LEGUME SOCIETY

Legumes for a Sustainable World

ILS2 | Second International Legume Society Conference

11th - 14th OCT 2016
TRÓIA RESORT | PORTUGAL

ITQB
UNIVERSIDADE NOVA DE LISBOA

Second International Legume Society Conference

Legumes for a sustainable world

Book of Abstracts

11th – 14th October, 2016

Contents

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Welcome Addresses

Welcome Addresses

From the President of ILS (2011-2016)

The Legume Society was founded in 2011 after closure of former European Association for Grain Legume Research (AEP). Our mission was becoming the society of reference for ALL legumes WORLWIDE, this is, extending the range of crops covered and the area of reference.

After five difficult years with absolutely lack of sponsors and any kind of financial support, we can proudly realize that Legume Society has consolidated with great success and has a promising future. This was possible only thanks to the voluntary work of a number of committed people.

We have been able to establish a solid and reliable series of triennial legume-devoted conferences as well as a dissemination magazine (Legume Perspectives), with a real niche serving as a dissemination tool for the legume community.

First Legume Society Conference was successfully organized at Novi Sad, Serbia in 2013. Second is taking place now (2016) at Troia, Portugal, together with a number of satellite events. Third is already planned at Poznan, Poland in 2019. We are sure that this reliable series of multidisciplinary conferences will be of great interest to legume experts, extending it to stake holders. We should acknowledge the great efforts made by the local organizers of these events.

At the General Assembly a new Scientific Committee will be elected that will for sure bring the renewed energies needed to continue with Legume Society endeavor. We all shall offer our support and gratitude and wish them success for future.

Diego Rubiales

From the Local Conveeners

We cordially welcome you to the Second International Legume Society Conference in the International Year of Pulses.

In a world urgently requiring a more sustainable agriculture, food security and healthier diets, the demand for legume crops is on the rise. This growth is fostered by the increasing need for plant protein and for more sustainable and environmentally friendly sound agricultural practices.

Food, feed, fiber and even fuel are all products that come from legumes – plants that grow with low nitrogen inputs and in harsh environmental conditions.

The second ILS Conference is welcoming more than 370 attendees from 53 countries, showing the international recognition of the work developed by ILS and the global importance of research in legumes.

The general aim of the conference is to update and discuss the knowledge developed in legume research, in its various facets, from their genomes sequencing, their genetic resources, their environmental response and adaptation, to their use in agricultural systems.

We wish you a fruitful and rewarding conference and a pleasant stay in wonderful peninsula of Tróia.

Pedro Fevereiro, Carlota Vaz Patto and Susana Araújo

Organizers

International Legume Society

The **International Legume Society** was founded in 2011 with two primary missions. One of them was to treasure the rich legume research tradition of the former European Association for Grain Legume Research (AEP), with emphasis on carrying out its the triennial legume-devoted conferences. Another one is to fulfill a long-term strategy of linking together the research on all legumes worldwide, from grain and forage legumes pharmaceutical and ornamental ones and from the Old World to the Americas.

ITQB NOVA

The **Instituto de Tecnologia Química e Biológica António Xavier (ITQB NOVA)** is a research and advanced training institute of **Universidade Nova de Lisboa**. The mission of **ITQB NOVA** is to carry out scientific research and postgraduate teaching in life sciences, chemistry and associated technologies, for the benefit of human health and the environment. ITQB’s highly multidisciplinary nature makes it a leading centre for advanced training of researchers in Portugal.

Conveners

Pedro Fevereiro – ITQB NOVA

Carlota Vaz Patto – ITQB NOVA

Susana Araújo – ITQB NOVA

Diego Rubiales - Scientific Coordinator – IAS - CSIC

Scientific Committee

(in alphabetic order)

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Shiv Kumar Agrawal - ICARDA, Syria
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Diego Rubiales - CSIC, Spain
Fred Stoddard – Univ. Helsinki, Finland
Richard Thompson - INRA, France
Tom Warkentin – Univ. Saskatchewan, Canada

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(in alphabetic order)

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Program

October 10th-11th 2016: Satellite events (registration needed)

10th-11th October ***Ascochyta 2016 Workshop*** - Room *Arrábida IV*
(program in http://www.ascochyta2016.aweb.net.au/)

11th October 09:00-18:00h ***LEGATO project meeting*** *(partners only)* - Rooms *Arrábida III & Douro*
11th October 09:00-18:00h ***EUROLEGUME project meeting*** *(partners only)* - Room *Guadiana*
11th October 09:00-18:00h ***ABSTRESS project meeting*** *(partners only)* - Room *Atlântico.*

October 11th 2016: 18:00-20:00 ILS2 Conference Registration

October 12th 2016
08:00-12:00 Registration (cont.)

09:00-09:15 **Welcome address -** Room *Arrábida I & II*

09:15-10:30 Session 1, plenary: Legumes value chain: market requirements and economic impact - Room *Arrábida I & II*
Chaired by Eduardo Rosa (UTAD, Portugal) and Adrian Charlton (FERA, UK)

09:15-09:45 **Key lecture - Hakan Bahceci**: Forging a New Future for Pulses: Addressing research challenges with the momentum of the UN International Year of Pulses
09:45-10:00 P. Iannetta: Main-streaming pulses: exploring local solutions to supply chain limitations
10:00-10:15 F. Muel: Would the protein fraction be the future of oil and grain legume crops by 2030?

10:15-10:30 G. Dubois: Legume future from European Union perspective: Horizon 2020, EIP-AGRI and CAP

10:30-11:00 Coffee break

11:00-12:00 Session 2, plenary: Legumes and environment - Room *Arrábida I & II*
Chaired by Richard Thompson (INRA, France) and Diego Rubiales (CSIC, Spain)

11:00-11:30 **Key lecture - Marie-Hélène Jeuffroy**: Validating the environmental benefits of legumes requires a territorial approach

11:30-11:45 B. Cupina: Environmental impact of introducing legumes into cropping system

11:45-12:00 C. Watson: Sustainable management of grass-white clover leys in ley-arable farming systems

12:00-13:00 Poster viewing

13:00-14:30 Lunch

14:30-16:00 Parallel sessions - Room *Arrábida III*
Session 3, parallel: Beneficial legume-microbe interactions A
Chaired by Carmen Bianco (Univ. Bari, Italy) and Pedro Fevereiro (ITQB NOVA, Portugal)

14:30-15:00 **Key lecture - Jens Stougaard**: Receptor mediated signaling in legume symbiosis

15:00-15:10 J. Keller: Symbiotic genes expression in a context of nitrogen-fixing symbiotic specificity in *Lupinus*

15:10-15:20 M. Vosatka: Beneficial microbes associated with legumes

15:20-15:30 V. Bourion: Partner choice in a core collection of pea inoculated by a mix of five Rhizobium strains

15:30-15:40 M. Lepetit: Improving adaptation of legume-rhizobium symbiosis to the soil environment

15:40-16:00 General discussion on beneficial legume-microbe interactions

Session 4, parallel: Genetic resources - Room *Arrábida IV*

Chaired by Hari Upadhyaya (ICRISAT) and Rodomiro Ortiz (SLU, Sweden)

14:30-15:00 **Key lecture - Noel Ellis**: Where are we after 150 years of legume genetics?

15:00-15:10 E. von Wettberg: Using collections of wild relatives of chickpea to understand domestication

15:10-15:20 M. Carvalho: Characterizing the genetic diversity of cowpea accessions using a high-density SNP

15:20-15:30 K. Fischer: LupiBreed - Valorisation of novel genetic variability in narrow-leafed lupin

15:30-15:40 M. Nelson: Domestic bliss? Causes and consequences of a modern era domestication event

15:40-16:00 General discussion on genetic resources

16:00-16:30 Coffee break and Poster viewing

16:30-17:30 Parallel sessions

Session 5, parallel: Legumes value chain: market requirements and economic impact (cont.) - Room *Arrábida III*

Chaired by Frédéric Muel (Terres Inovia, France) and Pete Iannetta (JHI, UL)

16:30-16:40 L. Bedoussac: Evaluating cereal-legume intercrops towards sole crops

16:40-16:50 M. Magrini: Escaping from grain-legume socio-technical system lock-in

16:50-17:00 A. Bentaibi: Analysis of social and organizational aspects of food legumes chain

17:00-17:10 D. Lemken: The re-innovation of Mixed Cropping - who cares? - Trial willingness

17:10-17:30 General discussion on legumes value chain

Session 6, parallel: Root diseases - Room *Arrábida IV*

Chaired by Julie Pasche (North Dakota St. Univ., USA) and Nicolas Rispail (CSIC, Spain)

16:30-16:40 L. Gentzbittel: Quantitative response of *M. truncatula* to verticillium wilt.

16:40-16:50 M.L. Pilet-Nayel: Genetics of pea resistance to *Aphanomyces euteiches* in the genomics Era

16:50-17:00 C. Coyne: Progress on understanding genetic resistance to *Fusarium* root rot in pea

17:00-17:10 S. Chatterton: Molecular quantification of pathogenic *Fusarium* spp. in soil to predict pea root rot risk

17:10-17:30 General discussion on root diseases

17:30-18:30 Poster session 1: Slots of flash presentations (3 min + 2 min questions) from selected posters (topics of the day) - Room *Arrábida I & II*

Chaired by Alessio Cimmino (Univ. Naples, Italy) and Georg Carlsson (SLU, Sweden)

A. Seabra Pinto: Do consumers' value the new use of legumes?

C. Ghoulam: Intercropping legume-cereals is a system to value legume-rhizobia symbiosis

J. Fustec: Synergy between crop diversity and earthworm community improve crop yields

C. Lotti: A novel source of genetic diversity in cultivated chickpea as revealed by GBS and genotyping

M.G. Tobar-Pinon: Genetic diversity of the Gautemalan climbing bean collection

M. Ruland: Temporal and regional development of lentil populations by natural selection on-farm

A. Moussart: Effect of pea sowing date on aphanomyces root rot development and yield losses

A. Lesné: Construction and evaluation of Near-Isogenic Lines for resistance to *Aphanomyces euteiches* in pea

R. Tollenaere: Nested Association Mapping for resistance to *Aphanomyces* in *M. truncatula*

C. Bianco: The auxin indole-3-acetic acid (IAA) is more than a plant hormone

20:45 Third International Legume Football Cup

October 13th 2016

8:30-10:00 Session 7, plenary: Legumes in food and feed and other alternative uses - Room *Arrábida I & II*
Chaired by Maria Carlota Vaz Patto (ITQB NOVA, Portugal) and Ambuj B. Jha (Univ. Saskatchewan, Canada)

08:30-09:00 **Key lecture - Frédéric Marsolais**: Using beans with novel protein compositions for nutritional improvement

09:00-09:15 M. Bronze: The hidden phenolic content of faba beans

09:15-09:30 J.C. Jimenez-Lopez: Use of narrow-leafed lupin b-conglutin proteins in human food to tackle diabetes

09:30-09:45 C. Domoney: Genetic diversity in pea and its impact on strategies for seed quality improvement

09:45-10:00 A.F. Monnet: Understanding the structuring of wheat-legume cakes to promote product innovation

10:00-10:30 Coffee break and Poster viewing

10:30-12:00 Session 8, plenary: Frontiers in legume genetics and genomics - Room *Arrábida I & II*
Chaired by Roberto Papa (Univ. Le Marche, Italy) and Marta Santalla (CSIC, Spain)

10:30-11:00 **Key lecture - Judith Burstin**: Towards the genome sequence of pea: a tribute to Mendel

11:00-11:15 P. Wan: Genome sequencing of *Vigna angularis* provides insight into high starch and low fat

11:15-11:30 P. Annicchiarico: Genotyping-by-sequencing and its exploitation in forage and grain legume breeding

11:30-11:45 S. Kaur: Application of historical data from Australian lentil breeding program in genomic selection

11:45-12:00 G. Boutet: WGGBS in pea without reference genome and data assembly

12:00-13:00 Poster session 2: Slots of 3 min flash presentations (+ 2 min questions) from selected posters (topics of the day) - - Room *Arrábida I & II*

Chaired by Nuno Almeida (ITQB NOVA, Portugal) and Sara Fondevilla (CSIC, Spain)

E. Collado: Pea straw: an advantageous co-product in dairy goat diets

C. Arribas-Martinez: Nutritional and nutraceutical characterization of extruded gluten-free snacks

M. Książkiewicz: Genes involved in flowering time regulation in white lupin

R.V. Penmetsa: Mendel's enduring legacy: orthologs of two of his seven factors in multiple current day crop legumes

R. Papa: Bean Adapt: The genomics of adaptation during crop expansion in common bean

A. Sarkar: The *Lathyrus sativus* genome project

H. Bobille: Effect of soil water deficit on amino acid exudation in *Pisum sativum* roots

C. Le May: Plant disease complex: antagonism and synergism between pathogens

A. Cimmino: Necrotrophic effectors produced by fungal pathogens of legume crops

A. Quillévéré-Hamard: Genetic and phenotypic diversity of pea isolates of *Aphanomyces euteiches* in France

L. Aguirrezabal: Modelling the effect of assimilates availability on seed weight and composition in soybean

13:00-14:30 Lunch

14:30-16:00 Parallel sessions

Session 9, parallel: Legumes in food and feed and other alternative uses (cont.) - Room *Arrábida III*

Chaired by Ruta Galoburda (Latvia Univ. of Agriculture, Latvia) and Tom Warkentin (Univ. Saskatchewan, Canada)

14:30-14:40 E. Tormo: A meta-analysis to assess the effect of fine grinding, dehulling and pelleting

14:40-14:50 E. Mecha: Protein quality of different Portuguese varieties of common bean

14:50-15:00 L. Proskina: Economic factors of using the legumes in broiler chickens feeding

15:00-15:10 M.C. Serrano: Tocopherols and carotenoids diversity in a chickpea germplasm

15:10-15:20 A. Clemente: Bowman-Birk inhibitors from legumes and mammalian gut health

15:20-15:30 A.B. Jha: Evaluation of a pea genome wide association study panel for folate profiles by UPLC-MS/MS

15:30-16:00 General discussion on legumes in food and feed and other uses

Session 10, parallel: Frontiers in legume genetics and genomics (cont.) - Room *Arrábida IV*

Chaired by Bernadette Julier (INRA, France) and Kevin McPhee (North Dakota State Univ. USA)

14:30-14:40 C. Le Signor: A protein quantity loci approach combined with a genome-wide association study

14:40-14:50 M.C. Vaz Patto: Using genomics to decipher the grain legumes quality riddle

14:50-15:00 A.M. Torres: Strategies and advances to identify candidate genes for low vicine-convicine in faba bean

15:00-15:10 M. Santalla: Homologues of Arabidopsis genes involved in photoperiod response in common bean

15:10-15:20 P. Smykal: Wild pea *P. fulvum* and *P. elatius* chromosome segment substitution lines in cultivated pea

15:20-15:30 A. Campa: Delimiting the physical positions of anthracnose resistance clusters

15:30-16:00 General discussion on frontiers in genetics and genomics

16:00-16:30 Coffee break and Poster viewing

16:30-17:45 Parallel sessions

**Session 11, parallel: Frontiers in plant and crop physiology - **Room *Arrábida III*

Chaired by Christophe Salon (INRA, France) and Luis Aguirrezabal (CONICET, Argentina)

16:30-17:00 **Key lecture - Phil Mullineaux**: The identification of novel genes controlling plant - environment interactions

17:00-17:10 J. Vorster: Drought-induced transcriptome changes in soybean crown nodules

17:10-17:20 R. Metzner: In vivo monitoring of the development of legume roots, nodules and pods

17:20-17:30 G. Louarn: A common shoot developmental framework for perennial legume species

17:30-17:45 General discussion on frontiers in plant and crop physiology

Session 12, parallel: Integrated pest and disease management - Room *Arrábida IV*

Chaired by Jenny Davidson (PIRSA-SARDI, Australia) and Christophe Le May (INRA, France)

16:30-17:00 **Key lecture - Seid Kemal**: Integrated disease and insect pest management pest and in cool-season food legumes

17:00-17:10 A. Baranger: PISOM: Ideotypes, Systems, Surveys of pea and faba bean Main diseases

17:10-17:20 Y. Mehmood: The Australian *Ascochyta rabiei* population structure

17:20-17:30 W. Chen: Chickpea damping-off caused by metalaxyl resistant *Pythium* in the US Pacific Northwest

17:30-17:45 General discussion on integrated pest and disease management

17:55-19:00 ILS General Assembly - Room *Arrábida I & II*

20:45 Third International Legume Football Cup

October 14th 2016

8:30-10:00 Session 13, plenary: Frontiers in legume breeding - Room *Arrábida I & II*

Chaired by Wolfgang Link (Georg-August-University, Germany) and Gerard Duc (INRA, France)

08:30-09:00 **Key lecture - Scott Jackson**: Contribution of epigenetic variation to improvement

09:00-09:15 B. Julier: QTL detection for forage biomass of alfalfa in mixture with a forage grass

09:15-09:30 A. Charlton: Improving the resistance of legume crops to combined abiotic and biotic stress

09:30-09:45 M. Pazos: Integrated platform for rapid genetic gain in temperate grain legumes and wild *Cicer* species

09:45-10:00 A. Sarker: Broadening the genetic base of lentil

10:00-10:30 Coffee break and Poster viewing

10:30-12:00 Session 14, plenary: Frontiers in legume agronomy - Room *Arrábida I & II*

Chaired by Erik S. Jensen (SLU, Sweden) and Susana Araújo (ITQB NOVA, Portugal)

10:30-11:00 **Key lecture - Eric Justes**: Synthesis on the effects of grain legume insertion and cereal-grain legume intercrops in low input cropping systems in Southern France

11:00-11:15 E. Pelzer: Design and assessment of legume-based cropping systems with stakeholders in Europe

11:15-11:30 C. Porqueddu: Performance of legume-based annual forage crops in three Mediterranean regions

11:30-11:45 A. Lingner: Legume-based mixed cropping systems may have higher water use efficiency

11:45-12:00 G. Carlsson: Participatory development of grain legume-cereal intercrops for enhanced productivity

12:00-13:00 Poster session 3: Slots of 3 min flash presentations (+ 2 min questions) from selected posters (topics of the day) - - Room *Arrábida I & II*

Chaired by Sofia Duque (ITQB NOVA, Portugal) and Angel M. Villegas-Fernández (CSIC, Spain)

L. Wiesel: Starter fertilizers: Do they influence rhizobial populations in vining pea fields?

R. Bowness: Evaluation of agronomic practices on production of Clearfield red lentil in Alberta, Canada

R. Seljåsen: Nitrogen availability from peas and faba beans as pre-crops to broccoli followed by lettuce

J. Rebola Lichtenberg: Biomass production in mixed short-rotation woody cropping of *Populus* hybrids and *Robinia*

M. Ćeran: Discovering genetic signatures of selection in the elite soybean germplasm

J. Aper: Flower abscission rates of early-maturing soybean varieties

C. Holdt: Genetic studies of winter hardiness in pea

A. Scegura: Marker-assisted backcross selection of virus resistance in pea

J.J. Ferreira: Genetic resistance to powdery mildew in common bean

M. Pérez-de-la-Vega: RNA-seq analysis of gene expression in lentils in response to *Ascochyta lentis* infection

V. Vernoud: A transcriptomic approach identifies candidate genes for drought tolerance in pea

13:00-14:30 Lunch

14:30-16:00 Parallel sessions

Session 15, parallel: Frontiers in legume breeding (cont.) - Room *Arrábida III*

Chaired by Paolo Annicchiarico (CREA, Italy)

14:30-14:40 B. Taran: Genomic prediction for seed size in chickpea

14:40-14:50 L. Brünjes: Faba bean lines differ in their contribution as pollen donor to cross-fertilized seed

14:50-15:00 L. Pecetti: Assessing and overcoming genetic trade-offs in breeding grazing-tolerant alfalfa

15:00-15:10 T. Warkentin: Enhancing the nutritional quality of field pea

15:10-15:20 B. Rewald: Machine-learning approaches for root trait determination and differentiation of cultivars

15:20-15:30 R. Madhavan-Nair: An International network to improve mungbean breeding and production

15:30-16:00 General discussion on frontiers in legume breeding

Session 16, parallel: Advances in legume agronomy (cont.) - Room *Arrábida IV*

Chaired by Fred Stoddard (Univ. Helsinki, Finland) and Claudio Porqueddu (CNR, Italy)

14:30-14:40 G. Corre-Hellou: Ecosystem services provided by legumes and exploited by stakeholders

14:40-14:50 M. Guinet: Quantification of nitrogen fluxes and explanatory plant traits

14:50-15:00 N. Carton: Cereals as companion crops in cereal-grain legume intercrops: case of lupin

15:00-15:10 E. Journet: Intercropping lentil with spring wheat in organic farming

15:10-15:20 S. Guy: Diversification of USA dryland cropping systems using autumn-sown winter pea

15:20-15:30 J. Streit: Quantitative analysis of the root distribution in a faba bean-wheat intercropping system

15:30-16:00 General discussion on advances in legume agronomy

16:00-16:30 Coffee break and Poster viewing

Session 17, parallel: Legumes and environment (cont.) - Room *Arrábida III*
Chaired by Christine Watson (SRUC, UK)

16:30-16:40 E.S. Jensen: Soil nitrogen fertility and nitrogen acquisition in faba bean
16:40-16:50 D. Savvas: Impact of organic practices on growth, yield and greenhouse gas emissions
16:50-17:00 K. McPhee: Effect of simulated hail treatment on yield loss in chickpea
17:00-17:10 V. Verret: Meta-analysis of the effects of legume companion plants
17:10-17:20 S. Médiène: A tool integrating knowledge to select legume species for oilseed rape intercropping
17:20-17:30 V. Sánchez-Navarro: Nitrous oxide and methane fluxes from a cowpea-broccoli crop rotation
17:30-18:00 General discussion on Legumes and environment

Session 18, parallel: Resistance to biotic and abiotic stresses - Room *Arrábida IV*
Chaired by Weidong Chen (USDA-ARS, USA) and Laurent Gentzbittel (CNRS, France)

16:30-16:40 M. Dickinson: Exploring metabolic changes in legumes exposed to combined biotic and abiotic stress
16:40-16:50 K. Toyoda: The role of plant cell wall in resistance and susceptibility to pathogenic pathogen
16:50-17:00 J.M. Osorno: Detecting tolerant germplasm and QTLS associated with flooding stress in dry bean
17:00-17:10 S. Beji: Genome-Wide association mapping of frost tolerance in *Pisum sativum*

17:10-17:20 B. Ruge-Wehling: Marker-assisted breeding strategies for anthracnose resistance in lupin

17:20-17:30 D. Rubiales: Use of wild relatives in pea breeding for disease resistance

17:30-18:00 General discussion on resistance to biotic and abiotic stresses

18:00-19:00 Concluding session - Room *Arrábida I &II*
Poster and oral presentation awards
ILS Honorary member's awards

20:00 Farewell Dinner

October 15th 2016 (satellite events)

08:00-12:00 ***REFORMA project meeting*** *(partners only)* - Room *Douro*

08:00-12:00 ***IYP_Research Strategy write shop*** *(by invitation)* - Room *Atlântico*

Key Lecturers

Key Lecture - Session 1

12/10 - 09:15-09:45

Hakan Bahceci

Hakan Bahceci is the Chairman & Group CEO of Hakan Agro DMCC, a multinational agri-soft commodities supply company based in Dubai, UAE with processing facilities and offices in 26 countries. Hakan has over 25 years' of experience in global agri-soft commodities supply chain management. He currently serves as a Board Member of GAFTA (Grain And Feed Trade Association) and the Chairman of the Turkish Business Council in Dubai and Chair of GPC's IYP Committee. Hakan notably served as President of Global Pulse Confederation (CICILS IPTIC) between 2011-2015, as President of International Agri Food Network and as Chairperson of the Private Sector Mechanism at the UN Committee on World Food Security. Hakan holds a Bachelor's degree in English Literature and an MBA from Wollongong University, Australia.

Forging a New Future for Pulses: Addressing research challenges with the momentum of the UN International Year of Pulses

Bahceci, H

Key Lecture Session 2

12/10 - 11:00-11:30

Marie-Hélène Jeuffroy

Marie-Hélène Jeuffroy is a senior scientist in Agronomy. She defended her PhD in 1991 in ecophysiology, analysing and modeling yield formation in a pea crop. Then, she worked on nitrogen management in the cropping systems, with the aim of designing new practices or ideotypes taking into account various agronomic and environmental targets, and their use within the cropping systems. Then, she studied participatory methods for the design of decision-support systems and, more largely, technical innovations. A large part of her research concerned grain legumes, and their interactions with the cropping system.

Valuing the environmental benefts of legumes requires a territorial approach

Jeuffroy M-H[1], Hellou G[2], Magrini M-B[3], Pelzer E [1]

1 - UMR Agronomie INRA, AgroParisTech, Université Paris Saclay, 78850 Thiverval-Grignon, France

2 - LEVA, Univ. Bretagne Loire, Ecole Supérieure d'Agricultures (ESA), 49007 Angers, France

3 - AGIR, Université de Toulouse, INRA, INPT, INP- EI PURPAN, Castanet-Tolosan, France

Despite the environmental benefits of legume-based cropping systems largely described by scientists, and the great diversity of available species and crop practices showing possible adaptation to local environment, legume areas have strongly decreased since the 90s in Europe. However, their use as feed or food is highly recognized as beneficial for human health, nutritional qualities, and improved European autonomy for protein.

Based on surveys around various stakeholders at both national and local levels, including farmers, the reasons for that discrepancy have been identified in France. One main reason is that the environmental benefits are highly variable, according to the local situation, and farmers lack information and tools to take into account this variability in their crop management. Moreover, the benefits gained from legumes are most often measurable on the following crops, whereas the agricultural sociotechnical system enhances annual assessment of practices. Another reason is that some environmental benefits address global issues, which are not directly connected to the local stakeholders concerns. These observations call for the need of a shared vision of the benefits gained from legume crops among the stakeholders concerned by their possible development and use. We thus conclude that valuing the environmental benefits of legume crops requires a territorial approach.

Based on a combined approach mixing case studies in three territories and theoretical aspects, we show that gaining from these environmental benefits requires combine technical, but also organisational and economical innovations, within the territory, combining various levels of the agrifood system. When co-designed by the concerned actors within a territory, these coupled innovations appear adapted to the local conditions and stakeholders'activities and strategies, and thus allow to enhance the development of legume crops, taking benefit from a shared vision of the legume-based services.

Key Lecture Session 3

12/10 14:30-15:00

Jens Stougaard

Jens Stougaard is Professor of Molecular Biology and Genetics at Aarhus University and Director of the Centre for Carbohydrate Recognition and Signalling (CARB). Jens Stougaard leads a group studying genes regulating development of nitrogen fixing root nodules and mycorrhiza formation in legumes. Currently the mechanisms of Nod-factor perception, the function of receptors involved and the downstream signal transduction cascades are in focus. The plant model system used for this research is *Lotus japonicus* that is also used for investigating the long range signalling integrating root nodule development into the general developmental program of the plant. Genetics, genomics and biochemical methods are used to identify and characterise components of regulatory circuits. In order to improve the genetic analysis and to establish a system for reverse genetics, a large-scale insertion population based on the germ-line specific activity of the LORE1 retroelement is being established and made available to the community.

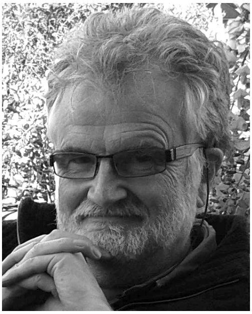
Receptor mediated signaling in legume symbiosis

Stougaard, J
Centre for Carbohydrate Recognition and Signalling, Department of Molecular Biology and Genetics, Aarhus University, Denmark

In the model legume *Lotus japonicus* a large family of LysM receptor kinases are predicted to mediate plant-microbe interactions. The function of some of these receptors in perception of microbial signal molecules including lipochito-oligosaccharides, exopolysaccharides and chitin will be presented. Biochemical approaches for characterization of ligand – receptor recognition in relation to host specificity in legume-rhizobia interactions will be discussed.

Key lecture - Session 4

12/10 - 14:30-15:00



Noel Ellis

Thomas Henry Noel graduated with a B.Sc First class Honours in Biological Sciences (1976) and a Ph.D. (1979) with his thesis "Examination of the variation of the structure of satellite DNAs".
Since 2000 is was Head of the Applied Genetics Department (2000 – 2001), Associate Head of the Crop Genetics Department, John Innes Centre (2001 – 2011), Professor of Crop Genetics, IBERS, at the University of Aberystwyth (2011 – 2013) and Director, of the CGIAR Research Program on Grain Legumes (2013 – 2015).
Noel's research interests have focused on the genetic basis of the inter- and intra-specific evolution and diversification of legumes at both genomic and phenotypic levels, developing approaches for the isolation of genes identified by their phenotype.
Noel has promoted research networks through the EU FP6 integrated project 'Grain Legumes' (2004-2008), the CGIAR's activities in legumes (2013 - 2015) and his activities in AEP and ILS.

Where are we after 150 years of legume genetics?

Ellis, N

Genetic resources come in a variety of forms, but can be classed broadly into designed or natural populations. Designed populations include segregating individuals or lineages derived from controlled crosses, following Mendel's lead. Systematic mutant populations are another powerful analytical tool and can provide useful allelic variation. These can be interrogated either from the point of view of phenotypic variation to determine the corresponding genotype, or using allelic (sequence) variation in order to determine the consequent phenotypic variation. Natural populations, on the other hand, are often represented by selections from wild material. There will be some structure in the wild material, reflecting its population history, and some structure will derive from the sampling strategy. For crop genetic resources wild material is augmented by diverse landraces and the combined material is often held in a germplasm collection. Much effort has been devoted to understand population structure in natural populations in the hope that this can enable genetic analysis; essentially this is a surrogate for designing population structure. These germplasm collections are widely viewed as useful sources of allelic diversity, because the alleles they contain have survived selection.

This presentation will discuss the interrelationship between different population types for the characterization of the genetic determination of traits and emphasise the continuing role of genetic analysis in the era of extensive genome sequence information.

Key Lecture - Session 7

13/10 - 8:30-10:00

Frédéric Marsolais

Frédéric Marsolais is a Research Scientist at the London Research and Development Centre of Agriculture and Agri-Food Canada (AAFC), and an Adjunct Research Professor at the Department of Biology of the University of Western Ontario in London, Ontario, Canada. Dr. Marsolais graduated with a B. Sc. in Microbiology and an M. Sc. in Biology from Laval University, and a Ph. D. in Biology from Concordia University. Prior to joining AAFC, he was an NSERC Visiting Fellow at Duke University, and the University of North Carolina at Chapel Hill. Dr. Marsolais' research focuses on protein biochemistry in common bean, including protein quality and seed protein composition. His laboratory also investigates the metabolism of sulphur and amide amino acids in relation with seed protein accumulation.

Using beans with novel protein compositions for nutritional improvement.

Marsolais, F

Agriculture and Agri-Food Canada. London Research and Development Centre.

A series of genetically related lines of common bean (*Phaseolus vulgaris*) integrate a progressive deficiency in major storage proteins, the 7S globulin phaseolin and lectins. SARC1 integrates a lectin, arcelin-1, from a wild accession. SMARC1-PN1 is deficient in phaseolin. SMARC1N-PN1 combines a deficiency in major lectins. Sanilac is the recurrent parental background. The changes in protein composition lead to an increased concentration of essential sulfur amino acids, methionine and cysteine, at the expense of the abundant non-protein amino acid, S-methylcysteine. Genomic research was performed to understand the basis for variations in protein profiles. Reads obtained from next generation sequencing technologies were aligned to reference sequences, and subjected to de novo assembly. The results identified polymorphisms responsible for the lack of specific storage proteins, and those associated with large differences in storage protein accumulation, including compensatory changes. We also performed research to identify genetic markers of phaseolin deficiency, map interspecific introgressions from P. coccineus and determine whether the increased concentration of sulfur amino acids may be combined with good agronomic characteristics. Variation in pectin acetylesterase expression in the seed coat, which may affect the properties of dietary fiber, has also been characterized.

Key Lecture - Session 8

13/10 - 10:30-11:00

Judith Burstin

Judith BURSTIN is Director of research at INRA UMR1347 Agroecology Dijon-France. The major goals of her program are to gain a better understanding of the effects of pea genes that are relevant to agriculture and to develop the tools required for more efficient pea improvement. Her research focuses on deciphering the control of seed yield and quality in the context of climate change. Her program integrates a broad range of research projects that include whole genome studies, mapping, positional cloning, and marker-assisted selection. Dr. Burstin has published >45 peer reviewed papers and 7 book chapters. Recent accomplishments of Dr. Burstin's research are the development of genomic resources for pea, such as the pea GeneAtlas and a high density and resolution 15k consensus genetic map. These tools will serve for cloning the genes that control several important traits in pea and for the establishment of the pea genome sequence. Dr. Burstin has led large consortiums of public-private collaborative programs for the last 15 years.

Towards the genome sequence of pea

Madoui M.-A.[1], Labadie K.[1], Kreplak J.[2], Aubert G.[2], d'Agata L. [1], Capal P.[3], Fournier C.[2] , Kougbeadjo A.[2], Vrana J.[3] , Gali K. K.[4] , Taran B.[4], Belser C.[1], Le Paslier M-C.[5], McGee R.[6], Edwards D.[7] , Batley J.[7] , Bendahmane A. [8], Bergès H.[9], Barbe V.[1] , Tayeh N.[2], Klein A.[2], Lichtenzveig J.[10] , Aury J-M.[1], Coyne C.J.[11], Warkentin T. [4] ,Dolezel J.[3], Wincker P.[1] , Burstin J.[2]

1 - CEA - Genoscope, Evry, France
2 - INRA, UMR1347 Agroécologie, Dijon, France.
3 - Institute of Experimental Botany, Olomouc, Czech Republic
4 - University of Saskatchewan, Saskatoon, SK, Canada
5 - INRA, US1279 EPGV, CEA-IG/CNG, EVRY, France
6 - USDA-ARS, Pullman, WA
7 - University of Western Australia, Perth, Australia
8 - INRA, Evry, France
9 - INRA - CNRGV, Castanet Tolosan, France
10 - Curtin University, WA, Australia
11 - USDA-ARS Western Regional Plant Introduction Station, Pullman, WA

Pea (*Pisum sativum* L.) was the original model organism for Mendel´s discovery of the laws of inheritance and kept this model status until the advent of molecular biology at the end of the 20th century. Pea is also one of the world's oldest domesticated crops. It is currently the third most widely grown pulse crop, as its seeds serve as a protein-rich food for humans and livestock alike.

While several legume species genome's draft sequences have been produced, progress in pea genomics has lagged behind largely as a consequence of its complex and large genome size. The pea genome is large (ca 4.45 Gb), probably resulting from recent expansion of retrotransposons followed by sequence diversification.

The Pea Genome International Project has undertaken several complementary strategies in order to produce a high-quality draft sequence of the species. We will present how this draft sequence opens the way to renew strategies in pea breeding.

Key Lecture - Session 11

13/10 - 16:30-17:00

Phil Mullineaux

Phil Mullineaux obtained his PhD from the University of Wales in 1981 and was a postdoctoral fellow, first at the University of Edinburgh and the John Innes Institute (now the John Innes Centre) until 1986. After this he was appointed as a Group Leader and from this time embarked on studying the response of plants to environmental stress and their associated subcellular and systemic signalling especially the role of reactive oxygen species and antioxidants. Phil moved as Professor of Plant Molecular Biology to the University of Essex in 2004, primarily to expand his experience of plant physiology. The work has continued at Essex and expanded to trying to understand the basis of the balance between growth and stress defence that every plant must achieve. In the context of this Congress, Phil has been and is a contractor in European Union FPV –FPVII projects (AIR1-CT92-0205 [ESTIM], FOOD-CT-2004-506233 and FP7-KBBE-2011-289562 [ABSTRESS] respectively). Therefore he has considerable experience of projects with both academic and industrial partners. His current EU project (ABSTRESS) of which he is a partner aims to understand the interaction between drought stress and Fusarium infection in legumes and other crop species and has strong crop genomics and Bayesian modelling components. His many publications can be found on his Google Scholar page (https://scholar.google.co.uk/citations?hl=en&pli=1&user=_yM2sFkAAAAJ)

The identification of novel genes controlling plant - environment interactions

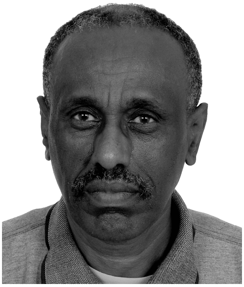
Mullineaux, P
School of Biological Sciences, University of Essex, UK

I will report an approach we have been using in the FP VII project ABSTRESS in which we have used time series transcriptomics data and dynamic modelling methods to identify candidate genes in the model legume Medicago truncatula (Mt) that uniquely respond to a combined drought stress and Fusarium oxysporum infection and move rapidly to pea. This is built on a method developed and published for Arabidopsis. The dynamic modelling, in an unbiased way, allows us to identify genes with high numbers of connections to other genes in inferred transcriptional networks. Such genes, therefore, may be of more significant interest than genes that are only differentially expressed in response to the combined stresses. These are termed hub genes and we identified 36 such candidates in Mt. The orthologs for 22 of these Mt genes ware identified in pea and we confirmed for 11 of them that the pea genes responded more strongly to the combined stress than either single stress. Mutants in these 11 pea hub gene orthologs have been, or are being identified by TILLING, with the aim of determining if altered phenotypes of the pea mutants to Fusarium and/or drought infection is manifested under field conditions. Therefore, ABSTRESS has been taking a novel approach to identifying genes in model species and determining if their counterparts in crop species can be fast-tracked though to field testing and eventual incorporation into breeding programmes. This communication will report our progress to date.

Key Lecture - Session 12

13/10 - 16:30-17:00

Seid Ahmed Kemal



Seid A. Kemal is a Legume Pathologist in the Biodiversity and Integrated Gene Management Program at ICARDA Morocco, Research Platform working with teams of food legume breeders, IPM experts and Agronomists. He received his BSc degree (in Agriculture majoring Plant sciences) from Addis Ababa University and MSc (Crop Protection) degree from Alemaya University of Agriculture, Ethiopia. He earned his PhD degree from the Department of Biology, University of Saskatchewan, Canada. He has served as Lecturer in Crop Protection in Alemaya university of Agriculture. He was leading the National Pulse Research Team in the Ethiopian institute of Agriculture Research and contributed in the releases of high yielding, disease resistant kabuli chickpea and lentil in Ethiopia. His major areas of interest are developing resistant sources to foliar and soil borne diseases of food legumes; disease epidemiology and integrated pest management. He authored and co-authored scientific articles on diseases of cool season food legumes and supervised and supervised over 20 graduate students.

Integrated disease and insect pest management pest and in cool-season food legumes

Ahmed, S
Biodiversity and Integrated gene Management, International Center for Agricultural Research in the Dry Areas, Rabat, Morocco

Cool-season food legumes (faba bean, chickpea, field pea and lentil) are key commodities in cereal-legume mixed cropping system in North Africa, West and South Asia and East Africa. The crops are key sources of protein; incomes, animal feed and improve soil fertility to small holder farmers. The major biotic factors affecting crop yield are fungal diseases, virus, parasitic weeds and insect pests. New diseases and insect pests are emerging due to climate variability and farming system changes. Major investment are being made in developing resistant cultivars in many countries. Other pest management option are cultural practices, bio- fumigation, application of pesticide and bio-pesticides and integration of two or more options to manage pests to reduce yield and quality gaps in small holder farmers. The development of resistant cultivars is not possible for most pathogens and insect pests due to wide host. Integrated pest management (IPM) is mainly applied to pests with wide host ranges and cultivars with partial resistance. IPM has many benefits farmers by increasing yield, reducing costs of production, delay development of more aggressive pathogen populations and reduce environmental and health hazards of pesticide uses. IPM options are demonstrated through different platforms (Farmer Field Schools, Innovation platforms, etc) where farmers and other stakeholders are involved to improve their knowledge and skills. In this presentation, the status of IPM research and adoption in managing the impact of pests of food legume crops of small holder farmers are reviewed.

Key Lecture - Session 13

14/10 - 08:30-09:00

Scott A. Jackson

Scott A. Jackson is the Georgia Research Alliance Eminent Scholar and Professor of Plant Functional Genomics at the University of Georgia. He is the Director of the Center for Applied Genetic Technologies and has appointments in the Institute for Bioinformatics, Plant Biology and Crop and Soil Sciences. His research focuses on the application of genomics for crop improvement and the understanding of basic biological processes, such as chromosome and genome evolution, domestication and polyploidy. His lab works primarily with rice and several legumes and is international in scope with work in Asia, Africa and South America. His lab has generated more than 135 publications encompassing basic to applied aspects of plant and crop genetics.

Genetic and Epigenetic Variation in Legumes and their Role in Improvement

Jackson S.
Georgia Research Alliance and University of Georgia

Epigenetic variation, non-sequence-based variation, has been of great interest in plant and animal research. Using soybean and common bean, we are exploring the level of epigenetic variation in breeding germplasm as well as association panels. Using sodium bisulfite DNA sequencing, Methyl C sequencing, we have sequenced more approximately 200 soybean and common bean accessions including landmark cultivars from the past 80 years of soybean improvement in the US, parents of the public soybean NAM (nested association mapping) population, landraces, a common bean GWAS panel and undomesticated relatives. Using these data, including RNA-seq and small RNAs, we determined differentially methylated regions (DMR) for all three methylation contexts (CG, CHG and CHH). These DMRs were then analyzed for their genomic context: exonic, UTRs, upstream, downstream, and intergenic or repeat (e.g. transposable elements). I will discuss these data in context of DMR variation (inherited and de novo) within and between species, varieties, landraces and wild soybean as well as their potential contribution to breeding/selection over the past 80 years and their contribution to variation.

Key Lecture - Session 14
14/10 - 10:30-11:00

Eric Justes

Eric Justes (Male, born in 1965, Senior researcher at INRA, France), is an agronomist and modeller specialised in soil science, ecophysiology and agroecology with experience in legume insertion in arable cropping systems as sole or intercrops, i.e. species mixtures of cereal-grain legumes and catch/cover crops. His expertise covers water and nitrogen cycling, management in arable systems and design of innovative low inputs, organic and diversified cropping systems. He has published over 60 articles in ISI journals (https://www.researchgate.net/profile/Eric_Justes). He is currently head of the VASCO research team (VArieties and Cropping System for an agrOecological production at INRA, AGIR lab, Toulouse), coordinator of French and European projects and is involved in dissemination activities to agricultural advisors.

Synthesis on the effects of grain legume insertion and cereal-grain legume intercrops in low input cropping systems in Southern France

Justes E., Plaza-Bonilla D., Gavaland A., Léonard J., Mary B., Nolot JM., Perrin P., Peyrard C., Raffaillac D.

Six cropping systems (CS) of three 3-year rotations based on durum wheat and sunflower inserting 0, 1 (pea or fababean) and 2 grain legumes (GL) (pea and soybean), and with or without cover crops (CC) were compared at INRA Toulouse from 2004. This experiment is still on going for a twelfth year. We demonstrated that 6 key points. 1) Pea as a preceding crop increased durum wheat grain production by 8% compared to sunflower as a preceding crop with a mean reduction of N fertilization of 45 kg N ha^{-1}. 2) Inserting GL in the rotations significantly affected the amount of C and N inputs to the soil that were lower than with cereals and consequently led to a decrease in soil organic-C (SOC) and –N contents. 3) N leaching simulated using the STICS model was higher when increasing the number of GL (from 22 to 52 kg N ha^{-1} after two rotation cycles of 6 years, for 0 to 2 GL respectively). 4) However, CC insertion i) reduced N leaching (from 15 to 18 kg N ha^{-1}), ii) mitigated SOC loss, and iii) did not affect durum wheat grain protein concentration or yield. 5) Daily measured N_2O emissions over the whole 3-year rotation were low but significantly higher under the CS including fababean than for the cereal-based CS (1.12 vs. 0.78 kg N_2O-N ha^{-1} year^{-1}) despite a lower N fertilization. Then, in such conventionally-tilled systems, properly designed cropping systems that simultaneously insert grain legumes and cover crops reduce N requirements of the following durum wheat, stabilize SOC content but do not decrease N_2O emissions at the rotation level.

Session Abstracts

Session 1, plenary: Legumes value chain: market requirements and economic impact - Room *Arrábida I & II*

Chaired by Eduardo Rosa (UTAD, Portugal) and Adrian Charlton (FERA, UK)

09:15-09:45 **Key lecture - Hakan Bahceci**: Forging a New Future for Pulses: Addressing research challenges with the momentum of the UN International Year of Pulses

Oral Communications

09:45-10:00 Oral –S1

Main-streaming pulses: exploring local solutions to supply chain limitations

Black K.[1,2], Walker G.[2], White P.[1], Karley A.[1], Ramsay L.[2], Ramsay G.[3], James E.[1], Squire G.[1] , Iannetta P.[1].

1 - Ecological Sciences, The James Hutton Institute, Invergowrie, Dundee, DD2 5DA, Scotland UK pete.iannetta@hutton.ac.uk
2 - Yeast Research Group, Abertay University, Dundee DD1 1HG, Scotland
3 - Tay Bees and Honey Ltd. - www.taybees.co.uk

In the UK, peas and faba beans are the main pulses produced and their commercial success needs improved if they are to compete more effectively in the market place. One solution is to use pulses as a raw material for higher value products. For example, UK farmed salmon production is 160,000 T/y with a farm gate value of £600m and feed use is set at 200kT/y. Production is set to increase dramatically and pulse protein sources are in demand. However, feed manufactures utilise the protein component and other key aspects of the UKs supply chain are limiting uptake by aquaculture. Bean dehullers and millers are not co-localised and centralising processing would improve commercial efficiency; processing facilities to fractionate locally grown pulses into their component starch and protein portions remain to be established in the UK, and; the value achieved for the starch byproduct must be maximised as it accounts of the bulk (ca. 60%), of the pulse by weight. However, we report on novel processing steams for whole faba beans in brewing and distilling, and the development of byproducts for animal- and aquaculture-feeds. The UKs brewing and distilling industries are very important economically at £10 billion annually in tax revenues; a value seconded only by farmed salmon. Can our approach help align major UK supply chains and the perception of pulse-use as a cultural norm?

Acknowledgements-The Scottish Government, EU-FP7 Legume Futures, InnovateUK see www(dot)beans4feeds(dot)net.

10:00-10:15 Oral – S1

113 Would the protein fraction be the future of oil and grain legume crops by 2030?

Muel F., Pilorgé E.

Terres Inovia, Institut Technique des oléagineux, des protéagineux et du chanvre. Av L. Brétignières, F-78850 Thiverval, Grignon, France, f.muel@terresinovia.fr

To support the reflections of the French professionals of vegetable oils and proteins, a prospective study was carried out to 2030 horizon (15 years), to shed light on the opportunities that will draw the oil and grain legume crops, and the areas of growth for the French and European vegetable oil and protein sector. The thinking was organised in the form of four different scenarios for 2030, which illustrate different logical evolutions of the context and related key issues, under the pressure of demographic, economic and socio-political constraints. Most of these scenarios seem favorable to the development of grain legumes in Europe, and it is clear that the economic value of the protein fraction is a key aspect of the future of grain legumes and oilseeds. Moreover, the EU might be able to become self-sufficient in protein consumption for both feed and food.

10:15 – 10:30 Oral - S1

Legume future from European Union perspective: Horizon 2020, EIP-AGRI and CAP

Dubois G.
European Commission - DG AGRI

Posters

P1 – S1

Do consumers' value the new use of legumes? An experimental auction with legume fortified maize bread.

Seabra Pinto A.[1], **Brites C.**[1],**Vaz Patto C.**[2], **Cunha L.**[3]

1 – Instituto Nacional de Investigação Agrária e Veterinária, INIAV, Oiras, Portugal

2 – Instituto de Tecnologia Química e Biológica, ITQB, Universidade Nova de Lisboa, Oeiras, Portugal

3 - Sense test

Legumes have a significant potential for a more sustainable and healthy food. Pulses, when blended with cereal proteins, may offer a promising alternative source for nutritional and functional proteins. In this context, manufacturers perceived that consumers are making more conscious and healthful food choices and they are moving away from artificial ingredients and towards introducing products high in desirable attributes like fiber and protein. Environmental and socio economic concerns also influence purchase decisions. Indeed, consumers believe that health and environmental attributes are important, but are they willing to pay more for the benefits they provide? Under the research work in experimental economics considered in the European Project LEGATO an experimental procedure was used to elicit consumers' willingness to pay with regard to legume fortified maize bread "Broa". This product is specific Portuguese maize bread, very well-known and eaten separately during the meals. A sample of Portuguese consumers participated in an experimental auction and they evaluated five different breads in three different treatments. The incentive compatible elicitation mechanism used was the original Surplus Comparison Mechanism (SCM) that takes into account the influence of the diversity of products actually available on the market and their comparison. This study contributes to a better understanding of consumers' perceptions and their behaviours regarding new uses of legumes.

P2 – S1

Establishment of a knowledge transfer network for cultivation and utilisation of field peas and field beans in Germany – DemoNetErBo

Jacob I.[1], Vogt-Kaute W.[1], Stevens K.[2], Zerhusen-Blecher P.[2], Quendt U.[3]

1 - Naturland Fachberatung, Eichethof 1, 85411 Hohenkammer, Germany
2 - University of Applied Sciences Südwestfalen, Lübecker Ring 2, 59494 Soest, Germany
3 - Hesse Department of Agriculture Affairs (LLH), Kölnische Straße 48, 34117 Kassel, Germany

Starting in March 2016, a knowledge transfer network consisting of 75 conventional as well as organic farms growing field peas (*Pisum sativum*) or field beans (*Vicia faba*) is currently established in Germany. Cultivation of peas and beans has been on a rather low and stagnating level in Germany in the past years. This is due to some challenges during cultivation, but also to low economic incentive for the farmers. This network (DemoNetErBo) shall expand and enhance the cultivation as well as the usage of field peas and field beans sustainably and improve the value gained by the farmers when growing peas and beans. Special focus is therefore on the development and presentation of legume value chains for feed and food production spanning all levels from breeding until the usage by the consumer. Hence, the farms are demonstrating diverse best practice examples for cultivation, processing, and utilisation of those two grain legumes. The overall aim of this project is to meet the growing need for regionally produced non-GMO protein crops.

The project is supported by funds of the Federal Ministry of Food and Agriculture (BMEL) based on a decision of the Parliament of the Federal Republic of Germany via the Federal Office for Agriculture and Food (BLE) under the Federal Protein Crop Strategy.

Session 2, plenary: Legumes and environment - Room *Arrábida I & II*

Chaired by Richard Thompson (INRA, France) and Diego Rubiales (CSIC, Spain)

11:00-11:30 **Key lecture - Marie-Hélène Jeuffroy**: Validating the environmental benefits of legumes requires a territorial approach

11:30-11:45 ORAL – S2

Environmental impact of introducing legumes into cropping system in temperate regions

Cupina B.[1], Krstc Dj.[1], Antanasovic S[1]., Mikic A.[2], Eric P.[1]
1 - University of Novi Sad, Faculty of Agriculture
2 - Institute of Field and Vegetable Crops

The use of legumes in cropping system is one measure that has been taken in agricultural production to increase environmental protection and to encourage sustainable use of natural resources. Legumes offer many benefits to sustainable agriculture and the integration of legumes into cropping systems brings costs and benefits, both internal and external to the farm. For ecological reasons, legumes are gaining increasing importance. Legume can be easily included in a crop rotation and, in contrast to grasses and crucifers, contribute additional N to the nutrient cycle by symbiosis. Some of this N can be used later as animal feed in the form of protein in herbage while the rest of the accumulated N can be taken up by subsequent crops. On the basis of experiments conducted in Serbia it can be concluded that the management decision concerning the use of legumes as cover crops should be based on the balance between farm profitability and environmental sustainability. The effect of legumes on cash crop yield and quality is mainly positive. N mineralization should be regulated in accordance with the N demands of the subsequent crop. In animal production areas, legumes can be an important source of quality forage or can be used for mulching. In such cases and in rotation with corn or Sudan grass, legumes should fulfil the following requirements: low-cost production, yield and quality, N uptake during periods critical for leaching and no negative effects on subsequent crops.

11:45-12:00 Oral – S2

Sustainable management of grass-white clover leys in ley-arable farming systems

Watson C.A.[1,2], **Walker R.L., Rees R.M., Topp CFE**[2]
1 - SLU, Sweeden
2 - SRUC, Sweeden

In ley-arable systems, grass-clover leys provide symbiotically fixed nitrogen which is released through mineralization to supply N for other crops in the rotation. The management of the ley is critical in terms of both N fixed and herbage yield and quality. Here we address the impact of age of ley on N fixation and clover content and the impact of pH on clover content. We report measurements in two long-term crop rotation experiments in the north-east of Scotland. An organically managed crop rotation experiment established in 1991 and a conventionally managed rotation experiment established in 1961 with pH treatments ranging from 4.5 to 7.5. The differences in nitrogen fixation resulting from the age of the ley (age 1, 2, and 3) have been assessed over four years. The total above ground N fixed was in the region of 72–156 kg N/yr. The results indicate that the rate of N fixation is affected by the interaction between the age of the sward and the sample time, and the year and the sample time. The age 3 swards tended to have a higher rate of fixation at the start of the season but which declined earlier in the season than in swards age 1 and 2 years; however, it is not clear from these data if total N fixation increases or decreases with the age of ley.

Posters

P3 – S2

Biological Nitrogen Fixation: Adoption rates of legume technologies among smallholder farmers in Northern Ghana and enabling factors that influence farmers' decision to adopt

Kwateng G. , Svensson S.
Dept. of Business and Economics, Swedish University of Agriculture Sciences, Ulls Väg 28, P.O. BOX 7012, 75007

Several studies have been conducted to understand the adoption potential of legume technology and factors that affect adoption (Shelton and Franzel, 2005; Mwangi and Kariuki, 2015). The study by Mwangi and Kariuki (2015) reveals that institutional factors, human specific factors, technological factors and economic factors have great potential to improve adoption among smallholder farmers. A study by Mafongoya et al. (2006) suggest that, improving agriculture yields is building and maintaining soil fertility in spite of low income and labor constraint faced by smallholder farmers. Similarly, a review by Adjei-Nsiah et al. (2007) show that legumes are able to improve soil fertility due to their ability to fix N2 and produce N-rich residues that may be rich to the soil. The effective ways in restoring such depleted soil is by improving inorganic fertilizers and manure to overcome nutrient depletion (Snapp et al., 2010). However, these products are not readily available for use by smallholder farmers. At the same time, Sanchez (2002) estimates the high cost of inorganic fertilizers in Africa to be two to six times compared to the cost in Europe, North America, or Asia. This is partly true in the case of Ghana where subsidies have been removed by the Government of Ghana (Adjei-Nsiah et al. 2008)

P4 – S2

The multifunctional role of legumes in vineyards and orchards

Vymyslicky T.[1], Pavlousek P.[2]
1 - Agricultural Research, Ltd., Czech Republic.
2 - Mendel University in Brno, Czech Republic.

Legumes have many positive ecological rules. In vineyards and orchards they eliminate soil and wind erosion and serve as feed source for pollinators, insect and animal species. Maybe the most important role is their ability to fix atmospheric nitrogen and supply other plants with nitrogen. Pure legume stand is able to fix up to 200 kg of N per hectare. Within a research project "Different ways of vineyard greening and management and their influence on reduction of soil erosion and quality of production" the role of legumes have been studied in six selected vineyards in the south-eastern part of the Czech Republic. The main aim of the project is development and testing of new cover crops legume mixtures intended for use in vineyards both in organic and integrated production. Species-rich mixtures both for inter-rows and for space under grape plants serve to promote biodiversity in vineyards. Cover crops mixtures have a positive effect on physical and chemical soil properties, growth and development of the grape plants, yield and quality of grapes and wines. At the end of the project the final composition of tested mixtures will be specified considering specific soil and climatic conditions. Suitable technologies of planting and a system of stand treatments including the above mentioned positive effect of legumes, as atmospheric nitrogen fixators, on the consumption of nitrogenous fertilizers and thus effective management of mineral nutrition will be emphasized.

P5 – S2

Environmental impact of introducing legumes into cropping system in temperate regions

Cupina B., Vujic S., Krstic D., Mikic A., Eric P.
University of Novi Sad, Faculty of Agriculture, Novi Sad; Institute of Field and Vegetable Crops, Novi Sad

The use of legumes in cropping system is one measure that has been taken in agricultural production to increase environmental protection and to encourage sustainable use of natural resources. Legumes offer many benefits to sustainable agriculture and the integration of legumes into cropping systems brings costs and benefits, both internal and external to the farm. For ecological reasons, legumes are gaining increasing importance. Legume can be easily included in a crop rotation and, in contrast to grasses and crucifers, contribute additional N to the nutrient cycle by symbiosis. Some of this N can be used later as animal feed in the form of protein in herbage while the rest of the accumulated N can be taken up by subsequent crops. On the basis of experiments conducted in Serbia it can be concluded that the management decision concerning the use of legumes as cover crops should be based on the balance between farm profitability and environmental sustainability. The effect of legumes on cash crop yield and quality is mainly positive. N mineralization should be regulated in accordance with the N demands of the subsequent crop. In animal production areas, legumes can be an important source of quality forage or can be used for mulching. In such cases and in rotation with corn or Sudan grass, legumes should fulfil the following requirements: low-cost production, yield and quality, N uptake during periods critical for leaching and no negative effects on subsequent crops

P6 – S2

Genetic Studies of Winter Hardiness in Pea (*Pisum sativum* L.)

Holdt C., McPhee K.
North Dakota State University, USA

Production of dry pea has increased in North Dakota and other states in the Great Plains due to their high protein content and ability to symbiotically fix atmospheric nitrogen. Fall sowing allows the pea crop to avoid high summer temperatures during the bloom period and increase seed production. Fall-sown pea crops would benefit northern states, however; extreme cold winter temperatures limit their success. This research aims to aid the development of winter hardy peas by developing improved screening methods to identify increased levels of winter hardiness. An RCBD with six and four replicates was used to evaluate 62 germplasm lines and 160 RILs, respectively. Two week old seedlings were acclimated for four weeks at 4°C and subjected to the freezing cycle. Temperatures ramped down from 3°C to -8°C at 1°C/hr and increased at the same rate after a one hour freeze at -8°C. Individual plants were given an injury score every three days during the 21 day recovery period and Area Under the Injury Curve values were calculated. Phenotypic data for freezing response will be used to conduct QTL analysis using a SNP based map of the Shawnee/Melrose population. Statistically significant differences were detected ($P<0.01$) among the 62 germplasm lines. Results of the QTL analysis will be presented. Development of improved protocols and molecular tools to detect winter hardiness in controlled environment will increase the productivity of breeding programs focused on winter peas.

P7– S2

Soil compaction evaluation in no-tillage plots under wheat-chickpea rotation

Masmoudi Y. A.

Institut National de la Recherche Agronomique (INRA), 126, Rue Moulay Ismail Derb Omar, Settat, Morroco

This work consists on evaluating compaction of soil under no-tillage system and wheat-chickpea rotation system. The penetration pressure and depth pressure were taken using portable penetrometer (30° cone). Measurements were done in the middle and extremities of the trial. As reference, compaction was done in adjacent field practiced using conventional tillage. On field measurements (in the number of three) were made between January and march 2016 according soil state, with different soil water content (dry, medium, wet). The results showed an increasing of penetration forces according to the maximum depths reached from the three measurements (the middle, extremities and reference) are respectively located between [13-38 cm], [21-52 cm] and [18-50 cm]. However, the depths recorded in the extremities of the same plot were respectively small [3-19 cm], [4-24 cm] and [7-25 cm]. Penetration depths recorded in the conventional plots are located respectively between [20-74 cm], [16-89 cm] and [20-75 cm]. These results showed that there is a significant compaction in the extremities of no-till plots, regardless of the state soil moisture also there is the important number of passages made by the agricultural tractors when they turn on the plots.

P8 – S2

Fumonisins associated with cowpea (*Vigna unguiculata*): Occurrence and phytotoxicity

Kritzinger Q.[1], **Aveling T. A. S.**[1,2], **Kotze R. G.**[1], **Crampton B. G.**[1,2]

1 - Department of Plant and Soil Sciences, University of Pretoria, Pretoria 0002, South Africa.

2 - Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria 0002, South Africa. quenton.kritzinger@up.ac.za

Research regarding mycotoxins and cowpea is a relatively unexplored field, especially in South Africa. In 2003, the natural incidence of fumonisins in cowpea seed was reported for the first time with total fumonisin levels ranging from 0.12-0.61 µg/g. Additional samples showed levels of 7.85–56.50 µg/g. This paper reports on our research activities regarding the occurrence of fumonisins on cowpea, with emphasis on the phytotoxic nature of fumonisin B1 (FB1). We found that germination and emergence of seeds imbibed in various FB1 concentrations were significantly decreased. Seedling mass was reduced by all FB1 concentrations. Chlorophyll content was higher in leaves of seedlings raised from seeds imbibed in FB1 when compared to the controls. Transmission electron microscopy of FB1 treated seed tissue revealed ultrastructural deteriorations including compaction of the cytoplasm and separation of the plasmalemma from the cell wall. FB1 is known to inhibit the formation of sphingolipids, and we therefore tested whether it would have an effect on expression of the ceramide synthase gene, the product of which plays a role in sphingolipid biosynthesis. However, semi-quantitative reverse transcriptase PCR suggested that there were no significant differences in ceramide synthase gene expression between control and FB1 treated cowpea root and shoot samples. Contaminated cowpea seed could affect food security, thus appropriate prevention and control strategies should be developed.

P9 – S2

Analysis of wild pea (*Pisum sativum* subsp. *elatius/humile*) seed dormancy levels

Hýbl M.[1]**, Kopecký P.**[1]**, Pechanec V.**[2]**, Brus J.**[2]**, Toker C.**[3]**, Smýkal P.**[4]

1 - Crop Research Institute, The Centre of the Region Haná for Biotechnological and Agricultural Research, Olomouc, Czech Republic.

2 - Department of Geoinformatics, Palack_ University in Olomouc, Olomouc, Czech Republic.

3 - Department of Field Crops, Akdeniz University, Antalya, Turkey.

4 - Department of Botany, Palack_ University in Olomouc, Olomouc, Czech Republic.

Seed dormancy and germination characteristics may vary within species in response to several environmental factors. In the wild, many seeds will only germinate after certain conditions have passed.

The objective of the study is to understand the genetic basis of adaptation to environmental conditions influencing dormancy release and the timing of seed germination, as a critical moment in a plant’s life, with fundamental consequences on fitness, using wild pea (*Pisum* sp.) model. Fifty geographically different wild pea lines were scored at fluctuating temperatures of 40/15°C, 30/10°C, 20/5°C regimes and variation in dormancy was recorded. In addition, 20 selected genotypes were tested for germination in semi-natural conditions of eastern Turkey. Similarities as well as differences to laboratory results were found, possibly related to soil temperature oscillations and rainfall pattern. These lines were also analysed anatomically for seed coat structure using SEM, light microscopy on cryosections and seed surface imaging. Simultaneously selected bioclimatic, topographic and humidity conditions will be extracted based on geographical coordinates from available layers. For each attribute will be generated descriptive statistics and calculated basic regression relationship. Results be subjected to model testing relationship with dormancy levels.

Acknowledgement: funding originates from Grant Agency of Czech Republic project Nr. 16-21053S.

P11 – S2

Agronomic performance of white clover genotypes in sole and mix cropping with ryegrass and chicory

Heshmati S., Isselstein J.
Georg-August-Universität Göttingen

White clover (*Trifolium repens* L.) is recognized as the most important forage legume in the temperate zones of the world. The cultivation of clover in mixture with ryegrass (*Lolium perenne*) is a common practice because there are a number of potential advantages of mixtures as compared to monocultures. The inclusion of a forb as a third component may provide further production advantages, in the present investigation the hypothesis was tested that the performance of mixtures is dependent on growth characteristics of white clover that vary among different clover genotypes. Eight novel genotypes of whit clover were grown on two sites either as monoculture or as binary mixtures with ryegrass and or chicory or as multi species mixtures with ryegrass and chicory. Herbage was harvested two times in the sowing year and four times in the first main production year. The mixtures produced high-accumulated total dry matter yields than the clover monocultures. The multi species mixture was not better performing than the binary mixtures. For the accumulated yield no significant effect of the factor clover genotype and the interaction clover genotype x cultivation was found. However, if single harvest were considered, clover genotype showed significant effects. A detailed analysis of the growth characteristics of the white clover genotypes is on the way and is intended to enable the identification of clover traits that are relevant for the mixture performance.

P12 – S2

Effect of environment on total phenol and tannin content and their relationship with other seed components in soybean [*Glycine max* (L.) Merrill] genotypes

Jhajj K. K.[1], Gill B. S.[1], Sharma S.[2]

1 - Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana-141004, India

2 - Department of Basic Sciences and Humanities, Punjab Agricultural University, Ludhiana-141004, India

Soybean [*Glycine max* (L.) Merrill] is an important agricultural and dietary commodity worldwide. The most important organic components of soybean seed are proteins (about 40%) and oil (about 20%). With the exception of isoflavonoids, few studies have been carried out on the other phenolic classes present in soybean. The present investigation was carried out to study the effect of environmental conditions (different photoperiod and temperature regimes) on the presence of phenolic compounds in soybean genotypes. Seventeen soybean genotypes were grown under three different planting dates i.e. March 1(D1), June 5 (D2) and August 7 (D3) to expose seed development stages to three different environmental conditions. Pooled analysis of variance over the three environments (sowing dates) showed that genotypes, sowing date and genotype x sowing date interactions were significant ($P < 0.01$) for phenol and tannin content. Both total phenol and tannin content were found to be lowest in case of March sowing (D2) with average of 27.1 mg/g and 12.4 mg/g, respectively which implied that when seed developed under high temperature and photoperiod, the phenol content was low as compared when seed filling takes place at low temperature and photoperiod. Correlation coefficients of both components with some other seed quality characters were also estimated. Mild to strong significant associations were observed for some of the nutritional and antinutritional seed characters.

P13 – S2

Mineralization kinetics and greenhouse gas emissions from legume crop residues added to soil

Oliveira M.[1], Rebac D.[1], Coutinho J.[2], Trindade H.[1]

1 - Centre for the Research and Technology of Agro-Environmental and Biological Sciences, University of Trás-os-Montes and Alto Douro, (CITAB-UTAD);
2 - Centro de Química de Vila Real

After harvesting legume crops for grain, the remaining biomass is high in N and C and can increase soil fertility for the following crop when left on the field. However, this process stimulates soil microbial activity, which may result in the loss of C and N by nitrate leaching and by the emission of ammonia (NH3) and greenhouse gases (GHG) carbon dioxide, methane and nitrous oxide (N2O). The bio-chemical composition of the residues and the method of application to the soil can influence the N mineralization rate and GHG emissions.

An 8-month laboratory soil incubation experiment is being performed. Treatments consist of three legume straws (cowpeas, fava beans and peas) added to soil at a fixed concentration of 7,5 t/ha by two different methods: incorporation and surface deposition. Two temperatures (10 and 20ºC) are being tested. Soil samples are collected periodically for mineral N analysis. Gaseous emissions from kilner jars were measured in the first 21 days with an INNOVA photoacoustic field gas monitor.

Results for the first 21 days show significantly higher cumulative NH3 emissions for pea and fava bean residues left on surface than cowpea residue, either incorporated or left on surface. Ammonia emissions at 10ºC were significantly higher than at 20ºC.

Incorporation of cowpea residue produced significantly higher cumulative N2O emissions in the first 21 days than all other treatments.

Further results from the on-going experiment are needed before drawing conclusions.

P14 – S2

Functional traits diversity and fitness evaluation in response to salt stress in some *Medicago* spp wild populations.

Amokrane M.S.Y.[1,2,4], Kadri A.[1,2,3], Laouar M.[1], Ben C.[4], Julier B.[5], Gentzbittel L.[4], Abdelguerfi A.[2]

1 - ENSA, Laboratoire d'Amélioration Integrative des Productions Végétales, Alger, Algérie
2 - ENSA, Laboratoire des Ressources Génétiques et Biotechnologies, Alger, Algérie
3 - Université de M'sila, Département d'Agronomie, Faculté des Sciences, BP166 Ichebillia, M'sila, Algeria
4 - EcoLab, Université de Toulouse, CNRS, INPT, UPS, Toulouse, France
5 - URP3F, INRA, 86600 Lusignan, France

Land salinity is one of the major abiotic constraints that affect negatively crop production worldwide. *Medicago* genus, mostly composed by annual species, is of a real interest in improving soil fertility and maintaining pastures for livestock. We assessed adaptive traits for salt tolerance in 40 contrasted populations belonging to 6 *Medicago* species. In a common site, trial was performed in saline and non-saline soils where functional and fitness traits were recorded. Only *M. ciliaris* populations survived in the saline soil, highlighting the negative effect of even low salt levels at plant lift. ANOVA and PCA revealed that lifting rate, length branch at flowering time and total pod number might be involved in salt tolerance. The response to salt stress of *Medicago* was further studied by analyzing germination kinetics of 37 populations under five ranges of NaCl concentrations from 0 to 200 mM, during 7 days. Kaplan-Meier survivor curves and Cox PH models indicated that time to 50% germination, germinability and germination synchrony are affected by the increase of salts. The risk of non-germinated seeds depends on species, populations and NaCl concentrations. Altogether, these results show that both salt level and exposition duration affect the phenotypical traits. Local adaptation may partly explain the patterns of salt tolerance. *M. ciliaris* is the most tolerant species, with a relatively high level of intraspecific variability for most studied traits.

P15 –S2

UMT ALTER’N : Knowing alternative nitrogen sources (legumes and organic waste products) in order to manage cropping systems with low nitrogen losses and less dependent on synthetic fertilizers

Schneider A.[1], Colnenne C.[2], Cadoux S.[1], Cellier P.[3], Drouet J.-L.[3], Houot S.[3], Jeuffroy M.-H.[2], LeGall C.[1], Reau R.[2]

1 - Terres Inovia, DEO
2 - INRA Agronomie
3 - INRA Ecosys

Labelled by the Ministry of agriculture as an UMT (technological mixed unit) in 2015, ALTER’N is a thematic partnership framework between Terres Inovia and INRA (Agronomie and Ecosys units in Grignon). ALTER’N aims to enhance the capacity for strategic advice for inserting legumes (which fix atmospheric nitrogen) and for recycling residual organic fertilising matters into crop systems that should be both competitive and with low nitrogen losses. The objective is to produce references and to deliver knowledge and operational tools. It should contributes that the actors of agricultural and environmental world are able to make the diagnostic of possible nitrogen losses of their crops systems and the conception and management of more N-efficients systems. Priority is given to knowledge synthesis by strengthening joint analysis, so as to deliver validated items for systems, which use these nitrogen sources as complements of the application of industrial mineral nitrogen.

P16 – S2

How heat stress affects the physiology and reproductive biology of summer and winter-season food legume crops?

Nayyar H.[1], Gaur P.[2], Kumar S.[3], Singh S.[4], Bindumadhava H.[5], Nair R.M.[6], Prasad P.V.V.[7], Siddique K.H.M.[8]

1 - Department of Botany, Panjab University, Chandigarh, 160014 India
2 - ICRISAT, Patancheru 502 324, Greater Hyderabad, Telangana, INDIA
3 - ICARDA, Rabat 10112, Morocco
4 - P.A.U., Ludhiana 141004, Punjab, India
5 - Plant Physiology, World Vegetable Center, South Asia Hyderabad, India.
6 - World Vegetable Center, South Asia, ICRISAT campus, Patancheru 502 324 Greater Hyderabad, Telangana, INDIA
7 - Kansas State University, Kansas Manhattan, USA
8 - The UWA institute of Agriculture, The University of Western Australia, Perth WA 6001, Australia

High temperature (heat stress) is a major concern for the productivity of food legumes, grown in winter as well as summer-season. Our studies have indicated a marked damage to reproductive stage resulting in reduction in pod set and seed yield of chickpea, lentil (cool-season legumes) and mungbean (warm-season legume) under high temperatures. Studies done in controlled and outdoor environments (late sowing) revealed that temperatures >35/20°C (as day and night) were highly detrimental. The degree of damage varies depending upon the duration and severity of stress. Among the reproductive components, pollen grains were more sensitive, became deformed and showed reduction in pollen viability, reduced germination and pollen tube growth. Stigma receptivity and ovule viability were also inhibited, which affected the pollen germination on stigma surface and restricted tube growth through style, impaired fertilization to cause flower abortion. Assessment of the physiology of leaves and anthers indicated decrease in sucrose production in both the organs due to inhibition of enzymes, which possibly affected the structural and functional aspects of the pollen grains. Oxidative stress increased markedly in anthers due to heat stress, which possibly affected the pollen development and its function. Genetic variation for stress tolerance exists in our target legume crops, which needs further probing and use of heat tolerant germplasm in breeding programs.

Session 3, parallel: Beneficial legume-microbe interactions - Room *Arrábida III*

Chaired by Carmen Bianco (Univ. Bari, Italy) and Pedro Fevereiro (ITQB NOVA, Portugal)

14:30-15:00 **Key lecture - Jens Stougaard**: Receptor mediated signaling in legume symbiosis

Oral Communications

15:00-15:10 Oral – S3

Symbiotic genes expression in a context of nitrogen-fixing symbiotic specificity in the *Lupinus* genus

Keller J.[1]**, Cabello-Hurtado F.**[1]**, Salmon A.**[1]**, Imperial J.**[2]**, Aïnouche A.**[1]

1 - UMR CNRS 6553 Ecobio, OSUR (Observatoire des Sciences de l'Univers de Rennes), University of Rennes 1, 263 av. du Général Leclerc, 35042 Rennes, France

2 - Departamento de Biotecnología (ETSIA) and Centro de Biotecnología y Genómica de Plantas (CBGP), Universidad Politécnica de Madrid, 28040 Madrid, Spain

Ability of legumes to fix atmospheric nitrogen thanks to their symbiosis with bacteria has a major role for natural and agricultural ecosystems. Genes involved in the different steps of symbiosis formation have been extensively studied in economically important or model species. One striking aspect of this legume-rhizobial mutualistic association is the symbiotic specificity. In order to explore the complexity of the symbiotic specificity, a transcriptomic study is conducted on a group of non-model species from genus *Lupinus* (Genistoids) usually forming nitrogen-fixing symbiosis with *Bradyrhizobia*. In addition, specific features of symbiosis have been observed in this genus, such as: the absence of infection threads; a unique mode of bacteria penetration; and the occurrence of several cases of symbiotic specificity. Transcriptomes from root/nodules of three lupine species cultivated with two different strains of bacteria were generated, assembled and annotated. Using alternative approaches to estimate the expression level of either individual or clusters of transcripts, numerous differentially expressed (DE) genes have been detected. Careful analysis of these DE transcripts and clusters revealed the presence of many genes involved at different steps of the symbiosis genetic network, such as genes involved in the perception of symbiont signals and interaction with NOD factor receptors. This provides new insights on gene expression in a context of symbiotic specificity.

15:10-15:20 Oral – S3

Beneficial microbes associated with legumes

Vosatka M.[1], Rozmos M.[1], Latr A.[1], Ma Y.[2]

1 - Symbiom Ltd
2 - University of Coimbra, Portugal

Symbiotic rhizobia, plant growth promoting rhizobacteria (PGPR) and arbuscular mycorrhizal fungi (AMF) are common associates of majority of legumes. The trials undertaken within Eurolegume project by SYMBIOM Ltd. (producer of AMF inocula) confirmed the mutual compatibility between the microbial inoculants (rhizobia, PGPR and AMF) in pea and faba bean plants in terms of their establishment in the roots as well as the impact of drought stress on plant development and yield parameters. Interestingly, there was no difference found between the irrigation regimes in terms of dry biomass of faba bean. Positive effects were observed regarding seed weight per plant of faba bean. In addition, the leaf analysis showed an increase of the content of phosphorus in all microbial treatments for pea under 100% irrigation regime. Suitable combination of rhizobia and AMF for these legumes plus chickpea and cowpea have been tested and their effects on growth and stress resistance evaluated. Feasible application modes are developed for microbe delivery to cultivation. Potential of largescale application of inocula in legume production is considered.

Project has received funding from the European Union´s Seventh Framework Programme for research, technological development and demonstration under grant agreement no 613781. Providing of legume seeds and rhizobia by Dr. Rui Oliveira from University of Coimbra is acknowledged as well as collaboration with other Eurolegume partners.

15:20-15:30 Oral – S3

Partner choice in a core collection of pea inoculated by a mix of five *Rhizobium leguminosarum* sbv. *viciae* strains

Bourion V., de Larambergue H., Aubert V., Chabert-Martinello M., Siol M., Duc G., Burstin J.
INRA, 21000 Dijon, Fance

Pea is the third most important grain legume worldwide. The crop natural ability to use, as main nitrogen resource, the atmospheric N2 symbiotically assimilated by *Rhizobium leguminosarum* sbv. *viciae* (Rlv) in the plant nodules is a major component of its attractiveness. However, the symbiosis may not be optimal because natural Rlv populations are quantitatively and qualitatively heterogeneous, with strains varying in competitiveness and efficiency of nitrogen fixation. The variability of pea-Rlv partner choice was investigated within a collection of 104 pea accessions co-inoculated with a mix of five diverse Rlv strains. Analyses of the genetic structure of the pea collection - genotyped using the GenoPea 13K SNP Array - uncovered different genetic groups representative of the pea geographic origin or history of selection. Proportions of nodules formed with each strain were estimated in each pea accession. Differences in the Rlv choice were observed between the different pea genetic groups, revealing changes in partner choice during domestication and breeding selection. Additional experiments performed on a subset of pea accessions showed that in most cases competiveness for nodulation of a given pea-Rlv symbiotic association could not be related to its nitrogen fixation efficiency. Further studies involving larger pea panel and mix of Rlv strains together with a higher density SNP genotyping will be carried out to identify specific loci underlying the partner choice trait.

15:30-15:40 Oral – S3

Improving adaptation of legume-rhizobium symbiosis to the soil environment

Lepetit M., Brunel B., Heulin K., Lahmidi N.A., Le Quéré A., Pervent M., Tauzin M.

Laboratoire des Symbioses Tropicales et Méditerranéennes, UMR 1342 INRA-IRD-CIRAD-UM-Montpellier SupAgro, Campus International de Baillarguet TA-A82/J, 34398 Montpellier

A major hallmark of legume crops is adaptation to mineral N limitation by developing root symbiotic nodules with N_2-fixing rhizobia. Their use may reduce nitrogen fertilizer inputs. However nodules are highly sensitive to soil constraints. Soils do not necessarily shelter symbiotic partners for optimal N_2 fixation. Local water deficit and other stresses suppress rapidly the activity of nodules directly exposed to them in soils. Consequently yields of symbiotic legumes are frequently highly fluctuating. There is a need for breeding strategies.

A first strategy is to select rhizobium/legume associations that display the most efficient N_2 fixation and allow success for rhizobium inoculation at sowing. Bacteria forming nodules are not necessarily efficient and may display different levels of competitiveness for nodulation when they are in mixture, as it is generally the rule in soils.

The second strategy is to identify genetic determinants that allow plants to compensate a partial suppression of its symbiotic activity due to a localized soil constraint (notably drought). Several systemic mechanisms adjusting the symbiotic capacity to the plant N demand are involved. Compensatory responses may vary according to the symbiotic partner. Recent progress toward these two objectives using *Medicago truncatula/Sinorhizobium* as model system and pea/*Rhizobium leguminosarum* as agronomical target will be presented.

This work has been supported by Peamust (ANR) and Legato (EU FP7 KBBE) grants.

P17 – S3

Seed coating of grain legumes with inocula of arbuscular mycorrhizal fungi and plant growth-promoting bacteria.

Pinto L.M.[1], Cambra R.[1], Rocha I.[2], Ma Y.[2], Marques G.[3], Látr A.[4], Vosátk M.[5], Freitas H.[2], Oliveira R.S.[1,2]

1 - Department of Environmental Health, Research Centre on Health and Environment, School of Allied Health Sciences, Polytechnic Institute of Porto, Vila Nova de Gaia, Portugal.
2 - Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, Coimbra, Portugal.
3 - CITAB - University of Trás-os-Montes and Alto Douro (UTAD), Department of Agronomy, Vila Real, Portugal.
4 - Symbiom Ltd., Lanskroun, Czech Republic. 5 Institute of Botany, Academy of Sciences of the Czech Republic, Pr_honice, Czech Republic.

Beneficial soil microorganisms such as plant growth-promoting bacteria (PGPB) and arbuscular mycorrhizal fungi (AMF) can improve plant growth, nutrition and yield. Seed coating techniques have the potential to allow the use of minor amounts of inoculum, resulting in cost reduction and efficiency increase. The aim of this study was to assess whether seed coating can be used as a feasible microbial inocula delivery system for grain legumes. Seeds of chickpea (*Cicer arietinum* L.) and cowpea [*Vigna unguiculata* (L.) Walp.] were coated with inoculum of PGPB, AMF or a mixture of both. Seed germination rate and the number of viable PGPB and the number of propagules of AMF per seed of chickpea and cowpea were determined. Results showed that both microbial inoculants were viable after being coated onto seed of chickpea and cowpea. Seed coating may represent a sustainable approach for application of beneficial microorganisms in the production of grain legumes.

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P182– S3

Finding of superior *Rhizobium* strains for field pea and faba bean in Estonian soils

Toom M.[1], Narits L.[1], Sooväli P.[1], Põllumaa L.[1], Mäe A.[1]

1 - Estonian Crop Research Institute

The increased global N fixation from legumes requires the selection and development of effective inoculant strains of root-nodule bacteria that suit with legume host and the target edaphic environment.

Within the framework of the project EUROLEGUME (Enchancing of legumes growing in Europe through sustainable cropping for protein supply for food and feed) the trials with selecting appropriate Rhizobium strains were carried out.

The root nodules of Faba bean (*Vicia faba*) 'Jõgeva' and field pea (*Pisum sativum*) 'Mehis' were collected from pot grown plants containing soils from different Estonian regions. Strains of Rhizobium were isolated by standard methods. The composition of bacterial community were determined by 16S rRNA sequencing.

The effect of Rhizobial strains on nodulation and growth of bean and pea was examined in test tubes with seedling agar. Also the pot experiment with inoculated and uninoculated soil was carried out to evaluate the nodulation efficiency, plant growth, seed yield, nitrogen and protein content. Further, the acetylene reduction assay will be applied to estimate biological N2 fixation activity.

Acknowledgements: The project EUROLEGUME, Grant no 613781

P183 – S3

Phenotypic and molecular identification of rhizobia nodulating faba bean (*Vicia faba* L.) and cowpea (*Vigna unguiculata* (L.) Walp) plants

Pereira S.[1], Mucha A.[1], Sharma L:[1], Pereira G.[2], Duarte I.[2], Rosa E.[1], Marques G.[1]

1 - CITAB- University of Trás-os-Montes and Alto Douro (UTAD), Department of Agronomy, Vila Real, Portugal.
2 - Instituto Nacional de Investigação Agrária e Veterinária (INIAV), Elvas, Portugal.

Within the diversity of leguminous plants, cowpea and faba bean are very important in Europe, and in Portugal. In this work, 37 rhizobia isolates of cowpea and 27 rhizobia isolates of faba bean were collected in different geographic regions and edaphoclimatic conditions. The phenotypic characterization of the isolates was performed accordingly to their colony characteristics, Molecular identification of these isolates, after checking their ability to colonize other plants in vitro, was performed by 16S rDNA sequences. Other methods such as genomic fingerprinting using the repetitive sequence-based polymerase chain reaction (repPCR) method, with REP, ERIC and BOX primers and nifH and nodC sequences from selected isolates were used when necessary to increase the discriminating power. Although the genus *Bradyrhizobium* is more common in cowpea, in this work we have also isolated strains of *Rhizobium* that do not cluster with the existing species that have been identified. In the bacteria collected from faba bean nodules, some isolates belonging to the genus *Burkholderia* were identified.

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P184 – S3

Yield formation of Faba beans (*Vicia faba* L.) depending on double inoculation with rhizobia and mycorrhiza fungi

Senberga A., Dubova L., Alsina I.

Latvia University of Agriculture

Legumes are able to fix the necessary amount of atmospheric nitrogen because of symbiotic relationship with soil bacteria rhizobia. While rhizobia ensure legumes with nitrogen, the uptake of mineral elements (particularly phosphorus) can be enhanced by mycorrhiza fungi. Legume inoculation with mycorrhiza increases protein accumulation and also the activity of nodules.

Aim of the study was to examine the effectiveness of triple symbiosis and to test if double inoculation of faba beans with rhizobia together with mycorrhiza can enhance the quantity and quality of the crop. Four different faba bean cultivars were used (Bartek, Karmazyn, Fuego, Lielplatone). Rhizobia strains (RP023, RV407) were provided by the Institute of Soil and Plant Sciences (Latvia). Commercial mycorrhiza preparation was obtained from Symbiom Ltd. (Czech Republic).

Fresh weight, height and the level of bean root infection with rhizobia and mycorrhiza were detected during the flowering phase. After harvesting, the crop yield and protein content of beans were measured. Obtained data shows that crop yield and protein content depend on bean cultivar, microorganism inoculant and on the weather conditions during the vegetation period. Bean inoculation with rhizobium strain RV407, which is originally isolated from beans, was the most effective. Treatment with mycorrhiza showed a positive impact on yield formation. The highest protein content was detected in the faba bean cultivar Lielplatone.

P185 – S3

Intercropping legume-cereals is a system to value legume-rhizobia symbiosis toward agriculture sustainability

Mouradi M.[1], Makoudi B. [1], Kabbadj A. [1], Farissi M.[2], Bouizgaren A.[3] and Ghoulam C.[1]

1 - Unit of Plant biotechnology and Symbiosis Agrophysiology, Faculty of Sciences and Techniques, PO box 549, Gueliz, Marrakech, Morocco;

2 - Université Sultan Moulay Slimane, Faculté Polydsciplinaire, B. P. 592, Mghila, Beni Mellal, Morocco;

3 - Institut National de la Recherche Agronomique (INRA), Unité d'Amélioration Génétique des Plantes, B.P. 533, Guéliz, Marrakech, Marroco

Intercropping legume-cereal is one of the main farming systems that optimize use of common limiting resources. Our study aims to assess the benefit of faba bean-rhizobia symbiosis on barley plant growth as intercropped species particularly under soil nitrogen (N) and phosphorus (P) deficiency. The study was carried out in farmers 'fields using two *Vicia faba* varieties and one barley variety grown as intercropped species in N and P deficient soils in the Haouz area of Morocco. We considered sole crop of faba bean; sole crop of barley and intercropped faba bean-barley as alternate rows with plant densities of 30 and 50 plants per m2 respectively for faba bean and barley. The trials were conducted without chemical fertilization. At faba bean plant flowering stage, the trials were assessed. The results showed that faba bean plant growth and nodulation were positively correlated to phosphorus accumulation in different plant parts, whereas the phosphatases activities in nodules and roots were higher in intercropped faba beans than sole crop. For barley, plant biomass significantly increased when grown as mixed culture with faba bean in comparison to the corresponding sole crop controls. Indeed, this study proved that intercropping system stimulates the activity of phosphatases and increases P availability in the rhizosphere of both species. Thereby, in intercropping system, faba bean-rhizobia symbiosis improved barley plant growth through increase of nutrients availability.

P186 – S3

Chickpea and lentil co-inoculation with selected plant growth promoting rhizobacteria and rhizobia: impact on nodulation and growth

Benjelloun I.[1,2], Thami-Alami I. [2], El Khadir M.[2], Udupa S.M.[3], Aurag J.[4], Berraho E.[4], Douira A.[1]

1 - Laboratoire de Botanique, Biotechnologie et de Protection des Plantes, Département de Biologie, Faculté des Sciences de Kenitra, Université Ibn Tofayl, BP 242, Kénitra, Morocco. i.benjelloun@hotmail.fr

2 - Institut Nationale de la Recherche Agronomique (INRA), B.P.415, Rabat, Morocco

3 - ICARDA-INRA Cooperative Research Project, International Center for Agricultural Research in the Dry Areas (ICARDA), B.P. 6299, Rabat, Morocco

4 - Laboratoire de microbiologie et de biologie moléculaire (LMBM) Université Mohammed V Faculté Des Sciences, Rabat Agdal

Food legumes play a substantial socio-economic role and occupy an important place in the diet of Moroccan population. However, the yield remains low. Chickpea (*Cicer arietenum*) and lentil (*Lens culinaris*) are in the second rank in Morocco, after faba bean with a strong local and international demand. Culture and productivity of these two crops in Morocco depends largely on the chemical fertilization. To enhance the productivity and limit the use of chemical fertilizers, it is necessary to support the use of biofertilizers based on nitrogen fixing bacteria and phosphate solubilization Rhizobacteria for an economic and ecologically- sustainable agriculture.

A field experiment co-inoculation test of lentil and chickpea with rhizobia (L3 and L43 for the lens and Pc72 and Pc100 for chickpea) and plant growth promoting bacteria (M131 and P1S6) was carried out in two sites in Morocco, Merchouch (clay-silty) and Ain Sbit (clay-sandy) in a Randomized Complete Block Design (RCBD) with four replications of each treatments. 16 treatments were applied in each site to each culture: two Rhizobia strains S1 and S2, two PGPR strains (M131 and P1S6), two N levels (N0 and N 120) and two phosphate levels (P0 and P80).

Results showed that inoculation with rhizobia P72 and P100 for chickpea and L3 and L43 for lentil improved significantly grain and straw yield of both cultures in both sites.

P187 – S3

Synergy between crop diversity and earthworm community improve crop yields

Drut B., Cassagne N., Cannavacciuolo M, Fustec J.
UR LEVA, Ecole Supérieure d’Agricultures, Angers, France

Biodiversity may influence productivity of the plant cover through above- and belowground interactions. Our study aimed to analyze simultaneous effects of plant cover diversity and of earthworms on wheat performances. Mesocosms filled with soil were sown with either 6 wheat plants of the same cultivar, or 6 plants of 3 different wheat cultivars, or 3 wheats of 3 different cultivars with 3 clover plants (*T. hybridum*). They were inoculated or not with earthworms (n=5): i) 5 endogeic earthworms, ii) 5 endogeic and 2 anecic earthworms, iii) no earthwoms. Above-and belowground plant biomass and N concentrations were measured. The Relative Interaction Index was calculated to highlight the strength of competition between plants. The cultivar mixture had no influence on the wheat performance, but with clover, competition decreased to the benefit of wheat biomass and N accumulation. Earthworms also decreased competitive strength between wheats in mixed cultivars as well as in intercrop. In the presence of clover, wheat biomass and N were increased thanks to niche complementarity. Endogeic earthworms changed the interaction between plants and highly reduced belowground competition, suggesting that plant cover diversity and earthworms work synergistically to improve wheat yields. The addition of earthworm functional diversity had no effect on wheat intercropped with clover, which suggest that the benefit from interactions reached a threshold.

P188 – S3

The use of nitrogen fixing bacteria as “elite inoculants” in biodiverse legume pastures

Soares R. [1]**, Fareleira P.** [1]**, Pereira P.**[1]**, Silva A. R.**[2]**, Barradas A.**[2]**, Crespo D.**[2]**, Videira e Castro I.**[1]

1 - INIAV, I.P., Oeiras, Portugal
2 - Fertiprado, Vaiamonte, Portugal

The improvement of pastures in the montado (cork oak) ecosystem is based on the establishment of biodiverse permanent pastures rich in legumes, by sowing a diversity of selected and improved species, in which inoculated legumes with rhizobia are preponderant. This is considered as a powerful management tool, being legumes important components of the strategy for increasing productivity and sustainability, using symbiotic nitrogen fixation as a major process of providing nitrogen to the soils. Nodulation and N2 fixation in these symbioses need that host and microorganisms are well matched. The selection for the optimal combination of rhizobia and the host legume usually results in more effective symbioses. Despite the large numbers of rhizobial strains that nodulate host legumes, only some strains are symbiotically effective on their hosts. The aim of this work was to select autochthonous rhizobia strains isolated from several *Trifolium* sp. and *Medicago* sp. grown in the South of Portugal, towards their future use as elite inoculants. Experiments in controlled environment conditions were performed to evaluate the symbiotic effectiveness of different species of *Trifolium* and *Medicago* inoculated with several rhizobia strains. Molecular identification was performed using the sequence of 16S rRNA and recA genes. The performance and competitiveness of selected strains were evaluated in natural field conditions.

This work was supported by the project PRODER 54971.

P189 – S3

The auxin indole-3-acetic acid (IAA) is more than a plant hormone

Bianco C.[1], **Andreozzi A.**[1], **Rubino S.**[1], **Esposito R.**[2], **Angelini C.**[3], **Defez R.**[1]

1 - Institute of Biosciences and BioResources, CNR, via Pietro Castellino 111, 80131 Napoli, Italy

2 - Institute for Applied Mathematics Mauro Picone IAC, CNR, via P. Castellino 111, 80131 Napoli, Italy

3 - Institute of Genetics and Biophysics "A.B.T.", CNR, via P. Castellino 111, 80131 Napoli, Italy

RNA-seq analysis was applied to compare, under free-living conditions, the transcriptome of the IAA overproducing *S. meliloti* RD64 strain with the wild type *S. meliloti* 1021 one. Quantitative real-time PCR analysis was used to validate RNA-seq experiments and to evaluate, under microaerobic and nitrogen-limited conditions, the expression levels of genes directly involved in nitrogen fixation and metabolism. Our results showed that IAA overproduction by rhizobia directly or indirectly leads to the activation of key genes of nitrogen fixation process including the main nitrogen fixation regulator fixJ, the two intermediate regulators fixK and nifA, and several other genes, known to be FixJ targets, whose expression normally occur in nitrogen fixing root nodule. The gene coding for the sigma factor RpoH1 and other genes involved in stress response, regulated in RpoH1-dependent manner in *S. meliloti*, were also induced in RD64 cells. Under microaerobic condition, quantitative real-time PCR analysis revealed that the genes fixJL and nifA were up-regulated in RD64 cells as compared to 1021 cells. We speculate that IAA could be a plant signal used to induce the expression of rhizobia nitrogen fixation genes inside root nodules. We also hypothesize that the bacterial IAA-overexpression might improve the nitrogen fixation in different plant-bacteria associations that could poorly establish a microaerobic environment.

P190 – S3

Symbiotic genes expression in a context of nitrogen-fixing symbiotic specificity in the Lupinus genus

Keller J.[1], Cabello-Hurtado[1] F., Salmon A.[1], Imperial J.[2], Aïnouche A.[1]
1 - UMR CNRS 6553 Ecobio, OSUR (Observatoire des Sciences de l'Univers de Rennes), University of Rennes 1, 263 av. du Général Leclerc, 35042 Rennes, France
2 - Departamento de Biotecnología (ETSIA) and Centro de Biotecnología y Genómica de Plantas (CBGP), Universidad Politécnica de Madrid, 28040 Madrid, Spain

Ability of legumes to fix atmospheric nitrogen thanks to their symbiosis with bacteria has a major role for natural and agricultural ecosystems. Genes involved in the different steps of symbiosis formation have been extensively studied in economically important or model species. One striking aspect of this legume-rhizobial mutualistic association is the symbiotic specificity. In order to explore the complexity of the symbiotic specificity, a transcriptomic study is conducted on a group of non-model species from genus *Lupinus* (Genistoids) usually forming nitrogen-fixing symbiosis with Bradyrhizobia. In addition, specific features of symbiosis have been observed in this genus, such as: the absence of infection threads; a unique mode of bacteria penetration; and the occurrence of several cases of symbiotic specificity. Transcriptomes from root/nodules of three lupine species cultivated with two different strains of bacteria were generated, assembled and annotated. Using alternative approaches to estimate the expression level of either individual or clusters of transcripts, numerous differentially expressed (DE) genes have been detected. Careful analysis of these DE transcripts and clusters revealed the presence of many genes involved at different steps of the symbiosis genetic network, such as genes involved in the perception of symbiont signals and interaction with NOD factor receptors. This provides new insights on gene expression in a context of symbiotic specificity.

Session 4, parallel: Genetic resources - Room *Arrábida IV*

Chaired by Hari Upadhyaya (ICRISAT) and Rodomiro Ortiz (SLU, Sweden)

14:30-15:00 **Key lecture - Noel Ellis**: Where are we after 150 years of legume genetics?

Oral Communications

15:00-15:10 Oral – S4

Using expanded collections of wild relatives of chickpea to understand domestication and improve climate resilience.

von Wettberg E.[1], Chang P.[2], Singh V.[2], Cordeiro M.[2], Greenspan A.[3], Alford B.[4], Carrasquilla N.[3], Dacosta-Calheiros E.[1], Warschefsky E.[1], Rouf Mir R.[5], Bukun B.[6], Kahraman A.[7], Aydoğan A.[8], BergerJ.D.[9], Nuzhdin S.V.[2], R Varma Penmetsa R.V.[10], Cook D.R.[10]

1 - Florida International University, Miami, FL,
2 - University of Southern California, Los Angeles, CA,
3 - University of California, Davis, CA,
4 - University of California Davis, Davis, CA,
5 - SKUAST JAMMU, JAMMU, India,
6 - Dicle University, Diyarbakir, Turkey,
7 - Harran University, Urfa, AZ, Turkey,
8 - Turkish Ministry of Agriculture, Ankara, Turkey,
9 - Plant Industry, CSIRO, Floreat, WA, Australia,
10 - University of California at Davis, Davis, CA

Like many other annual crops, chickpea (*Cicer arietinum*) underwent a substantial population bottleneck when domesticated from its wild progenitor (*Cicer reticulatum*) approximately 10 thousand years ago. During this bottleneck several key domestication traits such as indehiscence were positively selected by early farmers. However, the small effective population sizes of early agriculture and the ecological transition to the protected habitat of a cultivated field likely relaxed selection on much of the cultivated chickpea genome. We document both positive and relaxed selection on the cultivated chickpea genome, utilizing a recently assembled expanded collection of the wild progenitor of chickpea as well as its sister taxa *Cicer echinospermum*. A thorough survey of the source populations for the wild relatives as well as their habitats allows inference into the levels of standing variation available to early farmers, and environmental factors that shifted with the advent of agriculture in the fertile crescent. Our work shows the need for in-depth collections of crop wild relatives and landraces shielded from modern breeding to make informed inferences about domestication.

15:10-15:20 Oral – S4

Characterizing the genetic diversity of cowpea accessions using a high-density SNP array

Carvalho M.[1], Castro I.[1,2], Matos M.[2,3], Lino-Neto T.[4], Close T.[5], Munoz-Amatriain M.[5] and Carnide V.[1,2]

1 - Centre for Research and Technology of Agro-Environment and Biological Sciences (CITAB), University of Trás-os-Montes and Alto Douro (UTAD), 5000-801 Vila Real, Portugal.

2 - Department of Genetics and Biotechnology, University of Trás-os-Montes and Alto Douro (UTAD), 5000-801 Vila Real, Portugal.

3 - Biosystems & Integrative Sciences Institute (BioISI), Sciences Faculty, University of Lisbon, Campo Grande, 1749-016 Lisbon, Portugal.

4 - Biosystems & Integrative Sciences Institute (BioISI), Plant Functional Biology Center (CBFP), University of Minho, Campus de Gualtar, 4710-057 Braga, Portugal.

5 - Department of Botany and Plant Sciences, University of California Riverside, Riverside, California 92521-0124 USA.

Cowpea, native to Africa, is a legume crop well adapted to hot and drought-prone environments, and a primary source of protein for millions of people in the developing world. Characterization of genetic diversity within cowpea germplasm is important for the preservation of genetic resources and their use in crop improvement. We used the Illumina Cowpea iSelect Consortium Array containing 51,128 SNPs to genotype 96 cowpea accessions including: 33 local landraces and cultivars from Portugal, and 63 landraces collected worldwide (a total of 24 countries). A total of 44,056 high-quality SNPs were polymorphic among the samples and used for genetic diversity analyses. Both STRUCTURE and principal component analysis identified four subpopulations, mainly differentiated by accessions geographical origin. Most Portuguese accessions were clustered together with those from other southern European and northern African countries, indicating genetic similarity among them. However, two Portuguese cowpeas did not belong to this subpopulation and instead were categorized as ‘admixed’ (1 accession) or belonged to another subpopulation (1 accession). These accessions could be used as sources of diversity in plant breeding programs.

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15:20-15:30 Oral – S4

LupiBreed - Valorisation of novel genetic variability in narrow-leafed lupin

Fischer K.[1], Roux S.[1], Jansen G.[2], Ulrich H-J.[2], Dieterich R.[3], Wehling P.[1], Ruge-Wehling B.[1]

1 - Julius Kühn-Institut, Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Agricultural Crops, Groß Lüsewitz, Germany,

2 - Julius Kühn-Institut, Federal Research Centre for Cultivated Plants, Institute for Resistance Research and Stress Tolerance, Groß Lüsewitz, Germany,

3 - Saatzucht Steinach GmbH & Co. KG, Bocksee, Germany

Narrow-leafed lupin provides a source of protein and fibre with exceptional functional properties, which may be used for a variety of purposes including the production of high-quality vegetable foods.

To keep lupin growing economically attractive to the farmer, further improvement of grain and protein yield is mandatory. This may be accomplished by plant breeding. However, genetic variability of advanced breeding materials of narrow-leafed lupin is limited. To generate novel genetic variants we started an EMS-based mutagenesis program using current varieties. Novel growth types with potential for higher yield were selected and propagated to phenotypically stable lines. Performance tests over three years and three replications were started in 2015 to record agronomical relevant traits such as grain yield, protein yield, pod shattering, and anthracnose resistance. Statistical analysis of field data (2015) revealed M lines with higher yield and higher protein contents compared to the initial ‘wild type’. Among these, some M lines those also expressed reduced pod shattering and/or reduced anthracnose infestation. The selected M lines are currently crossed with genotypes carrying defined anthracnose resistance genes. This breeding program is assisted by molecular markers and expected to result in novel, high-performing cultivars.

15:30-15:40 Oral – S4

Domestic bliss? Causes and consequences of a modern era domestication event in narrow-leafed lupin

Nelson M. [1,2], **Mousavi M.** [2], **Taylor C.** [2], **Bayer P.** [2], **Kamphuis L.** [3], **Berger J.** [3], **Clements J.** [4], **Hane J.** [5], **Edwards D.** [2], **Erskine W.** [2], **Cowling W.** [2]

1 - Royal Botanic Gardens Kew,
2 - UWA (University of Western Australia),
3 - CSIRO (Commonwealth Scientific and Industrial Research Organisation),
4 - DAFWA (Department of Agriculture and Food of Wetern Australia), 5 Curtin University, Australia

The taming of wild plants to become productive agricultural crops was a gradual process taking hundreds or thousands of years for most of our major crop species. It involved progressively accumulating domestication traits (such as removal of seed dormancy and reducing seed dehiscence) that made the plants increasingly more useful and productive to people. Narrow-leafed lupin (*Lupinus angustifolius L.*) is exceptional in that its domestication was both recent and rapid, starting humbly as a green manure and fodder crop in the Baltic States in the 19th Century and then rapidly being transformed into a high-quality grain crop in the 20th Century. This was achieved through fixation of a handful of domestication alleles: reduced seed dehiscence (lentus and tardus), removal of seed dormancy (mollis), altered time of flowering and maturity (Ku), and reduced seed alkaloid content (iucundus). Both ancient and modern domesticates share this is common: seriously depleted genetic diversity due population bottlenecks. Narrow-leafed lupin, as a 20th Century domesticate, is unique among legume grain crops in that these bottleneck events are all documented in the scientific literature.

Here we will outline the value of lupin as a model for understanding plant domestication, what is known about the molecular mechanisms of domestication traits, and the impact domestication had on genome-wide diversity in this modern era legume crop species.

Posters

P18 –S4

Genetic resources of food legume crops in Algeria

Gaad D.
National High School of Agriculture, Algeria

Food legume genetic resources play a very important and diverse role in food security, farming systems and poverty alleviation, particularly in developing countries. They are ideal crops for achieving food and nutritional security for poor consumers. Food legumes also serve as a feed crop in many farming systems. In Algeria, Lentil (*Lens culinaris*), Chickpea (*Cicer arietinum*), Pea (*Pisum sativum*), Fababean (*Vicia faba*), and common bean (*Phaseolus vulgaris*) are the main food legume crops grown under rainfed condition. Thiers area is estimated at 10000 HA. The paper discusses the characteristics of the main food legume cultivated in Algeria, the major issues related to their genetic resources maintenance, use and importance of their biodiversity.

P19 – S4

Evaluation of faba beans genetic resources for food and feed

Lepse L., Kronberga A., Olle M., Kokare A., KonošonokaI I., Pereira M.G., Bebeli P.
Pūre Horticultural Research Centre, Latvia

Faba beans (*Vicia faba* L.) become more and more popular due to nutritional value as protein source for food and feed and due to its agricultural service crop properties – biological nitrogen fixation, soil biological activity increasing and break crop in monoculture systems.

During the first two years of trials (2014 and 2015) genotypes and landraces of European origin of faba bean where investigated in terms of their genetic diversity and productivity parameters. Samples of locally grown commercial varieties and old cultivars where compared with genetic resources accessions from gene banks and collected in collection missions.

The yield parameters revealed that the number of pods per node varied between 0.9 and 2.6 in average. The highest number of pods per node were found in the cultivars \`Favel\`, \`Solberga\`, \`Gerd\`, Fb-2939, and \`Gubbestad\` for broad beans and in \`Bauska\`, \`Lövånger\`, \`Lielplatones\`, \`Valmiera\`, VF_013 and \`Gloria\` for field beans. The genotypes with the highest seed weight per plant were \`VF_001\`, \`VF_003\`, \`VF_004\`, \`VF_005\`, \`VF_009\` and \`Gerd\` in broad beans and for \`Prieku_u-32\` and \`Lielplatones\` in field beans. Overall, it was found that the most promising broad bean cultivar accessions are \`VF_001\` \`VF_54\` and field beans \`Prieku_u-32\` \`Gubbestad\`, \`Lielplatones\`.

The research was funded by the European Union's 7th Framework Programme for research, technological development and demonstration under grant agreement No 613781, EUROLEGUME.

P20 – S4

Morphological and physiological characterization of 15 accessions of cowpea

Fernández J.A.’ Martos-Fuentes M., Weiss J., Egea-Gilabert C., Egea-Cortines M.

Universidad Politécnica de Cartagena. Instituto de Biotecnología Vegetal

Cowpea (*Vigna unguiculata*) is a South African crop, used both for human and animal consumption. The aim of this work was the morphological and physiological characterization of 15 accessions of cowpea for further selection in a breeding program. We analysed 6 local accessions of cowpea from Spain, 6 from Portugal, 2 from Greece and a reference breeding line from USA (IT97K-499-35). Descriptors were used for the characterization according to the International Board for Plant Genetic Resources. From all descriptors analysed, the most important was seed protein content, which ranged between 17% and 26%. Seed weight per plant ranged between 5g and 40g, and the cultivar with the largest pod reached 65cm more than the shortest. Therefore, significant differences between cultivars were found for seed weight per plant, pod length and seed protein content, indicating that the genetic variability of cultivars plays an important role in plant performance.

P21 – S4

Evaluation of pea genetic resources for food and feed

Kronberga A., Olle M., Pereira M.G., Kokare A., Konošonoka I., Lepse L.

Institute of Agricultural Resources end Economics, Latvia

As cultivation history of pea is very long, a broad gene pool is developed during centuries. However, a tremendous amount of genetic resources is not evaluated until now for its potential benefits in regard to biochemical and morphological features.

During the first two years of trials (2014 and 2015) genotypes and landraces of European origin of pea where investigated in terms of their phenotypic diversity. Samples of locally grown commercial varieties and old cultivars where compared with genetic resources accessions from gene banks and collected in collection missions.

Field trials were established in Latvia, Estonia and Portugal. Broad variation was stated between locations and traits for genotypes included in evaluation. So plant length varied between 16.8 cm and 186 cm. The number of days to reach the full ripening ranged from 89 and 110 days. 100 seeds weight showed large variance ranging from 7.9 g to 38.1 g. Average seed weight per plant varied between 0.5 g plant-1 and 15.5 g plant-1. Protein content in dry pea grains varied between 18.8% and 33.5%. In accessions grown in ECRI protein content in seeds varied between 22.1 % and 33.5%.

The research was funded by the European Union’s 7th Framework Programme for research, technological development and demonstration under grant agreement No 613781, EUROLEGUME

P22 – S4

Genetic Diversity of Croatian Common Bean Landraces

Carović-Stanko K. [1,2], **Liber Z.** [2,3], **Vidak M.**[1], **Barešić A.**[1], **Grdiša M.**[1,2], **Radosavljević I.**[2,3], **Šatović Z.**[1,2]

1 - University of Zagreb, Faculty of Agriculture, Department of Seed Science and Technology, Svetošimunska cesta 25, HR-10000 Zagreb, Croatia
2 - Centre of Excellence for Biodiversity and Molecular Plant Breeding, Svetošimunska 25, HR-10000 Zagreb, Croatia 3 - University of Zagreb, Faculty of Science, Department of Botany, Marulićev Trg 20/II, HR-10000 Zagreb, Croatia * kcarovic@agr.hr

In Croatia common bean is a traditional grain legume, grown by small farmers in low input agriculture systems. The majority of the production is still based on local landraces adapted to the specific growing conditions and agro-environments and showing a great morphological diversity. Local landraces are in danger of genetic erosion caused by complex socio-economic changes in rural communities. The low profitability of farms and their small size, the advanced age of farmers and the replacement of traditional landraces with modern bean cultivars and/or other more profitable crops have been identified as the major factors affecting genetic erosion.

Three hundred accessions belonging to seven most widely used morphotypes (landraces) were genotyped by microsatellite markers in order to assess the genetic diversity and population structure of Croatian common bean germplasm. PCR-based phaseolin type analysis was used to trace the origin of accessions to Mesoamerican and Andean domestication centres. One-third of accessions showed phaseolin type I ("S"), predominant in germplasm of Mesoamerican origin while the rest of accessions belonged to Andean domestication centre characterized by the phaseolin type II ("H" or "C"; 22%) or III ("T"; 47%). A model-based structure analysis based on microsatellite markers revealed the presence of three clusters, for the most part, in congruence with the results of phaseolin type analysis.

P23 – S4

Identification of genes involved with resistance to *Fusarium oxysporum* in chickpea (*Cicer arietinum*) ecotypes from Central Italy

Fierro M.[1], De Curtis F.[1], Rubio J.[2], Millán T.[3], Gil J.[3], Lima G.[1]

1 - Dipartimento Agricoltura, Ambiente e Alimenti, Università degli Studi del Molise, Via F. De Sanctis, 86100 Campobasso, Italy.

2 - IFAPA Centro ""Alameda del Obispo"" Area de Mejora y Biotecnología, Avda. Menendez Pidal Apdo. 3092, 14080 Córdoba, Spain

3 - Departamento de Genética, Universidad de Córdoba, Campus Rabanales Edificio C5 2a Planta, 14071 Córdoba, Spain.

Chickpea (*Cicer arietinum* L.) is a self-pollinating diploid cultivated species genetically distinguished in two subpopulations: Desi and Kabuli. It is the third most important grain legume in the world covering 11.5 million ha of cultivated surface. In Italy, the annual mean yield of chickpea is around 1.9t/ha^{-1} and the cultivated surface is actually increasing. The crop is mainly carried out by small farmers so that the use of local ecotypes is widespread. Due to different selective pressure some of these ecotypes are often affected by serious pathogens as *Fusarium oxysporum* f. sp. ciceris (Foc) that often produces significant reduction of yield. In this regard, the aim of this work was to characterize by pathogenicity tests in growth chamber and genetic molecular analysis the resistance to Foc of 18 chickpea ecotypes from central Italy.

The pathogenicity tests evidenced that an ecotype (Longano) displays full resistance to Foc, another (S.Elia a Pianisi) shows partial resistance and other 16 ecotypes were all susceptible. Genetic analysis evidenced the presence of a 6 ecotypes cluster, including the ecotype Longano and distinguished from others ecotypes. Moreover, in some ecotypes new alleles in the microsatellites TA27 and TA59 were identified. These microsatellites are known to be associated with a gene involved with Foc resistance and located on LG 2 of chickpea genetic map.

P24 – S4

Variability of fat content and fatty acids profiles in seeds of white lupin (*Lupinus albus* L.) collection

Rybiński, W.[1], Święcicki, W.[1], Bocianowski, J.[2], Barzyk, P.[3], Börner, A.[4], Starzycka, E.[5], Starzycki, M.[5]

1 - Institute of Plant Genetics, Polish Academy of Sciences, Pozna_, Poland.
2 - University of Life Sciences, Pozna_, Poland
3 - Plant Breeders/ Wiatrowo, Poland.
4 - Leibniz Institute of Plant Genetics and Crop Plant Production, Gatersleben, Germany.
5 - Institute of Plant Breeding and Acclimatization, Department of Oil Plants, Pozna, Poland.

The paper presents an attempt to assess the variability of fat content and fatty acids (FA) composition in seeds of white lupin (*Lupinus albus* L.) domestic collection. The initial material comprised accessions originated from 30 countries. According to data given by accession donors the material was divided into four groups of origin: cultivars (CV), landraces (LR), wild relatives (CO) and cross derivates plus mutants (XD-M). The average fat content for analyzed accessions is 9.81 %. Fat content ranged from 6.9 % to 14.1%. In respect to unsaturated fatty acid (UFA), monounsaturated oleic acid in each of estimated group of accessions was predominant and most abundant (55.7%) in broad range of minimum-maximum values from 41.2% to 66.2%. The second examined monounsaturated fatty acid was erucic acid (1.74%) found in seeds of all studied accessions. Exceptions were four genotypes in CO group defined similarly to rapeseeds as “zero erucic” forms. Among polyunsaturated fatty acids (PUFA) dominated linolenic FA (ω – 6) followed by linolenic FA (ω – 3). Both FA were in the range 13.7-33.2% and 5.6-12.8% with mean values on the level 19.6% and 10.1% respectively. As a consequence, the examined seeds showed a very favourable ω–3/ω–6 FA ratio (0.51), ranging from 0.21 to 0.87, much higher than that of most vegetable oils. Fat content was positively correlated with stearic and oleic fatty acids and negatively with palmitic, linolic, linolenic and erucic acid.

P25 – S4

Grain legume participatory research: the Alvaiázere grass pea agronomic trials example

Gonçalves L.[1], **Almeida N.F.**[1], **Lourenço M.**[2], **Julião N.**[3], **Vaz Patto M.C.**[1]

1 - Instituto de Tecnologia Química e Biológica António Xavier, Universidade Nova de Lisboa, Av. da República, 2780-157 Oeiras, Portugal.
2 - Câmara Municipal de Alvaiázere, Praça do Município, 3250-100 Alvaiázere, Portugal.
3 - Simões & Ramos Lda, Estrada Nacional 110, 3250-404 Rego da Murta, Portugal.

There is a great potential to reduce European external dependency on plant proteins by the re-introduction of grass pea (*Lathyrus sativus*) into drought-prone areas. In Portugal, grass pea is part of the traditional heritage of dryland communities and is helping to revitalize dry agricultural regions such as Alvaiázere. However due to its underuse, has suffered strong genetic erosion and there is lack of productive, locally adapted varieties.

Under the scope of QUALATY project and in order to identify interesting sources of important agronomic traits for this region, we gather a collection of 150 different grass pea accessions from all over the world (with 12 representatives of the national grass pea traditional varieties). This collection was tested under field conditions using a participatory α-latice design experiment involving farmers, researchers and the local government. Accessions are being evaluated for morphological and agronomic characters (passport data, plant descriptors, agronomic characters, performance and yield) and other end-users important traits.

Data will be submitted to a multivariate analysis, performing a comparative assessment of the accessions behavior in this region and allow discriminate outstanding pre-breeding materials to be incorporated in future grass pea breeding programs. The established participatory research net will contribute to faster and wider adoption of the project research findings and elevate local knowledge to the status of science.

P27 – S4

Production and physical characterization of sixteen cowpea accessions

Fernandes H.A.[1], Abade F.[2], Castro C.[3], Carnide V.[1,4], Ribeiro C.J.[3]

1 - Centre for the Research and Technology of Agro-Environmental and Biological Sciences (CITAB), University of Trás-os-Montes and Alto Douro (UTAD), Quinta de Prados, 5001-801 Vila Real, Portugal. hortenseaf@hotmail.com

2 - University of Trás-os-Montes and Alto Douro (UTAD), Quinta de Prados, 5001-801 Vila Real, Portugal.

3 - University of Trás-os-Montes and Alto Douro (UTAD), Department of Agronomy, Quinta de Prados, 5001-801 Vila Real, Portugal. cribeiro@utad.pt

4 - University of Trás-os-Montes and Alto Douro (UTAD), Department of Genetics and Biotechnology, Quinta de Prados, 5001-801 Vila Real, Portugal.

Cowpea (*Vigna unguiculata* L.) is an annual crop of warm season mainly produced tropical and subtropical regions. However it is produced in Mediterranean region, also. There are a lot of germplasm accessions that must be evaluated by their productivity and adaptation to specific conditions. So, sixteen cowpea accessions were sowed at Vila Real at 2014 season to quantify production and physical attributes like weight, color parameters and force to cut the pod and the seed. This work was performed to obtain preliminary results for preparing the next steps for further selection and freezing objectives aiming the improvement of the intake of protein from vegetal origin in human diet.

The main results showed some differences among accessions in total production and texture properties related to the cutting force, reinforcing the idea of different adaptation to the local conditions. These results reveal the potential use of cowpea as an alternative crop to other species and the need to study its behavior under freezing conditions.

It was clear that some accessions presented highest amount of production at the beginning of the harvest season while others presented a regular production along the season. There was enough evidence of a large period of flowering and a quite long harvest time in the accessions evaluated which is not favorable to a mechanical harvest.

P28 – S4

Genetic diversity of root-nodulating bacteria isolated from Greek cowpea varieties

Fotiadis C., Ntatsi G. , Savvas D. , Tampakaki A.
Department of Crop Sciences, Agricultural University of Athens, Athens, Greece.

Cowpea (*Vigna unguiculata*) forms nitrogen-fixing root nodules with slow-growing rhizobial species also named “cowpea miscellany” which generally belong to the *Bradyrhizobium* genus. Despite that much research has been done on cowpea-nodulating bacteria in various countries around the world, very limited information is available on cowpea rhizobia in European soils. Given the importance of cowpea in sustainable agriculture and the lack of data on their rhizobia in Europe, we performed for first time an analysis on the phylogeny and genetic diversity of indigenous cowpea-nodulating rhizobia in Greece. The diversity and phylogeny of isolated strains were investigated by ERIC-PCR fingerprinting and multilocus sequence analyses (MLSA) of eight housekeeping genes. Phylogeny of nodulation (nodC) and nitrogen-fixation (nifH) genes of rhizobia was also studied. The sensitivity of the strains to different antibiotics, their tolerance to different levels of salinity, pH, temperature and their ability to nodulate soybean and common bean plants were also assessed. Based on ERIC-PCR fingerprinting and MLSA analyses, the isolated strains were grouped into four well-supported clusters belonging to the branch of the genera *Bradyrhizobium*, *Ensifer*, and *Rhizobium*. Finally, our results indicated that some of the strains studied might represent novel species, indicating that an as yet unknown diversity of rhizobia may exist in Greek soils.

P29 –S4

Molecular characterization of the U.S. *Phaseolus acutifolius* A. Gray collection using Amplified Fragment Length Polymorphism (AFLP) and Targeted Region Amplification Polymorphism (TRAP) markers

Kisha T. [1], **Bhardwaj H. L.** [2]

1 - USDA-ARS
2 - Virginia State University

Tepary bean (*Phaseolus acutifolius* A. Gray) is a short life-cycle annual desert legume indigenous to northwestern Mexico and southwestern USA and is considered drought and heat tolerant. The Western Regional Plant Introduction Station currently maintains 211 accessions of tepary bean. Molecular genetic relationships among 195 accessions of the *Phaseolus acutifolius* A. Gray collection were assessed using Targeted Region Amplified Polymorphic (TRAP) markers designed from sequences of genes associated with heat and drought tolerance and random Amplified Fragment Length Polymorphic (AFLP) markers. Although TRAP markers target specific genes, they have been shown to produce random genetic differences among accessions. Indeed, the correlation among the matrices produced by each marker was R = 0.81. Genetic relationships were compared to drought stress using measurements of variable fluorescence to maximum fluorescence (Fv/Fm). Cluster analysis using NTSys-pc and STRUCTURE of the combined marker set found 3 major groups and 7 sub-groups, but there was no association of drought tolerance with any group. Although the tepary bean has been used in interspecific crosses with common bean for heat tolerance and disease resistance, accessions have also been identified with prolific seed production, which could also increase yield in common bean.

P30 – S4

Structure of genetic diversity in a world collection of white lupin landraces

Nazzicari N., Annicchiarico P., Ferrari B.

Council for Agricultural Research and Economics (CREA), Research Centre for Fodder Crops and Dairy Productions, 29 viale Piacenza, 26900 Lodi, Italy.

White lupin was domesticated in the Aegean islands, from where it spread across southern Europe, North and West Africa, and Near East. Its genetic resources are limited to the primary gene pool. The rescue of white lupin as a major grain legume, justified by its outstanding protein content, is hindered by limited breeding work that suffers, inter alia, from lack of information on the structure of crop genetic diversity. The aim of this study was investigating the structure of landrace genetic diversity across diversity layers relative to variation among: (i) seven major cropping regions (Madeira-Canaries, Portugal, Spain, Maghreb, Egypt, East Africa, Near East), (ii) landraces within cropping region (8-10 sampled landraces per region), and (iii) genotypes within landrace (3-4 sampled genotypes per landrace). Overall, 243 genotypes were characterized by a genotyping-by-sequencing approach that provided 2178 polymorphic SNP markers per genotype (for a 10% genotype missing data threshold). An analysis of molecular variance indicated the following ranking of variance components: genotype variation within landrace > landrace variation within region > variation between regions. This result, not expected for this predominantly self-pollinated crop, highlights the importance of exploiting also within-landrace diversity. Landrace multi-dimensional scaling ordination displayed mainly a latitudinal gradient, along with outstanding variation within Near East.

P31 – S4

Conservation and regeneration of the annual pasture legumes and *Lupinus* spp. Spanish active collections

Maya-Blanco V., Gragera-Facundo J., Lozano-Ruiz M. J., González-López F.
CICYTEX, Junta de Extremadura, Spain

In the germplasm bank of the Instituto de Investigaciones Agrarias Finca La Orden-Valdesequera (CICYTEX) there are two official national active seed collections: the annual pasture legumes and the Lupinus spp. collections, including 6290 and 1950 accessions, respectively.
Basic issues of this germplasm bank are preservation, multiplication and documentation of their accessions.
About preservation, the condition of the stored sample seeds of the accessions are being revised every year changing hermetic seals or regenerating silicagel if necessary.
Furthermore, the multiplication of the accessions that are low germination capacity or their stored samples have less than 4000 seeds (2000 for *Lupinus* spp.) or are not duplicated in the base collection (CRF) or are new accessions are going on. Along these multiplications, the new accessions are characterized and basically evaluated.
For documentation, the germplasm databases are being maintained and updated.

P32 – S4

Assessment of genetic diversity of soybean accessions using SSR markers

Peric V.[1], Nikolic A.[1], Zoric M.[2], Mikic A.[2], Drinic S. M.[1]
1 - Maize Research Institute “Zemun Polje”, Belgrade, Serbia
2 - Institute of Field and Vegetable Crops, Novi Sad, Serbia

Soybean is a plant species characterized by an extremely narrow genetic base, as a consequence of self-pollination, a long process of domestication and artificial selection. A key phase in maintaining diversity and successful utilization in breeding is the genetic and phenotypic characterization of accessions available in collections. Soybean collection in Maize Research Institute "Zemun Polje" maintains more than 500 accessions from different regions of the world. The aim of this study was to investigate the level of genetic variation in collection, through the sample of 90 soybean genotypes originated from 15 countries, classified in 5 geographical groups (DOM-Serbia, EUR-European, USA-North American, CAN-Canadian, EXO-China and Japan). Twenty SSR primer pairs were selected for the molecular analysis. To assess the genetic relations among accessions, cluster analysis employing UPGMA method was performed. Distribution of genetic variation between and within 5 groups was calculated by AMOVA (analysis of molecular variance). Molecular analysis revealed a moderate polymorphism of SSR loci. Grouping pattern showed a high level of agreement with pedigree data, and, to a certain extent, with geographical origin of genotypes. AMOVA for five geographical groups of genotypes showed that low, but highly significant portion of variation has been attributed to differences between groups. Canadian genotypes were significantly differentiated from all observed geographical groups. No significant genetic differentiation between domestic and USA group of genotypes was observed, as well as between DOM and EUR group of genotypes.

Acknowledgement: The project TR-31068 of the Ministry of Education, Science and Technological Development of the Republic of Serbia

P33 – S4

Temporal and regional development of lentil populations by natural selection on-farm

Ruland M., Becker H.C., Horneburg B.
Georg-August-Universität Göttingen

On-farm management of plant genetic resources allows for evolutionary adaptation to site-specific conditions by natural selection. However, knowledge about the development of genetic diversity by on-farm management at multiple sites is still scarce. Lentil is an autogamous species with an outcrossing rate of 0 to five percent.

In a long-term experiment, three old lentil cultivars were exposed to ten generations of natural selection at three farms under rainfed conditions. Two of the selection sites were on poor or marginal soils. Populations in generation 0, 5, and 10 were tested in field plots at all three selection sites.

Results indicated

i) higher mean yield for the 10th generation,

ii) no significant site-specific adaptive effect ("home field advantage") on yield, but

iii) an overall higher yield for seed and straw of populations developed at the most stress prone selection site;

iv) significant site-specific changes in seed weight for both larger and smaller seeds were observed for one cultivar.

Seed weight, leaf size, and flowering time were traits contrasting the populations of different generations and provenances within the cultivars.

Genotyping was done with SNP markers (KASPar) for all populations by using one seed each of 100 single plant progenies per population. Calculations for genetic diversity parameters are in progress.

P34 – S4

Perspectives of pulses genetic resources collection in Portugal

Barata A.M.[1], Reis A.[1], Gaspar C.[1], Rocha F.[1], Lopes V.[1], Pereira G.[2], Duarte I.[2]

1 - Banco Português de Germoplasma Vegetal /INIAV, I.P., Quinta de São José, S. Pedro de Merelim, 4700-859 Braga, Portugal

2 - Instituto Nacional de Investigação Agrária e Veterinária, I.P. (INIAV). Apartado6, 7350-951 Elvas, Portugal

Pulses are multifunctional crops with large importance for agriculture, environment and culture in the Mediterranean countries. Today, in Portugal the average consumption of pulses/ per capita is 4 Kg.

Pulses genetic resources collection in Portugal, contains 6,359 accessions from nine species included in the Annex 1 of the International Treaty on Plant Genetic Resources for Food and Agriculture.

Pulses genetic resources collection, comprises genetic material, farmer knowledge and heritage profile. The collection began 4 decades ago, as a result of 126 collecting missions and assessment of local practices and uses. The pulse collection was evaluated for morphological, molecular and biochemical markers. Breeding programs have been implemented and led to the registration of new varieties In the National Varieties Catalogue.

All the results are documented and the passport data is in the public domain through the GRIN-GLOBAL platform.

The pulses national collection has a valuable role in creating a diverse economically viable agro-food value chain: Organic farming; Sustainable Intensive agriculture programs, helping to address challenges posed by climate changes; Development of new products associated to new uses in the Mediterranean diet.

The genetic basis of pulses in our agricultural landscapes can be enlarged by promoting genetic materials more resilient and reintroducing traditional varieties in the value chain, making them commercially viable.

P35 – S4

Genetic diversity of the guatemalan climbing bean collection

Tobar-Pinon M.G. [1,2], **McClean P.E.**[1], **Moghaddam S.M.**[1], **Lee R.**[1], **Osorno J.M.**[1], **Villatoro-Merida J.C.**[2]

1 - Department of Plant Sciences, North Dakota State University, Fargo, USA
2 - Instituto de Ciencia y Tecnología Agropecuaria (ICTA), Guatemala

Common bean (*Phaseolus vulgaris* L.) is the most important legume crop for human consumption in the world, and is the primary source of protein in the daily diet in Central America. In Guatemala, it occupies 184,000 hectares or 17.8% of available production acreage where 8 of 10 native children suffer from chronic malnutrition, the highest level in Latin America. For this reason, food security plays a key role in the development of a healthy country. At this point, bean breeders are challenged to increase seed yield and maintain seed quality while breeding for resistance to several diseases whose incidence has increased due to climate change. Race Guatemala of common bean includes climbing beans from the highlands of Guatemala where poverty is the highest, and it is a resource of new alleles for bean improvement. The objectives of this research are to evaluate and describe the population structure, genetic diversity, and genetic differentiation of a Guatemalan climbing bean collection of 376 inbred lines using SNP markers, and to perform a genome-wide association study to map important agronomic traits. The population structure will also be characterized by neighbor-joining and principal components analyses, and differentiation will be estimated by FST, and expected heterozygosity (He).

P36 – S4

Characterization of genetic diversity of a European collection of Pea (*Pisum sativum* L.)

Barcelos C., Pereira G., Meneses M., Duarte I.,
Instituto Nacional de Investigação Agrária e Veterinária, I.P. (INIAV) Apartado 6, 7350-951 Elvas, Portugal

In order to integrate the germplasm collections in the plant breeding programs, the characterization and evaluation of genetic diversity is essential. INIAV participates in the FP7 project EUROLEGUME, where one of the main objectives is evaluate the performance of the local genetic resources of pea accessions. Seventy-six pea accessions provided by the partners INIAV (Portugal), AREI (Latvia), ECRI (Estonia) and one reference variety from INRA-France were evaluated in the experimental field of INIAV (38°53'N, 7°09'W). The characterization was performed using three qualitative traits (plant pigmentation, flower and seed colour) and six quantitative traits (days to flowering and to maturity, duration of flowering, plant yield, 100 seed weight and plant height). Data were analysed by numerical taxonomy techniques, using NTSYS-pc package, version 2.01.The results showed that there is considerable morphological variation among the genotypes. Concerning the quantitative traits, the most variable character was 100 seed weight. The number of days to start flowering is negatively correlated with duration of flowering period and plant yield. The accessions that needed more days to start the flowering stage are from Latvia. In Portugal conditions, the most promising pea accessions that can be included in breeding programme are the Portuguese variety Grisel, the accessions Erme, Mehis, Seko, Tasuja, Herko, Looming from Estonia and k-6972, k-4822, k-6973 from Latvia.

P37 – S4

Morphological characterization of a European collection of faba bean (*Vicia faba* L.)

Pereira G., Barcelos C., Meneses M., Duarte I.
Instituto Nacional de Investigação Agrária e Veterinária, I.P. (INIAV) Apartado 6, 7350-951 Elvas, Portugal

Faba bean is an important legume crop well adapted to most climatic areas of Europe and widely used for feed and food. In Portugal, the major objectives of faba bean breeding programme are to develop varieties with high yield potential, early maturity and tolerant to the major diseases (*Botrytis fabae* and *Uromyces fabae*). INIAV participates in the FP7 project EUROLEGUME, where one of the main objectives is evaluate the performance of the local genetic resources of faba bean accessions. 16 faba bean accessions provided by the partners INIAV (Portugal), AREI (Latvia), ECRI (Estonia) and PHRC (Latvia) were evaluated in order to identify accessions with particular behavior that could be exploited by plant breeders. The faba bean experiment was conducted in the experimental field of INIAV-Portugal (38°53’N, 7°09’W). Characterization was performed using six quantitave traits (days to flowering and to maturity, duration of flowering, plant height, plant yield, 100 seeds weight) and three quality traits (flower and seed colour, growth habitat). Data were analysed by numerical taxonomy techniques, using NTSYS-pc package, version 2.01. In this collection, the major accessions were more productive than minor accessions. Portuguese accessions originated shortest plants than the accessions from Latvia and Estonia. The most promising faba bean accessions for further evaluation are Portuguese accessions Fb 3268, Fb 395, Favel, Fb 2939 and the accessions Valmiera, Tolea from Latvia."

P38 – S4

A novel source of genetic diversity in cultivated chickpea as revealed by genome-wide marker discovery and genotyping

Lotti C. [1] **Pavan S.**[2]**, Montemurro C.**[2]**, De Giovanni C.**[2]**, Ricciardi F.**[1]**, Bardaro N.**[2]**, Mazzeo R.**[2]**, Sonnante G.**[3]**, Marcotrigiano A.R.**[2]**, Ricciardi L.**[2]

1 - Dept. of the Sciences of Agriculture, Food and Environment University of Foggia, Via Napoli 25, I-71100 Foggia, Italy
2 – Dept. of Soil, Pant and Food Sciences, Section of Genetics and Plant Breeding. Faculty of Agriculture, University of Bari. Via Amendola 165/A, 70126 Bari, Italy;
3 - Institute of Bioscience and Bioresources- RNC, Via Celso Ulpiani, 70125- Bari

The accurate description of plant biodiversity is of utmost importance to efficiently address efforts in conservation genetics and breeding. Here we report the successful application of a genotyping-by-sequencing (GBS) approach in chickpea, resulting in the characterization of a cultivated germplasm collection of 82 accessions with 3187 high-quality single nucleotide polymorphism (SNP) markers. A body of evidence, based on genetic structure, principal component, and hierarchical clustering analyses, indicate the identification of a previously unnoticed gene pool, corresponding to black-seeded genotypes traditionally cultivated in the South East of Italy. This pool adds up to the other two characterized by previous literature and corresponding to the commercial seed types desi and kabuli. Fixation index estimates for individual polymorphisms highlight loci and genomic regions that might be of significance for the diversification of agronomic and commercial traits. Overall, our findings provide information on the genetic relationships in cultivated chickpea and identify germplasm of great interest for the scientific community and chickpea breeding, which is limited to a great extent by narrow genetic diversity.

P39 – S4

Medicago truncatula exhibits a novel type of quantitative disease resistance to *Verticillium* wilt involving a network of co-regulated genes related to PAMP-triggered immunity

Ben C.[1], Toueni M.[1], Le Ru A.[2], Gentzbittel L.[1] and Rickauer M.[1]

1 - EcoLab, Université de Toulouse, CNRS-INP-UPS, Toulouse, France

2 - Research federation « Agrobiosciences, Interactions et Biodiversité », 24 Chemin de Borde Rouge, BP 42617, 31326 Castanet-Tolosan, France

Molecular and cellular responses to *Verticillium alfalfae* were investigated in the model legume *Medicago truncatula*. Whereas initial root colonization was similar in resistant and susceptible lines, resistant line A17 eliminated the fungus before 7 days post-inoculation, in contrast to susceptible F83005.5 that became heavily colonized. A transcriptomic study of root response during early stages of the interaction showed that line A17 had higher basal expression of defense related genes, and responded to inoculation with up-regulation of only a small number of genes. The susceptible line in contrast exhibited a disorganized response involving a large number of up- and down-regulated genes from different functional classes. Hormonal control of resistance, as hypothesized from gene expression patterns, was experimentally assessed.

A co-expression network analysis highlighted 5 modules of co-expressed genes in the resistant line, whereas no such structured gene expression was found in the susceptible line. One module was particularly associated to the inoculation response in A17, containing the majority of the genes induced in A17 and notably genes associated to PAMP-triggered immunity. Eleven transcription factors from this module were described to respond to other root pathogens in *M. truncatula*. Taken together, the results suggest that resistance in *M. truncatula* line A17 might be due to PAMP-triggered defense mechanisms, which add to a pre-existing high basal defense level.

P40 – S4

Autoecology of legume species from five genera in Algeria and possibilities of recovery to improve the pastoral production

Abdelguerfi A.[1], Laouar M[2].

1 - E.N.S.A Laboratoire d'Amélioration Intégrative des Productions Végétales, El-Harrach, Alger, Algérie
2 - E.N.S.A Laboratoire des Ressources Génétiques et Biotechnologies, El-Harrach, Alger, Algérie

Algeria is characterized by great diversity of environments. Variations in temperature, altitude, rainfall (amount and distribution), soil type (texture, salinity), fashioned plants with very specific adaptations. Knowledge of these adaptations would be a major asset in the context of the valorization of these genetic resources. The autecology and distribution of species from five genera, *Medicago*, *Trifolium*, *Scorpiurus*, *Hedysarum* and *Onobrychis*, were studied. Several bio-prospections were conducted in Algeria and on 749 sites autecology was carried out. According to the genus, the main effect ecological factor of the presence-absence of species change. The ecological needs and limits of species could be applied for the development and/or improvement of pastures and fallow. Additional to the ecological aspects, the adaptation and stability production of species were takes into account.

P41 – S4

Phenotypic Variability for Agromorphological Traits in a Lentil Recombinant Inbred Line Population

Toklu F., Özkan H., Karaköy T., Hatipoğlu R.
Cukurova University Agricultural Faculty, Field Crops Department, 01330, Adana, Turkey.
fapet@cu.edu.tr

Lentil is one of the important members of food legumes, has significant role in human nutrition and animal feed in the world. Turkey is the primary gene center of lentil, contrary to this there is very limited research done for development of cultivar with high efficiency, high quality, and suitability for mechanized harvesting.

Due to above mentioned reasons, the objective of this work are to develop linkage map saturated with genomic SSR markers and to identify the QTLs for agromorphological and quality traits. In this manuscrip, only agromorphological traits evaluated because of the genomic studies are going on. One hundred fifty five recombinant inbred lines (RILs) at the F8 stage developed through single seed descent method from cross between two Turkish red lentil landraces Karacadağ x Silvan were used as plant material. 155 recombinant inbred lines were grown at two locations (Adana/Kozan, Sivas) according to Augmented block design in the field experiment.

In conclusion, considerable diversity was observed for the days to flowering, flowering duration, days to maturity, plant height, biological yield, number of the pods per plant, grain yield per plant, seed diameter and 1000 grain weight at both locations.

P42 – S4

Phenotypic variability for agromorphological traits in a lentil recombinant inbred line population

Özkan H
Çukurova University, Turkey

Lentil is one of the important members of food legumes, has significant role in human nutrition and animal feed in the world. Turkey is the primary gene center of lentil, contrary to this there is very limited research done for development of cultivar with high efficiency, high quality, and suitability for mechanized harvesting.

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Session 5, parallel: Legumes value chain: market requirements and economic impact (cont.) - Room *Arrábida III*

Chaired by Frédéric Muel (Terres Inovia, France) and Pete Iannetta (JHI, UL)

16:30-16:40 Oral – S5

Evaluating cereal-legume intercrops towards sole crops by combining argumentation and simulation

Thomopoulos R.[1], Bedoussac L.[2], Moulin B.[3]
1 - INRA, IATE Joint Research Unit / INRIA GraphIK, Montpellier, France
2 - AGIR, Université de Toulouse, INPT, INP-PURPAN, INRA, ENFA, 31320, Auzeville, France
3 - Laval University, Quebec, Canada

Intercropping (IC) cereal and legume is a practice particularly suited in low nitrogen input systems where it optimizes the use of N resources leading to improved and stabilized yields and increased cereal protein content [1]. Nevertheless, IC is only slightly adopted by farmers. Indeed, their potential economic advantage remains questionable because it depends on many factors (crop prices, cost to separate the grains or input prices and subsidies).

In the context of decision support [2], our work aims at proposing a systematic approach to assess various options available to farmers combining: i) a qualitative model based on arguments expressed by actors and ii) a quantitative simulation technique based on systems to compare different scenarios.

Simulations were performed to assess and compare the direct margin expected using actual observations and then 3 independent scenarios under the following "what if" hypotheses: i) same subsidies, ii) increased cost of inputs and iii) decreased cost of sorting.

This study illustrates the interest of the proposed approach and opens new perspectives, such as including information about product price, fertilizer price and Life Cycle Assessment data in order to help for the support of these alternatives in a context of price volatility, environmental concerns and climate change.

[1] Bedoussac et al., 2015. Agronomy for Sustainable Development 35(3): 911-935

[2] Thomopoulos R., Croitoru M., Tamani N., 2015. Ecological Informatics 26(2): 182

16:40-16:50 Oral – S5

Escaping from grain-legume socio-technical system lock-in: some evidence from socio-economic innovation trends in France.

Magrini M.
INRA, 24 Chemin de Borde Rouge - CS 52627, Castanet Tolosan, 31326, France

Grain-legumes can potentially decrease global warming, as they do not need nitrogen fertilizers that are responsible for half of all agricultural greenhouse gas emissions. As diversifying crops in the simplified arable systems in France, they also allow to decrease numerous environmental impacts of these systems. Moreover, grain-legumes have many functional and nutritional properties both as feed and food. But despite those benefits, grain-legumes prouction continues to fall. Some authors explain this situation as a technological lock-in that has resulted from the co-evolution of cropping systems toward homogenization and intensive use of agrochemical inputs, public policies, and market dynamics that promoted cereals during the half of the 20th century. Mobilizing theories on transitions from economics and strategic management, the objective of this communication is to review the current main drivers that could allow escaping from this lock-in, and to analyze several socio-technical niche innovations, both at the upstream and the downstream of the supply chains, that could foster grain-legumes production. In particular attention will be given to the way those innovations could create more value for these crops and so, to develop higher incentives for farmers to cultivate them. Those innovations case studies are focus on France but the insights of this analysis could be considered more largely at the European scale.

16:50-17:00 Oral – S5

Analysis of social and organizational aspects of food legumes chain

Bentaibi A.
Institut National de la Recherche Agronomique, Morroco

The specific objectives of this work are summarized in: i) analysis of the roles and tasks according to gender in the production system; ii) identification of forms of collective and individual organization to manage production systems; iii) identification of the OPA able to drive the actions of the initiative and contribute to the rehabilitation of food legumes.

The approach is based on a methodology based on the combination of an analysis of the existing documentation and participatory research through workshops and discussions with farmers and agricultural organizations present in the study area represented by five sites drivers.

Despite their importance, the authorities have not paid much interest in the development of these crops. They were considered second-rate cultures and their interest is limited to their role as preceding crop. While legumes are cash crops that generate substantial benefits to rural households. Through their rehabilitation is possible to rehabilitate forms of social organization that can play a crucial role in their development.

Small producers account for a majority of farmers and contribute strategically to food security, but their development is still limited by: (i) lack of access to capital for investment, (ii) the uncertainty of the markets in which they changing and (iii) the lack of institutions and organizations, including collective actions for return on investment.

17:00-17:10 Oral – S5

The re-innovation of Mixed Cropping – who cares? – Trial Willingness among German farmers

Lemken D.
University Göttingen

Mixed cropping (MC), the growing of two or more coexisting crops in one field, specifically the mix of cereal and grain legumes, can contribute to a more sustainable agricultural land use. Despite a variety of ecological benefits and promising grain productivity, applications are scarce among German farmers (ca. 0.007 % of land use). R&D and agriculture machineries evolve around monocultures. Many stakeholders believe substantial technical barriers to hinder the industrialization of MC. In consideration of MC's potential we analyze farmer's trial willingness to identify a profile of "early adopters" within the farming sector. The subsequent telephone interviews were quoted in respect to a representative geographical distribution of farmers within Germany. A proportional odds model regressed the hypothesized drivers upon the gradual change to carry out MC-trials. Preliminary results point to a significant role of land ownership and prior adoption of legumes. The latter implies a strong dependence of MC's implementation on legume adoption pattern. The perception of technical barriers and the perception of MC's usefulness are also major drivers. Research and visionary agribusinesses will need to identify the implementation costs of the technical barriers and quantify monetary advantages of the MC-approach before a communicational strategy for MC can and should be developed, otherwise diffusion will remain marginal.

Session 6, parallel: Root diseases - Room *Arrábida IV*

Chaired by Julie Pasche (North Dakota St. Univ., USA) and Nicolas Rispail (CSIC, Spain)

16:30-16:40 Oral – S6

Insights into the relative contribution of micro-evolution and phenotypic plasticity in the quantitative response of the model legume *M. truncatula* to *verticillium* wilt.

Gentzbittel, L.[1], Ben C.,[1] Sbeiti A.[1], Mazurier M.[1], Toueni M., Negahi A., Sarrafi A., Benameur S., Tardin M.-C.[2], Gras M.-C.[2], Rickauer M.[1]
1 - EcoLab, Université de Toulouse, CNRS, INPT, UPS, Toulouse, France
2 - R2n – Centre de Recherche Le Bourg, 12510 Druelle, France

The model legume *Medicago truncatula* was used as a host to study resistance to *Verticillium*, a soil-borne pathogen that causes substantial yield losses in many crops including alfalfa (*Medicago sativa*). *Verticillium* wilt response in *M. truncatula* is a quantitative disease resistance, regulated by QTL differing across resistant accessions and vary according to the fungal strains, as revealed by a genetic analysis in a multi-cross, multi-strain, multi-site design. This suggests that distinct genetic mechanisms control *Verticillium* wilt resistance.

To deepen the analysis, we assessed the genetic variability of susceptibility to Verticillium within the *M. truncatula* species, in a collection of 237 lines from around the Mediterranean Basin. Disease functional parameters and plant colonization by the fungus allowed identifying the genomic localization of the most frequent resistance alleles within the species.

The capacity of pathogens to adapt to new environments is a well-known threat to durability of crop resistance. Using a common-garden experiment in greenhouse, we showed that moderate increases (+3°C) or decreases (-5°C) of temperature during infection significantly impact early response, but not final fitness, suggesting plasticity in response to the pathogen.

We also experimentally adapted a *V. alfalfae* strain to higher temperature and show that increase in aggressiveness is rapid and efficient, confirming that climate change may quickly affect plant-microbe interactions.

16:40-16:50 Oral – S6

Genetics of pea resistance to *Aphanomyces euteiches* in the genomics Era

Pilet-Nayel M-L.[1], Desgroux A.[1], Lavaud C.[1], Lesné A.[1], Boutet G.[1], Aubert G.[2], McGee R.J.[3], Coyne C.J.[4], Bourion V.[2], Burstin J.[2], Baranger A.[1]

1 - INRA-UMR1349 IGEPP, PISOM-UMT INRA/Terres Inovia, France
2 - INRA, UMR 1347 Agroécologie, France
3 - USDA-ARS, Grain Legume Genetics Physiology, USA
4 - USDA-ARS, Plant Germplasm Introduction, USA

Common root rot, caused by the oomycete *Aphanomyces euteiches*, is a major soil borne disease of pea in many countries. The large pea genomic and plant resources recently developed have deepened the knowledge of genetics of partial resistance to *A. euteiches*. A dedicated panel of Aphanomyces genetic resources genotyped with a 13K-SNP array (Tayeh et al, 2015) was used in a genome-wide association study (GWAS) of partial resistance. Results identified a total of 52 small sized LD-based confidence intervals associated with the resistance, including 14 consistent QTL regions at which marker haplotypes were defined from the panel (Desgroux et al, 2016). This study validated six of the seven main resistance QTL previously identified, for which Near-Isogenic-Lines (NILs) were created by back-cross assisted selection (Lavaud et al, 2015). The fingerprint of the NILs using the 13K-SNP array showed that QTL introgressions could cover several smaller GWAS intervals, suggesting the presence of several linked genes or a single imprecisely located locus underlying a QTL. The genomic location of the major QTL Ae-Ps7.6, which effect was confirmed on slowing down symptom appearance and root colonization by the pathogen (Lavaud et al, 2016), was refined by GWAS and fine mapping. The unprecedented genomic resources recently developed in pea provide new markers closely-linked to Aphanomyces resistance loci, for accelerating progress in breeding future pea resistant varieties.

16:50-17:00 Oral – S6

Progress on understanding genetic resistance to *Fusarium* root rot in pea

Porter L.[1], Boutet G.[2], Pilet-Nayel M.-L.[2], Baranger A.[2], McGee R.[1], Ma Y.[3], Coyne C.[4]

1 USDA ARS Grain Legume Genetics, Pullman, WA USA;
2 INRA;
3 Washington State University;
4 USDA ARS Western Regional Plant Introduction Station.

Several species of Fusarium cause root rot of pea, a major constraint for pea production. One species, Fusarium solani f.sp. pisi has been an important pathogen in the U.S., Canada and New Zealand production regions. Infested fields result in stunting, yellowing and necrosis of susceptible plants. High levels of useful partial resistance is available in pea germplasm for this Fusarium root rot, but the multigenic resistance presents a challenge for population improvement in pea breeding programs. Two recombinant inbred line populations, segregating for Fusarium root rot resistance, were phenotyped. One was screened under field conditions and the other in controlled conditions. Using composite interval mapping, six QTL were identified controlling a significant proportion of the variance and two QTL were identified under both conditions. Use of the discovered co-dominant flanking markers for improving Fusarium root rot resistance will be discussed.

17:00-17:10 Oral – S6

Molecular quantification of pathogenic *Fusarium spp*. in soil to predict pea root rot risk in the field

Chatterton S.[1], Heynen M.[1], Safarieskandari S.[2], Zitnick-Anderson K.[3], Pasche J.S.[3].

1 - Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, Lethbridge, AB T1J 4B1, Canada.

2 - Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada.

3 - Department of Plant Pathology, North Dakota State University, Fargo, ND 58108, U.S.A.

Root rot of field pea causes severe yield loss in the Canadian prairies, where 1.5 million hectares of peas are grown annually. A recent survey revealed that 40 % of fields were positive for *Aphanomyces euteiches*, while 80-90 % were also infested with *Fusarium spp*. Pathogenicity tests indicated that while *A. euteiches* was the most damaging, *F. avenaceum* and *F. solani* were also highly virulent. To assess risk of root rot prior to planting peas, the relationship of DNA quantity of *Fusarium spp*. to inoculum potential and disease severity was evaluated. Soil was inoculated with increasing concentrations of *Fusarium inoculum*, and an aliquot was removed for DNA extractions prior to planting peas for root rot assessments. DNA quantity in soils was measured using real-time PCR assay, and *F. avenaceum* and *F. solani* DNA concentration was correlated to disease severity. This assay was then used to quantify DNA in soil and stubble collected from commercial field samples and related to root rot severity recorded during the growing season. *F. avenaceum* was detected in soil at concentrations that do not induce disease. However, concentrations in stubble from previously grown crops were at disease-causing levels. Similar analysis is underway for *F. solani*. Results are being validated in pea fields during the 2016 growing season, and will be used to develop a soil test to predict risk of developing Fusarium root rot, in conjunction with *A. euteiches* quantification.

Session 7, plenary: Legumes in food and feed and other alternative uses - Room *Arrábida I & II*

Chaired by Maria Carlota Vaz Patto (ITQB NOVA, Portugal) and Ambuj B. Jha (Univ. Saskatchewan, Canada)

08:30-09:00 **Key lecture: - Frédéric Marsolais**: Using beans with novel protein compositions for nutritional improvement

Oral Communications

09:00-09:15 Oral – S7

The hidden phenolic content of faba beans

Bento da Silva A.[1], Cardoso C.[2], Mecha E[1], Vaz Patto M.C.[1], Bronze M.R.[1,2,3]

1 - Instituto de Tecnologia Química e Biológica (ITQB), Oeiras, Portugal.

2 - Research Institute for Medicines and Pharmaceutical Sciences (iMED), Pharmacy Faculty, University of Lisbon, Lisbon, Portugal

3 - Instituto de Biologia Experimental e Tecnológica (iBET), Oeiras, Portugal

Faba bean (*Vicia Faba*, L.) is one of the most ancient crops extensively cultivated nowadays. These grain legumes are rich in carbohydrates, proteins, fat and have significant amounts of phytochemicals, such as (poly)phenols known for their beneficial health benefits, namely in cardiovascular diseases, type II diabetes and cancer. Faba beans are particularly rich in flavonoids, as (+)-catechin, (-)-catechin and (-)-epigallocatechin, and hydroxycinnamic acids, such as ferulic and p-coumaric acids.

Phenolic content evaluation of faba beans is usually based on the free phenolic fraction. However, in legumes there are some phenolics not directly extractable, as they are part of cell walls, considered as dietary fibres, due to the rich content in polysaccharides. As conjugated and bound phenolic compounds may be bioavailable after ingestion of faba beans in humans, in order to study the soluble-conjugated and the bound phenolic compounds fractions, a 50% ethanolic extract was prepared from a faba bean genotype. The extract and the residue were submitted to acidic and alkaline hydrolyses and the total phenolic content of the (1) soluble-free, (2) soluble-conjugated and (3) insoluble fractions were determined by Folin-Ciocalteau method Characterization of the main phenolic compounds was performed by LC-MS. The antioxidant activity of these fractions was also determined by ORAC method. Results are discussed in terms of bioaccessibility and health benefits of faba bean consumption.

09:15-09:30 Oral – S7

Use of narrow-leafed lupin b-conglutin proteins in human food to tackle diabetes through modulation of the insulin pathway

Lima-Cabello E.[1], Alche V.[2], Robles-Bolivar P.[1], Alche J.D.[1], Jimenez-Lopez J.C.[1,3]

1 - National Council for Scientific Research (CSIC); 2Estacion Experimental del Zaidin; Department of Biochemistry, Cell and Molecular Biology of Plants

Lupin is a worldwide important PULSE with a wide range of agricultural and health benefits (nutraceutical properties), i.e. prevention of cardiovascular diseases, obesity, dyslipidemia. Sweet lupines seem to be particularly promising as innovative food ingredients and as an important source of proteins for humans.

The aim of the current study was to evaluate the potential interaction between human insulin and b-conglutin proteins from narrow-leafed lupin (NLL), and to assess the modulatory response of genes involved in the insulin pathway, and the inflammatory response in type 2 diabetes (T2D) patients to such conglutin proteins.

Our results indicate that particular variants of b-conglutins up-regulate by ~2.5-fold the levels of mRNAs from insulin-activation meditated kinase genes and increase protein synthesis of several gene products (IRS-1/P38/AKT/GLUT-4) in the insulin pathway, possibly through their interaction with insulin. Interestingly, various b-conglutins promote down-regulatory effect in pro-inflammatory genes (IL-1b, iNOS), suggesting the potential therapeutic use of NLL proteins from the b-conglutin family in the prevention and treatment of T2D and other insulin-resistant conditions, and the potential role of these proteins in the regulation of inflammatory processes.

Acknowledgements:

EU Marie Curie grant ref. PIOF-GA-2011-301550; the Spanish MINECO grant ref. RYC-2014-16536; and “Junta de Andalucía” for the ERDF grant ref. P2011-CVI-7487.

09:30-09:45 Oral – S7

Genetic diversity in pea and its impact on strategies for seed quality improvement

Domoney C.[1], Rayner T[1], Moreau C.[1], Ambrose M[1], Clemente A.[1,] Isaac P.G.[3]

1 - John Innes Centre, Norwich Research Park, UK
2 - Estación Experimental del Zaidín, Granada, Spain
3 - IDna Genetics Ltd, Norwich Research Park, Norwich NR4 7UH, UK

Considerable genetic variation exists in *Pisum sativum* L. (pea), which has potential for trait improvement but remains under-utilised in breeding programmes. Our fundamental research on seed quality in pea identifies allelic variation in genes that control some economically important traits, and is providing tools and resources, which may be exploited ultimately within breeding programmes to improve end uses. Natural germplasm and induced mutant populations of pea are equally valuable resources for isolating variants of genes involved in determining seed quality.

High-throughput screening methods have been deployed to identify induced mutations and natural variation in genes that control seed compositional and visual traits. Although reduced seed trypsin-chymotrypsin inhibitor mutants were recovered among induced mutant populations, a high-throughput germplasm screen identified an extremely rare null mutant, a *Pisum elatius* accession, where both of the closely linked genes that encode the major seed inhibitors showed deletion of coding sequence. Combining this variant with null seed lectin and pea albumin 2 mutants provides opportunities for considerable gain in nutritional quality in pea seeds.

Visual traits can influence economic value for food crops. Loss of color from seeds may be reduced by disrupting the regulation of the chlorophyll degradation pathway, while avoiding perturbations in chlorophyll turnover, which can diminish yield.

09:45-10:00 Oral –S7

Understand the structuring of wheat-legume cakes to promote product innovation and to design new formulation tools for the industry

Monnet A.F.[1,2], Jeuffroy, M.-H.[2], Michon, C.[1]

1 - UMR Ingénierie Procédés Aliments, AgroParisTech, INRA, Université Paris-Saclay, 91300 Massy, France.

2 - UMR Agronomie, INRA, AgroParisTech, Université Paris-Saclay, 78850 Thiverval-Grignon, France.

The agronomical and nutritional benefits of cereal-legume associations are promising to improve the sustainability of wheat and legumes supply chains. Innovate by growing and processing both grains together would enhance commercial outlets and thus legume production. Pastries and cakes are mass-market products (0.7% of total food production at European scale) in which legumes-wheat mix flour could be used. Our aim was to develop a reverse engineering approach based on the understanding of cake structure formation at different length scales. Such approach would allow the design of new products and the proposal of practical formulation tools for the processing industry. The influence of the partial replacement of wheat flour by pea flour on the structure properties of soft cakes made under industrial-like conditions was investigated. The batters containing pea-wheat mix flours (P-W) were less dense then control ones (W). However, the air gained was lost during baking and the P-W cakes had higher densities than W cakes. However, the honeycomb structure of P-W cakes was finer and more homogeneous than W cakes. Moreover, the P-W cakes aerated cake crumb was softer than W cake one that is a quality criteria. These results are discussed versus pea and wheat flours characteristics (damaged starch, protein content and quality) and versus the evolution of the dough during the different process steps. The first parameters of the formulation tool are proposed.

P43 – S7

Sustainable sanitation methods for keeping overall quality of minimally processed fava seeds

Collado E.[1], Artés-Hernández F.[1,2], Artés F.[1,2], Aguayo E.[1,2], Fernández J.A.[1,3], Gómez P.A.[1]

1 - Institute of Plant Biotechnology. Universidad Politécnica de Cartagena. Campus Muralla del Mar. 30202, Cartagena (Murcia), Spain;

2 - Postharvest and Refrigeration Group. Department of Food Engineering, Universidad Politécnica de Cartagena. Paseo Alfonso XIII, 48, 30203, Cartagena (Murcia), Spain.

3 - Department of Horticulture. Universidad Politécnica de Cartagena, Paseo Alfonso XIII, 48, 30203, Cartagena (Murcia), Spain

Fava beans (*Vicia faba*) are high in proteins and rich in energy with important health promoting compounds. Due to their thick peel, whole immature pods cannot be eaten. Fresh seeds are highly perishable being proper sanitation and modified atmosphere packaging (MAP) very important.

In this study, fresh seeds from tender pods (cv. Palenca) were immersed in chlorine (4ºC, 150 ppm, pH 6.5) or, alternatively, in an ascorbic acid (4ºC, 0.05 mol L-1 pH 2.75) or in a lemon juice (4ºC, 30 ml 100 mL-1, pH 2.5) solution. Seeds (125 g) were packaged in 20x15 cm OPP 35 µm-thick bags. Then, bags were stored at 1º and 4ºC.

After 10 days, atmospheres within packages were 5 kPa CO2/16 kPa O2 and 6 kPa CO2/15 kPa O2 at 1 and 4°C, respectively for chlorine and 4 kPa CO2/17 kPa O2 for ascorbic acid and lemon juice, independently on the temperature. Microbial growth was higher for seeds treated with ascorbic acid (2.3 and 1.1 log CFU g-1 using chlorine, 2.4 and 1.5 log CFU g-1 for those seeds immersed in lemon juice, and 3.0 and 3.1 log CFU g-1 with ascorbic acid, for mesophilics and enterobacteria at 1ºC, respectively). Moreover, growth was about 1 log CFU g-1 lower at 1º than at 4ºC. Sensory quality and colour were acceptable until day 7. Then, browning was the main defect, without differences between treatments. Data presented here indicate that fava seed can be MAP stored at temperatures between 1º to 4ºC for one week. More research is needed for avoiding browning and extending shelf life.

P44 – S7

Comprehensive evaluation of field pea lines within the framework of the FP7 project LEGATO

Narits L.
Estonian Crop Research Institute

A wide-range testing of new breeding materials is an essential tool source for the knowledge of breeders. The overall aim of the project ""LEGumes for the Agriculture of TOmorrow"" (LEGATO) is to contribute to the increased sustainable reintroduction of grain legumes in European cropping systems. The project focuses on identification and testing of novel legume breeding lines of major grain legumes cultivated in Europe possessing valuable characters such as disease and pest resistance and quality for human consumption.

Twelve field pea varieties and seven breeding lines from six European countries were tested in field trials in Estonia. Evaluation of morphological and economical characters, resistance for biotic and abiotic stresses and quality was carried out. According to the results, two breeding lines are comperable to better varieties holding the potential for the future. Work with lines is continuing.

Acknowledgements: The project LEGATO, Grant no 613551.

P45 – S7

Annual vetches and grasspea as suitable crops for drylands of Iran

Alizadeh K.[1], **Kumar S.**[2]

1 - Dryland Agricultural Research Institute (DARI), Maragheh, Iran
2 - International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco

Studies on some *Vicia* species and *Lathyrus* in different agro-climatic zones of the country were conducted in the Dryland Agricultural Research Institute (DARI). Selection of suitable vetch species and their varieties for hay production in different agro-ecological zones along with soil conservation practices was a critical decision in the forage crops establishments in the rainfed conditions. It is intended to increase the productivity and stability of rainfed forage crops to ensure food security and improve rural livelihoods in dryland areas. This report recommends take advantage of annual vetch as well as grasspea crops in wheat rotation to overcome different forms of land degradation in dryland areas. This can contribute to improve the capability base of natural resources, and enhance the productivity and sustainability of the existing agricultural systems. Considerable genetic variation exists for forage and grain yields in the germplasm of vetches (*Vicia spp*.) and grass pea (*Lathyrus spp*.) under different environments. In general, grass pea is suitable for drier environments whereas vetches such as *Vicia panonica* and *Vicia villosa* are more suitable for cold highlands because of their ability to tolerate cold stress.

P46 – S7

Choosing the right time to harvest whole crop faba bean

Kuoppala K.[1], **Manni K.**[2], **Känkänen H.**[1], **Rinne M.**[1]

1 - Natural Resources Institute Finland (Luke), FI-31600 Jokioinen, Finland.
2 - Häme University of Applied Sciences, FI-31310 Mustiala, Finland.

Producing whole crop silage from grain legumes provides an opportunity to utilize them more efficiently for ruminants under Northern European conditions where the short length of the growing season limits the ripening of the seeds. Three cultivars of faba bean (*Vicia faba*), Fanfare, Honey and Pyramid, were grown in Tammela, Finland (N 60°) as a randomized plot experiment with four replicates. They were sown at June 2, 2015. No fertilization or plant protection was used. The herbage samples were taken biweekly from July 28 to September 22. The chemical composition and the concentration of digestible organic matter (DOM) of the samples were analyzed by NIRS. Morphological analysis was made by manually separating the leaves, stems and pods after sampling.

Average dry matter (DM) yield increased from 3150 to 12800 kg DM/ha (mean 147 kg DM/d) during the sampling period. The proportion of leaves and stems decreased and that of pods increased with progressing growth. Largest changes occurred during the fastest growth between two first samplings, when average DOM decreased from 715 to 598 g/kg DM (8.9 g/day). After that DOM remained relatively stable under 600 g/kg DM. Postponing harvest increased the DM yield until the late autumn with little effect on DOM but harvesting conditions were better earlier.

This work was done in the project "Protein Knowledge Centre provides solutions for protein self-sufficiency in Häme Region" also known as Protein Forum.

P47 – S7

Investigations on crude protein and amino acids in organically produced field pea (*Pisum sativum* L.) varieties

Aulrich K., Böhm H., Witten S.

Thünen Institute of Organic Farming, Federal Research Institute for Rural Areas, Forestry and Fisheries

The content of essential amino acids in grain legumes is of special interest for monogastric animal feeding in organic farming. Therefore, we investigated the influence of variety on the contents of crude protein (CP) and amino acids (AA) as well as the relation between CP and AA in field peas.

Samples of 73 peas of 5 varieties (Alvesta, Auckland, KWS La Manscha, Navarro, Salamanca) were collected from field trials of organically managed experimental sites in Germany in 2011 - 2013. The contents of CP and AA were analyzed with NIRS. Pearson correlation analyses and mixed procedures were conducted in SAS 9.4. Variety affected CP and AA in peas. Alvesta had the lowest content of CP (21%) and almost all AA per kg dry matter ($p<0.001$). KWS La Manscha had the highest content of CP (23%) and all AA per kg dry matter ($p<0.001$). However, KWS La Manscha had the lowest amount of total AA and each AA except arginine per 100g CP. There was a high negative relationship between CP and most of the AA in the CP of field peas ($r < -0.63$***). Only arginine was positively correlated with CP ($r=0.61$***), while histidine and leucine were not related with CP content. Tryptophan and the non-essential AA glutamic acid were less strongly negatively correlated with CP ($r=-0.49$***). The results indicate that higher CP contents could lead to more non-protein-nitrogen and an altered relation between AA. Thus, attention should be paid to amino acids rather than on CP in pea varieties used as feedstuffs.

P48 – S7

Forage quality and yields of some perennial legumes

Knotova D.[1], Pelikan J.[1], Skladanka J.[2]
1 - Agricultural Research, Ltd., Czech Republic.
2 - Mendel University in Brno, Czech Republic

In two harvest years two Czech varieties of alfalfa (Holyna and Tereza), two varieties of red clover (Spurt and Amos), Hungarian clover (variety Panon) and goat's rue, Lithuanian variety Gale were tested. The experiment was established by the method of randomized blocks in four replications. The yields of both green and dry matter were acquired in all evaluated species. Some quality indicators (% content of ash, crude protein, fibre, ADF, NDF, fat, sugars and nitrogen) were determined from the biomass obtained in the first cut. Mycotoxin content in the harvested biomass was also determined.

P49 – S7

The incidence of yeasts and fungi in the legumes' feeding stuffs for dairy cows.

Konosonoka I.H., Proskina L., Osmane B., Cerina S.
Latvia University of Agriculture, Latvia

In Latvia grown peas and beans meal, conventional feedstuffs and imported protein rich feed included in dairy cows' feeding trial control group ration were micologically evaluated. In total 42 samples of different dairy cows' feeding stuffs were analysed. All these samples were tested for total count of yeasts and fungi, presence and count of *Aspergillus spp*. and *Fusarium spp*. The assessment of pea meal, bean meal, soybean meal, rape cake, mixture of pea and bean meal, fodder, and hay on the yeast load showed the lowest counts in pea (2.81 log10 cfu g-1) and bean (3.22 log10 cfu g-1) meal samples, whilst the highest corresponded to hay (6.99 log10 cfu g-1) samples. The results obtained on the evaluation of the fungi load of feeding stuffs samples showed that the lowest fungi load corresponded to rape cake samples. Bean meal, pea meal, and mixture of pea and bean meal samples were contaminated with microscopic fungi in a similar low degree, 3.28, 3.53 and 3.74, accordingly. The highest count of fungi was observed in hay (5.99 log10 cfu g-1) samples. Fungi from the genera Fusarium were not found in the feedstuff samples. *Aspergillus flavus* and *Aspergillus fumigatus* were isolated from the peas and beans meal samples in relatively low numbers.

P50 – S7

The physicochemical properties of extruded rice based snacks fortified with bean and carob bean

Pedrosa M.M.[1], Arribas C.[1], Burbano C.[1], Muzquiz M.[1], Cuadrado C.[1], Cabellos B.[1], Guillamón E.[2].

1 - Food Technology Department, SGIT-INIA, Ctra de La Coruña, Km 7.5. 28040 Madrid, Spain. mmartin@inia.es

2 - Centre for the Food Quality, INA, Campus Universitario Duques de Soria, 42004 Soria, Spain

Consumers are increasingly worried about the quality of the food that ingest and look for a major diversity that can improve their health and reduce the risk of suffering certain diseases. So, the development of functional food is an area of great interest and represents a permanent challenge for the food industry.

FAO and FDA consider breakfast's cereal or snacks an effective way for the incorporation of nutrients. Rice has been used in a wide variety of extruded products due to their starch content since it is responsible of the high expansion rates and the mechanical properties of extrudates. The inclusion of legumes in their formulation increase nutrient and dietary fibre content, but produces important changes in the physicochemical properties of the extrudates. This change must be evaluated in order to optimize production parameters and to obtain products with optimum physical and sensory characteristics.

In this study, extrudates with different proportions of rice, bean and carob bean were developed. The incorporation of legumes produced a significant increase in the density and a reduction of the expansion index. The highest modifications corresponded to the inclusion of carob bean flours. The pasting properties, texture and colour values are also significantly affected, since a reduction in the starch content takes place in the flour mixtures, together an increase in the protein and fibre content.

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P51 – S7

Nutritional and nutraceutical characterization of extruded gluten-free snacks made from rice, bean and carob bean flour mixtures.

Arribas C. [1]**, Guillamón E.**[2]**, Burbano C.**[1]**, Muzquiz M.** [1]**, Cuadrado C.** [1]**. Cabellos B.** [1]**, Pedrosa M.M.** [1]

1 - Food Technology Department, SGIT-INIA, Ctra de La Coruña, Km 7.5. 28040 Madrid, Spain, arribas.claudia@inia.es

2 - Centre for the Food Quality, INA, Campus Universitario Duques de Soria, 42004 Soria, Spain.

Consumers are becoming aware of the importance of diet in relation to health problems, but a large proportion of the population lacks an adequate intake of fruits and vegetables. Legumes, such as beans and carob bean, are currently considered gluten-free functional foods since they are a rich source of nutritional and bioactive compounds with health-promoting activity.

Breakfast cereals and snacks are the major convenience foods produced by extrusion and they are an integral part of the daily food intake of the majority of the world's population. One of the strategies to reduce energy density of foods is to increase their content of dietary fiber. Taking into account the nutrient profile of legumes and mainly, the high fibre content, they seem to be ideal for inclusion into new food formulations.

In this study, it has been developed and analysed the extruded product containing different proportions of rice (50-80%), bean (20-40%), and carob bean (5-10%). The incorporation of pulses produced an increase in the protein, fat, carbohydrates and dietary fibre contents in the flour mixtures. After extrusion a significant reduction was observed in the fat and dietary fibre content. The protein content only showed slight variations, whereas in vitro protein digestibility was improved. Protease inhibitors were abolished after extrusion and inositol phosphates content showed reductions higher than a 15%.

This study was supported by the Project RTA2012-00042-C02.

P52 – S7

Phenolic content and antioxidant activity in gluten-free extruded composite flours of rice and different legumes

Guillamón E. [1], **Arribas C.** [2], **Burbano C.** [2], **Muzquiz M.** [2], **Cuadrado C.** [2], **Cabellos B.** [2] **and Pedrosa M.M.** [2].

1- Centre for the Food Quality, INA, Campus Universitario Duques de Soria, 42004 Soria, Spain, guillamon.eva@inia.es.

2 - Food Technology Department, SGIT-INIA, Ctra de La Coruña, Km 7.5. 28040 Madrid, Spain

The incorporation of plant foods to the habitual diet is the latest trend in a health strategy to prevent and treat diseases. Cereals, particularly rice, and legumes are the most consumed plant food in the world. Fortified cereal flour with legumes provides the opportunity to develop new foods for increasing their nutritional value and incorporating bioactive compounds. Among the physiological active substances present in legumes, phenolic compounds have attracted much attention. Their mechanisms of action are commonly related to their excellent antioxidant properties. The extrusion/cooking is an efficient processing technique to obtain new food, with a clear improvement of their texture and flavor. The aim of this study was to evaluate the effect of extrusion of flours containing different portion of rice (50-80%), bean or pea (20-40%), and carob bean (5-10%) on total phenols, anthocyanin, flavonol and tartaric ester contents and their antioxidant activity (ORAC). The incorporation of legumes, particularly pea and carob bean, produced an increase in total phenols and some of phenolic compounds, as well as in antioxidant activity. Extrusion affected to antioxidant activity and content of some phenolic compounds. A significant positive correlation between the antioxidant activity and the total phenols or, some of the phenolic compounds was observed.

This study was supported by the Project RTA2012-00042-C02.

P53 – S7

Study of imbibition properties and composition of legumes flours in relation to its technological competence. Case: food gluten-free baked

Lopera-Cardona S., Alvarez R. C., Gallardo C., Salamanca R., Yanez S., de la Hoz S.
Group of the Stability of Medicines, Cosmetics and Food, Fac. of Pharmaceutical Chemistry, Universidad de Antioquia, Calle 67 Nº 53-108, Bloque 2, Medellín, Colombia.
seneida.lopera@udea.edu.co

Legumes are characterized by their endosymbiosis with nitrogen fixing organisms, becoming a rich source of protein. The aim was to study pulses flours of *Pisum sativum*, *Cicer arietinum* and *Lens culinaris*, and Water absorption capacity and minimum gelation concentration, using methods of the AOAC The protein profile by Osborne and Bradford methods. Gluten were determined according CODEX STAN 118. Product prototypes were developed, with flour of lentil, evaluated the s volume according to the AACC method. The results showed that the protein content was higher than 26.6±2%, being and the lipid content was the lower in all flours, 3.1±0.4%. In germinated flour lentil, the MGC decreases and WAC increases, in relation to flour ungerminated that could be related to efficiency in gel formation and structure. The albumin protein fraction, contained in all flours on average of 19.25±4 µg/µL, by enzymes and proteins of higher digestibility according to studies reviewed. Chickpea flour showed the highest value of 44.39±2 µg/µL globulins, as storage proteins. All flours showed prolaminas and gluten lower than 12.63 ppm, in this order; lentil germinated> chickpea> pea> Lentil, less than 20 ppm, suitable to be labeled as gluten-free. Product prototypes are perceived with a soft touch, an apparent darker color and specific volume of 2.21cm3/g, similar to the control of wheat. As a general conclusion, the findings present an opportunity for legumes in diversification of consumption.

P54 – S7

Intercropping sainfoin with annual crops for forage production and weed control

Milošević B., Karagić D., Mihailović V., Katanski S., Milić D., Vasiljević S., Živanov D.
Institute of Field and Vegetable Crops, Novi Sad, Serbia

Sainfoin in combination with forage pea, faba bean or oat, provides a superb feed for domestic animals such as cows, lactating ewes, goats, etc. As well, one of the benefits of this kind of variety mixture is reducing the weeds in forage.

The aim of this study was to examine the potential of intercropping sainfoin with annual crops (forage pea, faba bean and oat) for forage production. The trial with three replications was carried out at Experimental Field of Institute of Field and Vegetable Crops Novi Sad at Rimski Anevi. Sainfoin was the under sown crop, and forage pea, faba bean and oat were the companion crops. Control variant was pure stand of sainfoin. At the harvestable stage of sainfoin, forage yield (t ha^{-1}) and weed proportion (%), were monitored.

In all replications, sainfoin mixture with forage pea, faba bean and oat produced the highest green forage yield per hectare in comparison to control. The average green forage yield in mixture with oat (16.9 t ha-1) was significantly higher than in forage pea (10.2 t ha-1) and faba bean (11.4 t ha-1) mixture. The significantly lowest weed proportion has been achieved in sowing with oat (1.5 %), while pure crop had the highest weed percentage (6.4 %, respectively).

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P55 – S7

Intercropping legumes with legumes and its effects on yield components

Živanov D., Karagić Đ., Milošević B., Vasiljević S., Đorđević V, Savić A., Mikić A.
Institute of Field and Vegetable Crops, Novi Sad, Serbia

The experimental trial was established in the experimental field of the IFVCNS, using completely randomized block design with three replications. The plot size was 5m2 and the seeding ratios was 50:50%. Pea +faba bean, pea + fenugreek and grass pea + white lupin were mixed together, and mechanically sown in rows at the same depth. A total of ten plants randomly chosen per plot in three replications were estimated for the yield components (the number of pods, number of seeds and seed weight per pod.

The average number of pods (7.6/8.2), number of seeds (26.9/30.1) and seed weight (6g/7.2g) per pea plant in a mixture with faba bean and fenugreek was significantly higher than in sole crop, where the average number of pods was 5.2, number of seeds 19.2, and seed weight 4.7g. However, in the same mixture the average number of pods (12.3/13.8) and seeds (29.7/57.7) per faba bean and fenugreek plants were significantly higher than in intercrop. Moreover, the fenugreek had the significantly higher seed weight (0.9g) in mixtures than in a sole crop. The sole crops of grass pea and white lupin had the significantly higher number of pods (18.5/9.2), seeds (44.1/29) and seed weight (7.25/13.2) then in mixture.

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P56 – S7

Characterization of saponin production in developing seeds of *Vicia faba* and *Pisum sativum*

Marais J.[1], Vernoud V.[1], Le Signor C.[1], Lacaille-Dubois M-A.[2], Thompson R.[1]

1 - INRA, UMR1347 Agroécologie, INRA Centre de Dijon, Rue Sully, F21000 DIJON, France

2 - Université de Bourgogne-Franche Comte, EA 4267, FDE/UFC, Laboratoire de Pharmacognosie, Faculté de Pharmacie, F21079 DIJON, France

Legume seeds are increasingly in demand as an inexpensive source of protein for incorporation in foodstuffs. However, protein fractions prepared from pea (*Pisum sativum*) and faba bean (*Vicia faba*) seeds contain significant quantities of saponins, which may confer an undesired bitter flavor on the final food product. Saponins have also been implicated in abiotic and biotic stress responses, hence a further interest in studying their accumulation and genetic control in these species. We have identified pea genes putatively involved in saponin biosynthesis in developing pea seeds, and optimized an extraction method for use in following saponin accumulation and distribution in seeds of pea and faba bean.

Acknowledgement. This project is supported by the FUI (Fonds Unique Interministériel) AAP no. 18 LEG'UP.

P57 – S7

Intercropping field pea with perennial legumes for forage production

Katanski S., Milić D., Karagić D., Milošević B., Vasiljević S., Mikić A., Mihailović V.

Institute of Field and Vegetable Crops, Novi Sad, Serbia

One of the most important problems in establishing perennial legumes are weeds in the stages of the early growth and development of a perennial legume. Field pea is a short term, annual crop and can reduce weed invasion, and also it can provide increased forage yield in the first cut in the first year. The goal of this study was to examine the potential of intercropping field pea with perennial legumes for forage production. The trial with three replications was carried out at Experimental Field of Institute of Field and Vegetable Crops Novi Sad at Rimski an_evi in 2015. Alfalfa and red clover were the under sown crops, and field pea was the companion crop. Control variants were pure stand of alfalfa and red clover and their mixture with oat. At the harvestable stage of pea, forage yield (t ha-1) and weed proportion (%) were monitored. On average, intercropping with oat produced the highest green forage yield (22.6 t ha-1 alfalfa and 18.9 t ha-1 red clover). Forage yield was higher when perennial legumes were sown with pea than grown as the pure crops (10.0 t ha-1 vs. 6.4 t ha-1, 10.8 t ha-1 vs. 8.7 t ha-1). The lowest weed proportion has been achieved in sowing with oat (0.4 % alfalfa and 0.3 % red clover), while pure crops had the highest weed percentage (13 % and 46 %, respectively).

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P58 –S7

Application of legumes in development of crunchy protein-rich snack bars.

Galoburda R., Puiskina E., Muizniece-Brasava S.
Latvia University of Agriculture

Energy, cereal or chocolate bars available in the market typically have high carbohydrate (54–70 g, on average 65 g per 100 g of product) and fat content (7–23 g per 100 g of product). The aim of the current study was to develop crunchy legume bars with increased protein and reduced carbohydrate and fat content. Extruded snacks produced from Latvian grey peas (*Pisum sativum* L.) of the variety ‘Bruno’, broad beans (*Vicia faba* L.) of the variety ‘Barteks,’ and cowpeas (*Vigna unguiculata* L.) of the variety ‘Fradel’ from Portugal were used as a basis for new product development. After sensory evaluation, the highest consumer acceptance among developed products received snack bars made from grey peas, which were selected for further study. Suitability of the following packaging materials was evaluated – polypropylene (PP), metalized polypropylene (metPP), and polylactide (PLA). Study revealed a small change in colour of the product during 90 days of storage at room temperature; the product became darker. The least changes in product color were observed in metPP packaging. Moisture content decreased, but product hardness increased, in a close correlation (r=0.98). The pH during storage did not change significantly. Water activity (aw) in the new crunchy protein-rich snack bars was less than 0.49. Microbial safety of product was proved by microbiological analyses performed during its storage. Nutritional and energy value of pea snack bar was experimentally detected.

P59 – S7

Biomass production in an improved sustainable mixed short-rotation woody cropping of *Populus hybrids* and *Robinia pseudoacacia*

Rebola-Lichtenberg J., Ammer C.
University of Göttingen

The rising demand on bionenergy leads to a necessity for optimization of biomass production. Hardwood short-rotation coppice crops are used as a source for carbon-neutral energy. Mixed cropping is seen as an improvement towards higher ecological complexity. Intercropping - the cultivation of different crops on the same land at the same time- may lower the dependence on additional input by recovering the internal regulation of a natural ecosystem and enhancing the crop systems stability.

Due to their rapid high woody biomass production the fast-growing *Populus* hybrids are particularly used as elements for bioenergy production in monocropping systems. *Robinia pseudoacacia* L. is a lesser known species for energy plantations, but has the promising ability to fix nitrogen.

This study aims to throw light on a potential facilitation and complementarity between the N-demanding species poplar (*Populus* spp.) and the N-fixing legume species black locust (*Robinia pseudoacacia*) on biomass increment. Along with tree measurements, the crown structure and leaf-area-index will be analyzed as indication for tree interaction. The poplar hybrids that benefit most from this type of crop mixture will be identified.

P60 – S7

Relationship between physicochemical components

Karayel R.[1], Bozoglu H.[2]

1 - Blacksea Agricultural Research Institute, Samsun

2 - Ondokuz Mayıs University, Faculty of Agriculture, Agronomy Department, Samsun

This study was conducted to determine relationships in between some physicochemical properties of 4 control varieties and 44 local pea lines which has been collected from Blacksea Regions and obtained from Gene Bank of Eagean Agriculture Research Institute. Relationship between properties was determined by correlation and path analysis. It was determined that cooking time was very significantly and positive correlated with water absorption capacity, swelling capacity, dry matter rate passed to cooking water, seed length, protein rate in seed, tryptophan quantity in seed, ash rate in seed and P quantity in seed; significantly and positive correlated with 100 seed weight, amylose rate in seed and Ca quantity in seed; very significantly and negative correlated with fragmentation ratio of seed after cooking and starch rate in seed. It was determined that dry matter rate passed to cooking water (0.5637) and water absorption capacity (0.5459) have positive and highest direct effects; starch rate in seed (-0.3548) and K quantity in seed (-0.2900) have negative and highest direct effects on cooking time in the and of path analyses. Starch rate in seed have effected negative to cooking time (0.641**) in other words the increaser starch rate in seed, the shorter cooking time. According to the path analysis, direct effects of starch rate in seed to cooking time is % 28.4736 and it was seeing the property doing highest indirect effect is water absorption capacity (%16.9914).

P61 – S7

Micropropagation of forage legume elite genotypes: solutions and prospects

Duque A.S.[1], Costa O.C.[1,2], Medalhas M.[2], Silva A.R.[2], Araújo S.S.[1], Barradas A.[2], Crespo J.P.[2], Fevereiro P.[1,3]

1 - Plant Cell Biotechnology Laboratory, Green-it Unit, Instituto de Tecnologia Química e Biológica António Xavier (ITQB), Apt. 127, 2781-901 Oeiras, Portugal;
2 - Fertiprado-Sementes e Nutrientes Lda., 7450-250 Vaiamonte, Portugal;
3 - Departamento de Biologia Vegetal, Faculdade de Ciências da Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal

There is an ever-increasing demand for high quality forage legumes, essential to feed livestock. Micropropagation may be useful to preserve elite allelic compositions in allogamous and auto-incompatible species. For clonal multiplication of elite genotypes micropropagation processes for *Trifolium incarnatum*, *T. resupinatum*, *T. michelianum*, *T. isthmocarpum*, *T. alexandrinum* and *Hedysarum coronarium* were developed. Axillary shoot development was induced by cultivating disinfected nodal segments on agar solidified MS basal medium, supplemented with sucrose and 0.0-1.8μM benzyladenine. Micropropagated shoots were rooted on MS medium without growth regulators and 80 to 100 % were successfully acclimated. A very prone to etiolate T. resupinatum genotype stood out by presenting an extremely etiolated-like phenotype with long, weak stems and sparse leaves, together with high percentages of in vitro flowering. To reverse the etiolation like effect and flowering induced by in vitro culture, zeatin, benzyladenine and gibberellic acid supplementation was tested. Supplementation with 9.12μM zeatin reversed the etiolation-like phenotype, inhibited in vitro flowering and improved acclimation in this *T. resupinatum* genotype. To investigate the photosynthetic performance of in vitro propagated *T. resupinatum* elite genotypes, gas-exchange measurement coupled to pigment quantifications are also being conducted at Fertiprado trial fields and greenhouse.

P62 – S7

Intercropping of Pea and Cereals in Organic Farming

Hunady I., Hochman M.
Agritec Plant Research Ltd.

The legume-cereal intercropping (LCI) may be advantageous to increase self-sufficiency with animal fodder in organic farming and reduce the possible dependency on imported soybeans and extracted soy meal. Finally, the reintroduction of LCI growing as major crop appears to be very promising way to stabilize yields, decrease weed and pests pressure.

Field experiments with plot trials with intercropped leafy and afila pea varieties and spring cereals (wheat, barley) were carried out in the Czech Republic over four consecutive cropping seasons (2008–2011). Different varieties and pea-cereal combinations were tested to find useful varieties for intercropping and optimal pea to cereal ratio (pea to cereal ratios 80:20, 60:40, 40:60, 20:80). The results demonstrate that pea-cereal intercrops compared to sole crops produce high yields of grains especially when intercropped at the pea to cereal ratio of 60:40 and 40:60. To determine land use efficiency, the land equivalent ratio (LER) was evaluated. It emerged that LER values must be interpreted carefully and should not be used when yield levels of intercropped pea-cereal components are extraordinarily low or high.

P63 – S7

Whole chickpea flour and crude mucilage addition affect kefir quality and antioxidant capacity during storage.

Ouldsaadi L.[1], Mahtout R.[1], Boudjou S.[1], Zaidi F.[1], Hassissene N.[1], Oomah B.D.[2], Hosseinian F.[3]

1 - Departement des Sciences Alimentaires, Faculté des Sciences de la Nature et de la Vie, Université de Bejaia, 06000 Bejaia, Algérie

2 - Formerly with National Bioproducts and Bioprocesses Program, Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Summerland, BC, Canada, V0H 1Z0

3 - Food Science Department of Chemistry Carleton University and Nutrition Canada. nadhassi1@gmail.com

This study investigated the capability and efficiency of the whole chickpea and his crud mucilage to enhance bacterial survival and growth in kefir as well as the antioxidant activity of samples.

The results showed that kefir samples supplemented with flour and mucilage enhanced significantly ($P < 0.05$) higher viability of bacteria (8.36 log cfu/mL) and acidity (0.82%TTA) than the control. An overall pH decline of 0.2 was observed during cold storage period. The mucilage from crude chickpea exhibited strong antioxidant activity; ORAC value of 267.45 ± 3.3 _molTrolox equivalent /g, in agreement with high TPC. This study demonstrated that chickpea flour and his mucilage acts as a good source of prebiotic, enhancing lactic acid bacteria growth in kefir model in addition of their high antioxidant beneficiary.

P64 – S7

Uses of faba beans and chick peas in food (pasta, bread and kefir)

Ouazib M.[1], Tazrart K.[1], Moussou N.[1], Boudjou S.[1], Ouldsaadi L.[1], Mahtout R.[1], Hosseinian F.[2], Lamacchia C.[3], Haros M.[4]; Garzon R.[5]; M Rosell C.M.[5], Hassissen N.[1], Zaidi F.[1]

1 - Département des Sciences Alimentaires, Faculté des Sciences de la Nature et de la Vie, Université de Bejaia, 06000 Bejaia, Algerie

2 - Food Science Department of Chemistry Carleton University and Nutrition Canada

3 - Dipartimento di Scienze degli Alimenti, Università degli Studi di Foggia, Via Napoli, 25, 71100 Foggia, Italy

4 - Institute of Agrochemistry and Food Technology (IATA-CSIC), Av. Agustín Escardino 7 Parque Científico, 46980 Paterna-Valencia, Spain

5 - Food Science Department, Institute of Agrochemistry and Food Technology (IATA-CSIC), C/ Agustin Escardino, 7, 46980, Paterna, Valencia, Spain. idiazdiraf@yahoo.fr

Pasta, bread and kefir are very popular food in several countries around the world, easy to prepare and well accepted by all age groups.

The incorporation of broad-bean flour in maccheronccini pasta resulted in a significant increase in protein levels, fiber, resistant starch, ash and minerals. In vitro protein digestibility increased proportionally with the broad-bean substitution level. Lower glycemic index (GI) for enriched pasta compared to traditional pasta and white bread is noted.

Bread made with raw chickpea flour had the highest proximate component content but the lowest in vitro protein digestibility. Finally about sensory properties, no significant ($p<0.05$) differences were observed in texture, after-taste, aroma and overall acceptability among the different breads. Concerning appearance, breads made with raw and germinated chickpea were more appreciated, however, bread made with cooked chickpea flour, was tastier than other breads. Processing of chickpea beans could be used for obtaining gluten free breads with good nutritional characteristics.

Whole ground faba bean was investigated for its capability and efficiency to enhance bacterial survival and growth during kefir storage. Bacterial count was strongly and positively correlated with lactic acid content and inversely associated with pH.

P65 – S7

The influence legumes in combined organic fertilizers on spring cereals productivity and quality.

Kadžiulienė Ž., Arlauskienė A. and Šarūnaitė L.
Lithuanian Research Centre for Agriculture and Forestry

Legumes and organic fertilisers are tools for supporting of nutrient cycling in low-input systems. Yield benefits to subsequent crops are the major component of pre-crop value of legumes, however management of legume is complicated and use in crop rotations is insufficient. Also using only the nitrogen fixed by legumes, it is not easy to meet the nitrogen needs of other crops at the right time. It is therefore important to find out measures that may contribute to grain yield and quality improvement. The experiments were carried out on Endocalcari-Ephypogleyic Cambisol in Dotnuva (55˚24' N, 23˚50' E), and on a heavy loam Cambisol at the Joniškėlis Experimental Station (56º21' N, 24º10' E). The study aims to combine legumes and newer forms of organic fertiliser as cow manure pellets and find out the effect on spring cereals productivity and quality. Grain yield of spring wheat was affected by using manure pellets and biomass of incorporated red clover in both locations. Cattle manure pellets used for cultivation of oats and spring wheat had a positive impact on barley yield.

P66 – S7

Evaluation of edamame in Latvia

Zeipina S., Lepse L.
Pūre Horticultural Researche Centre. Latvia

The difference between soybeans (*Glycine max*) and edamame is in the stage of maturity when the beans are harvested. Vegetable soybean also called edamame is an important vegetable. Beans are harvested before full maturity when bean pods are green and just started becomes yellow. Edamame is a valuable food for vegetarians and vegans due to its high nutritional value. Edamame has 376 calories, 17 grams total fat, 28 grams total carbohydrates per cup. Preliminary investigations with the aim to clarify edamame growing possibilities in Latvia were carried out in Pūre Horticultural Research Centre Ltd. in 2015. Five Japanese cultivars were tested: 'Sappon Miclin', 'Soya Comachi', Kaohsiung No 9', 'Chiba Green' and 'Midori Giant'. Meteorological conditions in vegetation period of 2015 were suitable for soya growing. Fresh pod yield ranged between 1.3 – 5.2 t ha^{-1}, higher yield was obtained for 'Midori Giant'. In organoleptic assessment variety 'Chiba Green' showed slightly better results than other varieties.

Session 8, plenary: Frontiers in legume genetics and genomics - Room *Arrábida I & II*

Chaired by Roberto Papa (Univ. Le Marche, Italy) and Marta Santalla (CSIC, Spain)

10:30-11:00 **Key lecture - Judith Burstin**: Towards the genome sequence of pea: a tribute to Mendel

11:00-11:15 Oral – S8

Genome sequencing of adzuki bean (*Vigna angularis*) provides insight into high starch and low fat accumulation and domestication

Wan P.
Beijing University of Agriculture

Adzuki bean (*Vigna angularis*) is an important legume crop, and is grown in more than thirty countries of the world. The seed of adzuki bean, as an important source of starch, digestible protein, mineral elements and vitamins, is widely used in a variety of foods for at least a billion people. Here, we generated a high quality draft genome sequence of adzuki bean by whole genome sequencing. The assembled contig sequences reached to 450 Mb (accounting for 83% of the genome) with an N50 of 38 kb, and the total scaffold sequences were 466.7 Mb with an N50 of 1.29 Mb. Of them, 372.9 Mb of scaffold sequences were assigned to the 11 chromosomes of adzuki bean using a single nucleotide polymorphism genetic map. A total of 34,183 protein-coding genes were predicted. Functional analysis revealed that significant differences in starch and fat content between adzuki bean and soybean were likely due to transcriptional changes, rather than copy number variations, of the genes related to starch and oil synthesis. We detected strong selection signals in domestication by the population analysis of 50 wild and cultivated adzuki beans. The genome sequence of adzuki bean will facilitate the identification of agronomically important genes, and accelerate the improvement of adzuki bean. In summary, our results provide insight into evolution and metabolic differences of legumes.

11:15-11:30 Oral – S8

Genotyping-by-sequencing and its exploitation in forage and grain legume breeding.

Annicchiarico P. [1], **Nazzicari N.** [1], **Wei Y.** [2], **Pecetti L.** [1], **Brummer E. C.** [2]
1 - CREA, Italy
2 - Univ. of California, Davis

Genotyping-by-sequencing (GBS), compared with SNP array platforms, may drastically reduce genotyping costs, and is applicable also to relatively small experiments. However, it may require optimization for specific crops, to maximize the number of usable markers. Exploiting GBS-generated markers may require optimization too (e.g. to cope with missing data). This study aimed (i) to compare the value of different GBS protocols for three legume crops (alfalfa, pea, white lupin) that contrast for genome size, ploidy and breeding system; (ii) to show various successful applications of GBS data on legume species and some of their challenges. Preliminary work on alfalfa highlighted the greater interest of ApeKI over PstI:MspI DNA digestion. We compared all different combinations of KAPA or NEB Taq polymerase with primer extensions that are progressively more selective on restriction sites, identifying GBS protocols of general value across the three legume species. We assessed genomic selection accuracy for predicting forage yield-based alfalfa breeding value and pea grain yield in different growing environments, considering different missing value imputation strategies and statistical models (Ridge regression BLUP, SVR, Bayesian methods). We tested the usefulness of GBS data to assess alfalfa cultivar distinctness, which offers advantages over phenotypic trait-based distinctness. GBS proved useful also for exploring the genetic structure of white lupin landrace germplasm.

11:30-11:45 Oral – S8

Application of historical data from Australian lentil breeding program to enable rapid implementation of genomic selection

Pembleton L.[1], Sudheesh S.[1], Braich S.[1], Rodda M.[2], Slater T.[1], Forster J. W.[1,3], Cogan N. O. I.[1,3], Spangenberg G.[1,3], Kaur S.[1],*

1) AgriBio, Centre for AgriBioscience, Agriculture Victoria, DEDJTR, 5 Ring Road, La Trobe University, Bundoora, Victoria 3083, Australia. sukhjiwan.kaur@ecodev.vic.gov.au

2) Grains Innovation Park, DEDJTR, PMB 260, Horsham, Victoria 3401, Australia

3) La Trobe University, Bundoora, Victoria 3086, Australia.

Genomic selection (GS) has recently emerged as an evolutionary approach in crop breeding that can accelerate genetic improvement through the ability to predict the phenotypic performance early in the breeding cycle, reducing the generation interval. Here we evaluate for the first time its efficacy for breeding lines from the Australian lentil breeding program. A total of 864 advanced breeding lines were evaluated infield annually in a range of environments from 2010-2014 for economically important traits such as grain yield and grain weight. Genotyping was performed using a whole genome genotyping-by-sequencing transcript approach. Over 200,000 SNPs were initially identified from sequencing key ancestor lines of the PBA breeding program, and were used for SNP variant calling in the breeding lines. The ability to genomically predict the observed phenotypic performance in each progressive year, and within-year clustered environments was explored by using lines from previous years, as the reference population and applying a range of GS models i.e. GBLUP, BayesA and BayesB. Accuracies achieved for grain yield and weight were moderate to high (c. 0.35-0.70), reflecting the relative heritabilities of these two economically important traits. The genomic estimated breeding values and prediction equations developed are now being implemented within the lentil breeding program to design optimal crossing schemes to increase genetic gain and reduce the overall generation interval.

11:45-12:00 ORAL – S8

Legume-based mixed cropping systems may have higher water use efficiency than mono crop systems WGGBS in pea without reference genome and data assembly: a successful strategy at low sequencing coverage for SNP discovery, genotyping and genetic mapping.

Boutet G.[1,9], Alves Carvalho S.[1], Peterlongo P.[2], Falque M.[3], Lhuillier E.[4,6], Bouchez O.[4,7], Lavaud C.[1,9], Uricaru R.[1,8], Lesne A.[1,9], Pilet-Nayel M-L.[1,9], Rivière N.[5], Baranger A.[1,9]

1 - INRA, UMR 1349 IGEPP, BP35327, Le Rheu Cedex 35653, France

2 - INRIA Rennes - Bretagne Atlantique/IRISA, EPI GenScale, Rennes, 35042 France

3 - INRA, UMR 320 GQE–Le Moulon, INRA - Univ Paris-Sud - CNRS - AgroParisTech, Ferme du Moulon, 91190 Gif-sur-Yvette, France

4 - GeT-PlaGe, Genotoul, INRA Auzeville F31326, Castanet-tolosan, France

5 - Limagrain Europe, route d'Ennezat, CS90126, Chappes 63720, France

6 - INRA, UAR1209, Castanet-Tolosan, France

7 - GenPhySE, Université de Toulouse, INRA, INPT, INP-ENVT, Castanet Tolosan, France

8 - University of Bordeaux, CNRS/LaBRI, F-33405 Talence, France

9 - PISOM, UMT INRA/Terres Inovia, BP35327, Le Rheu Cedex 35653, France

Our objective was to develop a comprehensive SNP resource in a species lacking a sequenced reference genome (*Pisum sativum*), by developing a whole genome genomic DNA genotyping by sequencing (WGGBS) strategy for high-throughput SNP discovery, genotyping and genetic mapping.

Over four hundred thousand SNP markers were identified from sequencing 4 pea lines (7x coverage), among which 63,353 were successfully genotyped and mapped through genome sequencing of 48 RILs (3.5x coverage), without prior genome reduction or assembly to a reference genome (Boutet et al., 2016).

A subsequent KASP™ assay on 1438 pea lines, with a subset of 1000 SNPs chosen for their mapping positions within QTL confidence intervals for biotic stress resistance, showed that almost all generated SNPs were highly designable and that most (95 %) delivered highly qualitative genotyping results. It allowed refining map genomic regions and QTLs associated with traits of interest identified from RIL populations.

Using rather low sequencing coverages and the development and optimization of appropriate tools such as discoSnp in SNP discovery or custom R scripts using CARHTA GENE for genetic mapping, we made available a large set of polymorphic markers internal to and bordering QTL confidence intervals. This provides an unprecedented resource that could significantly speed up genetic studies and marker assisted breeding for non-model species. Boutet et al. (2016) BMC Genomics 17:121

P67 – S8

Validation of quantitative trait loci for height-related traits in faba bean.

Atienza S.G.[1], Ruiz-Rodriguez M.D.[2], Cruz-Izquierdo S.[2], Torres A.M.[2], Cubero J.I.[3], Avila C.M.[2].

1 - Inst. Agric. Sostenible (CSIC)
2 - IFAPA-Centro Alameda del Obispo (Córdoba)
3 - University of Córdoba

Most faba bean genotypes show indeterminate growth habit. These genotypes may become very tall when water is available. Indeed faba bean crops may grow to a height of 2 m at maturity although faba bean crops are not usually that tall. Excessive plant height (PH) may result in plant lodging. Besides, the crop may result in poor pod set due to predominant vegetative growth, uneven maturity.

Accordingly shorter genotypes are important in faba bean breeding. Other height-related traits are also important. The height of the lower flower (HLF) and the height of the lower pod (HLP) are important agronomic traits. Pods located near ground may remain unharvested and they may be more affected by disease incidence.

Previous studies in our group identified preliminary quantitative trait loci (QTL) for these traits in the population derived from the cross VF6 x Vf27. In this work we have validated QTL for PH, HLP and HLF at field conditions. Besides, the role of candidate genes for height-related traits in model species was investigated in relation with these QTL.

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P68 – S8

Genotyping of *Pisum sativum* L. and *Vicia faba* L. by SNP analysis using next generation sequencing,

Martos-Fuentes, M.; Appeltans, J; Maes, I; Mezaka, I.; Egea-Gilabert, C.; Fernández, J.A.; Egea-Cortines, M. and Weiss, J.
ETSIA Universidad Politécnica de Cartagena

SNPs (single nucleotide polymorphism) are an important source of polymorphisms throughout the genome and therefore a valuable type of marker to study genetic distances. We have chosen 45 markers for Pisum sativum and 60 for Vicia faba, identified in QTL mapping projects. We used Next Generations Sequencing with the IonTorrent Semiconductor Sequencer. We developed a barcoding system that allowed us efficient amplifications and sequencing all SNPs for 12 plants from both species on a single Ion Torrent chip. The method is based on two consecutive conventional PCRs. In the first one, SNP specific primers were used to amplify the specific region, adding a bead specific sequence (P1) to one end and a common sequence “B” to the other end. The second PCR was performed using P1 as forward primer and an adaptor “A” + “B” specific sequence as reverse primer. The adaptor “A” contains the barcode of 4 nucleotides, differentiating for 12 plants. First rounds of sequencing showed that 40 of the 60 SNPs in V. faba and 37 of the 45 SNPs in P. sativum gave reliable sequence results. Some DNA extractions failed to give sequencing reactions. The percentage of polymorphic SNPS was 70% both for P. sativum and V. faba and the percentage of heterozygosity was 54% in P. sativum and 67% in V. faba. SNP sequence information of a total of 72 varieties will be finally used for phylogenetic reconstruction in order to obtain information about similarities at the molecular level.

P69 – S8

Using GBS-GWAS to Identify Loci Controlling Forage Yield and Nutritive Value in a Diploid Alfalfa Mapping Panel

Sakiroglu M.[1], **Brummer E.C.**[2]

1 - Department of Bioengineering, Kafkas University, Kars, Turkey.
2 - Department of Plant Sciences, The University of California-Davis, USA.

Alfalfa is one the most widely cultivated forage legumes worldwide and improving alfalfa forage yield and nutritive value are major global breeding goals. Genotyping-by-sequencing (GBS) provides cost effective genotyping that enable high resolution genome-wide association studies (GWAS). We previously used a panel of 365 diploid individuals and 89 SSR markers to map 23 forage yield and nutritive value-related traits over two years. The limited marker number, unsurprisingly did not identify any associations. Using GBS, we were able to conduct a true GWAS. More than 15,000 genome-wide SNPs passed the quality criterion after filtering and were used for subsequent analyses. We have detected a number of associations for all the traits evaluated and the top associations were located on the *Medicago truncatula* genome. A SNP in a coding region of a cell wall biogenesis gene associated with several cell wall related traits and we suggest that it may be the true causative polymorphism. Two other SNPs residing in meristematic development and early growth genes were found to associate with the total biomass yield. None of the SNPs associated with regrowth after harvest or with spring regrowth were mapped to *M. truncatula* genome. *M. truncatula* is an annual species related to alfalfa that typically has limited ability to regrow. The alleles we identify with the major impact on forage yield and nutritive value can be rapidly incorporated into our breeding program.

P70 – S8

Unravelling seed development in the common bean (*Phaseolus vulgaris*) integrating transcriptomics and proteomics data

Parreira J.R.[1], Bouraada J.[2], Fitzpatrick,M.A.[2], Silvestre S.[3,4], Bernardes da Silva A.B. [3,4], Marques da Silva J. [3,4], Almeida A.M.[1,5], Altelaar A.F.M.[2], Fevereiro, P. [1,4], Araújo, S.S.[1,6]

1 - Plant Cell Biotechnology Laboratory, ITQB - NOVA,

2 - Biomolecular Mass Spectrometry and Proteomics, Bijvoet Centre for Biomolecular Research, Utrecht Institute for Pharmaceutical Sciences, University of Utrecht, Netherlands Proteomics Centre, Padualaan 8, 3584CH Utrecht, The Netherlands.

3 - Plant Functional Genomics Group, Biosystems and Integrative Sciences Institute (BioISI), Faculdade de Ciências, Universidade de Lisboa

4 - Departamento de Biologia Vegetal, Faculdade de Ciências da Universidade de Lisboa, Campo Grande, 1749-016, Lisboa, Portugal.

5 - Ross University School of Veterinary Medicine, P.O. Box 334, Basseterre, Saint Kitts and Nevis.

6 - Plant Biotechnology Laboratory, Department of Biology and Biotechnology, 'L. Spallanzani', University of Pavia, via Ferrata 1, 27100 Pavia, Italy.

Common bean (*Phaseolus vulgaris*) is an important staple food worldwide. We conducted a proteomic and transcriptomic analysis to unravel the molecular mechanisms of *P. vulgaris* seed development (SD).

A gel-free proteomic assay (LC-MS/MS) was done on seeds at 10, 20, 30 and 40 days after anthesis, spanning from late embryogenesis until desiccation. At the early SD stage an accumulation of proteins related with protein metabolism, glycolysis, TCA, stress and nucleic acid metabolism was observed, reflecting an extensive metabolic activity. At mid-SD the accumulation of storage, signaling, starch synthesis and cell wall-related proteins stood out. In the later stages, an increase in proteins related to redox, and to a lesser extent protein degradation/modification/folding and nucleic acid metabolisms reflect that seed desiccation-resistance mechanisms were activated. Clues on maintenance of genome integrity during SD were unveiled, such as proteins involved in chromatin remodeling (histone H2A) and DNA repair (proliferating cell nuclear antigen).

In parallel, we also investigated changes in gene expression profiles during SD. For this purpose, we performed a Massive Analysis of cDNA Ends (MACE) at the same time points.

The integration of information from both analyses enhances our knowledge on the SD molecular mechanisms. This knowledge may be used in the design and selection of common bean seeds with desired quality traits.

P71 – S8

A high-density genetic linkage map and QTL analysis of ascochyta blight resistance in chickpea

Deokar A.A., Sagi M., Tar'an B.

University of Saskatchewan, Saskatoon, Canada, amit.deokar@usask.ca

Ascochyta blight causes significant yield loss in chickpea (*Cicer arietinum* L.) crop worldwide. To determine the genetic basis of resistance to ascochyta blight in chickpea, we constructed a high-density genetic linkage map using genotyping-by-sequencing (GBS) and Illumina GoldenGate SNP genotyping approach on a chickpea recombinant inbred line population (CPR02) derived from a cross between the Ascochyta blight partial resistant chickpea cultivar 'Amit' and a highly susceptible cultivar 'ICCV 96029'. Genotyping data of 664 segregating SNPs were generated using 1,536 GoldenGate assays. Single enzyme (ApekI) based GBS and paired-end sequencing generated over 224.4 million reads with an average of 1.7 million reads per line, which facilitated identification of 2,828 high quality segregating SNPs. Combining SNP genotyping data from both platforms, CPR02 linkage map consists of 3,460 SNP markers, distributed on eight linkage groups, covering a genetic distance of 867.9 cM. The CPR02 population was evaluated in greenhouse and open field conditions and investigated the quantitative trait loci (QTL) associated with ascochyta blight disease resistance. A total of six QTLs for resistance to ascochyta blight, located on chromosome 2, 3, 4 and 5 were identified. The identified QTLs explained 26.0% (greenhouse study), 39.9% (field study 2014) and 55.8 % (field study 2015) of the total estimated phenotypic variation. Candidate genes physically located in the genomic region associated with QTL were identified and genetically mapped to validate their colocalization with the identified QTLs. This study provides useful genetic and genomic resources for marker-assisted breeding and better understanding genetics of ascochyta blight resistance in chickpea.

P72 – S8

Genes involved in flowering time regulation in white lupin (*Lupinus albus* L.): transcriptome profiling, linkage mapping and phylogenetic inference

Książkiewicz M.[1], Rychel S.[1], Tomaszewska M.[1], Nelson, M.[2], Naganowska B.[1], Wolko B.[1]

1 - Institute of Plant Genetics of the Polish Academy of Sciences, Poznan, Poland.

2 - Royal Botanic Gardens, Kew, Millennium Seed Bank, Wakehurst Place, Ardingly, United Kingdom

White lupins are valuable grain crops with high protein and oil content, low alkaloid and low fibre. Nevertheless, their cultivation involves a long vegetative period, which may be reduced in early flowering accessions. However, this trait appears to be under polygenic, recessive control, difficult to manage in plant breeding.

Insight into European Lupin Collection led to identification of vernalization independent, early flowering breeding lines, mutants and cultivars. Late lines, which flowered about 5-6 weeks later, were from wild populations. Mining of the *Lupinus albus* transcriptome for flowering regulation genes tagged 34 of 53 *Arabidopsis thaliana* homologs. Protein-based hidden Markov model annotation resulted in prediction of full-length proteins for 27 genes. The number of predicted copies varied from 1 (AGAMOUS-LIKE 19, EARLY FLOWERING 1 and 3, FRIGIDA, FLOWERING LOCUS Y, VERNALIZATION INDEPENDENCE 3) to 8-10 (EARLY FLOWERING 6, EARLY IN SHORT DAYS, VERNALIZATION 1). Massive analysis of cDNA ends of 20 lines differing in flowering time was performed to survey flowering regulation pathway and to upgrade white lupin gene index. Representative homologs were localized in the reference linkage map. Phylogenetic inference encompassing legume family revealed complex pattern of independent, lineage-specific duplications.

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P73 – S8

Physicochemical and cooking properties of dry bean (*Phaseolus vulgaris* L.) and soybean (*Glycine max* L. Merr.) seeds

Boros L., Wawer A.
Plant Breeding & Acclimatization Institute -NRI , 05-870 Radzików, Poland.

Physicochemical and cooking properties were determined in 23 dry bean local populations together with 2 cultivars from the Polish Genebank and in 9 soybean genotypes adapted to northern latitude, which included seven cultivars and two breeding lines. Wide variation among local populations of dry bean were observed in seed weight, hydration capacity, swelling capacity and electric conductivity with CV% values 30, 32, 33 and 35 respectively, suggesting that there are considerable levels of genetic diversity. Substantial variations were found in seed coat content (CV% 14) and cooking time (CV% 17) among dry bean populations. Tested soybean genotypes differed significantly for all evaluated traits, however with much lower variation among genotypes, except for cooking time, as compared to dry bean, indicating narrow genetic diversity.

Few significant correlation coefficients were common for both species e.g. seed coat content was negatively correlated with hydration and swelling capacities and positively with conductivity of soaking water. Cooking time was negatively correlated with conductivity of soaking water and with hydration index. The results showed substantial variability in dry bean and soybean in cooking time. From breeding standpoint, high variability suggest that it should be possible to obtain appreciable responses in selection for this trait and develop cultivars with decrease in cooking time.

P74 – S8

The *Lathyrus sativus* genome project.

Sarkar A., Edwards A., Emmrich P. M. F., Martin C., Wang T. L.
The John Innes Centre, Norwich, NR4 7UH, United Kingdom.

Grass pea (*Lathyrus sativus*) is a hardy, drought tolerant legume grown for animal feed, food and fodder on poor soils with minimal inputs. It serves as an insurance crop for marginal farmers in the Indian subcontinent and Africa. It is a diploid (2n=14) with an estimated genome size of 6.9 Gbp (Bennett and Leitch, 2005. Annals of Botany 95: 45-90). Its main drawback is the presence of a neurotoxin (beta-ODAP), which can cause neurolathyrism in people subsisting on a predominantly grass pea diet for an extended length of time.

We are currently sequencing the grass pea genome of a European line (LS007). A TILLING population is also being created for this line. A de novo shotgun sequencing strategy has been adopted based on the construction of a PCR-free library (using the Discovar protocol) and mate-pair libraries for Illumina sequencing. The draft genome will be annotated using ours and others' transcriptome data and data from completed genome sequences of related legumes.

The genome sequence will be valuable for the identification of the genes in the beta-ODAP biosynthesis pathway, as well as for traits of agronomic importance. The data will also provide insights into comparative genomics across legumes, help in the development of high quality genetic and physical maps for marker-assisted and genomic selection strategies and enable a genome-editing platform for grass pea.

P75 – S8

Bean adapt: the genomics of adaptation during crop Expansion in bean

Papa R.[1], **Jackson S.A.** [2], **Gepts P.** [3], **Graner A.**[4], **Fernie A.R.**[5]
1 - Marche Polytechnic University, Ancona, Italy
2 - University of Georgia, Athens, GA
3 - University of California, Davis, CA
4 - Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany
5 - Max Planck Institute of Molecular Plant Physiology, Potsdam-Golm, Germany

BEAN_ADAPT is a three-year project funded through the 2nd ERA-CAPS call, ERA-NET for Coordinating Action in Plant Sciences. The main aim of this project is to dissect out the genetic basis and phenotypic consequences of the adaptation to new environments of the common bean (*Phaseolus vulgaris* L.) and its sister species, the runner bean (*Phaseolus coccineus* L.), through the study of their introduction, from their respective centers of domestication in the Americas, and expansion through Europe, as a recent and historically well-defined event of rapid adaptation. A large collection (11,500 accessions of both species) from three major genebanks, will be characterised by genotyping-by-sequencing (GBS), to define the population structure and to obtain subsets of genotypes for phenotyping (field and growth chamber) and for a deeper genomic–transcriptomic–metabolomic characterisation. We will use a multidisciplinary approach: genomics (WGS and RNAseq), population/quantitative genetics, biochemistry, plant physiology on the subset of samples. Differential expression analysis, analysis of the co-expression patterns, and GWAS will be used to identify genes and metabolites putatively associated with adaptation, while genotypic information obtained from RNA-seq data will be used, with GBS and WGS data, to test for signatures of selection. Among the main outcomes of the project are the development in *P. vulgaris* of haplotypes of all 10,000 accessions (HapBean).

P76 – S8

Mendel's enduring legacy: orthologs of two of his seven factors in multiple current day crop legumes

Penmetsa R. V.[1], Carrasquilla-Garcia N.[1], Stonehouse R.[2], Mir R. R. [3], Sani G.[1], Rezaei M.[2], Chang P.[1], Cordeiro M.[4], Ta'ran B.[2], von Wettberg E.[5], Cook D.[1], Bett K.[2]

1 - University of California, Davis, USA
2 - University of Saskatchewan, Saskatoon, SK, CANADA
3 - Sher-e-Kashmir University of Agricultural Sciences & Technology, Jammu, INDIA
4 - University of Southern California, Los Angeles, USA; 5 Florida International University, Miami, USA

We characterized morphological variants for seed color in chickpea and lentil. Analysis of sequence variation in candidate genes from biological pathways suggested by the morphological phenotypes, cross-legume synteny, mining of draft whole genome sequence data, and sequence characterization of germplasm suggest that morphological variation in chickpea and lentil are likely from orthologs of Mendel's A and I loci for purple versus white flower color and yellow versus green cotyledons. The identification of the molecular basis for the chickpea and lentil morphological variation has practical implications for crop improvement. The growing evidence for conserved function across legumes suggests a facile route to the identification of the molecular basis of morphological variation in other legumes with limited genomics and sequencing resources.

P77 – S8

5-azacytidine and hydroxyurea affect germination and seedling development

Paiva J.A.[1], Pagano A.[2], Gualtieri C.[1,2], Gomes C.[1], Fevereiro P.[3], Araújo S.S. [2,3], Balestrazzi A.[2]

1 - Department of Integrative Plant Biology, INSTYTUT GENETYKI ROŚLIN POLSKIEJ AKADEMII NAUK, ul. Strzeszyńska 34, 60-479 Poznan, Poland

2 - Department of Biology and Biotechnology 'L. Spallanzani', via Ferrata 1, 27100-Pavia Italy

3 - Plant Cell Biotechnology Lab, ITQB NOVA Av. da República, 2780-157 Oeiras Portugal

Epigenetic marks, metastable changes in gene expression and function that do not result from changes in DNA sequence, are mediated by DNA methylation, histone modifications, and small interference RNAs. Cytosin-5 methylation (Cy5Met) is a major and dynamic epigenetic modification, which is established and maintained by multiple, interacting cellular machineries. Cy5Met of promoter regions and gene bodies is very important in gene expression regulation (by cis and trans acting). We are interested in to investigate how the modification of DNA methylation patterns impact on plant development, namely on seed development and germination and on secondary cell walls modification, in the legume model plant *Medicago truncatula* Gaert. In this preliminary essay we test the effect of different concentrations of 5-azacytidine (100, 50, 25, 0 uM; demethylation agent) and hydroxyurea (50, 10, 1 and 1mM; hyper-methylation agent) on germination of *M. truncatula*. We observed a significant reduction of the growth between the higher concentration and water for both treatment, and for 50mM hydroxyurea germination occur but no further development and growth of the seedlings were observed. These phenotypic results will be presented and discussed together the global levels of methylation and gene expression of some genes related with chromatin remodeling.

P78 – S8

Genetic variability study and kasp marker mapping analysis revealed a new haplotype determining pale hilum Hc in *Vicia faba*

Khamassi K.[1], **Jeddi F.B.**[2], **O'Sullivan D.M.**[3]

1 - University of Carthage, Field Crop Laboratory, National Agricultural Research Institute of Tunisia, Rue Hédi Karray 2049 Ariana, Tunisia

2 - University of Carthage, National Institute of Agronomy of Tunisia. 43 av. Charles Nicole, 1082 Cité Mahrajène – Tunis

3 - School of Agriculture, Policy and Development, University of Reading, Whiteknights, UK

Phenotyping and genotyping of the Tunisian faba bean populations vs two local commercial varieties (Badï and Bachaar) and world diversity collection, revealed significant diversity. Consequently, three individuals carrying Pale Hilum (PH) were identified within two Tunisian populations. Several studies mentioned that PH trait was in linkage with low vicine-convicine (VC) gene (VC-) that reduces 20 fold these two antinutritional factors. Thus, VC were quantified in the three Tunisian PH individuals as putative candidate for VC-gene, Badï and Bachaar and other PH-varieties from different origins and compared to the check varieties Disco and Melodie carrying PH and VC-. Results showed that the PH trait in the Tunisian individuals is not associated with zero VC. However, some of them were distinguished by their significant lower VC levels compared to the Tunisian and international commercial cultivars. A separate genetic mapping study using a segregating biparental population developed previously at NIAB (UK) was carried out. This analysis allowed the identification of new kasp marker linked to pale hilum traits segregating in the population. Genotyping of the F2 generation and plant and seed phenotyping over F2:3 and F3:4 generations were conducted. The Mendelian factors Hc, controlling Hilum colour, were located in linkage groups 2. The mapped marker for Hc allowed the identification of a new haplotype within the Tunisian individuals that differ from the European PH cultivars.

P79 – S8

Identification of the translocation breakpoint between chromosome 4 and 8 in the genomes of *Medicago truncatula* A17 and A20

Szabó Z.[1], Balogh M.[1], Miró K[1], Debelle F. [3], Cook D.R.[4], Ellis T.H.N., Kiss G.B.[1,2], Kaló P.[1]

1 - NARIC, Agricultural Biotechnology Institute, Gödöll_, Hungary
2 - AMBIS Biotechnology and Research Ltd, Szeged, Hungary
3 - INRA, Toulouse, France
4 - University of California Davis, Davis, California, USA

Extensive genomic resources have been developed for *Medicago truncatula* in the last two decades that made this species one of the model legumes. A previous genetic analysis of the F2 mapping population derived from the cross of *Medicago truncatula* A17 and A20 detected an unusual linkage phenomenon between markers located in the lower arms of chromosome 4 and 8 (Choi et al. 2004). It was found that some markers displaying high degree of genetic linkage showed cruciform-like linkage and no linear genetic map could be constructed based on the detected recombination events between these markers. The map position of these markers were resolved by positioning them to either linkage group 4 or 8 using the mapping population of M. sativa. A subsequent study indicated that accession A17 of *M. truncatula* carries a translocation between chromosome 4 and 8 that resulted in reduced viability of F1 pollens (Kamphuis et al., 2007) when crossing with other *M. truncatula* accessions.

In order to pinpoint the breakpoint of the translocated chromosomal segments in A17, a study was initiated using further genetic mapping of another segregating population of *M. truncatula* combined with the systematic sequencing of BAC clones using recently developed genetic markers around the breakpoint of the chromosomal rearrangement. We are going to present how the identification of the translocation breakpoint has been progressed.

P80 – S8

Lifting the curse of the grass pea

Emmrich P. M. F., Sarkar A., Edwards A., Martin C., Wang T. L.
The John Innes Centre, Norwich, NR4 7UH, United Kingdom.

Grass pea (Lathyrus sativus) is a legume crop with exceptional yield stability in the face of drought, flooding and poor soils. This hardiness gives the crop great potential for food security, especially in the face of climate change. However, this ancient food and feed crop has not received sufficient attention from breeders due to its association with the neurological disease Lathyrism, which is caused by the toxin beta-ODAP, which is produced by the plant.

We are working to remove this crucial limitation on the utilisation of grass pea by developing low/zero-toxin genotypes. To this end, we have screened natural germplasm and an EMS-mutagenized population, identifying new genotypes with lower toxin levels than existing varieties. In addition, we have sequenced transcriptomes derived from seven tissues of grass pea. By interrogating this dataset, we have identified candidate genes for some of the metabolic enzymes involved in the beta-ODAP synthesis pathway, which we are now testing biochemically. This may allow us to elucidate the genetic basis of the production of beta-ODAP and pave the way for the first ever toxin-free grass pea varieties.

P81 – S8

MicroRNA expression during induction of *M. truncatula* somatic embryogenesis

Costa S.F.[1], Costa O.C.[1], Fevereiro P.[1,2], Duque A.S.[1]

1 - Instituto de Tecnologia Química e Biológica António Xavier, Universidade Nova de Lisboa, Av. da República, 2780-157 Oeiras, Portugal

2 - Departamento de Biologia Vegetal, Faculdade de Ciências, Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal

Plant somatic embryogenesis (SE) is a highly complex development process essential for genetic engineering, plant improvement and clonal propagation.

A highly embryogenic line of *M. truncatula* cv Jemalong (M9-10a) was derived from a non-embryogenic line (M9), as a result of somaclonal variation. These two lines are ideal tools for studying embryogenesis as they share an extremely similar genetic background, differing essentially at the level of SE ability.

MiRNAs play crucial roles in plant SE since they modulate gene expression to enable pattern formation during plant embryogenesis. Quantitative PCR is a standard methodology for quantifying miRNA due to its specificity and reproducibility. However its accuracy relies on the use of on proper data normalization.

Here we compare the expression profiles of five siRNAs (Mt si4, si41, si65, si106 and si190) with the commonly used U6 snRNA during SE induction process in M9/M9-10a lines to find candidate reference sRNAs, using NormFinder and geNorm algorithms. We identified si65 and si106 as the best normalizers.

Selected si65/si106 were subsequently used for data normalization with Pfaffl analysis of five conserved miRNAs (mir159a, mir166a, mir166g, mir167a and mir172a) during 21 days of SE induction. Our results show significantly differences in miRNAs expression profiles between M9/M9-10a lines over time. Moreover, selected siRNAs could be considered more appropriate than the U6 snRNA for qPCR data normalization

P82 – S8

Novel in vivo protocol for evaluation of constitutive and seed specific promoter activity in immature legume seeds

Švábová L. [1], van Haesendonck G. [2], Navrátil O.[2], Plchová H.[2], Jindřichová B.[2], Ploužková T.[2,3], Čeřovská N.[2], Griga M.[1], Moravec T.[2]
1 - Plant Biotechnology Department, Agritec Plant Research Ltd., Šumperk, Czech Republic
2 - Laboratory of Virology, Institute of Experimental Botany CAS, Prague, Czech Republic
3 - Department of Biochemistry, Charles University, Prague, Czech Republic

Leguminous seeds are attractive expression systems for production of recombinant proteins such as edible vaccines or antibodies. Nevertheless, efficient and stable genetic transformation of legumes is still not a routine and the whole process to obtain T0 transformants may take 9 to 12 months. In addition the reasonable production of recombinant proteins of interest must be directed to the seeds, by organ-specific promoters. Novel in vivo protocol was developed to assess various promoter activity of different constructs containing gus reporter gene in combination with promoters 35S, nosP, gly, βcon and ole for soybean and pea. In the preliminary series of experiments we studied the effect of co-cultivation treatments (sonication) and chemical additives (acetosyringone, dithiothreitol, L-cysteine). The protocol was carried out in non-sterile conditions on plants grown in the glasshouse. Agrobacterium suspension was applied to scored seeds in pods and wrapped with parafilm for 6 days. Quantitative gus assay was done on harvested seeds to evaluate transient gene activity of constructs. Using novel in vivo protocol we were able to achieve sufficient expression of recombinant DNA in immature seeds and to perform their quantitative comparison. The protocol could be improved using changes in Agrobacterium strain, sonication time/intensity, presence/absence of chemical additives.

Acknowledgement: This research was financially supported by CSF, grant No. 15-10768S.

P83 – S8

Fine mapping of Ascochyta blight resistance in chickpea

Verma P.
National Institute of Plant Genome Research, New Delhi, India

Ascochyta blight (AB) is a devastating disease that affects chickpea (Cicer arietinum), a major legume crop. Conferring resistance in chickpea to AB is a prominent aim of chickpea breeders. Studies conducted in the past using classical markers have pointed out that resistance to AB is partial or incomplete with its inheritance being quantitative. We adopted NGS resequencing-based multiple QTL-seq approach to identify QTLs for AB resistance in chickpea using population bulks derived from two crosses, one inter-specific and the other intra-specific. We focused on two major QTLs and proceeded to confirm the NGS data with classical QTL analysis using thirteen polymorphic markers. We could bring down the area of one of the major QTLs to a narrow region of 28 Kb, which harboured four genes. Expression analysis of these four genes under AB stress showed induced expression of two genes in the resistant variety, both belonging to the same family and they interact physically in-planta. Interestingly, this gene family was also identified in other minor QTLs responsible for AB. These genes were further employed for functional characterization. The area under this QTL was sequenced in different accessions of chickpea that are either resistant or susceptible to AB for association of the trait to the gene(s). Markers developed by us can be used in breeding programmes and other population studies.

P84 – S8

Mutations in the MFN genes lead to an increased production of pods and seeds in pea

Martínez-Fernández I.[1], Fourquin C.[1], Berbel A.[1], Dalmais M.[2], Smykal P.[3], Annichiarico P.[4], Bendahmane A.[2], Madueño F.[1], Ferrandiz C.[1]

1 - Instituto de Biología Molecular y Celular de Plantas, CSIC-UPV, Valencia, Spain

2 - Unité de Recherche en Génomique Végétale, UMR INRA-CNRS, Evry Cedex, France

3 - Department of Botany, Faculty of Sciences, Palack_ University in Olomouc Olomouc, Czech Republic.

4 - Research Centre for Fodder Crops and Dairy Productions, ARC, Lodi, Italy

Annual legume plants, such as pea, go through a vegetative phase in which it the shoot apex produces nodes with lateral vegetative branches. After floral transition the shoot apex becomes a primary inflorescence that, while it is active, produces flowering nodes, with lateral secondary inflorescences with flowers. The production of pods and seeds depends on the number of flowering nodes formed by the plant.

We have identified two genes, which we named MORE FLOWERING NODES (MFN), encoding homologous transcription factors that control the period of time in which the primary inflorescence apex is active and, therefore, the number of flowering nodes. Homozygous plants with null mutations in MFNa or MFNb, grown under optimal greenhouse conditions, produce up to twice the number of pods and seeds than their corresponding wild-type parental line, without affecting flowering time.

To understand whether the MFN genes can be used to increase the production of seeds in pea, we are analysing in detail the phenotype of the mfn mutants. In addition, to analyse their performance in commercial varieties, we are currently introgressing the mfn mutant alleles into several pea elite cultivars. Finally, we are also looking for new mfn alleles, potentially more advantageous, in collections of wild pea accessions and cultivars to establish their possible correlation with the number of flowering nodes.

We expect that MFN genes can be used as a useful tool to increase yield in grain legumes.

Session 9, parallel: Legumes in food and feed and other alternative uses (cont.) - Room *Arrábida III*

Chaired by Ruta Galoburda (Latvia Univ. of Agriculture, Latvia) and Tom Warkentin (Univ. Saskatchewan, Canada)

14:30-14:40 Oral – S9

A meta-analysis to assess the effect of fine grinding, dehulling and pelleting on the nutritive value of peas and faba beans for poultry

Tormo E.[1], Heuzé V.[2], Peyronnet C.[1], Tran G.[2], Chapoutot P.[2,3]
1 - Terres Univia, 11 rue de Monceau, CS 60003, 75378 Paris Cedex 08, France
2 - AFZ, 16 rue Claude Bernard, 75231 Paris Cedex 05, France
3 - UMR MoSAR, INRA, AgroParisTech, Université Paris-Saclay 75005 Paris France

The nutritive value of pea (P) and faba bean (FB) can be improved by mechanical and heat treatments, such as grinding, dehulling and pelleting. Data were collected from 18 publications and processed by meta-analysis to assess these effects and obtain within-sample or within-trial prediction models. Fine grinding improved starch digestibility (STd) and metabolisable energy content (AMEn) of P and FB in non-pelleted diets, with a greater effect for broilers than for roosters: a reduction of the median diameter of 100 mm lead to an increase of 4.2 *vs* 1.4 points % of STd and of 169 *vs* 39 kcal/kg DM of AMEn for broilers *vs* roosters. Dehulling improved AMEn for colored and white-flowered FB, but only for tannin-rich P. Protein digestibility (CPd) was improved for tannin-rich varieties of both grains. Crude protein content (CP, %DM) is the best criteria to predict AMEn and CPd: AMEn = 106.4 CP - 484 (FB data, N=20; Nsample=10; R^2=0.97; RSD=82) for FB; CPd = 3.06 CP - 19.2 (N=16; Nsample=8; R^2=0.95; RSD=2.0) for both tannin-rich grains. Pelleting improved feed AMEn and Std, however the gain obtained by pelleting (DAMEn, DSTd, % initial values) was negatively correlated with initial grain values (AMEn0, Std0): DAMEn = 117 - 0.037 AMEn0 (N=30; Ntrial=13; R^2=0.95; RSD=2.1) for P and DAMEn = 50 - 0.015 AMEn0 (N=12; Ntrial=2; R^2=0.69; RSD=3.1) for FB. Due to lack of data on STd, only one model was obtained for both grains: DStd = 83.6 - 0.894 Std0 (N=23; Ntrial=10; R^2=0.97; RSD=1.5).

14:40-14:50 ORAL – S9

Protein quality of different Portuguese varieties of common bean (*Phaseolus vulgaris* L.): the missing data for breeding

Mecha E.[1], **Figueira M.E.**[2], **Vaz Patto M.C.**[1], **Bronze M.R.**[1,2,3]

1 - Instituto de Tecnologia Química e Biológica, Universidade Nova de Lisboa, Av. Da República, EAN, 2780-157 Oeiras, Portugal.

2 - Faculdade de Farmácia, Universidade de Lisboa, Av. das Forças Armadas, 1649-019 Lisboa, Portugal.

3 - Instituto de Biologia Experimental e Tecnológica, Apartado 12, 2781-901 Oeiras, Portugal.

emecha@itqb.un.pt

Common bean (*Phaseolus vulgaris* L.) is consumed worldwide as a rich source of inexpensive vegetable protein, particularly relevant for preventing protein deficiency status in developing countries (where animal protein is not always available).

Characterized by their high content in aminoacids such as lysine and low content in sulphur containing aminoacids, common beans complemented by cereals provide all the essential aminoacids and can be used as an alternative to animal protein in human diet.

Genetics and environment have been pointed as determinant factors in protein quality of common beans, affecting aminoacid composition. Despite the interest of breeders in improving protein quality of common beans, the diverse Portuguese traditional varieties remain understudied. Characterization of such varieties will contribute to the development of interesting germplasm and tools for future breeding approaches. In order to analyse protein quality of Portuguese germplasm, 108 different varieties were multiplied in a randomized controlled field trial and aminoacids' content determined in triplicate, after chemical hydrolysis, using High Performance Liquid Chromatography (HPLC) coupled to Fluorescence (FL) detection. To estimate protein digestibility, a fast screening method based on enzymatic hydrolysis and pH variation was applied. Final data, treated by multivariate analysis, allowed systematization of data and bridge the gap of knowledge in protein quality of common beans.

14:50-15:00 Oral – S9

Economic factors of using the legumes in broiler chickens feeding

<u>Proskina L.,</u> Sallija C., Konosonoka H.I
Latvia University of Agriculture

The productivity, meat quality and production cost of broiler chickens are directly associated with crude protein in a diet fed to the broiler chickens as well as its content, biological value and price. Soybean protein, which is a relatively expensive imported feedstuff, makes up, on average, 25% of any poultry diet. In the EU Member States, feed protein imports comprise 70% of the total feed imports, which contributes to production cost increases. An analysis of domestic protein-rich feedstuffs shows that faba beans and peas contain, respectively, 200-230 g kg-1 and 260-380 g kg-1 crude protein, which allows replacing imported protein rich feed with domestically produced protein-rich feedstuffs, thereby reducing feed production cost and the proportion of imported feed in livestock diets. The research aim is to identify economic gains from feeding domestically produced faba beans and peas to broiler chickens. The research found that replacing imported soybeans with faba beans and peas in broiler chicken diets reduced feed costs by 0.06-0.16 EUR kg-1, increased the production efficiency factor (PEF) by 9.85-54.94 units as well as decreased the feed conversion ratio or the amount of feed consumed per kg live weight gain by 0.61-6.06% for the experimental groups, compared with the control group.

15:00-15:10 Oral - S9

Tocopherols and carotenoids diversity in a chickpea germplasm collection exploited in chickpea breeding in Europe

Serrano C.[1], Carbas B.[1], Vaz Patto M.C.[2], Brites C.[1]

1 - INIAV, Instituto Nacional de Investigação Agrária e Veterinária, 2784-505 Oeiras, Portugal

2 - ITQB NOVA, Instituto de Tecnologia Química e Biológica, 2780-157 Oeiras, Portugal

Chickpea (Cicer arietinum L.) is considered the 5th valuable legume in terms of worldwide economic importance and a cheap source of protein, which can be largely explored by the processing industry for enhancing food nutritional value.

This grain legume is also a good source of important vitamins such as the vitamin A precursor, β-carotene, and Vitamin E like tocopherols (α-T, β-T, γ-T, δ-T) and their tocotrienol counterparts (α-T3, β-T3, γ-T3, δ-T3).

The objective of this research was to examine the variation of bioactive compounds like tocopherols and carotenoids in 86 chickpea accessions representing the chickpea germplasm diversity in use by the European breeders. These analyses were performed under the FP7-EU LEGATO project.

The tocopherols and carotenoids in chickpea flours were quantified by normal phase high performance liquid chromatography. The tocopherols were expressed in the fat fraction and mean concentration for γ-tocopherol was 626.59 μg g-^{1}, followed by α-tocopherol 139.11 μg g^{-1} and δ-tocopherol 31.96 μg g^{-1}. The highest concentration of the different tocopherols determined in the fat fraction was found in LEGCA717 for γ-tocopherol (1078.76 μg g^{-1}) followed by LEGCA602 (216.75 μg g^{-1}) for α-tocopherol, while the highest contend of δ-tocopherol was found in LEGCA674 fat fraction (57.35 μg g^{-1}).

The carotenoids were expressed in whole flours and the mean for lutein was 5.43 μg g^{-1} folowed by zeaxantin 4.38 μg g^{-1}.

15:10-15:20 Oral – S9

Bowman-Birk inhibitors from legumes and mammalian gut health

Clemente A. [1], **Marín-Manzano M.C.** [1], **Arques M.C.** [1], **Olías R.** [1], **Rubio L.A.** [1], **Domoney C.** [2]

1 - Estación Experimental del Zaidín (CSIC), Granada, Spain.
alfonso.clemente@eez.csic.es
2 - John Innes Centre, Norwich, United Kingdom.

Bowman-Birk inhibitors (BBI) from legumes, such as soybean, pea, lentil and chickpea are resistant to mammalian gut proteolysis; their intrinsic ability to inhibit serine proteases is not significantly affected by the metabolic/enzymatic activity of gut microbiota. In vitro and in vivo studies have proven that soybean BBI and homologous proteins can exert a protective and/or suppressive effect against inflammation and cancer development within the gastrointestinal tract.

We have investigated the effects of a pea albumin extract enriched in BBI (PPIC) in a mouse colitis model. Macroscopic and histological studies, together with analysis of colonic expression of pro-inflammatory markers, showed that a severe inflammatory condition was ameliorated in extent and severity by PPIC.

We have described a significant concentration- and time-dependent decrease in the proliferation of human colorectal adenocarcinoma cells, following treatment with BBI variants from pea, lentil and soybean. A major pea protease inhibitor, TI1, expressed in *Pichia pastoris*, and related engineered mutants having modified inhibitory activity suggest that BBI proteins are taken up by colon cancer cells and exert their anti-proliferative properties via protease inhibition. Serine proteases that become active in early stage of colorectal carcinogenesis are likely to represent a primary target of BBI.

15:20-15:30 Oral – S9

Evaluation of a pea genome wide association study panel for folate profiles by UPLC-MS/MS

Jha A.B., Purves R.W., Gali K., Tar'an, B., Vandenberg A., Warkentin T.D.

Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada. ambuj.jha@usask.ca

Folates are important cofactors in several metabolic functions including the biosynthesis of nucleic acids. Pulse crop seeds are rich in folates. In our previous studies, six different folates were quantified by ultra-performance liquid chromatography coupled with mass spectrometry (UPLC-MS/MS) in seeds of four cultivars each of common bean, lentil, chickpea and pea developed at the Crop Development Centre (CDC), University of Saskatchewan. Compared to the other crops, pea had a relatively low concentration of total folates. A wider survey of pea accessions may reveal useful variation for improvement of folate concentration or profile. With this objective, research is in progress to evaluate a pea genome wide association study panel of 177 accessions developed at the CDC consisting of cultivars and land races from North America, western and eastern Europe, and Australia for folates using UPLC-MS/MS. These accessions were genotyped by genotyping by sequencing and an Illumina GoldenGate array, and have been grown at Saskatoon, North Dakota, Washington State, Czech Republic and Serbia. Using genome-wide association and candidate gene approaches, folate profiles will be associated with genotyping data to identify significant SNPs for marker-assisted selection.

Session 10, parallel: Frontiers in legume genetics and genomics (cont.) - Room *Arrábida IV*

Chaired by Bernadette Julier (INRA, France) and Kevin McPhee (North Dakota State Univ. USA)

14:30-14:40 Oral – S10

A protein quantity loci approach combined with a genome-wide association study revealed regulators of protein accumulation in legume seeds

Le Signor C.[1], Aime D.[1], Sanchez M.[1], Young N.D.[2], Prosperi J-M.[3], Thompson R.D.[1], Buitink J.[4], Burstin J.[1], Gallardo K.[1]

1 - Agroécologie, AgroSup Dijon, INRA, Univ. Bourgogne Franche-Comté, F-21000 Dijon, France

2 - Department of Plant Biology, University of Minnesota, St. Paul, Minnesota, 55108, USA

3 - UMR AGAP, Equipe Génomique évolutive et gestion des populations, Institut national de Recherche Agronomique (INRA), Montpellier, 34060, France

4 - IRHS, INRA, AGROCAMPUS-Ouest, Université d'Angers, SFR 4207 QUASAV, 7 49071 Beaucouzé cedex, France

The seeds of grain legumes provide proteins (20-40% protein content depending on species) for human nutrition and animal feed. The nutritional and technological quality of legume seeds is mainly determined by the composition and functional properties of the seed protein fractions. By accounting for up to 70% of total proteins in mature seeds, the globulins are major determinants of seed quality. In pea, which is one of the grain legumes most cultivated in Europe, the variability in the abundance of globulin polypeptides across lines is significant, which might enable a wide range of food application.

To provide knowledge about the molecular determinants underlying differences in seed protein composition, we have used the model legume species *M. truncatula* for which extensive genetics and genomics resources were available (Young and Bharti, 2012), along with comprehensive transcriptomics data related to seed development (Benedito et al., 2008; Thompson et al., 2009). A PQL approach identified the genomic regions controlling variations in seed protein composition, and a translational approach exploiting the resources developed for *M. truncatula* and pea provided a set of candidate genes underlying PQLs conserved between the two species. The candidate gene selection was then refined by genome-wide association studies (GWAS), which enabled the identification of nucleotide variations associated with variations in globulin synthesis and/or maturation.

14:40-14:50 Oral – S10

Using genomics to decipher the grain legumes quality riddle

Vaz Patto M.C.[1], Alves M.L.[1], Mecha L.[1], Bento da Silva A.[1], Leitão S.T.[1], Almeida N.[1], Gonçalves L.[1], Diego Rubiales[2], Bronze MR[1,3,4]

1 - Instituto de Tecnologia Química e Biológica, Universidade Nova de Lisboa, Oeiras, Portugal.

2 - Institute for Sustainable Agriculture, CSIC, Cordoba, Spain.

3 - iBET, Instituto de Biologia Experimental e Tecnológica, Portugal, 4iMED, Faculdade de Farmácia, Universidade de Lisboa, Portugal.

Today's consumers are increasingly concerned with food quality and sustainability. Grain legumes could play an important role in answering these concerns. Grass pea (*Lathyrus sativus*) is a promising source of calories for drought-prone areas while common bean (*Phaseolus vulgaris*) is the most important edible legume worldwide. Yet the nonalignment of breeding objectives and end-users preferences is hampering their use in Europe.

Breeding for improved end-user´s quality is a complex task due to trait interaction. Particular metabolites act as antinutrients as well as health-promoting agents, influencing both taste and consumers' acceptability.

Under the scope of LEGATO, BEGEQA and QUALATY projects, we studied the genetic basis of several of these dual action bioactive compounds (as phenolic compounds, phytic acid or -ODAP) as a primary step for devising innovative quality breeding approaches for common bean and grass pea.

To reach these goals, 100 grasspea and 150 common bean accessions were repeatedly field trialed. Seed metabolites contents were analyzed using different analytical approaches and DNA screened using NGS-based SNP genotyping. A genome-wide association study, joining bioactive compounds content phenotypes with genomic information, is ongoing using mixed linear models to account for population structure and familiar relatedness.

Functional markers will be identified conferring consumer-driven quality traits, to redirect breeding towards more attractive varieties.

14:50-15:00 Oral – S10

Strategies and advances to identify candidate genes controlling low vicine-convicine in faba bean (*Vicia faba* L.);

Gutiérrez N.[1,2], Bakro F.[2], Atienza S.[3], Avila C.M.[2], Torres A.M.[2]

1 - ZAYINTEC, edificio PITA - Universidad de Almería, 04120, Almería, Spain;

2 - IFAPA, Centro Alameda del Obispo, Área Mejora y Biotecnología, Apdo. 3092, 14080, Córdoba, Spain

3 - Instituto de Agricultura Sostenible-CSIC, Alameda del Obispo s/n, 14004, Córdoba, Spain

Vicine and convicine (v-c), limit the use of faba bean as food and feed. A single gene vc-, responsible for a 10-20 fold reduction in v-c, 10 cM apart from the white hilum has been described (Duc et al. 1989; 2004). Khazaei et al. (2015), reported a QTL for v-c content on chromosome I (Chr I) and although several closer markers were identified (Gutierrez et al. 2006) no candidate genes are so far available. The identification of suitable candidate genes is limited for the lack of knowledge of the pathway for the v-c biosynthesis and the large faba bean genome size (~13 Gbp). In an attempt to determine which enzymes or transcriptional regulators could be encoded by the vc-gene, we are applying a combination of genetic linkage and comparative genomic approaches. To facilitate high-throughput genome profiling DarTSeq (Kilian et al. 2012) has been applied in a RIL population from the cross Vf6 (high v-c) x vc- (low v-c) generating more than 10.000 markers. For the assignment of the linkage group to specific chromosomes, 58 EST anchor marker from the reference consensus map (Satovic et al. 2013) were assayed and 14 of them could be mapped. On the other hand, 37 SNPs, from the KASPar assay platform (Semagn et al. 2014) belonging to Chr I, were genotyped and 9 of them, resulted polymorphic. The moderate conservation of the faba bean Chr 1 with the Medicago Chr 2 confined the target region between Medtr2g005900 and Medtr2g026550. To fine mapping the v-c position, primers for 61 new candidates were designed using both the Medicago (29) and the faba bean (32) transcriptome sequences (Ocaña et al. 2015) and 12 genes could be mapped. The forthcoming linkage analysis may provide potential candidate genes for the target trait.

15:00-15:10 Oral – S10

The homologues of *Arabidopsis* FLOWERING LOCUS T and GIGANTEA genes are involved in the control of photoperiod response of flowering in common bean

González A.M.[1], Yuste-Lisbona F.J.[2], Fernández-Lozano A.[2], Bretones S.[2], Sussmilch F.C. 3, Weller J.[3], Lozano R.[2], Santalla M.[1]

1 - Grupo de Biología de Agrosistemas (www.bas-group.es). Misión Biológica de Galicia-CSIC. P.O. Box 28. 36080 Pontevedra, Spain

2 - Departamento de Biología y Geología (Genética), Centro de Investigación en Biotecnología Agroalimentaria (BITAL). Universidad de Almeria. 04120 Almeria, Spain

3 - School of Plant Science, University of Tasmania, Hobart, Tasmania 7001, Australia.

In the common bean short-day plant, seasonal flowering is a crucial aspect of maximizing reproductive fitness. Expansion to higher latitudes or changes in day length has been accompanied by earlier flowering under long-day and a reduction in photoperiod responsiveness that enables plants to anticipate approaching seasonal variation in the surrounding environment. In the model species Arabidopsis thaliana, flowering time is determined by day-length–dependent induction of the FLOWERING LOCUS T (FT) gene, which encodes a floral-inductive mobile signal, and GIGANTEA (GI) gene acting upstream of FT. The characterization of common bean homologues of Arabidopsis photoperiodic flowering pathway genes is reported with the end goal of accelerating common bean breeding by understanding the genetic basis of adaptation. The expression of common bean GI and FT homologues under short- and long-day conditions was examined using qRT–PCR in common bean lines, which exhibit different day length responses. The PvFTa3 and PvFTb1 homologues showed similar expression patterns independently of the analyzed genotype, whereas significant differences were found in the GI homologue PvGI1 gene. It is proposed that these differences could contribute to the different day length responses. Together, our results indicate that key genes controlling photoperiodic flowering in Arabidopsis are conserved in common bean, and a role for these genes in the photoperiodic control of bulb initiation is predicted.

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15:10-15:20 Oral – S10

Wild pea *Pisum fulvum* and *Pisum elatius* chromosome segment substitution lines in cultivated *P. sativum* genetic background

Lenka S.[1], Gregoire A.[2], Smykal P.[1]

1 – Dep.of Botany, Palack University in Olomouc, lechtitel 27, 783 71 Olomouc, Czech Republic.

2 - INRA, Dijon, France

Plant evolution under domestication has altered numerous traits, introducing domestication bottleneck resulting in high degree of relatedness, leading to narrower genetic base of cultivated germplasm, prone to pests and diseases. The study of genetic diversity showed that although wide diversity is captured among cultivated pea, wild material provides yet broader diversity (Smýkal et al. 2013, 2015). The chromosome segment substitution lines (CSSL) containing genomic segments of wild pea (*Pisum fulvum* WL2140 or *Pisum elatius* L100) in the cultivated pea (*P. sativum* subsp. *sativum* cv. Terno or cv. Cameor) genetic background were developed. These lines have been molecularly analyzed using microsatellite and gene-specific markers at 2 to 82 cM spacing at early generations (BC2-3F2-4). There were 5 to 14 segments per line, with mean of 9.6. Higher density genotyping of 50 selected BC3F6 *P. fulvum*/Terno CSSL lines using pea 13.2k Pea SNP (Tayeh et al. 2015) and further 100 lines using DARTseq approach is in progress. Establishment of such permanent introgression library will allow phenotypic characterization of unlimited number of target traits, which, coupled together with higher density markers, will provide means for QTL and gene identification and subsequent incorporation in desired genotypes. Field testing of agronomical performance of 50 lines of *P. fulvum*/Terno CSSL lines is under way.

This work received funding from the European Community's Seventh Framework Programme (FP).

15:20-15:30 Oral – S10

Delimiting the physical positions of anthracnose resistance clusters Co-2 and Co-3 using GbS in a set of common bean near-isogenic lines

Campa A., Murube E. and Ferreira J.J.
Plant Genetic Group, SERIDA, Asturias, Spain

Genotyping by sequencing (GbS) analysis was used in a set of bean near-isogenic lines (NILs) and the corresponding parents, in order to delimit the introgressed genomic regions and approach to genes conferring anthracnose resistance. GbS analysis provided 50504 SNPs with known physical position, distributed along the 11 common bean chromosomes. Introgressed regions tagging SNPs were detected at the beginning of chromosome 4 in six NILs derived from resistance sources A493 and A321, both carrying an anthracnose resistance locus at the Co-3 cluster. Among the six NILs there is a common introgressed region of 1.32 Mb between physical positions 0.4-1.30 Mb. In silico exploration into this region in the reference genome showed 31 genes associated to disease responses (R genes) that are candidate genes to be controlling the resistance. Two neighboring regions including 2 or 4 blocks were delimited in chromosome 11 when common regions were investigated in ten NILs derived from resistance sources A252 and SanilacBc6Are, both with an anthracnose resistance loci at the Co-2 cluster. In this case, the regions introgressed from both sources are quite different, showing only a common region of 0.09 Mb, between 46.9-47.1 Mb, that included 16 annotated R genes. Large scale genotyping supplied by GbS analysis has enabled to discard more than 99.8% of the genes annotated in the bean reference genome, showing that can be rapid way to approach to genes controlling important traits using NILs.

Session 11, parallel: Frontiers in plant and crop physiology - Room *Arrábida III*

Chaired by Christophe Salon (INRA, France) and Luis Aguirrezabal (CONICET, Argentina)

16:30-17:00 **Key lecture - Phil Mullineaux**: The identification of novel genes controlling plant - environment interactions

17:00-17:10 Oral – S11

Drought-induced transcriptome changes in soybean (*Glycine Max*) crown nodules

Vorster J., Cilliers M., van Wyk S., van Heerden R., Kunert K.
University of Pretoria, Department of Plant and Soil Sciences, Forestry and Agricultural Biotechnology Institute

Biological nitrogen fixation is an important attribute of legumes. However, root nodule formation and their life span are negatively affected by drought stress. There is an increasing need for selection of improved drought tolerant soybean cultivars to address future food security. In this study we investigated the response of soybean root nodules exposed to various levels of water deficit conditions on a physiological and transcriptomic basis. We found just over 100 genes in the nodule transcriptome that were up regulated over all drought treatments. The most highly up-regulated genes as a result of drought stress were a D11-LEA group 2 protein (Glyma.05G112000) and an inositol 3-alpha-galatosyltransferanse (Glyma.19G227800). We are particularly interested in the role of cysteine proteases drought induced senescence. We identified eight C1 and three C13 cysteine proteases induced by drought stress. One protease (Glyma.05G055700), a beta-leguamin C13 cysteine protease was highly expressed under drought stress conditions compared to natural senescence and could provide a possible marker for drought induced nodule senescence. Overall the results identified genes that are responsible for causing premature senescence of soybean root nodules as a consequence of drought.

17:10-17:20 Oral – S11

In vivo monitoring of the development of legume root system, nodule and pod development

Metzner R., Chlubek A., Dautzenberg M., Breuer E., Windt C., Pflugfelder D., Jahnke S.

Institute for Bio- and Geosciences (IBG) 2: Plant Sciences, Forschungszentrum Jülich GmbH, 52425 Jülich, Germany.

Quantitative non-invasive measurement of structural and functional development of plant organs allows for deep phenotyping and dynamic investigation of plant performance under stress. While this can be done straightforward for leaves or stems other plant parts, such as seeds enclosed in pods or roots and nodules hidden in soil, are more difficult to investigate. Their development, however, is critical for yield and performance under stress and direct observations in conjunction with genetic and metabolomics approaches may therefore hint on the underlying mechanisms. Here, we apply a set of three non-invasive techniques for studying such developmental processes. 1) Low-field nuclear magnetic resonance relaxometry with portable devices (pNMR) is used to monitor dry matter and water content in pods over periods of several weeks. 2) Magnetic Resonance Imaging (MRI) is taken to study the structural development of roots and nodules in soil filled pots over several weeks. 3) Positron Emission Tomography (PET) with the short-lived radiotracer 11C is used to analyze the partitioning of photoassimilates and its dynamics among roots and nodules. The application of all three techniques to pea and bean plants grown in soil will be presented. We also discuss their potential to provide a direct view on the effects of genotype or rhizobial strain on plant performance under stress and on biological nitrogen fixation.

17:20-17:30 Oral – S11

A common shoot developmental framework for perennial legume species with contrasting morphogenesis

Faverjon L. , Louarn G.
INRA, URP3F, Lusignan, France

A wide range of legumes species is used for forage production in sown grasslands. Yet, despite their close phylogenetic relationship, they display a wide range of growth habit, morphologies and competitive abilities. Little is known about the elementary traits, which make temperate forage legumes differ so substantially in their growth habit. In the present study, we compared the patterns of shoot organogenesis and of organ growth of six contrasting forage species (namely alfalfa, birdsfoot trefoil, sainfoin, Kura clover, red clover and white clover) during their vegetative phase. An experiment was carried out over two years in a greenhouse under non-limiting water and soil nutrients. Phytomer initiation and shoot branching appeared driven by temperature and highly deterministic in all the species in the absence of competition for light. The temporal sequence of organ growth differed between species. However, organ growth was highly coordinated within a phytomer in all the species, and was independent of the position and axis order when expressed in phyllochronic time. By contrast, organ dimensions at maturity were dependent on phytomer position, and followed a regular function of the rank for all the organs. Overall, a very similar developmental pattern was followed by all the species, but they differed greatly in the absolute values taken by their developmental traits.

P85 – S11

Conglutin proteins as biomarkers for the study of the biochemical and physiological changes occurring during lupin seed germination and seedling growth

Robles-Bolivar P.[1], Alche J.D.[1], Jimenez-Lopez J.C.[1,2]

1 - National Council for Scientific Research (CSIC)

2 - Estacion Experimental del Zaidin; Department of Biochemistry, Cell and Molecular Biology of Plants josecarlos.jimenez@eez.csic.es

Narrow-leafed lupin, NLL (*Lupinus angustifolius* L.) is mainly characterized by its adaptation to drought stress, and the absence of the vernalization required for early flowering and maturity. This legume crop is highly beneficial for agriculture i) acting as a disease break in cropping rotations, and as control of grass weeds; ii) fixing nitrogen, and enriching the soil for subsequent crops.

Despite the abundant knowledge about its agricultural traits, scarce information is known about the NLL seed germination process.

In the present work, we have studied the different steps of NLL seed germination by means of microcopy and biochemical methodological approaches. A large amount of storage proteins is accumulated in protein bodies (PBs), and mobilized during germination. We have analyzed the roles of particular conglutins families of proteins (b and g) in the endosperm and cotyledon tissues, in order to better understand the key molecular and physiological processes in NLL germination, with a focus on the regulatory signalling and metabolic pathways after seed imbibition and until early stages of seedling growth.

The knowledge generated in this study provides evidences for the structure-functional changes, and physiological tightly regulated events occurring during germination in the NLL seed tissues.

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P86 – S11

Effect of methanol on some morpho-physiological traits and yield of chickpea (*Lens culinaris* L.)

Paknejad F.

Amir moshiri Department of Agronomty, Karaj Branch, Islamic Azad University, Karaj, Iran

Lentil, having a high protein (22 to 23 percent) in its seeds is considered as important source of vegetable protein. Methanol is a substance that increases the CO2 fixation in plants tricarbonic. Methanol is relatively smaller compared with the CO2 molecule that easily by plants, are absorbed and used. In order to investigate the effects of methanol on qualitative and quantitative traits of lentils in dry conditions was conducted experiment in Khodabande 94-1393. This experiment was conducted in a randomized complete block design with 3 replications. The treatments included control, 5, 10, 15, 20 and 25 percent by volume of methanol. The results showed that methanol significant effect on the length of branches, leaf dry weight per plant, number of leaves, number of pods per plant, number of seeds per pod, hundred seed weight, biological yield, grain yield, relative water content and carotenoid content at a level one per cent on plant height, Number of branches, harvest index, chlorophyll content and leaf area index at the level of five percent. The highest hundred-grain weight was related to treatment, 25 percent by volume with 6.33 grams and the lowest 5 percent by volume to treatment with 3.96 gr. 25 percent by volume methanol treatment.

P87 – S11

The regulation of carbon assimilation and nitrogen fixation during nodule development

Khahlu T., Vorster J., Taylor N.

University of Pretoria, Department of Plant and Soil Sciences, Forestry and Agricultural Biotechnology Institute

Soybean nodules play a pivotal role in fixing atmospheric nitrogen and using that for their growth and development. Nodules have a short lifespan, which limits the ability to fix nitrogen and affects overall growth. There is a need to study nodule development and senescence to improve soybean plant physiology. Of interest to this study, is how carbon assimilation and nitrogen fixation are affected during nodule senescence. This is important to understand because the knowledge of how these two processes affect each other is still limited. Two soybean cultivars, Williams 82 and the commercial cultivar PHB 94Y80R (Pioneer) were used for the trial conducted at the Forestry and Agricultural Biotechnology Institute (FABI). Plants were sampled at time points: four, six, eight and ten weeks. Photosynthesis measurements including A/Ci and light response curves were taken to quantify carbon assimilation. The ureide assay was used to determine nitrogen fixing ability of the nodules at said time points. To identify gene expression profiles for the sucrose synthase enzyme, RNAseq data from van Wyk (2015) was used. Nine genes were identified and each had at least two gene copies. The overall photosynthesis decreased from four to ten weeks, the same trend was mirrored by the ureide assay results. Four genes namely: Glyma13g17421, Glyma17g05067, Glyma09g08550 and Glyma19g40041 with the highest transcript numbers were chosen for further expression studies with studies with RT-qPCR.

P88 –S11

Effect of soil water deficit on amino acid exudation in *Pisum sativum* roots

Bobille H., Cukier C., Robins R.J., Limami A. M., Fustec J.
UR LEVA-ESA, UMR SESAN-IRHS, Univ. Angers, France

As part of rhizodeposition, root exudation may aid plants cope with abiotic stress by helping establish positive plant-soil interactions. But, relationships between plant physiology and exudated compounds are poorly documented. We hypothesize that amino acid (AA) exudation by roots may be quantitatively and qualitatively altered by water deficit (WD), as a physiological response of plants to stress. *Pisum sativum* plants grown in unsterilized soil were stem-labeled (cotton-wick) with 15N-urea for 72 h, then subjected or not to water deficit (WD). The assimilation of 15N into AAs and their fingerprint were quantified by GC-MS in both rhizosphere and roots. There was no significant effect of WD on either dry matter or N content in the plants. But, after 24 h of WD the concentration of all AAs increased in the roots, accompanied by a dramatic rise in isotopic enrichment. Furthermore, the release of proline, alanine, glutamate and valine and the translocation of 15N proline, 15N-serine, 15N-threonine, 15N-glutamate and 15N-asparagine into the rhizosphere were increased significantly in WD. These results support the idea that, under WD, recently assimilated N is rapidly translocated to the roots, and part of this is exudated. Serine and proline are well known to be involved in the plant response to stress, the latter as an osmoprotectant of macromolecules. It can be suggested that the early exudation of proline would increase the water holding capacity to facilitate water uptake.

P90 – S11

Modelling the effect of assimilate availability on seed weight and composition in oilseeds: the case of soybean

Bianculli, M. L., Echarte, M.M., Aguirrezábal, L.A.N.

Laboratorio de Fisiología Vegetal, Unidad Integrada Balcarce (INTA-FCA, UNMdP), Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET). laguirre@mdp.edu.ar

Pods and seeds of species like soybean are green during their development so that local effects of solar radiation on grain weight and composition could be expected. On the contrary, sunflower seeds are non-green and the effects of solar radiation on weight and composition were exclusively mediated by assimilates produced by leaves. The aims of this work were to build a general model to explain the effects of solar radiation on weight and composition of grains of oilseeds which differ in the photosynthetic capacity of their reproductive structures (e.g. soybean and rape vs. sunflower) and in their canopy architecture (e.g. soybean vs. rape and sunflower) and to apply it to account for experimental data. The model was built based on results of field experiments where the amount of assimilate supplied by vegetative structures and/or the amount of solar radiation reaching the pods were modified. Weight, oil content and fatty acid composition of soybean seeds depend on assimilate availability to their filling. Local effects of solar radiation reaching the pods also depend on the amount of assimilates coming from vegetative organs. On the other hand, only the incident solar radiation on pods accounts for variation in seed weight and composition in rape while the role of leaves could be disregarded. The model was appropriated to describe soybean response to solar radiation and it is potentially useful to explain this response in other oilseeds.

P91 – S11

The expression profile of GA signaling repressor (LlDELLA) in generative organs of *Lupinus luteus*

Marciniak K.[1,2], **Kućko A.**[1], **Wilmowicz E.**[1,2], **Tretyn A.**[1,2], **Kopcewicz J.**[1]
1 - Chair of Plant Physiology and Biotechnology,
2 - Centre for Modern Interdisciplinary Technologies, Nicolaus Copernicus University in Torun, Poland

Gibberellins (GAs) control the proper development of generative organs in many plant species, including *Lupinus luteus*, the species cultivated in Poland, Australia and many Mediterranean countries. The key and negative regulators of GA signaling are DELLA proteins. Complex of GA with receptor (GID1) binds to the DELLAs and leads to their degradation via the UPS.

In this paper, the transcriptional activity of LlDELLA at different development stages of inflorescence, flowers and pods in *L. luteus* v. Taper was determined. During the development of the whole inflorescence a slight decrease of mRNA level was observed. In turn, there were no significant differences in the content of the LlDELLA transcripts in the six individual flower whorls of fully mature inflorescence. Following senescence and wilting of flowers (with small initially formed pods) and pods development, rapid decrease in the transcriptional activity of investigated gene was recorded. In plants with fully mature pods in each whorl, we observed approximately 3-fold lower level of gene expression compared to plants with fully developed flowers.

The profile of LlDELLA gene expression may be correlated with GA involvement in appropriate generative organs development. In the near future our results will determine the precise mechanism of the flower and pod development of *L. luteus*.

This research was funded by the program supported by Resolution of the Council of Ministers of Poland (RM-111-222-15)"

Session 12, parallel: Integrated pest and disease management - Room *Arrábida IV*

Chaired by Jenny Davidson (PIRSA-SARDI, Australia) and Christophe Le May (INRA, France)

16:30-17:00 **Key lecture: Seid Kemal**: Integrated disease and insect pest management pest and in cool-season food legumes

17:00-17:10 Oral – S12

PISOM (Ideotypes, Systems, Surveys of Pea and faba bean Main diseases)

Baranger A.[1,3], **Boutet G.**[1,3], **Brier C.**[2,3], **Le May C.**[1,3], **Pilet-Nayel M-L.**[1,3], **Moussart A.**[2,3]
1 - UMR IGEPP, INRA, Agrocampus Ouest, Université Rennes1, 35650 Le Rheu, France
2 - Terres Inovia, Avenue Lucien Bretignières, 78850 Thiverval Grignon, France
3 - UMT PISOM, Terres Inovia-INRA, 35650 Le Rheu, France

The French Technological Mixed Unit PISOM is a partnership tool between INRA, the National Institute for Agronomic Research and Terres Inovia, the technical institute for grain legumes. It aims at developing knowledge and tools to describe, predict and manage main pea and faba bean diseases.

Among considered issues is the impact of climate and systems changes on diseases incidence and severity at the regional or national scales. Surveys emphasize the effects of environmental conditions and cultural practices on the emergence and severity of diseases. Another purpose is the design of ideotypes to control diseases using individual plant or canopy traits, such as partial resistance, tolerance, architecture and phenology characters. Elucidation of the genetic control of these traits, and identification of linked molecular markers to trace them in breeding, open the way to more efficient and durable epidemics control. A third objective is to anticipate new cultural systems for sustainable disease management. This includes new cultural methods and rotations, and combining partially efficient methods.

PISOM invests in increasing the speed and quality of the research results transfer to stakeholders by supplying breeding lines, molecular markers, methodologies and cultural recommendations. Prospects include a better vision of emerging diseases and diseases risk assessment with a range of strategies based on species and plant traits, and their deployment in agricultural systems.

17:10-17:20 Oral – S12

The Australian *Ascochyta rabiei* population structure and evidence of a highly adapted and evolving haplotype

Mehmood Y.[1], Sambasivam P.[2], Ford R.[1,2]

1 - School of Natural Sciences, Griffith University, Queensland, Australia 4111.

2 - Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Victoria, Australia 3010

The Australian *Ascochyta rabiei* population has previously been found to be genetically narrow with only one mating type gene detected, potentially precluding evolution through recombination. In an effort to better understand the risk to currently used resistance sources through selective adaptation, the population was examined in greater detail. For this, a total of 416 isolates were hierarchically collected from within the major Australian chickpea growing regions and from commonly grown cultivars in 2013 and 2014. Genotyping via SSR loci indicated an overall low diversity (0.074), as previously observed. Although a large number of haplotypes were detected (78), more than 64% of the population belonged to a single dominant haplotype (ARH01). Pathogenic screening on a differential host set, ICC3996 (R), cv. Genesis090 (R), cv. PBAHatTrick (MR) and cv. Kyabra (S), revealed distinct isolate pathotype groups, with 17% of all isolates assessed identified as highly aggressive. Of these, over 63.33% belonged to the ARH01 haplotype. A similar pattern was observed at the host level, with 46% of all isolates collected from Genesis090 (R) identified as highly aggressive, of which 50% belonged to the ARH01 haplotype. This is very high compared to the percentage of aggressive isolates detected within other haplotype groups i.e. ARH125 (6% aggressive isolates) and ARH144 (3.33% aggressive isolates). This indicates the fitness of ARH01 to survive and replicate on our best resistance sources.

17:20-17:30 Oral – S12

Chickpea damping-off caused by metalaxyl resistant Pythium in the US Pacific Northwest

Chen W.[1], McGee R.[1], Paulitz T.[1], Porter L.[1], Vandemark G.[1], Guy S.[2], Schroeder K.[3]

1 - USDA-ARS, Pullman and Prosser, WA;
2 - Washington State University, Pullman, WA;
3 - University of Idaho, Moscow, ID, USA

Chickpea seed rot and damping-off is an important disease worldwide. Metalaxyl is an active ingredient in fungicides that have been used for decades to control plant diseases caused by Oomycetes, such as *Pythium* and *Phytophthora* diseases, and used in seed treatments to protect seeds from Pythium damping off. In 2014 and again in 2015 and 2016, we have observed that metalaxyl-treated chickpea seeds failed to germinate in a dozen or so fields in the US Pacific Northwest, requiring reseeding in several fields. The un-germinated seeds become soft, slimy, and coated by soil particles, and are often difficult to find because they just look like the soil. Pythium isolates obtained from rotten seeds are highly resistant to metalaxyl. Additionally, soils sampled from the areas where there was poor germination consistently showed Pythium populations with high levels of resistance to metalaxyl. Under controlled conditions, metalaxyl treatments failed to protect chickpea seeds from damping-off inoculated with metalaxyl-resistant Pythium isolates. All evidence shows that the poor germination of Kabuli chickpea is due to the Pythium populations resistant to metalaxyl. We are working to determine field prevalence of metalaxyl-resistance in chickpea production areas, identify alternative fungicides that can control or manage metalaxyl-resistant Pythium, and investigate mechanisms of metalaxyl resistance in Pythium.

P92 – S12

The incidence of diseases and pests of faba bean on different varieties according to different locations

Olle M.
Estonian Crop Research Institute, Estonia

The incidence and diversity of diseases and pests are changing in decades. Climate change results are consequent adverse effects, like increased frequencies of abiotic stresses (heat, drought) and increase of biotic stresses (pests and diseases). Therefore the aim of the study was to evaluate the diseases and pests incidence on different faba bean varieties in three different locations: Pūre (Pūre Horticultural Research Centre; Latvia), Priekuļi (Institute of Agricultural Resources and Economics; Latvia) and Jogeva (Estonian Crop Research Institute, Estonia). The incidence of Aphids (*Aphis spp*.), Seed weevils (*Bruchus spp*.), Chocolate spot (*Botrytis fabae*), Ascochyta blight (*Ascochyta fabae*), Rust (*Uromyces fabae*), Stem rot (*Sclerotinia spp.*) and Faba Bean Yellow Mosaic Virus were scored. Varieties of faba bean used in the trial: Gloria, Julia, Jogeva, Lielplatones and Bauska. The results showed that overall from varieties the most susceptible for diseases in different locations was Jogeva, followed by Gloria. The less susceptible varieties were Lielplatones and Bauska. However the distribution of diseases and pests differed between locations and in different years. In 2014 the disease damages were increased compared to 2015, probably because of different weather conditions. In Priekuļi only Ascochyta blight was present in notable percentage, while in Pūre and Jogeva mostly chocolate spot and seed weevil damaged plants.

P93 – S12

The relationship between sowing date of *Vicia faba* (field beans) and the level of damage caused by *Bruchus rufimanus* (bean seed beetle) in the UK

Ward R.L.[1] **and Brown P.**[2]

1 - Processors and Growers Research Organisation, The Great North Road, Thornhaugh, Peterborough, PE8 6HJ.
2 - Frontier Agriculture Ltd., Sandy Lane, Diss, Norfolk, IP22 4HY.

The bean seed beetle, *Bruchus rufimanus* (Boheman), is an economically important pest of *Vicia faba* bean crops throughout Europe and causes severe quality losses due to seed and produce damage. The beetle has one generation per year and insects emerge from over-wintering in the UK in April and May to feed in flowering bean crops. The females lay eggs on the outside of developing pods, predominantly at the base of the plant where pod-set starts. Hatching larvae bore through the pod walls and develop within the seed. When fully grown, larvae pupate and young adult beetles emerge, leaving a round hole in the bean. Following evaluation of data collected from UK field bean crop harvest samples between 2006 and 2014, and crop development evaluations at a number of field sites, a pattern emerged that indicated a relationship between the date of first pod set, and the amount of damage caused by the pest. A series of trials sown at three different timings was established in 2015 to further investigate this relationship. The results showed that damage reduction to harvested produce was up to 50% when drilling was delayed. This has provided a valuable addition to UK recommendations for control of the pest and may allow growers to reduce insecticide applications in field beans during the critical flowering and pod set period.

P94 – S12

Employment of varietal mixtures to reduce the incidence of diseases on grain legumes

Villegas-Fernández Á.M., Moral J., Rubiales D
Institute for Sustainable Agriculture, CSIC, Apdo. 4084, 14080, Córdoba, Spain

The employment of resistant varieties is one of the best options to control diseases in legumes, both in ecological and economical terms. Nevertheless, one of the problems associated to this practice is the appearance of pathogen strains that are able to overcome the plant resistance. This calls for an efficient and wise management of resistance genes in which diversification is always key.

We have focused on the use of varietal mixtures to reduce the impact of diseases in two important legume crops: pea and faba bean. Two field experiments were carried out for each crop, the assessed diseases being powdery mildew in pea and rust in faba bean. In both cases, a resistant monogenic variety was mixed with a susceptible one. Five treatments were tested, corresponding to growing proportions of the resistant variety: 0%, 25%, 50%, 75% and 100% (rows of the resistant variety were alternated with varying numbers of rows of the susceptible one depending on the desired proportion). Disease severity was recorded on the susceptible variety in each trial.

Results in both experiments show a significant negative correlation between disease severity on the susceptible variety and the proportion of the resistant one. Severity reduction is important when the resistant variety is grown every other row (50% proportion), reaching highest levels with 75% proportion. The dilution effect of inoculum due to the distance between susceptible plants is probably behind these results.

P95 – S12

Diversity of ascochyta blight disease complex of field pea and soybean in serbia

Petrović K. [1], **Riccioni L.** [2], **Valente M. T.** [2], **Đorđević V.** [1], **Živanov D.** [1], **Vidić M.** [1], **Miladinović J.** [1]

1 - Institute of Field and Vegetable Crops, 21000 Novi Sad, Serbia.
2 - Consiglio per la ricerca in agricoltura e l’analisi dell’economica agraria-Centro di ricerca per la patologia vegetale, I-00156 Rome, Italy

Soybean and field pea are the most important legumes worldwide. However, diseases are a strong limitation to obtaining stable yields, among which Ascochyta blight complex is one of the most significant and widespread pathogens. Three causal agents of pea diseases have been described: *Peyronellaea pinodes*, the most common and most damaging causal agent of blight; *P. pinodella*, the causal agent of foot rot; and *Ascochyta pisi*, causal agent of blight and pod spot. Only *A. sojaecola* is reported as causal agent of leaf spot on soybean. Taxonomy of *Peyronellaea* and *Ascochyta* species was the subject of many studies for a long time. Initial identification was based on morphological characteristics, which is difficult because morphological features often vary and "overlap", making it impossible to establish the appropriate taxonomic rank. Taxonomy of these species is currently redefined mostly by using DNA sequences. Based on the morphological characteristics, only *A. pisi* on pea and *A. sojaecola* on soybean were determined in Serbia, but the identification was not confirmed at the molecular level. The objectives of this study were to identify *Peyronellaea* and *Ascochyta* species that are found on field pea and soybean in Serbia, and provide a clear morphological profile for each species followed by molecular identification and pathogenicity test. The first results indicated the presence of several new species associated with Ascochyta blight complex on pea and soybean in Serbia.

P96 – S12

Plant disease complex: did antagonism and synergism between pathogens be the result of differentiated life traits?

Le May C.

Agrocampus, INRA, Domaine de la Motte BP 35327, Le Rheu, 35653, France

In a disease complex, different pathogen species commonly develop simultaneously in a field and can then infect the same host individuals. Co-occurring pathogens may affect each other, through antagonism and/or synergism. An important question is the ecological and pathological consequences of co-occurrence of pathogenic species within a disease complex. By using two pathogens (*Didymella pinodes* (Dp) and *Phoma medicaginis* var. pinodella (Pm)) of the Ascochyta blight complex, this study aimed at describing how co-occurrence affects the development of pathogens and disease severity. One of the main principles of ecology is competitive exclusion, the hypothesis given for explain this simultaneous presence is the niche differentiation by separation in time. In order to prove this hypothesis, the presence of a trade-off between the parasitic fitness and saprophytic fitness was also evaluated. Results indicated a low saprophytic fitness that would be offset by a higher parasitic fitness (aggressiveness, reproduction) for Dp while Pm seemed to invest more in the saprophytic fitness (survival, chlamydospores). Moreover, the presence of the two pathogens on the same host plant organ limited the disease development and their reproduction. Damages caused by the two pathogens, however, increased when plants that had been previously inoculated were inoculated with the other species. The development of one pathogen species can be affected by a subsequent pathogen inoculation.

P97 – S12

Effect of pea sowing date on aphanomyces root rot development and yield losses

Moussart A.[1,2,3]**, Even M.N.**[1,2,3] **and Baranger A.**[2,3]

1 - Terres Inovia, Avenue Lucien Bretignières, 78850 Thiverval Grignon, France
2 - UMR IGEPP, INRA, Agrocampus Ouest, Université Rennes1, 35650 Le Rheu, France
3 - UMT PISOM, Terres Inovia-INRA, 35650 Le Rheu, France

Successive sowings of a susceptible pea cultivar were realized from October to April, in a highly infested field and were subjected to aphanomyces root rot severity assessments until maturity. First symptoms on roots appeared at later plant stages in autumn-sown than in spring-sown plants due to more conducive climatic conditions to the disease from early spring.

The effect of inoculation of a susceptible pea cultivar at different plant stages on subsequent plant growth and yield components was then assessed in the greenhouse. The younger the plants were at the time of infection, the more damaging the disease was on yield components. Contamination after flowering had no impact on growth and yield components.

The effect of sowing dates (autumn-sown vs spring-sown) on yield losses was confirmed in a large field network (each site comprising a very infested and a healthy neighbouring fields). Autumn-sown showed no aerial symptoms and no or below 15% yield losses, whereas spring-sown always showed typical aerial symptoms (yellowing and stunting) and higher yield losses (from 10 to 68%).

The lower aphanomyces root rot impact in autumn-sown pea, due to the more advanced growth stage at the time of contamination, makes winter pea an alternative to spring pea in moderately infested fields. To secure yield and avoid pathogen multiplication, it is however advised not to cultivate winter pea in heavily (inoculum potential > 2.5) infested fields.

P98 – S12

Necrotrophic effectors produced by fungal pathogens of legume crops

Cimmino A.[1],[*] Fondevilla S.[2] , Masi M.[1], Villegas-Fernández A. M.[2], Rubiales D.[2], Evidente A.[3]

1 - Dipartimento di Scienze Chimiche, Università di Napoli Federico II, Complesso Universitario Monte Sant'Angelo, Via Cintia 4, 80126, Napoli, Italy.

2 - Institute for Sustainable Agriculture, CSIC, 14004 Córdoba, Spain.

3 - Dipartimento di Scienze Chimiche, Università di Napoli Federico II, Complesso Universitario Monte Sant'Angelo, Via Cintia 4, 80126, Napoli, Italy.

Despite their importance for the agriculture and the environment, the production of food legumes is decreasing in most of the Mediterranean farming systems. A major cause for this is the low and irregular yield as a consequence of biotic and abiotic stresses. Necrotrophic fungi, including essentially *Ascochyta* and *Botrytis* species, are among the main biotic constraints. Both fungal genus are well known phytotoxins producers. These toxins, belonging to different classes of natural compounds, are frequently involved in the development of disease symptoms.

In this communication the chemical and biological characterization of the necrotrophic effectors produced by *Didymella pinodes* and *Botrytis fabae* pathogens of pea and faba bean respectively, will be reported. Furthermore, the studies aimed to identify novel resistance sources in the respective hosts in sensitivity assays will be discussed, too.

P99 – S12

Biocontrol of emerging insect pests of legume crops

Evidente A.[1], Aznar-Fernández T. [2], Masi M.[1], Rubiales D.[2], Cimmino A.[1]

1 - Dipartimento di Scienze Chimiche, Università di Napoli Federico II, Complesso Universitario Monte Sant'Angelo, Via Cintia 4, 80126, Napoli, Italy.
2 - Institute for Sustainable Agriculture, CSIC, 14004 Córdoba, Spain.

Pea weevils (*Bruchus pisorum*) and pea aphids (*Acyrthosiphon pisum*) are insect pests of great economic importance for agriculture and represent one major cause of damage and loss in legume crops. *Bruchus pisorum* is specialist, feeding and developing almost exclusively on pea. *Acyrthosiphon pisum* feeds on several species of legumes worldwide and ranks among the aphid species in agriculture.

Recently, germplasm collections of pea have been screened under field conditions to identify sources of resistance to weevils and aphids in pea.

The identification of compounds with phagodeterrent activity, which are able to interfere with aphid host plant selection and host acceptance, is currently becoming of great interest for the design of innovative biotechnical strategies in control of phytophagous insects.

In this communication results obtained on the identification of metabolites responsible for antixenosis and/or antibiosis in pea resistant accessions to weevils and aphids will be reported. The effect of natural metabolites against these pests will be discussed, too.

P100 – S12

Toward the understanding of host differentiation of *Orobanche crenata* populations on legumes

Mentag R.
INRA - Centre Régional de Rabat, Rabat, Morocco.

Orobanche crenata represents a major biotic constraint to production of faba bean (*Vicia faba L.*) and lentil (*Lens culinaris* Medik.). While this parasitic plant species attacks both of these crops, the extent to which *O. crenata* biotypes specialize in parasitizing specific crops is unknown. To address this question, we studied natural populations of *O. crenata* seed produced on different hosts and quantified their host specificity to faba bean and lentil. The virulence of *O. crenata* populations on each host was investigated through field trials, pot and Petri dishes assays. Genetic diversity of the parasite populations was also assessed through molecular analyses. Evaluation under controlled conditions showed a greater affinity between host species and their associated *O. crenata* populations. The two legume host species showed distinct patterns of infestation. Faba bean was more sensitive to both *O. crenata* populations, while the specificity for lentil by lentil-grown *O. crenata* was evident by the final stage of the parasite life cycle as shown by Correspondence Factorial Analyses. Considerable internal variation (81%) within *O. crenata* populations growing on both legume species was also observed. These results indicate that *O. crenata* can adapt to specific host species, which is important knowledge when developing integrated pest management practices for parasitic weed.

P101 – S12

Genetic and phenotypic diversity of pea isolates of *Aphanomyces euteiches* in France

Quillévéré-Hamard A.[1,2], Le Roy G.[1,2], Moussart A.[2,3], Pilet-Nayel M.-L.[1,2], Le May C.[1,2]

1 - INRA-Agrocampus Ouest-Université Rennes 1, UMR1349 IGEPP, Le Rheu F-35653, France

2 - UMT PISOM INRA/Terres Inovia, Le Rheu F-35653, France 3 Terres Inovia, Thiverval Grignon F-78850, France

Aphanomyces euteiches is an oomycete pathogen that causes devastating root rot in many pea-growing countries. Crop rotations with resistant or non-host legumes and genetic resistance are the main ways to manage the disease, but require more knowledge about structuration of the pathogen population. The aim of this study was to evaluate the genetic and phenotypic diversity of *A. euteiches* isolates in France. A collection of 207 isolates was established from pea-infested fields located in eight French departments. The isolates were genotyped using 20 SSRs markers (Le May et al, 2016) and a subset of 34 isolates was evaluated for aggressiveness on a set of legumes (pea, faba bean, vetch, alfalfa) (Moussart et al., 2008). Results showed low genetic and phenotypic diversity between most of *A. euteiches* isolates and no geographical structuration. However, some isolates with specific molecular patterns were detected in one location with different crop histories in legumes. Most of the isolates were aggressive on all the four legumes tested but some of them showed low aggressiveness depending on the host. These results suggest low genetic flows between *A. euteiches* populations, in accordance with the biology of the pathogen. They open new prospects for investigating the role of host diversity on structuration of *A. euteiches* populations.

P102 – S12

Effect of intercropping field pea with spring cereals on temporal changes in pea aphid (*Acyrthosiphon pisum* Harris, 1776) abundances and distribution in crops

Seidenglanz M. [1], **Huňady I.** [2], **Šafář J.** [2], **Villegas-Fernández A.M.**[3]

1 - AGRITEC Research, Breeding and Services, Ltd., Department of Plant Protection, Zemědělská 2520/16, Šumperk, 78701; Czech Republic

2 - Agritec Plant Research Ltd., Department of Grain Legumes and Technical Crops, Zemědělská 2520/16, Šumperk, 78701; Czech Republic

3 - CSIC/IAS Instituto de Agricultura Sostenible, Avenida Menéndez Pidal s/n, Campus Alameda del Obispo, Córdoba, 14004; Spain

In the course of 2013 - 2015 abundances of pea aphid (*A. pisum*) and their natural enemies found on field pea plants, grown either as a monoculture or intercropped with spring cereals and some other legumes, were compared. Two types of trials were used: small plot trials and large plot trials. Pea aphid colonies in field peas intercropped with cereals developed differently than in pea monocrops. However, the small plot trials showed different results to the large plot trials. In the small plot trials on intercropped plots pea aphid numbers were higher during the first part of crop colonisation, but the decline in aphid populations also happened earlier. In the large plot trials pea aphid abundances were significantly lower in field pea – barley intercrops compared to monocrops during the whole duration of crop infestation. Pea aphid colonies encountered syrphid larvae attacks more frequently in intercrops than in monocrops.

P103 – S12

Determination of fungicide efficacy on rust of field pea

Markell S.[1], Halvorson J.[1], Berghuis B.[1], Humann R.[1], Meyer S.[1], Schuh C.[1], Haugen S.[1], Jordahl J.[1], Fitterer S.[2], Carruth D.[2].

1 - Department of Plant Pathology North Dakota State University Fargo, ND 58102 U.S.A
2 - BASF North Dakota Research Farm Davenport, ND 58021 U.S.A.

Dry edible pea (*Pisum sativum*) acreage in the two United States north central states of Montana and North Dakota has recently approached 0.5 M Ha. Reports of rust, caused by Uromyces viciae-fabae (Pers.) Schroet., have recently increased in the region and are cause for concern. The objective of this study was to evaluate the efficacy of numerous fungicides for the management of rust on field pea. Fungicide trials were conducted in Leonard and Fargo, ND in 2015 and 2016. All trials were arranged in a randomized complete block design with four replications, and included a varying number of treatments with different modes of action, including; QoI (FRAC 11), DMI (FRAC 3) and SDHI (FRAC 7). Trials were artificially inoculated with fresh U. viciae-fabae urediniospores and fungicides were applied after the occurrence of disease. Disease severity was determined visually by evaluating the percent of the canopy covered with pustules in each plot and/or the percent leaf area covered with pustules on ten arbitrarily selected plants within each plot. In 2015, disease severity in plots treated with Azoxystrobin, Pyraclostrobin, Prothioconazole, and Fluxapyroxad + Pyraclostrobin was statistically lower than the non-treated control plot in at least one location. In 2016, the number of treatments evaluated for efficacy on rust has been expanded and yield data will be taken, if possible.

Session 13, plenary: Frontiers in legume breeding - Room *Arrábida I & II*

Chaired by Wolfgang Link (Georg-August-University, Germany) and Gerard Duc (INRA, France)

08:30-09:00 **Key lecture - Scott Jackson**: Contribution of epigenetic variation to improvement

09:00-09:15 Oral – S13

QTL detection for forage biomass of alfalfa in mixture with a forage grass

Julier B.
INRA, Le Chêne - RD 150 CS 80006, Lusignan, France

The agronomic and environmental value of forage grass - legume mixtures has been proved but legume breeding is still mostly conducted in monoculture. A progeny of 200 F1 individuals obtained from two alfalfa parents (H1 and G4) contrasting by aerial morphology was evaluated for biomass and plant height under two cropping conditions in micro-sward (mixture with tall fescue and monoculture) for 8 consecutive cuts. Phenotypic data showed a large variation among individuals for all traits in all cuts. The correlation between traits recorded in mixture and in monoculture was positive but the large variation around the correlation indicated that some genotypes were relatively more performant either in mixture or in monoculture. A genetic map of each parent was obtained from SSR and DArT markers, by using the TetraploidMap software. QTL were found on each parent and each linkage group (LG). Most QTL were common to mixture and monoculture (LG 1 of H1; LG 1, 2 and 4 of G4) but some QTL were specific to the mixture condition (LG 3 and 7 of H1, LG 6 of G4). These results indicate a partial common genetic control for biomass in mixture and monoculture but also highlight a specific genetic control for performance in mixture. To create alfalfa varieties adapted to monoculture and mixed cropping conditions, both common and specific QTL for biomass could be used.

09:15-09:30 Oral – S13

Improving the resistance of legume crops to combined abiotic and biotic stress (ABSTRESS)

Charlton A.J.

Fera Science Ltd, National Agrifood Innovation Campus, Sand Hutton, York YO41 1LZ, UK

Crop varieties that are better able to tolerate the effects of climate change are key to a sustainable future for European legume farming. Modern phenotyping tools and more diverse germplasm are required to ensure efficient crop breeding.

Combined integrated systems biology and comparative genomics approaches were developed to conduct a study of the gene networks and metabolic pathways implicated in the interaction between drought stress and *Fusarium oxysporum* infection in *Medicago truncatula*. Plants subjected to combined stress were produced using a high throughput phenotyping platform equipped with molecular imaging technologies. Bayesian models were applied to metabolomics and transcriptomics data derived from *M. truncatula* to identify "hub" genes and key control points in metabolic pathways implicated in combined drought and disease response.

Thirty-six hub gene candidates were identified in *M. truncatula*. Genetic mapping identified 28 hub gene orthologs in pea. These have a similar gene expression profile in *M. truncatula* and pea when exposed to combined stresses. Using gene silencing technologies, these hub genes have also been demonstrated to correlate with a phenotypic response. Tilling and eco-tilling for mutants of the 28 pea genes is producing new germplasm for testing in field trials and ultimately breeding resistance to combined stress. Introgression and multiplication of the mutant seeds is currently being completed with field performance trials planned for 2017.

09:30-09:45 Oral – S13

Integrated platform for rapid genetic gain in temperate grain legumes and wild *Cicer* species

Pazos-Navarro M., Ribalta F., Tschirren S., Munday C., Edwards K., Bennett R., Wells S., Erskine W., Croser J.
Centre for Plant Genetics and Breeding, The University of Western Australia, 35 Stirling Hwy, Crawley, WA 6009, Australia

Pulse genetic improvement has historically been constrained by the long lifecycle of the plant resulting in slow genetic gain. In conventional breeding systems, one to three generations can been obtained in a single year, with six required for fixation of favourable genes. Our research has resulted in breakthrough technology to accelerate the traditional Single Seed Descent (SSD) system in five major grain legumes (chickpea, lentil, lupin, pea and faba bean) and in wild Cicer species as *C. echinospermum* and *C. reticulatum*. Accelerated SSD (aSSD) enables a turnover of 6-8 generations per year, more than halving the current fastest route (SSD) to homozygosity in these species. Key to this system is: (1) Plant growth under tightly-controlled environmental and physical conditions to rapidly initiate flowering; and (2) A world-first system for precocious germination without in vitro intervention. With the final goal of developing an integrated breeding platform, we have designed hydroponic selection screens (HSS) for key abiotic constraints, including salinity, aluminium and boron toxicity that can be fully integrated through the aSSD system. This breeding platform represents a step-change in the potential efficiency of plant breeding programs. The proposed technology will benefit complex genetic studies via the rapid development of recombinant inbred lines (RIL) and multi-parental advanced generation intercrosses (MAGIC) populations."

09:45-10:00 Oral – S13

Broadening the genetic base of lentil

Sarker A.[1], Nath R.[2], Ali O.[3]
1 - ICARDA, India
2 - BCKV, India
3 - BARI, Bangladesh

Lentil (*Lens culinaris* Medikus subsp. *culinaris*) is an important pulse crop grown and consumed in South Asia since time immemorial. Its seed is nutritious human food, plant residues are valued animal feed and its cultivation provides sustainable cereal-based cropping systems in the region. Lentils in South Asia have narrow genetic base with respect to morphological, phenological and stress tolerant traits. The International Center for Agricultural Research in the Dry Areas (ICARDA) and its partners in South Asia are engaged in broadening the genetic base of lentil with the aim to develop high yielding varieties suitable for cultivation under various crop production systems. ICARDA holds the largest collection of > 11,000 diverse lentil germplasm from 72 countries, which is the building block of an international breeding program. Targeted utilization of these materials in genetic enhancement research has resulted into construction of new genotypes, and development of improved cultivars in Bangladesh, India, Nepal and Pakistan. Some of these varieties have early seedling vigor, early maturity, robust root systems, high biomass, and have ability to adapt under mixed cropping, inter-cropping and no-till production systems. Additionally, high iron and zinc content varieties have been developed, super-early lentil genotypes have been identified to fit into rice-lentil-rice cropping system, and for successful cultivation in rice-fallows as a second crop.

P105 – S13

Challenges and progress in improving genetic resistance to mycosphaerella blight of field pea by conventional breeding

Bing D.
Agriculture and Agri-Food Canada, Canada

Mycosphaerella blight, caused by *Mycosphaerella pinodes* (Berk. & Blox.) Vestergr., is the most prevalent disease of field pea (*Pisum sativum* L.) worldwide. To date extensive research has not been able to identify any strong genetic resistance to the disease. Various breeding techniques applied to improving the resistance, progress and challenges over 10 years in the field pea breeding program at Agriculture and Agri-Food Canada are reviewed.

P106 – S13

Hay and seed yield performances of *Vicia sativa* subsp. *sativa* X *Vicia sativa* subsp. *macrocarpa* hybrids in F4 generation

Acikgoz E.
Uludag University, Faculty of Agriculture, Bursa, Turkey.

The *Vicia sativa* aggregate is a complex of six closely related taxa which combines cultivated, weedy and wild forms. Common vetch (*Vicia sativa* subsp. *sativa* L.) is widely grown for hay and seed production in the Mediterranean basin. Big leaf vetch (*Vicia sativa* subsp. *macrocarpa* (Moris) Arcang.) is usually found in the wetter areas of the Mediterranean region. It is late maturing subspecies with very large seeds and leaflets. Two white flowered common vetch accessions (W-1 and Soner) were crossed with two purple flowered big leaf vetch accessions (Ericek and ICARDA – 5283) under the greenhouse conditions in 2012.

Hybrids between the subsp. *sativa* x subsp. *macrocarpa* were highly sterile. F1 and F2 generations showed extremly low fertility in all combinations. But restoration of fertility occurred in the F3 generation and several lines were developed. The lines were evaluated under dryland conditions in a randomized complete block design with 3 replications. Large morphological variations were observed among the F4 lines. Some hybrids were superior in most yield components, biomass and seed yield than both parents and the check cultivars.

P107 – S13

Generation of linked markers for low vicine-convicine (lvc) and zero tannin (zt-1) traits and their use in Marker Assisted Selection (MAS)

Kiss G.B. [1]**, Winkler J.** [2]**, Adam E.**[2]**, Ferrari B.** [3] **and Paolo Annicchiarico**[3]

1 - AMBIS Ltd, Szeged, Hungary.
2 - Saatzucht Gleisdorf GmbH, Austria.
3 - CRA-FLC, Lodi, Italy.

Polymorphic PCR based genetic markers tightly linked to low vicine convicine content (lcv) and zero tannin (zt-1) traits were developed for several faba bean (*Vicia faba*) parents. These markers (VfVc12, VfVc13, VfZt12) were used to genotype individuals in several breeding populations to help marker assited selection for these traits. Results of the genotiping and evaluation of the results will be presented.

P108 – S13

Models with two predictor variables accurately predicts seed yield in diploid and tetraploid red clover (*Trifolium pratense*)

Vleugels T.[1], Ceuppens B.[1,3], Smagghe G.[3], Roldán-Ruiz I.[2], Cnops G.[2]

1 - Plant Sciences Unit – Genetics and Breeding, Institute for Agricultural and Fisheries Research (ILVO), Caritasstraat 39, 9090 Melle, Belgium.

2 - Plant Sciences Unit – Growth and Development, Institute for Agricultural and Fisheries Research (ILVO), Caritasstraat 39, 9090 Melle, Belgium.

3 - Ghent University, Faculty of Bioscience Engineering, Dept. of Crop Protection, Coupure Links 653, 9000 Ghent, Belgium.

Red clover (*Trifolium pratense* L.) is a valuable protein-rich forage crop. Tetraploid red clover cultivars produce more dry matter weight and have increased disease resistance compared to diploid cultivars and are therefore favoured by farmers. However, the disadvantage of tetraploid cultivars is their unsatisfactory seed yield, what makes seed production of tetraploids economically uninteresting.

We investigated the effects of 10 traits on seed yield in a set of 600 individual genotypes, derived from 15 diploid and 15 tetraploid cultivars. Our data and models show the importance of only two traits for the determination of the variation in seed number. The number of ripe flower heads per plant and the seed number per ripe flower head explained respectively 94.8% and 53.2% of the variation in diploid plants, and 88.1% and 64.9% in tetraploid plants. The latter two traits can be included in the breeding program to increase seed yield in red clover.

P109 – S13

Diverse winter faba beans in mixed crop stand with wheat

Siebrecht D., Martsch R., Link W.

Georg-August-Universität Göttingen, Department of Crop Sciences, Division of Plant Breeding

Mixed crop stands can show higher yields when compared with pure stands. Such yield increments are assumed to result from complementarity effects between crops. In particular, it is argued that mixed crop stands of legumes and non-legumes have the potential to the promote sustainability and resilience of our food and feed production. One such example is the mixed cropping of winter faba bean (*Vicia faba* L.) and winter wheat (*Triticum aestivum* L.). A detailed description and thorough understanding of mixing effects would allow plant production systems to better exploit this phenomenon, for instance via breeding. Will such yield increments be found in these mixed stands? If they are, how can this information be used to guide plant breeding efficiently? To address such questions, mixed stands of N=8 winter faba bean lines a nd N=3 winter wheat cultivars were compared with their corresponding pure stands within the framework of IMPAC^3 (a German research project based at the University of Goettingen). In 2015, field experiments at two locations near Goettingen were implemented. Mixtures and pure stands were conducted in a row intercropping design over 360 plots (10.5 m^2 each). Yield parameters were observed in detail. Preliminary results show significant yield surplus of mixed crop stands over pure stands. Moreover, there is a significant variation of this mixing effect caused by the different faba bean lines.

P110 – S13

Advancement of winter hardy peas and lentils breeding in Hungary – Benefits and possibilities.

Mendler-Drienyovszki N., Dobránszki J.
Research Institute of Nyíregyháza, University of Debrecen, Hungary.

Winter legumes are of great ecological and economical importance in the sustainable agriculture. Their sowing occurs in autumn so the plants can be strengthened already in the same year before the winter therefore their cultivation has less risk and resulting in higher yield than the spring planted legumes. Our breeding aim includes creating new, cold tolerant varieties that are suitable both for human consumption (winter hardy lentil) and animal feeding or even other special use (winter hardy pea). Beside cold tolerance the most important joint breeding aims included early maturation, plant height, high and stabile yield with good quality; in the case of winter hardy lentil also the seed colour. Two lines of generation F5 originating from new crossings belong in the 'super-early' maturity group. The winter hardy pea breeding lines have high plant height so the best practice may be growing them in combination with cereals. One of the results of the winter hardy lentil breeding is a variety-candidate called 'Pinklevi' and three additional breeding lines with different seed colours. The 'Pinklevi' is a cold tolerant variety-candidate belongs to the early maturity group. The main colour of the testa of the dry seed is pink and ochre. The size of the dry seed is medium, their weight is low. According to our previous studies and experiences these species are successfully grown also on acidic sandy soils.

P111 – S13

Role of L- histidine in protein-oil relationship in soybean seed

Djordjevic V., Ceran M., Miladinovic J., Balesevic-Tubic S., Petrovic K., Miladinov Z.

Institute of field and vegetable crops, Novi Sad, Serbia

In soybean, negative correlation between protein and oil is well documented but it is poorly explained. Three F2 and F2:3 populations were developed, crossing between one high protein line and three high yielding genotypes. Based on protein content, from each F2 population (approximately 150 lines per population) were selected ten high protein (HP) and ten low protein (LP) lines and amino acid analysis performed on F2:3 lines. Two of three populations have high negative correlation between protein and oil content (-0.81 and -0.82), while in one population this negative correlation was weak (-0.42). Among all analyzed amino acids, only content of L- histidine follow similar pattern. In populations with high negative protein-oil correlation, L- histidine was significantly lower in HP lines. On the other hand, in population with weak negative protein-oil correlation, content of L- histidine increased in HP lines. These findings can explain week negative correlation. Biosynthesis of L- histidine share biochemical reactions with oxidative phase of pentose phosphate pathway, which produces reducing equivalents (NADPH) necessary for biosynthesis of other compounds. Genotypes in this population can overcome this negative correlation by increased biosynthesis of reducing equivalents, necessary for protein and oil synthesis. This finding can be useful in further research, for breeding of better quality soybean and L-histidine can be useful biomarker.

P112 – S13

Discovering genetic signatures of selection in the elite soybean germplasm

Ćeran M., Đorđević V., Miladinović J., Balešević-Tubić S., Mikić A., Mikić S., Trkulja D.
Institute of Field and Vegetable Crops, Maksima Gorkog 30, Novi Sad, Serbia

Identification of genomic regions affecting soybean improvement has practical importance for future breeding, indicating positions of agronomically important genes or genes underlying adaptation. Genetic consequences of breeding in the environment of Central-East Europe were detected by analysis of ancestral and elite soybean varieties, using genetic hitchhiking mapping. As a result of long-term selection, significant reduction in genetic diversity of the elite population comparing to ancestral was observed. Population structure of analyzed varieties has been largely influenced by the pedigree, causing a low level of genetic differentiation between the populations. Nine microsatellite markers were considered as strong positive selection candidates, indicating regions involved in the improvement and adaptation to target environment. *In silico* analysis detected 264 previously mapped quantitative trait loci (QTLs) located in the identified selectively important regions. The largest number had an influence on the reproductive period, followed by seed characteristics, whole-plant performance and yield QTLs. Being the strongest candidates for selection, markers Satt557 and Satt357, located on Chromosome 6, revealed that E1 gene, which controls flowering time and time to maturity in soybean, seems to be a major contributor for adaptation to environmental conditions of Central-East Europe.

P113 – S13

Construction and evaluation of near-Isogenic lines for resistance to *Aphanomyces euteiches* in pea

Lavaud C.[1*], Lesné A.[1*], Riviere J-P.[1], Mangin P.[2], Roullet G.[3], Herbommez J.F.[4], Declerck P. [5], Furet G.[6], Boutet G.[1], Baranger A.[1], Pilet-Nayel M-L.[1]

*** Contributed equally to the work**

1 - INRA-UMR1349 IGEPP, PISOM-UMT INRA/Terres InoviaBP35327, Le Rheu F-35653, France
2 - INRA, Domaine Expérimental d'Epoisses, Bretenières F-21110, France
3 - Unisigma, GIE Recherche et Sélection, Froissy F-60 480, France
4 - KWS-Momont, Mons en Pévele F-59246, France
5 - RAGT2n, Louville la Chenard F-28150, France
6 - Limagrain Europe, Chartainvilliers F-28130, France

Common root rot of pea, due to *Aphanomyces euteiches*, is one of the most damaging diseases in many countries. The development of resistant varieties is a major objective to manage the disease. Consistent quantitative trait loci (QTL) controlling partial resistance were discovered from four pea RIL populations (Hamon et al, 2013). This study aimed to validate the resistance QTL effects in different genetic backgrounds, by creating and evaluating Near-Isogenic Lines (NILs) carrying resistance alleles at individual or combined consistent QTL. Five then two parallel marker-assisted back-cross selection schemes were developed, each consisting in transferring resistance alleles at one to three of the main QTL into three susceptible pea cultivars. A total of 157 then 36 BC5 or BC6 NILs, carrying zero to three resistance introgressions were obtained. The NILs were phenotyped for resistance to *A. euteiches* in controlled conditions at seedling stage. The first set of NILs was also phenotyped for resistance in multiple field environments. NILs carrying the major-effect QTL, individually or in combination with minor-effects QTL, had increased levels of partial resistance in both conditions. Several NILs carrying multiple minor-effects QTL also showed reduced levels of disease severity in the field. This study gives tools and information for the choice of resistance QTL to use in breeding to increase partial resistance to *A. euteiches* in future varieties.

P114 – S13

Comparison of vernalization response in wild *Cicer* species and cultivated chickpea

Kushwah A., Singh S.

Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, Punjab-141004, India

Wild *Cicer* species can contribute to enhance the levels of resistances to many stresses besides broadening the genetic base of cultivated chickpea (*Cicer arietinum* L.). Vernalization insensitivity is a key feature of domesticated chickpea, and its genetic basis is not well understood. In this study, the response to vernalization was studied in cultivated and wild *Cicer* species belonging to primary, secondary, and tertiary gene pools. A total of 46 germplasm accessions including 37 wild and 9 cultivated germplasms were used in this study. All the germplasm accessions were tested with (30 days at 4°C) and without vernalization (control). The difference in mean days to flower between control and vernalization treatments was used to assess the flowering vernalization response. The difference in mean days to germination and mean days to first podding between control and vernalization treatments was also recorded to know the effect cold treatment on days to germination and first podding. The wild germplasm accessions are vernalization-sensitive, late flowering genotypes while domesticated germplasm accessions are vernalization insensitive. Strong genotype by environment interaction effect on days to flower was observed for all the germplasm accessions. Chickpea breeders interested in using the wild progenitor as a donor of exotic traits should be aware of the possibility of introducing vernalization response alleles that may alter the phenology of their breeding materials.

P115 – S13

Screening of diverse lentil genotypes for total phenolic content

Gupta S., Dikshit H.K., Prakash P., Singh A., Aski M.
ICAR-Indian Agricultural Research Institute, New Delhi, India.

Phenolic compounds possess antioxidant activity and delay the oxidation of lipids, proteins, and DNA by inhibiting oxidizing chain reactions. Natural phenolic antioxidants can scavenge reactive oxygen and nitrogen species (RONS) thereby preventing the onset of oxidative diseases in the body. Eighty-five lentil genotypes comprising Indian released varieties/ advanced breeding lines and germplasm lines, Mediterranean landraces and ICARDA germplasm were evaluated for total phenolic content (TPC). Spectrophotometric technique, based on Folin-Ciocalteau reagent was employed and calculated as Gallic Acid Equivalents per gram of extract. The total phenolic content (TPC) of lentil genotypes varied from 0.756 (L-11-231) to 3.043 (IC262839, L-11-295) mg gallic acid equivalents (GAE)/g sample. This study will help breeders not only to develop lentil lines with better phyto-nutrient profile but can also be promising in phytomedicinal and pharmacological formulations.

P116 – S13

Breeding for intercropping: join applied genetics and agronomy for improved annual legume production

Mikić A.[1], Duc G. [2], Bedoussac L. [3], Ćeran M. [1], Corre-Hellou G. [4], De Ron A.M. [5], Đorđević V. [1], Floriot M. [6], Jeuffroy M.-H.[7], Justes E. [3], Lecomte C.[2], Mihailović V.[1], Mikić S.[1], Šarūnaitė L.[8], Vasiljević S.[1]

1 - Institute of Field and Vegetable Crops (IFVCNS), Novi Sad, Serbia

2 - Institut National de la Recherche Agronomique (INRA), UMR 1347 Agroécologie, Dijon, France

3 - Institut National de la Recherche Agronomique (INRA), UMR 1248 AGIR, Castanet-Tolosan, France

4 - Groupe ESA, Angers, France

5 - Consejo Superior de Investigaciones Científicas (CSIC), Misión Biológica de Galicia (MBG), Pontevedra, Spain

6 - Agri-Obtentions, Paris, France

7 - Institut National de la Recherche Agronomique (INRA), UMR 0211 Agronomie, Thiverval-Grignon, France

8 - Lithuanian Research Centre for Agriculture and Forestry, Institute of Agriculture, Akademija, Lithuania

Archaeology offers evidence that growing plants together, with annual legumes as usually inevitable component, could be the most ancient cropping system in all primeval agricultural centres. With a ten millennia long tradition, intercropping annual legumes, usually with cereals and for diverse uses, has remained important all over the world until today. There is a phenomenon that brings together legume breeders and agronomists: both are aware that there are differences in the agronomic performance of the mixtures of annual legumes and other field crops if diverse annual legume cultivars are used. Wishing to understand this phenomenon properly and define its economic significance, we are establishing a firm interaction between breeders and agronomists, in order to design such annual legume ideotypes that would have the best agronomic performance when intercropped with diverse plants for either forage or grain or biomass or any other use. Our major hypotheses are that the ideotypes for intercropping are the genotypes being the most competitive in the same environment compartments or taking profit of the complementary compartments. However demanding, this is feasible: the preliminary schemes for forage and grain production, developed mostly at IFVCNS, produced encouraging results in field conditions. Joint efforts of annual legume breeders and agronomists should be beneficial for both scientific community and result in enhancing the legume cultivation and production in general.

P117 – S13

The protein quantity and quality in breeding of soybean, chickpea and bean to create cultivars

Abugaliyeva A.I., **Didorenco S.V.**
LLP "Kazakh Research Institute of Agriculture and Plant Growing", Kazakhstan

The main legume seeds biochemical component is a protein.
Objective: To evaluate the potential of soybean, chickpea and bean cultivars for protein content and stability of its formation.
In Kazakhstan registry there are 30 soybean varieties, including 10 from Kazakhstan breeding, represented with 5 maturity groups from the early "00" to late-maturing "III".
On the protein content stability, Misula - leading variety in terms of state variety test 40,1 ± 0,7% and the Radost 1-39,8 ± 0,5%. The share of soybean genotypes with a protein content above 40% is maximum marked for varieties Perizat, Paradis, Khorol and Gallek, also for Atlanta, Renta, Ruzhica, Riza, Selecta 302, Cheremosh, Selecta 201, Iskra.
Soybean cultivars yield in a demonstration (domestic and foreign breeding) nursery varies depending on the genotype, growing year and maturing group from 1.0 t/ha to 6.2 t/ha. The protein content in soybean seeds as a whole ranged from 32.2% (LADA) to 46.9% (Horol). Maximum "protein content"observed for 00 and 0 maturing group.
Germplasm soybean set genotypes (Kazakhstan, Russia, Serbia, Ukraine, Moldova and the United States) are characterized by protein from 21.0 to 50.0% (Smena cvs and Karyagin Pamyat cvs). Chickpeas breeding nurseries on the protein content varied from 26,6% to 31,8%, bean from 21,5% to 26,9%.
A number of samples selected on the high Fe content: (Vavilov collection, KRIAPG, and foreign) methionine, cysteine content and balance 11S/7S globuline.

P118 – S13

New portuguese chickpea varieties

Duarte I., Pereira G., Barcelos C., Meneses M.
INIAV, Elvas, Apartado 6, 7350-951 Elvas. Portugal

An increase of grain legume production is essential for meeting food protein need in Europe.

Portugal is located in the West part of Iberian Peninsula (latitude 37º - 42º N and longitude 9º - 6º W); this southerly latitude gives it a Mediterranean type of climate, characterized by hot and dry summers and cool and wet winters so has suitable conditions to produce pulses crops, such as chickpea (Cicer arietinum L.).

Chickpea breeding is being conducted at INIAV-Elvas, Portugal since 1986. Five varieties have been released: 3 kabuli type (‘Elvar’, ‘Eldorado’ and ‘Elixir’) and 2 desi type (‘Elmo’ and ‘Elite’). ‘Elvar’ is the most cultivated variety in Portugal and south France.

Selection criteria include autumn/winter growth adaptation, high tolerance to Ascochyta rabiei and Fusarium oxysporum, adaptation to abiotic stresses (high temperatures and waterlogging) and seed size.

From 100 advanced lines, included on adaptation trials in the last 4 years, were selected 3 genotypes: 1 desi and 2 kabuli.

Those genotypes show good adaptation to different environmental conditions with high yield and tolerance to diseases.

These 3 advanced lines will be registered on the Portuguese Catalogue of Varieties.

P119 – S13

Application of NIRS technology to genetically analyse vicine and convicine content in faba bean (*Vicia faba* L.)

Puspitasari, W., Link W.
Department of Crop Sciences, Georg-August-University of Goettingen

Faba bean, being a grain legume, provides seed protein and starch for human and animal nutrition. However, faba bean seeds contain antinutritive compounds such as vicine and convicine that negatively affect digestibility. Moreover, vicine and convicine are the causative agents of favism (haemolysis) in such humans who are genetically deficient in glucose-6-phosphate-dehydrogenase. The purpose of the current experiments is to develop a valid near infrared spectroscopy (NIR) calibration for the quantitatively varying vicine and convicine content of such faba beans which do not have the low-vicine gene "vc—"; and to study their genetic variation of these compounds. Spectra and HPLC-results of milled seed of 147 winter faba bean inbred lines and 75 further faba bean lines were used to develop and validate the calibration. The currently available NIRS calibration equation is able to reasonably predict vicine and convicine content in faba bean with a standard error of calibration SEC = 0.07 and coefficient of determination RSQ = 0.91. Analyses are ongoing, yet we already by now see a large quantitative-genetic variation of vicine and convicine content.

P120 – S13

Methods for the development new pea lines

Dostalova R., Hunady I., Ludvikova M., Ondrackova E.
Agritec Plant Research Ltd., Sumperk, Czech Republic

The aim of this work was to increase genetic diversity of field pea. For the creation of new lines of peas were used unique genetic resources with accumulated resistance genes from the gene bank of AGRITEC. 69 new pea accessions were obtained from gene bank VIR St Petersburg.

Accessions were evaluated under field conditions, morphologically described using Descriptor list of genum *Pisum* L. and the incidence of diseases and pest infestations was evaluated.

Declared sources of resistance were tested in inoculation tests. Molecular analyses were performed to speed the breeding process. eIF4E (iso) corresponding loci SBM-1 (LG VI) and SBM-2 (LG II), mediating recessive resistance to several viral pathogens of the genus potyvirus (including PSbMV) were identified. Alleles of eIF4E gene were identified in selected genotypes of pea, involving all PSbMV donors used in practice. Based on sequence analysis PCR molecular markers, allowing the 100 % reliable identification of both the homozygous and heterozygous plants were designed, tested and selected.

Genetic diversity of pea accessions was determined using RBIP markers. Molecular detection of resistance to powdery mildew, *Fusarium* wilt and PEMV were carried out. Molecular detection of trypsin inhibitor activity was performed and results were compared with chemical analysis.

Suitable materials with high levels of biological properties were used in the hybridization process, obtained lines are using for breeding.

P121 – S13

QTL detection of pod-related traits in Pea (*Pisum sativum* L.).

Guindon M.F., Martin E.A., Cravero V.P., Cointry E.L.
IICAR-CONICET (Instituto de Investigaciones en Ciencias Agrarias de Rosario).

Pea is a self-pollinated, diploid (2n=14), annual crop produced worldwide for human consumption and animal feed. Pea breeding has been conducted with the aim of developing high yielding cultivars. QTL detection will provide additional tools to identify desirable alleles early in the breeding process, reducing the time of cultivar release. The purpose of this work was to detect and validate QTLs related to number (NP), length (LP) and diameter (DP) of pods in pea. A total of 50 SRAP marker combinations and 10 SSR were evaluated in 112 F2 individuals derived from a cross between DDR14 and Explorer commercial lines. The phenotypic traits were measured in the F2 population in 2013 and in their F3 families in 2014 and 2015. The normality of each trait was evaluated using the Shapiro-Wilk´s test. The mendelian segregation of each polymorphic molecular marker was verified with a $\chi 2$-test. Associations among mendelian markers and traits were detected by ANOVA single point analysis. Consistency of the associations found in F2 individuals and F3 families were evaluated to validate the QTLs. All the morphological traits presented normal distributions and 285 molecular markers showed mendelian segregation. The analysis allowed the validation of 11 QTLs: 3 markers associated to NP (5 to 10% of phenotypic variation explained), 4 markers related to LP (3 to 17%) and 6 markers related to pod diameter (4 to 11%). This work provides interesting information for use in pea breeding programs.

P122 – S13

Genetic assessment of mutant populations of Lentil and Chickpea

Laouar M.[1], Tabti D.[1], Tiliouine W[2]., Abdelguerfi A.[2]

1 - E.N.S.A Laboratoire d'Amélioration Intégrative des Productions Végétales, El-Harrach, Alger, Algérie

2 - E.N.S.A Laboratoire des Ressources Génétiques et Biotechnologies, El-Harrach, Alger, Algérie

3 - Division of Biotechnology and plant breeding, National Institute of Agricultural Research of Algeria (I.N.R.A.A.), Baraki, Algiers, 16000, Algeria. tiliwahiba@yahoo.fr

Lentil (*Lens culinaris* Medik.) and Chickpea (*Cicer arietinum* L.) are important foods legumes crops with high nutritional value and ecological importance. Algeria is the third (chickpea) and fifth (lentil) largest importer in the world. The productions are very low because specially the lack of adapted and productive varieties. Radio-mutagenesis is one of ways to create new variability for selection according to environmental conditions. Many useful genetic changes were induced by a mutagenic treatment. Gamma rays were the most used mutagen to change gene(s) in lentil and chickpea due to their easy application. Mutation was induced using gamma rays in two varieties Idlib-3 (lentil) and Ghab 4 (chickpea) by 100 and 258 Gy corresponding to the lethal doses (DL50) respectively. For each species, from 10000 seeds M1 we generated about 140 families M1 and about 4000 genotypes were characterized in the field. Yield, yield component and harbor variability, heritability, and genetic advance were assessed on putative mutant. The range of variability for main traits was high. High correlation showed between number of total pods and seed yield. About 3% of families' mutants (M2) showed superiority than the control for days to flowering, days to maturity and other traits. High heritability associated with high genetic advance was observed from seed yield and hundred seed weight; this indicates the expected effectiveness of selection for the traits under consideration.

P123- S13

Adaptation of Pea to contrasted French regions: simulation of pea varieties with the AZODYN-Pea crop

Bénézit M[1], Larmure A.[2], Munier-Jolain N.[2], Jeuffroy M.-H.[1]

1 - UMR Agronomie INRA, AgroParisTech, Université Paris Saclay, 78850 Thiverval-Grignon, France

2 - UMR agroécologie, Dijon

Pea (*Pisum sativum* L.) is a particularly sensitive crop regarding abiotic stress throughout its cycle (Schneider and Huyghe 2015). Climate change results in the increase of the unpredictability of both the frequency and the intensity of these stresses (Stocker et al. 2013). To avoid abiotic stress, breeders have been developing, for the last fifteen years, winter pea varieties sown during autumn, more resistant to frost with an earlier flowering date than spring pea, as well as varieties called “Hr”, photoperiod-sensitive, that can be sown even earlier than regular winter types. However, despite the progress of winter type breeding, winter pea surfaces seldom reached more than 25000ha since 2000. Our aim was to study the performances of the different types of pea in contrasted French regions, for various climates, in order to adapt the choice of the pea type to the frequency and intensity of abiotic stress. For this purpose, the crop model Azodyn-Pea (Jeuffroy et al. 2012) was adapted to simulate various types of pea. The model was then used for the evaluation of the three types over the past ten years in different French regions in order to identify which type is most suited to each environment (climate, region). Here we show the potential of winter pea for various French climates. Azodyn-Pea will also allow, in a second phase, the exploration of novel combinations of plant traits in order to design ideotypes and contribute to the development of new varieties within each type.

P124 – S13

Cost/Benefit Analysis of Marker Assisted Selection in a Field Pea Breeding Program.

Rosewarne G.M., Slater T., Pandey B., Kaur S.
Biosciences Research, Agriculture Victoria, Australia.

Many molecular markers are currently available in field peas and these are being applied in the Australian field pea-breeding program. As the breeding program operates on a fixed budget, the implementation of markers requires both genetic and economic analyses to develop cost effective models that give the best genetic outcomes. This paper compares costs of using phenotypic selection for a range of traits and compares those costs and theoretical genetic outcomes against deploying molecular markers to pyramid the same set of traits.

Efficient, controlled environment assays have been developed to screen for tolerance to salinity and boron, and for resistance to downy mildew (2 pathovars), *Pseudomonas syringae* pv pisi (race 3) and *P. syringae* pv syringae. These traits are simply inherited with one to two loci conferring each of the desired phenotypes. Costs for all assays (controlled environment and molecular) have been calculated based on consumables and staff time. Phenotypic selection involved applying different assays to large segregating populations in consecutive generations, (F2-F5) with all phenotypes confirmed on F5 families. Marker assisted selection applied all markers to enrich for appropriate alleles in the F2 generation, and confirmed homozygous status in the F5 generation. The application of markers was 1/6th of the cost of phenotypic selection and also gave better genetic outcomes with regard to the frequency of germplasm that recombined all traits.

P125 – S13

Genotype x environnement interaction in winter pea

Biarnès V., Pontet C.
Terres Inovia, Grignon, France

An analysis of genotype x environnement interaction has been made on the winter pea trials network of registered varieties, coordinated by Terres Inovia in 2015. 10 winter pea varieties, recently registrered, were sown in 25 sites in different french areas.

The main results are :

- Genotype x environnement interaction is about 4,3 % of the total variation observed for yields. It is higher than variety effect but much smaller than the environment effect, which explains more than 80 % of the total variation.
- Groups of varieties with similar behaviour and groups of environemnts with similar ranks of varieties have been found.
- Variables calculated from development stages and climate allow to explain genotype x environement interaction.

P126 – S13

Short duration pigeonpea hybrids to bridge decades old yield

Hingane A.J.[1], Rathore A.[1], Kumar C.V.S.[1], Chand U.[1], Singh S.J.[2]

1 - International Crops Research Institute for Semi-Arid Tropics, Patancheru, India-502324

2 - Sri Karan Narendra Agriculture University (SKNAU), Rajasthan Agriculture Research Institute (RARI), Durgapura, Jaipur, 302 018,India

Low yield in pigeonpea has always been a matter of concern for all the stakeholders over more than last five decades. But, development of CMS based hybrid technology in pigeonpea, has proved the potential to bridge this yield gap. Several medium duration hybrids have been released in states of India, yielding 25-40% higher yield than local varieties, but these hybrids are region specific due to its photo–thermo sensitive nature. Hence, need was felt to explore other possibilities to increase pigeonpea production and productivity. Recently developed photo-thermo incentive short duration varieties have helped to identify new production niches like wheat and rice cropping system in non-traditional states of India. But over years, productivity of these short duration varieties has also become stagnant. Considering this, a hybrid-breeding program was initiated at ICRISAT to develop location specific short duration hybrids. Nine short duration experimental hybrids along with two checks were evaluated for its yield and adaptability at ICRISAT, Patancheru and RARI, Durgapura Rajasthan for three years (2013-15) using GGE biplot analysis. Among the six environments evaluated, Patancheru (Pat-15) was identified as suitable location in discriminating short duration pigeonpea hybrids and can be considered as ideal testing location. ICPH 2364 followed by ICPH 3310 were earliest to mature while ICPH 2429 and ICPH 2433 were found to be high yielders and stable across both the locations.

Session 14, plenary: Frontiers in legume agronomy - Room *Arrábida I & II*

Chaired by Erik S. Jensen (SLU, Sweden) and Susana Araújo (ITQB NOVA, Portugal)

10:30-11:00 **Key lecture - Eric Justes**: Synthesis on the effects of grain legume insertion and cereal-grain legume intercrops in low input cropping systems in Southern France

11:00-11:15 Oral – S14

Design and assessment of legume-based cropping systems with stakeholders in Europe

Pelzer E.[1], Bourlet C.[1], Carlsson G.[2], Lopez-Bellido R.J.[3], Jeuffroy M.-H.[1]

1 - UMR Agronomie INRA, AgroParisTech, Université Paris Saclay, 78850 Thiverval-Grignon, France

2 - SLU, Department of Biosystems and Technology, PO Box 103, SE-230 53 ALNARP

3- University of Cordoba, Edificio C4 "Celestino Mutis", Ctra. Madrid-Cadiz km 396, 14071 Cordoba, Spain

Legume-based cropping systems have numerous environmental benefits, but stakeholders are often not aware of all of them. Moreover, there is a large range of available species that can be grown with various practices in the fields (sole or cover crop, intercrop, etc.).

Our aim was thus to design legume-based locally adapted cropping systems, in three European regions, valuing the diversity of legumes species and practices.

After describing the most frequent cropping systems in each region, local improvement targets were defined. Then, during a design workshop gathering scientists and a few advisors and farmers, knowledge on legume crops were shared, and then innovative cropping systems were designed.

With the aim of assessing them with the multi-criteria tool ®Masc (tool accounting for user’s preferences on sustainability), we surveyed stakeholders in each country (29) to gather their preferences on ranking of performance criteria (weight sets) and to collect their opinion on the feasibility of designed cropping systems. We then synthesized these weight sets into 4 MASC trees and each innovative cropping system was assessed according to those trees.

In the end, for each region, we identified legume-based cropping systems, which were assessed sustainable by the 4 stakeholder trees and said feasible. The whole study also allowed identifying lack of knowledge on legume crops and their effects on the following crops that should be completed for promoting legumes in Europe.

11:15-11:30 Oral – S14

Performance of legume-based annual forage crops in three Mediterranean regions

Porqueddu C.[1], Melis R.A.M.[1], Thami-Alami I.[2], Abbas K.[3], Pecetti L.[4], Annicchiarico P.[4]

1 - Istituto per il Sistema Produzione Animale in Ambiente Mediterraneo (CNR-ISPAAM), Sassari, Italy

2 - INRA - Centre Régional de Rabat, Rabat, Morocco

3 - INRAA - Agro-system East Division, Sétif, Algeria

4 - Centro di Ricerca per le Produzioni Foraggere e Lattiero-Casearie (CREA-FLC), Lodi, Italy

Legume-based forage crops may be pivotal for improving the sustainability of Mediterranean crop-livestock systems. The objective of this study was identifying key species and optimal crop composition across three drought-prone Mediterranean regions, on the basis of crop performance and farmers' acceptability. Cultivars of three legume species (field pea, semi-dwarf and tall types; Narbon vetch; common vetch) and two cereals (oat; triticale) were grown in Sassari (Italy), Sétif (Algeria) and Marchouch (Morocco) as pure stands and legume-cereal binary and four-component mixtures, assessing crop dry-matter yield (DMY), legume proportion and weed dry weight over two cropping years in four-replication experiments. Large farmer groups assigned acceptability scores (1=poor, 5=excellent) before harvesting. On average, binary and complex mixtures showed higher DMY than pure stands. Both pea types in pure stand or in mixture with oat, common vetch in mixture with oat and the complex mixture of vetch and cereal species, tended to combine high forage yield, high farmer acceptability score (around or over 4), and high weeds control. Pea-based binary mixtures had higher DMY than vetch-based ones (6.0 vs 5.2 t ha^{-1}). The mean legume proportion of binary mixtures was 53% for pea, 45% for common vetch, and 31% for Narbon vetch. Our results point to the particular interest of pea crops (in pure stand or in mixture) as an alternative to vetches in drought-prone Mediterranean environment.

11:30-11:45 ORAL – S14

Legume-based mixed cropping systems may have higher water use efficiency than mono crop systems

Lingner A. [1,2], **Dittert K.** [1], **Senbayram M.**[3]

1 - Institute of Applied Plant Nutrition, University of Göttingen, Germany,
2 - Centre of Biodiversity and sustainable Land Use, University of Göttingen, Germany,
3 - Institute for Plant Nutrition and Soil Science, Harran University of Sanliurfa, Turkey

Improving sustainability and productivity of agricultural systems is a major concern facing global change. The increasing probability of seasonal droughts and freshwater scarcity emphasizes the importance of crop traits such as water use efficiency (WUE). In this context, multi-species crop stands with legumes are less dependent on external inputs and may have higher resource use efficiency.

Our study aimed to evaluate two different agro-ecosystems: cropland and grassland, cultivated as mono or mixed cropping with legumes (faba bean and white clover). Canopy WUE in each treatment was determined via transparent chambers connected to a gas exchange system (GFS-3000, Heinz Waltz GmbH, Germany). Additionally, a Quadrocopter (Raptor, EagleLive Systems GmbH, Germany) equipped with a spectral camera (ADC Micro, Tetracam Inc., California) was used to measure normalized difference vegetation indices (NDVI).

The gas exchange data clearly showed that in cropland both net-photosynthesis and WUE were highest in mixed cropping (faba bean + wheat) in summer 2015, while during a temporal drought period the evapotranspiration was lowest. In pure white clover stands, net-photosynthesis was considerably higher than both in ryegrass and their mixed stands. NDVI values were almost similar when comparing pure legume stands and their mixed cropping, which was significantly higher than pure wheat or grassland stands. Both methods suggested that mixed cropping systems improved productivity and WUE.

11:45-12:00 Oral – S14

Participatory development of grain legume-cereal intercrops for enhanced productivity and reduced weed abundance in organic crop production.

Carlsson G.[1], Modig P.[2], Hunter E.[3], Jensen E.S.[1].

1 - Swedish University of Agricultural Sciences (SLU), Department of Biosystems and Technology, Alnarp, Sweden.

2 - Swedish Rural Economy and Agricultural Society in Skåne, Kristianstad, Sweden.

3 - SLU, Department of Work Science, Economy and Environmental Psychology, Alnarp, Sweden.

Grain legumes such as beans, lentils, lupins and peas are highly appreciated for their symbiotic nitrogen fixation and for providing high-quality food and feed, but perceptions of low or variable yields may limit farmers' interest to grow grain legumes. In addition, despite documented benefits of crop diversification in terms of yield stability and resource use efficiency, European agriculture is still mainly based on sole crops. We present results from an ongoing project together with organic farmers in southern Sweden, designed to evaluate the empirical generalizability of production benefits in intercropping systems. The work started by agreeing on objectives concerning evenness in crop maturity, low weed abundance and high crop quality, that need to be fulfilled in order for the participating farmers to grow more intercrops. Grain legume-cereal combinations that appear promising according to farmers' experience and scientific results were then identified, and their performance tested in on-farm trials and research-station field experiments. The results obtained so far show clear reductions in weed abundance with increasing proportion of the cereal component in lentil-oat and lupin-wheat intercrops, and higher total yields in intercrops than in sole crops. The results and experiences from the project will be discussed in the context of promoting the implementation of intercropping and enhancing the sustainability of Swedish organic grain legume production.

P127 – S14

The effects of legume crops (pea and faba bean) on yield and quality parameters of following cabbage crops under organic production conditions

Balliu A.[1], Liko J.[2], Rada Z.[1], Sallaku G.[1]
1 - Agricultural University of Tirana, Albania
2 - Technology Transfer Center of Lushnja,Albania

Forty day old broccoli and cauliflower seedlings were transplanted in three equal field blocks previously cultivated with respectively; wheat, field pea and faba bean. The common conventional production technology, including the use of chemical fertilizers was applied in wheat, but no fertilizers at all were used in faba bean or field pea blocks. Field transplanting of broccoli and cauliflower seedlings was conducted according to a three replications randomized block design at an equal planting density (0.6 m x 0.3m) and common organic production practices were applied throughout plant' growing cycle till the end of November 2015. A significantly higher above ground biomass was recorded in the cauliflower crops followed faba bean, versus both field pea and wheat, but no difference was found regarding broccoli. As well, significantly higher N total content and N-NO3 content was found in the leaves of broccoli and cauliflower crops followed faba bean compared with the respective crops followed either field pea or wheat. A significantly higher percentage of curd formation, as also the highest curd yield either in broccoli or cauliflower were harvested from the crops followed faba bean and then field pea. While a significantly higher average curd weight was found in cauliflower crops following faba bean, but not in broccoli, yet no differences were found regarding total N, P and K content in broccoli or cauliflower's curd due to pre crop plant.

P128 – S14

Suboptimal environment temperatures affect growth and the morphology of root system in pea (*Pisum sativum* L) plants

Sallaku G., **Balliu A.**
Agricultural University of Tirana,Albania

Seeds of three different pea genotype were sown in styrofoam transplant trays filled with vermiculite and latter placed in two different growth chambers, respectively at air temperatures of 10°C and 15°C. In both chambers the relative humidity was maintained at 90%, PPFD 180μmol m^2 s^{-1} and the photoperiod 12h. At DAS 7, 9 and 12, ten plant of each treatment were selected randomly, dissected and separated into roots and shoots. The root system was scanned and analyzed and subsequently, all plant organs were dried (65°C, 48 h) and weighted separately. The environment temperature has affected the dry matter accumulation of newly emerged pea plants. Low temperature has significantly reduced the overall plant dry matter, but it has favored a higher proportion of root dry matter versus the total plant matter. However, depend less of environment temperatures, root to whole plant ratio was gradually decreased alongside plant growth. The morphology of root system was also highly influenced by the environment temperature. Under suboptimal environmental temperatures, the root system of pea plants is less branched, i.e., the number of tips and forks was significantly reduced. Total root length, root projected area, root surface area and root volume were as well significantly smaller, while the average root diameter was strongly increased. Significant differences regarding root morphology parameters did also found among different genotypes.

P129 – S14

Foliar application of free amino acids improved alfalfa performance under rainfed conditions

Pooryousef M.[1] **and Alizadeh K.**[2]
1 - Department of Agronomy, Mahabad branch, Islamic Azad University, Mahabad, Iran
2 - Dryland Agricultural Research Institute (DARI), Maragheh, Iran

This work investigated the efficiency of free amino acid compounds to improve production of alfalfa (*Medicago sativa* L.) under rain-fed conditions during 2011-2012. Experiment was conducted as complete randomized blocks design with three replications at three already established alfalfa cv. Garayonja fields. There was two different spraying times including one spray at early 4-6 leaves stage and three times spraying started at 4-6 leaves stage with two weeks intervals. The experiment included 12 treatments resulted from factorial of six spray treatments and two spraying times. Spray treatments included Aminol-forte, Kadostim, Fosnutren and humiforte at 1 L/ha, along with water spray and no spray as control. Results indicated that increasing the spraying times of plants with amino acid compounds significantly ($P<0.01$) increased plant height, dry biomass weight and crude protein content compared to control. Different amino acid compounds showed different effects regarding the studied traits. The highest biomass achieved in using Kadestim and application of Aminol-forteh resulted to the highest crude protein content. It was concluded that foliar spray of free amino acids could enhance the quality and quantity of alfalfa in the rain-fed conditions.

P130 – S14

Evaluation of different organically cultivated grain legumes in Northern Germany

Böhm H., Aulrich K.
Thünen-Institute of Organic Farming

Field trials at the Thünen-Institute of Organic Farming in Northern Germany were conducted in the years 2011 to 2015 in a randomized block design with four replicates. Different grain legumes such as *Vicia faba* (field bean, cv Divine), *Pisum sativum* (pea, cv Respect), *Lupinus angustifolius* (blue lupin, cv Boruta) and *L. albus* (white lupin, cv Feodora) were compared to two varieties of *Vicia sativa* (common vetch, cv Ina and Slovena) as pure stand and intercropped with oat (cv Galaxy) and three different seed ratios (75% : 25%, 50% : 50% and 25% vetch : 75% oat of the respective seed rate in pure stand). In the years 2014 and 2015 peas, field beans and blue lupins were cultivated intercropped with 100% of the seed rate of grain legumes and 25% of the seed rate of oat.

White lupin showed the highest yield, crude protein (CP)-content and CP-yield, but the cultivation is not recommendable due to the high susceptibility to anthracnose. Yield of field bean is lower compared to white lupin but higher compared to the pea and blue lupin. The cultivation of vetch-oat intercrop is necessary due to the low lodging resistance. The seed ratio of 50% vetch and 50% oat had a higher lodging resistance and a better weed suppression compared to the intercropped vetch with 75% vetch in the seed rate. Yield of Slovena was higher compared to Ina. CP content of vetch (33.4%) was comparable to that of blue lupin (33.6%) and higher than in field bean (29.0%). Peas had the lowest level of CP (19.6%).

P131 – S14

Effect of sulfur fertilization and variety on yield and contents of crude protein and amino acids of organically produced blue lupins (*Lupinus angustifolius* L.)

Witten S., Aulrich K., Böhm H.

Thünen Institute of Organic Farming - Federal Research Institute for Rural Areas, Forestry and Fisheries

Grain legumes, like blue lupins, are important protein feedstuffs especially in organic farming. Their content of crude protein (CP) and essential amino acids (EAA) is of great interest. The sulfur-containing amino acids (SAA) methionine and cysteine are often limiting in common diets primarily for poultry. Therefore, we investigated, whether sulfur fertilization of blue lupins could enhance their contents of SAA and if it has other effects regarding crop yield, CP and further EAA.

Two branched (Boregine, Probor) and two determinated (Boruta, Sonet) blue lupin varieties were cultivated at an experimental station in Northern Germany in the years 2012, 2013, and 2015. The varieties were either grown with or without S fertilization (40 kg S ha-1; MgSO4). Samples were analyzed for CP and amino acids (AA) with NIRS. Statistical analyses were done with SAS 9.4 (proc glm).

The yield and the contents of CP and AA differed depending on variety in the observed years. Boregine showed the highest yield and Probor the highest CP content. Boruta had the lowest yield and CP content. Sulfur fertilization was able to increase the amount of SAA in some varieties but tended to decrease lysine and threonine content without affecting crop yield or CP content. This might be due to an altered storage protein ratio. Hence, sulfur fertilization could be beneficial by increasing SAA in blue lupin varieties. Further investigations on the effect of sulfur fertilization for other legumes are requested.

P132 – S14

Beans: from seed to seed

Sousa M.[1], Fernandes H.A.[2], Ribeiro C.J[3]

1 - Frescura Sublime Unipessoal Lda., Rua Cruz do Romeu, 510. Ronfe, 4805-406 Guimarães. sousamaf@gmail.com

2 - Centre for the Research and Technology of Agro-Environmental and Biological Sciences (CITAB), University of Trás-os-Montes and Alto Douro (UTAD), Quinta de Prados, 5001-801 Vila Real, Portugal.hortenseaf@hotmail.com

3 - University of Trás-os-Montes and Alto Douro (UTAD), Department of Agronomy, Quinta de Prados, 5001-801 Vila Real, Portugal. cribeiro@utad.pt

Leguminous species are part of the Portuguese gastronomic tradition and Mediterranean diet, but in recent decades their consumption suffered a sharp decline. So, it is very important the improvement of their consumption by using different stages of plant development, based on a best knowledge of the cultural practices and its relation to the quality of pods and seeds.

The use of ancient cultivars and good agriculture practices are important ways to preserve the genetic resources and making use of species and cultivars already used and adapted to our agricultural conditions and used by our ancestors. By this way, it will be possible to identify the best stages of pod and seed maturity for harvest and establish the time elapsed between sowing and the desired maturation stage.

The offer of new products with high degree of quality requires the monitoring of all cultural practices and the recording of all phases of production. The main objective of this work is to present the sequence of cultural practices between sowing and harvest at different development stages of pods and seeds from cowpea (*Vigna unguiculata*) and bean (*Phaseolus vulgaris*). Also, it will be recorded the vegetative and the reproductive phase of each species, presenting the cultural cycle for these plants produced at the North of Portugal.

The main use of the production is a freezing process of immature fruits and seeds instead of the common use as dried seed.

P133 – S14

Efficacy of different herbicide treatments in a trial located in Montijo (Extremadura, Spain)

Gragera-Facundo J., Lozano-Ruiz M. J., Maya-Blanco V., González-López F.

CICYTEX, Junta de Extremadura, Spain

The effect of four herbicide treatments has been tested in six different legume species in a trial located in a commercial farm located at Montijo. The applied treatments were: 1 (pendimetaline 33%, 3,5 L/ha + linuron 45% 1 L/ha, preemergence), 2 (pendimetaline 33%, 3,5 L/ha + linuron 45% 1 L/ha + imazamox 4% 3 L/ha + aclonifen 60% 2,5 L/ha, preemergence), 3 (imazamox 1,67% plus pendimetaline 25% 3 L/ha + clomazone 36% 0,25 L/ha + aclonifen 60% 2,5 L/ha) and 4 (fluazifop-butil 12,5% 1,5 L/ha, posteemergence). Legume species were white lupin, chickpea, pea, field bean, vetch and *Vicia ervilia*. Herbiciede treatments 2 and 3 control very well broad leaf weeds, without detectable effects over grass weeds. In lupin and chickpea the highest grain yield was recorded under the treatment 4. For the rest of legumes, the highest grain yields were recorded under the treatment 2, that was the second highest grain yield for lupin and chickpea. Phytotoxicity sympthoms were detected when the treatments 2 and 3 were applied.

P135 – S14

Nitrogen availability from peas and faba beans as pre-crops to broccoli followed by lettuce, in Norwegian field trials

Seljåsen R.[1], Torp T.[2] and Vågen I.M.[1]

1 - Norwegian Institute of Bioeconomy Research, Division of food production and society, Norway
2) - Department of Horticulture, Reddalsveien 215, 4886 Grimstad, Norway.

Meth: Organic field trial, 'spilt-split plot design' with 4 blocks. Whole plots (spring 2014) had legumes (pea or faba beans), and sub plots (autumn 2014) had 4 autumn soil treatments with combinations of legume residue incorporation and cover crop. The sub-sub plots (spring 2015) were with and without additional manure fertilization.
Res: The root biomass of both legume pre cops had equal nitrogen (N) concentration, but total root biomass was twice as high for fava beans as for peas (5.08 vs. 2.41 kg m^{-2}). Fava bean pre crop with biomass incorporation without cover crop gave the highest broccoli yield (4.10 t ha^{-1}) compared with pea pre crop with biomass incorporation and no cover crop (2.44 t ha^{-1}). Also the last crop in the rotation, lettuce, had 94% higher yield after fava beans (6.6 t ha^{-1}) compared to peas (3.4 t ha^{-1}). Rye as cover crop efficiently assimilated and conserved N during winter, shown by a 4 to 5-fold reduction in soil NO3-N, and nearly 2-fold reduction in soil N-min levels, compared to open soil. Additional manure application affected crop yield, with 3- and 2-fold increase in broccoli and lettuce, respectively.
Conc: Fava beans as pre crop resulted in higher yields of broccoli and lettuce the following seasons, compared to peas. This was explained by twice as much root biomass for that crop

P136 – S14

Evaluation of agronomic practices on production of Clearfield red lentil in Alberta, Canada

Bowness R.[2], Dubitz T.[2], Olson M.A.[1], Hoy C.[1], Henriquez B.[1,] Bandara M.[5], Kruger A.[5], Pauly D.[3], Middleton A.[3], Pfiffner P.[3], Gill K.[4], Pettyjohn J.P.[4]

1 - Alberta Agriculture and Forestry, Edmonton, Alberta, Canada
2 - Alberta Agriculture and Forestry, Lacombe, Alberta, Canada
3 - Alberta Agriculture and Forestry, Lethbridge, Alberta, Canada
4 - Smokey Applied Research and Demonstration Association, Falher, Alberta, Canada
5 - Alberta Agriculture and Forestry Food and Bio-Industrial Crops Branch, Alberta, Canada

Red lentil (Lens culinaris L.) is an important nutritional global commodity. It is the largest acreage pulse crop grown on the prairies and Canada is the leading exporter. As lentil fixes nitrogen from the air, it is a valuable crop for rotation. Field trials were conducted across Alberta from 2012-2015 to identify the best management practices for Clearfield red lentil. Treatments included a range of nitrogen rate applications combined with the presence or absence of rhizobial bacteria inoculation, five different seeding densities and the use of several imidazolinone herbicide formulations. Plots were assessed for agronomic and phenological traits. Results were variable across locations and years, however the results indicated that red lentil grows well in Alberta. Nitrogen application improved plant growth at low rates, but negatively affected nodulation and seed yield at levels above 30 kg N ha^{-1}. The optimum seeding density ranged between 120 to 160 plants m^{-2} but the yield response above 60 plants m^{-2} was not significant. In general all herbicides effectively controlled the weeds but some formulations caused a decrease in nodulation and seed yield. Considering the success of the red lentil studies, Clearfield red lentil is a great rotational option for Alberta producers when proper agronomic practices are followed.

P137 – S14

Effect of forage legumes management methods on variation dynamics of mineral nitrogen in the Lithuania’s Cambisol

Arlauskienė A.

Joniškėlis Experimental Station of the Lithuanian Research Centre for Agriculture and Forestry, Lithuania

The study was aimed to determine of perennial forage legumes (*Trifolium pratense* L., *Medicago sativa* L.) and their mixtures with festulolium (x *Festuliolium*), used as mulch, and their effect on mineral N variation in the clay loam Cambisol. The experiments were conducted in 2007-2012 in the crop sequence: perennial grasses – winter wheat – winter triticale. Management methods of the aboveground mass of perennial grasses were: removed from the field (cut twice); mixed management (first cut was removed from the field, second and third cuts – mulched); mulching (cut four times and mulched). The mineral N content variation in the soil depended on the incorporated mass of perennial grasses (mixed management), its C:N and lignin:N ratios (mixed management and mulching) and meteorological conditions (all methods). The compatibility of N release from incorporated organic matter and cereal N demand was established not every year. In favourable years, forage legumes and their mixtures with festulolium significantly increased mineral N in the soil for two years in spring. The effect of mulch was more prominent in the second year of cereal growing. Rainy summer and autumn led to increased mineral N content after incorporation of legumes total mulch. During the non-vegetation period of plants, mineral N content in the soil can be reduced by applying mixed management method or by using mixtures of forage legumes and festulolium as mulch.

P139 – S14

Seed yield stability assessment and QTL mapping for yield-related traits in narrow-leafed lupin (*Lupinus angustifolius* L.)

Górynowicz B., Kroc M., Święcicki W.
Institute of Plant Genetics, Polish Academy of Sciences, Poznan, Poland

Lupins are characterized by high potential of seed yield production, especially with reference to protein content. Unfortunately yield stability of lupins is variable influencing their growing area. Seed yield and its components are quantitatively inherited but also affected by both agricultural and weather factors. The aim of this study was to assess selected narrow-leafed lupin cultivars gathered in the current Polish National List of Varieties, regarding their yield stability. Moreover regions of Lupinus angustifolius genome governing the expression of seed yield components were identified.

In the assessment of seed yield size and quality 10 traditional and unbranched cultivars of narrow-leafed lupin were included. Field experiments were conducted in 2011-2014 in locations with different soil and weather conditions. Population of 89 RILs in F8 was assessed regarding four seed yield components (number of pods per plant, number of seeds per plant, yield and 1000-seed weight) during 4-year field trial (2012-2015) to identify QTLs.

As a result of this study we identified the most stable lupin cultivars regarding yield, which are Boruta and Graf. Less stable were Kalif, Kadryl and Regent, while as most unstable we found Zeus, Neptun, Sonet, Bojar and Dalbor cultivars. Moreover QTLs consistent across years responsible for seed yield and its components were identified.

Session 15, parallel: Frontiers in legume breeding (cont.) - Room *Arrábida III*

Chaired by Paolo Annicchiarico (CREA, Italy)

14:30-14:40 Oral – S15

Genomic based platform for chickpea breeding program at the University of Saskatchewan

Deokar A., Tar'an B.
Crop Development Centre/Department of Plant Sciences, University of Saskatchewan.
51 Campus Dr., Saskatoon, SK, Canada, S7N 5A8 bunyamin.taran@usask.ca

Important breeding objectives of chickpea consist of traits with different levels of genetic complexity. For simple traits such as herbicide resistance, growth habit and early flowering, MAS has been effective and allows selection for desirable breeding lines at early generation, thus, only selected lines continue for agronomic evaluation at later generations. The use of MAS for improving more complex traits in chickpeas, however, had very limited success. Genomic selection (GS) has become an important method of applying molecular markers for selection of complex traits in plants. We applied GS in chickpea and evaluated the effect of marker selection on prediction accuracy. A panel of 281 germplasm and elite lines was evaluated at multi locations in 2014 and genotyped by GBS generating a total of 4,524 SNPs (MAF >0.05). Genome wide association analyses were done to examine the genetic architecture of the traits being tested. Best linear unbiased estimates (rrBLUP) were calculated and input into the genomic prediction model for days to flowering, days to maturity, resistance to ascochyta blight, seed weight, seed iron concentration and grain yield. The effect of training population size on prediction accuracy was evaluated using a validation set comprised of randomly selected lines and training sets of 10-90% total population. The validation set was created by randomly sampling breeding lines without replacement. The correlation accuracy with varying training population sizes ranged from 0.20 for seed iron concentration to 0.80 for 1000 seed weight. For seed weight, the prediction accuracy increased from 70% to 80% when the size of the training population increased from 28 to 84 lines; further increase of the training population size did not significantly increase the accuracy.

14:40-14:50 Oral – S15

Faba bean lines differ in their contribution as pollen donor to cross-fertilized seed

Brünjes L., Link W.

Georg-August-Universität, Department of Crop Sciences, Plant Breeding, Von-Siebold-Str. 8, 37075 Göttingen, Germany

Faba bean (*Vicia faba* L.) is still a marginal crop in Germany due to insufficient yield level and yield stability. In this study, we aim at increasing both traits by increasing shares of heterosis in synthetic varieties. In partially allogamous crops such as faba bean, the share of heterosis in a synthetic can be increased by higher degrees of cross-fertilization. This degree is a central parameter in yield prediction and generally defined as the ratio between crossed seed and all seed. When using the degree of cross-fertilization to predict inbreeding and share of heterosis, genotype-specific degrees of cross-fertilization are considered while assuming that all genotypes contribute the same pollen dose to the cross-fertilized seeds. However, we expect faba bean genotypes to differ in paternal mating success assuming that genotypes have different success rates as pollen donors. To quantify the variation of both, the degree of cross-fertilization and of the paternal mating success, we have assessed these parameters in a polycross of eight faba bean lines, each grown with 64 individuals. Ten seeds per plant have been analyzed using eight SNP markers in order to identify the father genotype of each seed. Based on these results, the degree of cross-fertilization varied between 28 and 63 %, the paternal mating success between 8 and 19 %. We will include these differences in yield predictions of synthetics, to better manage and exploit heterotic yield increase in faba bean.

14:50-15:00 Oral – S15

Assessing and overcoming genetic trade-offs in breeding grazing-tolerant alfalfa

Pecetti L., Annicchiarico P.

Council for Agricultural Research and Economics – Research Centre for Fodder Crops and Dairy Productions (CREA-FLC), Lodi, Italy

Grazing-tolerant alfalfa is an important asset for sustainable intensification of Mediterranean-climate crop-livestock systems, but selection is challenged by marked cold-season dormancy and prostrate habit of tolerant material. This study assessed in different genetic backgrounds the size of genetic variation and genetically based trade-offs for various key traits and their implications for selection. Some 432 cloned F1 progenies issued by four crosses between erect/little dormant and prostrate/dormant genotypes were evaluated for dry-matter (DM) yield and final persistence under continuous, intense sheep grazing for three years. Both DM yield and persistence had negative genetic correlation with erect plant habit (rg range: –0.31 to –0.87), while persistence was inversely related also to cold-season growth (rg range: –0.33 to –0.73). Correlations of these traits with early DM yield under mowing, plant diameter and leaflet area were erratic or nil. DM yield under grazing and persistence showed large genetic variation (CVg range: 33.3 to 57.8%), and about 50% greater within- than between-cross variance. Morphophysiological traits had lower genetic variation and even greater relative size of within-cross variance. Selecting grazing-tolerant cultivars can exploit large genetic variation but requires extensive within-cross genotype evaluation to produce material with modest dormancy and relatively erect habit. Marker-assisted selection needs be explored to facilitate this task.

15:00-15:10 ORAL – S15

Enhancing the nutritional quality of field pea

Warkentin T.D.[1], Arganosa G.A.[1], Bangar P.[1], Liu X.[1], Shunmugam A.[2], Delgerjav T. [3], Diapari M.[4], Rehman A.[5], Jha A.B.[1], Ashokkumar K.[6], Purves R.W. [1], Thacker P.[7], Tar'an B.[1] Bett K.E.[1], and Glahn R.P.[8]

1 - Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada
2 - Agriculture and Agri-Food Canada, Saskatoon, SK, Canada
3 - Bayer Crop Science, Inc, Saskatoon, SK, Canada
4 - Agriculture and Agri-Food Canada, London, ON, Canada
5 - Cargill, Inc., Aberdeen, SK, Canada
6 - Department of Plant Biotechnology, Tamil Nadu Agricultural University, Coimbatore, TN, India.
7 - Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada
8 - USDA-ARS, Cornell University, Ithaca, NY, USA

Field pea seeds, like those of other pulse crops, are rich in protein, slowly digestible carbohydrates, and fiber. To further enhance their nutritional value, research is in progress to increase the concentration and bioavailability of key micronutrients. A 100 g dry weight serving of field pea supplied a substantial portion of the recommended daily allowance of Fe, Zn, and Se for adults. Association analysis identified nine single nucleotide polymorphisms (SNPs) associated with Fe concentration, and 2 SNPs associate with Zn concentration in pea. Field pea lines were identified with a 60% reduction in phytate-phosphorus concentration in seeds controlled by a single recessive gene mapped on pea chromosome 3. Iron bioavailability, assessed using a human cell culture assay, of progeny arising from crosses with the low phytate lines displayed up to 3-fold greater iron bioavailability than that of their progenitor. In some cases, iron concentration and lutein concentration were positively correlated with iron bioavailability. Total tract apparent availability of phosphorus and bone strength were higher for broiler chicks fed a low phytate pea diet than for birds fed a normal pea diet

15:10-15:20 ORAL – S15

Machine learning approaches allow for determination of important root traits and enhance differentiation of legumes cultivars

Zhao J.[1], Gaonkar B.[2], Bodner G.[3], Rewald B.[1]

1 - Department of Forest and Soil Sciences, University of Natural Resources and Life Sciences, Vienna (BOKU), Peter-Jordan-Straße 82, 1190 Vienna, Austria.

2 - Center for Biomedical image computing and Analysis, Department of Bioengineering, University of Pennsylvania, 3600 Market street, Philadelphia, PA 19104, USA.

3 - Division of Agronomy, Department of Crop Sciences, University of Natural Resources and Life Sciences, Vienna (BOKU), Konrad Lorenz-Straße 24, 3430 Tulln an der Donau, Austria.

Plant phenotyping intends measuring complex traits related to growth, yield, and adaptation to stress at different macroscopically scales of plant organization. Especially the modification of root system architecture (RSA) could contribute to improvements of desirable agronomic traits; RSA was described key to a second green revolution improving resource use efficiency of crops. Machine learning approaches are promising statistical tools for variable selection and group classification—reducing the workload for humans, but also ensuring objectivity and consistency in analyses. However, new approaches overcoming the difficulties of applying machine learning with unbiased root traits importance measure on small size samples and powerful classification methods are needed to improve the analyses of manually and image analysis-derived phenological data sets and identify candidate cultivars for wider agricultural use and/or future breeding efforts. Thus, we developed algorithms identifying the most discriminative root traits of three legume species with random forest models and differentiated cultivars and species with support vector machine analysis based on root traits.

Interestingly, discriminative root traits were unique in each species. The machine learning approach could accurately identify cultivars with root system architectures such as deep or shallow rooting which can be used for future breeding. Funded by FP7 grant agreement no 613781 (EUROLEGUME).

15:20-15:30 Oral – S15

An international network to improve mungbean breeding and production

Madhavan-Nair R.[1], Schafleitner R.[2], Douglas C.[3], Alam Md.M.[4], Garg A. P.[5], Shwe T.[6], Huttner E.[7]

1 - World Vegetable Center, South Asia.
2 - World Vegetable Center, HQ.
3 - Department of Agriculture and Fisheries (DAF).
4 - Bangladesh Agricultural Research Institute (BARI).
5 - Indian Institute of Pulse Research (IIPR).
6 - Myanmar Department of Agriculture Research (DAR).
7 - Australian Centre for International Agricultural Research (ACIAR).

Mungbean [*Vigna radiata* (L.) R. Wilczek var. radiata] is an important food legume in south, east and southeast Asia, where 90% of global production currently occurs. More than 6 million hectares are cultivated, producing up to 3 million metric tons of grain that is consumed directly as dhal, bean sprouts or noodles.

The World Vegetable Center holds the world's largest collection of *Vigna* species, with 11,591 accessions. Recently the Center developed a mungbean core collection comprising 1,481 accessions and a mini-core comprising 296 accessions. The core collection was developed based on phenotypic characterization, while the mini-core was developed by molecular characterization using 20 single sequence repeat (SSR) markers. Intra-specific and inter-specific hybridization methods are being utilised to tackle major problems in mungbean such as mungbean yellow mosaic disease, Cercospora leaf spot, powdery mildew, and bruchids. Also variation for nutritional quality as well as sprouting ability in mungbean are being explored.

The International Mungbean Improvement Network and its outcomes will help unlock the potential of mungbean to improve productivity of tropical agriculture in Australia and Asia. The project is an initiative of ACIAR, DAF, and the World Vegetable Center, and will initially partner with Bangladesh, India and Myanmar. The objectives of the project are to develop coordinated pre-breeding capability; conduct an extensive phenotypic characterisation of the mini core collection; screen for resistance to key biotic and abiotic stresses; genotype the mini-core at high density and identify marker traits associations and support these activities with an integrated plant breeding information system.

Session 16, parallel: Advances in legume agronomy (cont.) - Room *Arrábida IV*

Chaired by Fred Stoddard (Univ. Helsinki, Finland) and Claudio Porqueddu (CNR, Italy)

14:30-14:40 Oral – S16

Ecosystem services provided by legumes and exploited by stakeholders in three french territories

Corre-Hellou G.[1], Mauline M.[1], Naudin C.[1], Poret J.[1], Sorin S.[2], Pelzer E.[3], Médiène S.[3], Jeuffroy M.-H.[3], Bazot M.[3], Journet E.-P.[4-5], Lecloux E.[5], Justes E.[5], Larribeau A.[6], Garnaud D.[7]

1 - LEVA, Univ. Bretagne Loire, Ecole Supérieure d'Agricultures (ESA), 49007 Angers, France

2 - Terrena Innovation, 44150 Ancenis, France

3 - UMR Agronomie INRA, AgroParisTech, Université Paris Saclay, 78850 Thiverval-Grignon, France

4 - LIPM, Université de Toulouse, INRA, CNRS, Castanet-Tolosan, France

5 - AGIR, Université de Toulouse, INRA, INPT, INP- EI PURPAN, Castanet-Tolosan, France

6) - Qualisol, 82102 Castelsarrasin, France 7 S.C.A de déshydratation de la Haute Seine, 21450 Baigneux les Juifs

Legumes offer a wide array of services to be valued in production systems and supply chains: production of protein-rich seeds with interesting nutritional properties for both food and feed; beneficial preceding crop effects through the restitution of biologically fixed N and the time/space diversification of cropping systems. However the high variability of performances hinders anticipating and exploiting such services through adapted cropping system management. Today, stakeholders are lacking local references for diverse legume species and insertion modes. Hence approaches to insert more legumes in territories need to be assisted by identifying / characterising 1) the contrasted actors expectations, 2) services obtained by farmers in real farm context, 3) the main variability factors and levers to optimally exploit services, and by sharing results with actors. In 3 french territories (Pays de la Loire-PDL, Burgundy-B & Midi-Pyrénées-MP) observatories have been set up in partnership with farm cooperatives. Several species and insertion modes selected by local actors are being studied: spring/winter lupin as sole crop or intercropped with triticale (PDL); alfalfa and spring pea (B), soybean, and lentil as sole crop or intercropped with wheat (MP). A 2-year followup of the legume and the next crop has been performed in 2015-16 and is repeated on other plots in

2016-17. Performances variability has been analysed in relation with (a)biotic limiting factors and farmers practices.

14:40-14:50 Oral – S16

Quantification of nitrogen fluxes and explanatory plant traits during a two-year legume-cereal rotation

Guinet M., Voisin A-S., Nicolardot B.

UMR Agroécologie, AgroSup Dijon, INRA, Univ. Bourgogne Franche-Comté, F-21000 Dijon, France

In the context of agroecological transition, the reintroduction of legume crops should play a key role in cropping system sustainability by allowing a reduction of nitrogen (N) inputs. But few references are available concerning the agronomical and ecological services provided by a wide range of legume crops, particularly within crops succession scale. Thus, the main objective of our study is to quantify the N fluxes during and after the legume crops taking into account 10 legume crops (peas, lupin, faba bean, soybean...). Our experiment consists in i) quantifying symbiotic N fixation depending on the amount of soil inorganic N, the mineralisation of N present in legume crop residues after soil incorporation and N losses outside of the soil-plant system (leaching, emission of nitrous oxide), ii) identifying plant biological traits associated to N fluxes. Thus, different N fluxes were quantified during a two-year field experiment, i.e. the first year (2014) legume crops were implanted and followed by wheat the second year (14-15) after incorporation of legume residues. This experiment will be repeated in 2016-2017.The first results concerning legume pre-crop effects will be presented during the congress, considering the effect of preceding legume crops on wheat seed yield and N content. This effect will be related to legume aerial and below ground residues that were characterized by their biomass, C/N content and potential mineralization.

14:50-15:00 Oral – S16

Cereals as companion crops to improve weed control and overall productivity in cereal-grain legume intercrops: case of lupin

Carton N., Piva G., Naudin C., Corre-Hellou G.
UR LEVA-ESA, 55 Rue Rabelais, 49007 Angers, France

Low and unstable yields due to abiotic and biotic factors (notably weeds) are major obstacles to a broader adoption of grain legumes in European agricultural systems. There is a need to design alternative-cropping practices for grain legumes in order to secure their productivity and improve weed control while reducing herbicide use.

Intercropping, the growing of two or more species together on the same area of land at the same time may be a way to decrease yield variability and to increase competitive ability against weeds. A cereal crop can be seen as a companion crop providing services to the legume in cereal-legume intercrops.

We illustrate the benefits of intercropping legumes with a non-fixing crop to control weeds and increase overall productivity as compared to grain legume sole crops. The mechanisms explaining the benefits are presented, with a focus on the dynamics of nitrogen and light sharing between legume crop, non-legume crop and weeds. We also demonstrate the impact of plant traits on interactions using contrasted combinations of species and cultivars. This work shows the relevance of using trait complementarities when designing intercrops. The approach is illustrated with winter white lupin (*Lupinus albus* L.), which is well known for its high yield variability and low competitive ability against weeds. Lupin-cereal intercrops are compared with lupin sole crops both in controlled conditions and field experiments in Western France.

15:00-15:10 Oral – S16

Intercropping lentil with spring wheat to improve productivity and income in organic farming

Viguier L.[1,2], Bedoussac L.[2,3], Journet E.P.[2], JustesE.[2]

1 - Cooperative Qualisol, F-82100 Castelsarrasin, France
2 - INRA, UMR1248 AGIR, F-31320 Castanet-Tolosan, France
3 - ENFA, F-31320 Castanet-Tolosan, France
4 - CNRS, UMR2594 LIPM, F-31320 Castanet-Tolosan, France

The food legume lentil is attracting growing interest among organic farmers. However, its productivity is low and very variable notably due to its lodging sensitivity. We analysed the functioning and performances of lentil-spring wheat intercrops (IC) for yield improvement/stabilization. An organic field experiment was conducted at INRA-Toulouse, with 4 lentil cvs. and 2 of spring wheat grown as sole crops (SC) and IC at 4 seeding ratios (67/33%, 100/17%, 100/33% and 100/50% for lentil and wheat resp., compared to SC density). Total IC grain yield was 1.24 t/ha and was higher than the mean yield of the respective SCs, higher than that of lentil SCs (0.87 t/ha) and similar to that of spring wheat SCs (1.29 t/ha). This confirms the interest of IC in organic farming to improve yield due to the species complementarity for use of available resources. Lentil production was often lower in IC than in SC as a result of wheat competition. Hence to favour yield of lentil, the most profitable crop (3-4 times higher price), wheat density must remain low. Even with wheat density as low as 17% lentil lodging was reduced which may increase the amount of lentil harvested in IC vs. in SC. Thus lentil IC could be an efficient system to increase organic farmers net income in comparison to classical lentil SC. "Genotype by density by species" interactions were observed across IC combinations, calling for further study of the different cultivars responses in order to design optimized IC systems.

15:10-15:20 Oral – S16

Diversification and intensification of usa dryland cropping systems using autumn-sown winter pea

Guy S. O.[1], McGee R. J.[2], Lauver M. A.[1]

1 - Department of Crop and Soil Sciences, Washington State University, Pullman, WA, USA. sguy@wsu.edu

2 - Grain Legume Genetics and Physiology Research Unit, USDA-ARS, Pullman, WA, USA

In the USA states Washington, Oregon, Idaho, and Montana, 5.3 million cropped hectares average less than 450 mm annual precipitation. There are few alternative crops to winter wheat in low rainfall, but there is a strong interest in economically viable rotation crops where fallow is practiced. Autumn-sown peas (ASP) can now be marketed as a food quality allowing potential ASP production in low rainfall winter wheat areas. Spring-sown peas are lower yielding than ASP by 30-50% and mature later. Early maturity is important when crops mature under terminal drought and heat stress. Emergence can be a problem for winter wheat seeded deep to reach moisture. ASP consistently emerges from 15cm depths or more and forces through most crusting. Improved winter hardiness in ASP can rival winter wheat. Current ASP production in the dry areas includes cover crop and feed uses, and contracts are in high demand. Food quality ASP varieties will soon be released by USDA-ARS and private breeders that can be sold to open markets and hectarage should not be limited by contracts. ASP conducts biological N fixation, is a low energy and greenhouse gas emissions crop, will interrupt weed, disease and insect cycles, has a low water use, and can flourish under current crop management conditions. Spring sown pea rotated with wheat in higher rainfall areas revolutionized that cropping system. Similarly, ASP is poised to diversify and intensify crop production especially in the lower rainfall region.

15:20-15:30 Oral – S16

Quantitative analysis of the root distribution in a faba bean-wheat intercropping system by Fourier transform infrared (FTIR) spectroscopy

Streit J., Meinen C., Rauber R.

Georg-August-University Goettingen| Department for Crop Sciences | Devision of Agronomy

Intercrops often demonstrate higher yields compared to their sole crops due to complementary resource use e.g. in light or nutrients. Another reason for this effect could be a differing rooting system of both intercropping partners and therefore a shift in rooting patterns resulting in root mass overyielding. To study these species-specific rooting patterns, roots have to be identified to species level. In this study, Fourier transform infrared (FTIR) attenuated total reflection (ATR) spectroscopy was successfully used to discriminate specie specific root proportions in a faba bean-wheat intercropping system. Eight winter faba bean lines (*Vicia faba* L.) and one winter wheat cultivar (*Triticum aestivum* L.) grown in in a field trial of pure stands and mixtures were investigated in regard to their differences in root distribution down to 60 cm soil depth (4 repl.). FTIR spectroscopy was used to analyze absorption spectra of dried and ground roots. Roots of pure stands were used to prepare artificial samples of faba bean and wheat root mixtures to calibrate and validate a FTIR model which predicted the species proportion in root mixtures. Root absorption spectra showed species specific peak distributions. Faba bean and wheat root spectra were clearly separated by the cluster analysis. Preliminary results indicate a root partitioning of both species and a tendency of higher root biomass in mixtures than in sole stands (overyielding).

Session 17, parallel: Legumes and environment (cont.)

- Room *Arrábida III*

Chaired by Christine Watson (SRUC, UK)

16:30-16:40 ORAL – S17

Soil nitrogen fertility and nitrogen acquisition in fababean – long-term system effects

Carlsson G., Ernfors M., Mårtensson L.M., Jensen E.S.
Swedish University of Agricultural Sciences, Alnarp, Sweden.

Nitrogen (N) fertilization of legumes reduces symbiotic N2 fixation, but knowledge on the long-term effects of N fertilization in non-legume rotational crops on the symbiotic performance of grain legumes grown without fertilizer N is limited. In this study, fababean (*Vicia faba* L.) was grown in a six-year conventional crop rotation with cereals, oilseed rape and sugar beet, at the SITES Lönnstorp field experimental station in southern Sweden. The experiment started in 1994 and included three levels of N fertilization to the other crops than fababean: 0 (N0), 85 (N2) and 160 (N4) kg N/ha. Fababean were sampled in 2011 and 2012, after three full crop rotations, for determination of grain and straw yield, N accumulation from soil and symbiotically fixed N using the natural 15N abundance method. The average fababean grain and straw yields across N levels and years were 4.6 and 2.9 metric tons per ha, respectively, and there was no significant effect of N fertilizer level to other crops on fababean N concentrations. The total fababean accumulation of soil N increased with approximately 40 kg N per ha in the N4 system compared to the N0 system, while the percent N derived from N2 fixation was reduced from 67 (N0) to 54 (N4)%. The results are discussed in the contexts of N use efficiency at the cropping system and global N cycle levels.

16:40-16:50 Oral – S17

Impact of organic practices on growth, yield, greenhouse gas emissions and biological nitrogen fixation by three local pea and faba bean landraces

Savvas D.[1]*, Pappa V.A.[1], Yfantopoulos D.[1], Karkanis A. [2], Travlos I.[1], Bebeli P.J.[1], Ntatsi G.[1], BilalisD. [1]

1 - Department of Crop Science, Agricultural University of Athens, Athens, Greece.
2 - Department of Agriculture Crop Production and Rural Environment, University of Thessaly, Greece.

Legumes constitute an essential component of rotations in organic systems due to their ability to provide plant available N2 to agricultural ecosystems. However, there is a general need to increase grain legume protein production in Europe so as to meet the increasing demand while reducing resource utilization, thereby contributing to mitigation of global climate change. A field-based experiment with pea and faba bean was carried out in a field certified for organic agriculture from 11/2014 to 11/2015 within the framework of EUROLEGUME. The experiment was laid out in a split-plot design with 2 main treatments (conventional and organic farming system) and 4 sub-plots per main plot corresponding to 4 different pea and faba bean cultivars (peas: Onwards Amorgos, Andros and Schinousa; faba beans: Aguadulce, Andros, Lefkada, Mani). Standard inorganic fertilizer and sheep manure were used in the conventional and the organically treated plots, respectively. The aim of the experiment was to test the performance of each cultivar in organic farming crops as compared to conventional cropping, in terms of GHG emissions and biological N2-fixation efficiency. The results indicated significant differences in cumulative N2O fluxes between pea cultivars with Schinousa producing the highest N2O amounts and 'Andros' the lowest. Also, Lefkada showed similar cumulative fluxes in both systems. Furthermore, Schinousa exhibited the lowest BNF efficiency and Lefkada the highest in both systems.

16:50-17:00 Oral – S17

Effect of simulated hail treatment on yield loss in chickpea

McPhee K.
North Dakota State University, USA

Hail can have devastating effects on crops and dramatically reduce productivity and quality. This study evaluated the amount of damage and yield loss from simulated hail. This research will aid crop adjusters to quantify hail damage in chickpea fields at certain growth stages. CDC Frontier was grown at the Carrington Research Extension Center in North Dakota in 2015. Five treatment levels, untreated, 25, 50, 75, and 100%, were applied at vegetative, first flower, and late bloom growth stages. Treatment levels were established based on canopy height before treatment to remove 25% of canopy height for the 25% level and 40% of canopy for the 50, 75 and 100% treatments. Individual 30x30 cm samples of plant material were collected after initial treatment to determine biomass reduction and assess damage on individual plants. Post-harvest data, seed yield, one thousand seed weight, and seed size distribution, were collected to correlate with the level of damage. Average seed yields were 2482, 1719, and 1344 kg/ha for treatments at the vegetative, first flower, and late bloom stages, respectively. The average seed yield for the five injury levels, untreated, 25, 50, 75, and 100%, were 2482, 2102, 1649, 1536, and 1476 kg/ha, respectively. Hail events later in the season with increased level of damage reduces seed yield and correlation analyses showed that plant injury data will be useful in establishing procedures to aid insurance adjustment.

17:00-17:10 Oral – S17

Meta-analysis of the effects of legume companion plants on weed control and yield of the cash crop.

Verret V.
Unité mixte de recherche d'Agronomie - Inra - AgroParisTech - Versailles-Grignon

Companion plant (CP) intercropping involves growing a cash crop with another plant that is not harvested, that delivers services to the crop and the environment. CP can compete with weeds for light and nutrients, but may also compete with the crop. Here, we reviewed 476 observations from 34 studies of intercrops of an annual cash crop and a legume CP. We explored whether legume CP intercropping can control weeds while maintaining crop yield. Yield and weed biomass ratios were analyzed as response variables in linear mixed effect models with the type of cash crop (straw cereals, maize or other crops) and the methods used to establish the CP (living mulch, synchronized sowing or relay intercropping) as explanatory variables.

52% and 34% of the intercrops resulted in lower weed biomass and higher yield (win-win) compared to non-weeded (NW) or weeded (W) control treatments (CT) respectively. 13% and 27% of the cases had a higher weed biomass associated with a lower yield (lose-lose) compared to NWCT and WCT, respectively. In average, companion plants had no significant effect on cash crop yield, but significantly decreased weed biomass by 56% relatively to NWCT and 42% relative to WCT. In particular, intercropped maize yielded 37% more than NWCT thanks to good weed suppression. The use of legume CP generally enhance weed control without reducing crop yield, but the conditions giving rise to win-win situations should be explored further to encourage the spread of this technique.

17:10-17:20 Oral – S17

A tool integrating and sharing knowledge to select legume species for oilseed rape intercropping

Médiène S., Verret V., Felix J., Valantin-Morison M.
UMR 211 Agronomie, INRA-AgroParisTech, 78850 Thiverval-Grignon

Legumes companion plants can contribute to design cropping systems less reliant on synthetic inputs, as they can deliver ecosystem services: e.g. nitrogen supply, weed regulation. Researchers have to identify and bring new knowledge to farmers to help them designing innovative systems based on intercrops. Our work focuses on oilseed rape intercropped with frost-sensitive companion plants.

We present here the steps to elaborate a tool integrating and sharing knowledge to select candidate species for oilseed rape intercropping, according to their ability to deliver regulation and provision services:

- census of existing tools and potential users' needs
- identification of plant traits (both legume and non-legume plants) and agro-pedo-climatic characteristics that enable the realization of processes leading to services delivery (by literature review and participatory workshops between extension advisors, technical institutes and researchers)
- building a multi-attribute aggregation tree (DEXI software) to aggregate plant traits and agro/pedo/climatic characteristics into a rating of services delivery
- compiling 20 traits in a database, in addition to 13 agro-pedo-climatic elements asked to the user, used as input variables in the DEXI tree.

As output, the tool classifies companion plant species according to their potential to deliver ecosystem services and explains relationships between plant traits, services delivery and interactions with the environment in a pedagogical purpose

17:20-17:30 Oral – S17

Nitrous oxide and methane fluxes from a cowpea-broccoli crop rotation under conventional and organic management practices

Sánchez-Navarro V., Zornoza R., Faz A., and Fernández J.A.
Universidad Politécnica de Cartagena, ETSIA, Cartagena, Spain

This study was carried out in a cowpea-broccoli crop rotation with the aim of evaluating the effects of applying conventional and organic fertilizers on greenhouse gas emissions (N_2O and CH_4) and their relationship with soil properties. Two cultivars of cowpea (Black-eyed pea and Grey-eyed pea) were grown within a randomized complete block study with 4 replications in plots of 10 m^2 that rotated with broccoli. Gas samples were taken at different times (0, 30 and 60 minutes) once a week using the static gas chamber technique. Soil samples (0-30 cm) were taken from each plot at the end of the crop cycle to measure soil organic carbon (C), total nitrogen (TN), NO_3- and the enzyme activities. The results obtained from the cumulative N_2O fluxes did not show a clear pattern of N_2O emission as a function of management practice or cultivar. However, the cumulative CH_4 fluxes for both cowpea cultivars were higher under conventional management than under organic, with an average increase of 2758 mg m^{-2} in Black-eyed pea and of 1612 mg m^{-2} in Grey-eyed pea. Broccoli crop in rotation with cowpea showed the same pattern with regard to CH_4 emissions, with an increase of 529 mg m^{-2} in broccoli rotated with Black-eyed pea and of 1293 mg m^{-2} in rotated with Grey-eyed pea. We observed significant negative correlations between CH_4 and TN, β-glucosidase and β-glucosaminidase. Organic management contributed to reducing CH_4 fluxes, and promoted an increase in soil TN content and β-glucosidase .

Session 18, parallel: Resistance to biotic and abiotic stresses - Room *Arrábida IV*

Chaired by Weidong Chen (USDA-ARS, USA) and Laurent Gentzbittel (CNRS, France)

16:30-16:40 Oral – S18

Exploring metabolic changes in legumes exposed to combined biotic and abiotic stress

Dickinson M.[1], Rusilowicz M.[2], WilsonJ.[2], Charlton A.[1]

1 - Fera Science Ltd, National Agrifood Innovation Campus, Sand Hutton, York YO41 1LZ, UK

2 - York Centre for Complex Systems Analysis, University of York, York YO10 5GE, UK

The yield of legume crops is severely undermined by both drought and fungal infection. A current EU FP7-project (ABSTRESS) is using state-of-the-art plant breeding tools alongside the study of gene and metabolite expression data in legume species to study their resistance mechanisms to combined stresses. Metabolomics data can be used as markers for the expression of crucial hub genes associated with stress resistance, significantly reducing the time taken to develop new crop varieties able to withstand the challenges associated with climate change.

This presentation will discuss metabolomics data obtained from the model legume *Medicago truncatula* exposed to combined drought and Fusarium infection over 12 days. Metabolite profiles were obtained from both leaves and roots for every day over the 12 days and were acquired using liquid chromatography-high resolution mass spectrometry (LC-HRMS), with further metabolite annotation/identification by LC-HRMS/MSn. Biochemical changes observed in lipid, flavanoid and alkaloid metabolism in plants exposed to both stresses will be discussed.

To support findings, a second metabolomics experiment was undertaken in pea using an identical set up as the model. The data from this confirmatory study will also be discussed, highlighting changes in metabolites and subsequent pathways common to both sets of data, with particular focus on legumes exposed to combined stresses over time.

16:40-16:50 Oral – S18

The role of plant cell wall in resistance and susceptibility to pathogenic pathogen

Toyoda K.[1], Miki M.[1], Yamasaki S.[1], Yao S.[1], Matsui H.[1], Noutoshi Y.[1], Yamamoto M.[1], Ichinose Y.[1], Shiraishi T.[1,2]

1 - Okayama University, Japan
2 - Research Institute of Biological Sciences, Okayama, Japan

Successful colonization by an appropriate pathogen can be therefore achieved by the suppression or circumvention of PAMP-triggered immunity through the secretion of pathogen-derived effectors. In *Mycosphaerella pinodes*, which causes leaf spots (blights) of pea, two structurally related glycopeptide suppressors named supprescins A and B are secreted in the pycnospore germination fluid. Pure suppressors potently inhibit the ecto-ATPase (apyrase; EC3.6.1.15) of host cell wall, temporarily reducing the ability of the host cells to defend themself. The catalytic activity in extracts from the cell walls of pea was enhanced in vitro, with the consequent increase of ROS generation by extracellular peroxidase(s), when exposed to the fungal elicitor. Interestingly, the Blue-Native PAGE analysis for cell wall proteins from pea epicotyls demonstrated that cell wall-associated, ecto- ATPase(s) formed a large protein complex(es) ranging from 450 to 900 kDa, one of components was the hydrogen peroxide-producing copper amine oxidase (CuAO). The CuAO activity was coordinately regulated with ATP-hydrolyzing activity in vitro, by an elicitor and a suppressor from *M. pinodes*. Moreover, in vitro treatment of cell wall proteins with the suppressor caused an appearance of the apyrase monomer. It is thus likely that *M. pinodes* targets the host ecto-ATPase-containing protein complex(es) to attenuate cell wall-based, extracellular defense(s).

16:50-17:00 Oral – S18

Detecting tolerant germplasm and QTLs associated with flooding stress in dry bean (*Phaseolus vulgaris* L.)

Soltani A.[1], Moghaddam S.M.[1], Walter K.[1], Restrepo-Montoya D.[1], Schroder S.[1], Mamidi S.[2], Lee R.[1], McClean P.[1], Osorno J.M.[1]

1 - North Dakota State University, Department of Plant Sciences, Fargo, ND, USA
2 - HudsonAlpha Institute, Huntsville, AL, USA

Flooding is one of the most devastating abiotic stress, endangering food security. This stress can drastically modify several physiological pathways of plants, which will eventually affect seed yield. Even though dry bean is highly susceptible to flooding, there are a few efforts addressing this issue. To identify the potential mechanisms by which dry bean tolerate the flooding stress, we evaluated ~500 genotypes under greenhouse conditions at two growth stages: germination and seedling. Seven traits were evaluated and analyzed and used for a Genome-wide Association study (GWAS) was performed using ~150K SNPs. In general, results suggest that middle-American gene pool is using different physiological mechanisms than Andean gene pool to deal with waterlogging stress. Within each pool, significant differences were also detected among market classes. For instance, chlorophyll content was well preserved in pinto and great northern market classes (16% reduction). However black and small red market classes were more tolerant to flooding in germination stage. The results of GWAS indicate that tolerant to waterlogging stress is a polygenetic trait controlled by more than 30 loci. Among them, two QTL on Pv08/1.6 and Pv02/41.1, which control root weight and germination rate under flooding conditions were also reported to play similar role in soybean. Identifying tolerant genotypes along with the associated QTL will set the stage for improving waterlogging tolerance in dry bean.

17:00-17:10 Oral – S18

Genome-Wide association mapping of frost tolerance in *Pisum sativum*

Beji S.[1], Fontaine V.[2], Devaux R.[3], Negro S.[5,6], Bahrman N.[2], Aubert G.[4], Delbreil B.[1], Lejeune-Hénaut I.[2]

1 - USC ICV-AFP, Université Lille1, 59655, Villeneuve d'Ascq, France
2 - USC ICV-AFP, INRA, 80203, Péronne, France
3 - UE GCIE, INRA, 80203, Péronne, France
4 - UMR Agroécologie, INRA, 21065, Dijon, France
5 - UMR GQE, INRA, 91190, Gif sur Yvette, France
6 - UMR MIA-Paris, AgroParisTech, 75005, Paris, France

Genome Wide Association Mapping was performed in pea. Accessions from the pea reference collection where phenotyped for frost in field and controlled conditions, and genotyped using Infinium®BeadChip 15K SNPs (Tayeh et al., 2015). After applying filters of quality control, we obtained 363 accessions and 10739 loci for GWA study. Association analyses were conducted with FaST-LMM software using a mixed model that included a relatedness kinship matrix (K) and a population structure matrix (Q) to control for false positives. The K matrix was generated using two approaches. In the first one, the kinship matrix was estimated with all the 10739 markers. In the second approach, we estimated the kinship, called "K-chr", with all the markers other than those located on the same chromosome as the marker being tested (Rincent et al., 2014). Simulations revealed that Rincent's approach was more powerful than the mixed model taking into account a general kinship (estimated for all chromosomes). The GWA study identified 8 loci distributed over different chromosomes comprising 61 SNPs significantly associated with frost tolerance. Results confirmed 3 QTLs that were previously mapped using bi-parental populations and identified 3 novel tolerance loci. Several potential-candidate genes were found corresponding to these SNPs. Additionally, the analyses allowed to identify haplotypes with increased frost tolerance and accessions with favourable alleles for this trait.

17:10-17:20 Oral – S18

Marker-assisted breeding strategies for anthracnose resistance in lupin

Ruge-Wehling B.[1], Fischer K.[1], Dieterich R.[2], Rotter B.[3], Winter P.[3], Wehling P.[1]

1 - Julius Kühn-Institut, Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Agricultural Crops, Groß Lüsewitz, Germany.
2 - Saatzucht Steinach GmbH & Co. KG, Bocksee, Germany.
3 - GenXPro GmbH, Frankfurt/Main, Germany.

Anthracnose, caused by the fungus *Colletotrichum lupini*, represents the most important disease in lupin cultivation worldwide. To obtain high and stable yields it is necessary to plant resistant cultivars as there are no possibilities to overcome the fungus via pesticides. Sets of plant genetic resources of sweet narrow-leafed and yellow lupin were assessed in their susceptibility to anthracnose. In both lupin species breeding lines were identified which displayed a qualitative resistance, each governed by a dominant gene as revealed by genetic analyses of segregating F2 families and their F3 progenies. Multi-annual field-tests with the novel resistant resources of blue and yellow lupins confirmed its high and stable level of anthracnose resistance. The underlying genes were designated LanrBo (*L. angustifolius*) and Llur (*L. luteus*). Different resources were used for developing molecular markers for the resistance, namely, (I) anchor markers already mapped in *L. angustifolius*, (II) sequence information drawn from model genomes and (III) sequence information from differentially expressed cDNA derived from RNA-Seq. Linkage analysis allowed us to locate LanrBo on linkage group NLL-11 of *Lupinus angustifolius*. Two flanking markers resulted in a marker bracket with a joint recombination of less than 0.2 %. The two markers are already integrated in breeding programs. Highly polymorphic SNPs are available for Llur and are currently used for mapping.

17:20-17:30 ORAL – S18

Use of wild relatives in pea breeding for disease resistance

Rubiales D.[1], Barilli E.[1], Rispail N.[1], Castillejo M.A.[1], Aznar-Fernández T.[1], Fondevilla S.[1]

1 - Instituto de Agricultura Sostenible, CSIC, Avda. Menendez Pidal s/n 14004, Cordoba, Spain

Pea (*Pisum sativum* ssp. *sativum*) is a cool season legume crop produced worldwide, mainly in temperate regions whose seeds can be used to feed livestock or for human food. Pea yield can be constrained by a number of pests and diseases to which there is insufficient genetic resistance available. Wild relatives, including related subspecies of *P. sativum*, or even the most distant *P. fulvum* offers a reservoir of sources of resistance that can be exploited in pea breeding.

At CSIC at Córdoba we have screened large germplasm collections of *Pisum* looking for resistance to ascochyta blight, powdery mildew, rust, broomrape, fusarium wilt, aphid and weevil. This resulted in the identification of valuable sources of resistance that were introduced in our breeding program. As an example, a new gene (*Er3*) for powdery mildew resistance was identified in *P. fulvum* and introduced in pea, with a resistant cultivar ('Eritreo') already protected in European catalogue. Similarly, the first two broomrape resistant cultivars are now protected, and a number of breeding lines are being developed. Parallel to this applied approach, some of the identified resistances have been characterized at the histochemist, genetic and proteomic level.

P140 – S18

Er3 gene, conferring resistance to *Erysiphe pisi*, is located in pea LGIV.

Cobos M.J.[1], Rubiales D.[1], Fondevilla S.[1]

1 - Institute for Sustainable Agriculture-CSIC, Avda. Menendez Pidal s/n, 14004, Cordoba, Spain

Three genes for resistance to *Erysiphe pisi*, named *er1*, *er2* and *Er3* have been described in pea so far. *er1* gene is located in pea linkage group VI, while *er2* gene has been mapped in LGIII. SCAR and RAPD markers tightly linked to *Er3* gene have been identified, but the position of these markers in the pea genetic map was unknown. In this study the pea cv. Messire and a near isogenic line of Messire containing *Er3* gene (cv. Eritreo) were surveyed with SSRs with known position in the pea map. Two SSRs previously mapped in LGIV were polymorphic between cv. Messire and cv. Eritreo and between two contrasting bulks homozygous for *Er3* or *er3* alleles. Further linkage analysis confirmed that these SSRs were linked to *Er3* and to the RAPD and SCAR markers previously reported to be linked to this gene. Therefore, this study demonstrates that *Er3* gene is located in pea LGIV.

P141 – S18

Developing Drought and Heat Stress Tolerant Chickpea (*Cicer arietinum* L.) Genotypes

Yücel D., Angın N., Mart D., Türkeri M., Çatalkaya V., Yücel C.
Eastern Mediterranean Research Institute, Adana, Turkey.

Chickpea (*Cicer arietinum* L.) with high protein content is a vital food, especially in under-developed and developing countries for the people who do not consume enough meat due to low-income level. The objective of the proposed study to evaluate growing, yield and yield components of chickpea genotypes under Mediterranean condition so determine tolerance of chickpea genotypes against drought and heat stress. For this purpose, a total of 34 chickpea genotypes were used as material. The experiment were conducted according to factorial randomized complete block design with 3 reps at the Eastern Mediterranean Research Institute, Adana, TURKEY for 2014-15 growing season under three different growing conditions (Winter sowing, irrigated-late sowing and non-irrigated- late sowing). According to results of this experiment, vegetative period, flowering time, poding time, maturity time, plant height, height of first pod, seed yield and 100 seed weight were ranged between 68.33to 78.77 days, 94.22 to 85.00 days, 94.11 to 106.44 days, 198.56 to 214.44 days, 37.18 to 64.89 cm, 18.33 to 34.83 cm, 417.1 to 1746.4 kg/ha and 14.02 to 45.02 g, respectively. Among the chickpea genotypes, Aksu, Arda, Çakır, F4 09 (X 05 TH 21-16189), FLIP 03-108 were least affected by drought and heat stress. Therefore, these genotypes can be used as sources of drought and heat tolerance in further breeding programme for evolving the drought and heat tolerant genotypes in chickpea.

P142 – S18

Starter fertilisers: Do they influence rhizobial populations in vining pea fields?

Wiesel L.[1], Maguire K.[2], Ward R.L.[1], Francis S.[3]

1 - Processors and Growers Research Organisation, Great North Road, Thornhaugh, Peterborough, PE8 6HJ, UK

2 - Formerly at PGRO, now at Bayer CropScience Limited, 230 Cambridge Science Park, Cambridge, CB4 0WB, UK

3 - Fen Peas Ltd, The Old Farm House, Old Leake, Boston, PE22 9HR, UK

Pea yields have reached a plateau in many areas over recent years and one option to increase yields is the application of starter fertilisers. Starter fertilisers contain phosphorus, which promotes root growth and is essential for root nodulation to occur. Some starter fertilisers, however, contain nitrogen which is potentially damaging to rhizobial populations thereby not only reducing nitrogen fixation in the pea crop but also leaving reduced levels of soil nitrogen for the subsequent crop. The impact of starter fertilisers with and without nitrogen on vining pea yields and rhizobial populations in soils has been investigated in two subsequent years. Three field trials in early, mid and late-drilled crops were established each year. Yields tended to increase in mid and late-drilled crops and preliminary results suggest that the application of starter fertilisers did not affect rhizobial populations in soils. Application of starter fertilisers is not very costly to growers and any pea yield increase of greater than 73 kg/ha will result in an economic benefit for pea growers. If it can be shown that starter fertilisers do not negatively impact rhizobial populations the use of starter fertilisers holds great potential for the vining pea industry.

P144 – S18

RNA-seq analysis of gene expression in wild and cultivated lentils in response to *Ascochyta lentis* infection

García P., Sáenz de Miera L.E., Vences F.J., Vaquero F., González A.I., Polanco C., Pérez de la Vega, M.

Área de Genética, Fac. Biología, Universidad de León, 24071 León, Spain

Lentil ascochyta blight is caused by the fungal pathogen *A. lentis* and is an important disease in most lentil producing countries. Ascochyta is favoured by cool and wet conditions and can reduce crop yields, but also affects seed quality and hence their market value. Resistance to ascochyta blight have been identified both in cultivated and wild *Lens* species. We used the susceptible *L. c. culinaris* cultivar 'Alpo' and the resistant wild *L. odemensis* ILWL235 to investigate the differences in gene expression after infection.

Total RNA was isolated from the aerial parts of infected and non-infected 15-day-old plantlets that were collected 24 hours after the treatment. RNA-seq was performed using three biological replicates per each species and treatment on an Illumina HiSeq 2500. This yielded over 435 million 100 nucleotide paired-end reads, with an average of 18 million read-pairs per replicate. Alpo sequences were aligned to non-annotated lentil genome v0.8 using STAR tool and their transcriptome was assembled with TRINITY. Read counts for each replicate were then assessed for differential expression using the R package DESeq with RSEM mapping tool.

We found that 880 genes increased their expression after infection in both species while 23 decreased it. In the resistant L. odemensis the increase in 256 genes and the decrease in 207 genes were detected, while 1810 and 1053 genes showed, respectively, expression changes only in the susceptible cultivar.

P145 – S18

Characterization of Mildew resistance locus (Mlo) genes in wild species of lentil

Cano J., Fernández-Túñez C., Sáenz de Miera L.E., Pérez de la Vega M., Polanco C.
Área de Genética, Fac. Biología, Universidad de León, 24071 León, Spain

Powdery mildew is a widespread disease that can cause significant harvest losses in crop plants in temperate climates. Loss-of-function mutant alleles of specific MLO genes confer broad-spectrum powdery mildew resistance in monocots (barley) and dicots (*Arabidopsis thaliana*, tomato, and pea). SNARE genes are required for mlo-specified resistance. MLO genes are present as small families in plants and we previously identified 14 MLO gene family members in the lentil genome (*Lens culinaris culinaris* cv. CDC-Redberry) by sequence similarity-based homolog searches using the available sequences in pea and soybean.

The phylogenetic analysis revealed that three genes (LcMLO_01, LcMLO_02, LcMLO_10) were homologous of MLO genes associated with powdery mildew resistance in other species. A set of primers was designed in order to amplify the complete LcMLO_01 gene sequence from interesting lentil accessions and wild relative species. Here we present SNARE gene candidates in lentil and the sequences of LcMLO_01 in *L. c. orientalis*, *L. odemensis*, *L. tomentosus*, *L. nigricans*, and *L. lamotei*. Most of the nucleotide differences were detected in the 14 intronic regions but amino acid changes were also identified. The deduced protein sequences showed the presence of characteristic and conserved transmembrane motives and a conserved calmodulin-binding domain. A phylogenetic tree was constructed using the corresponding nucleotide sequences of this gene including cultivated lentil lines.

P146 – S18

Pea straw: an advantageous co-product in dairy goat diets

Collado E.[1], Fernández J.A. [2], Vivancos N.[3], Moya F. [4], Armero E.[5].
1 - Instituto de Biotecnología Vegetal
2 - Departamento de Producción Vegetal
3 - Departamento de Ciencia y Tecnología Agraria
4 - Kapra Sociedad Cooperativa, 5Departamento de Ciencia y Tecnología Agraria

Legume production offers us different co-products to use in animal nutrition. The nutritive value of the legume straw is higher than cereal straw with a slightly higher percentage of crude protein, higher digestibility, and lower percentage of neutral detergent fibre. The aim of this work was to replace cereal straw by pea straw and to analyse its effect on milk yield and milk quality in dairy goat. The experiment was carried out during July of 2015 in a commercial farm in Murcia (Spain). 200 goats were fed with cereal straw (cereal straw group or CSG) and in the diet of 200 goats cereal straw was replaced by pea straw (pea straw group or PSG). Milk yield and its quality were assessed with overall information from each group along the trial and with individual data nine days after the diet was modified. Feed intake was measured through overall information from each group. Considering overall measurements, PSG had a slightly higher milk yield, with a higher percentage of fat, and higher food intake than CSG. However when the results were analysed with individual data there was a trend to produce more milk in PSG, but it was not statistically significant, and no differences were observed in milk quality. Therefore, the use of pea straw in diets for dairy goats could enhance farm sustainability without affecting milk production, but possible modifications in milk quality, such as fatty acid or amino acid compositions, should be assessed in future researches.

P147 – S18

Genome-wide association study of common bean disease resistance in Portuguese germplasm.

Leitão S.T.[1], Alves M.L.[1], Rubiales D.[2], Vaz Patto M.C.[1]

1 - Instituto de Tecnologia Química e Biológica, Universidade Nova de Lisboa, Oeiras, Portugal
2 - Institute for Sustainable Agriculture, CSIC, Cordoba, Spain.

Common bean (*Phaseolus vulgaris* L.) is the world's most important grain legume for human consumption. Portugal holds a very promising common bean germplasm, which results from more than five centuries of natural adaptation and farmer's mass selection in the country, not yet fully explored in breeding. Fusarium wilt (*Fusarium oxysporum* f. sp. *phaseoli*) is among the diseases that cause major yield losses in this crop. In order to identify new sources of resistance and to unravel the associated genetic control we characterized the resistance to fusarium wilt of a collection of 150 Portuguese common bean accessions. Evaluation took place under growth chamber conditions, using a replicated complete randomized block design. Infection responses revealed great variability among the accessions with the identification of interesting sources of resistance. This collection was additionally screened with ~12000 molecular markers (SSR and SNPs from Illumina BeadChip and DArTseq arrays) uniformly distributed throughout the genome. A genome-wide association study, joining the disease resistance levels with the genomic information, is currently ongoing, using a mixed linear model approach accounting for population structure and familial relatedness. The putative statistically significant associations found will contribute to a more effective selection of common bean genetic resources in future disease resistance breeding programs.

P148 – S18

Nitrogen and phosphorus use efficiency in the recombinant afila lines of a mapping population of field pea (*Pisum sativum* L.)

Gawłowska M.[1], **Górny A.** [1], **Ratajczak D.** [1], **Niewiadomska A.**[2], **Święcicki W.** [1], **Beczek K.** [1], **Knopkiewicz M.** [3]

1 - Institute of Plant Genetics Polish Academy of Sciences, Poznań, Poland,
2 - University of Life Sciences, Poznań, Poland,
3 - Adam Mickiewicz University in Poznań

In European countries productivity of field pea is considerably affected by instabilities in water and nutrient accessibility. In these conditions, yield potential depends on plant physiological capacities to an efficient utilization of environmental resources (water, nutrients).

In field experiments, variance and co-variance between components of nitrogen and phosphorus efficiency was evaluated among lines of the Canadian mapping population [Carneval_MP1401] during the whole growth season under varied nitrogen nutrition.

The pea yield and nitrogen utiliztion efficiency (NERgen) were positively correlated in optimal and stress localizations (Wiatrowo, optimal conditions r=0.95, stress conditions: Wiatrowo r=0.50, Przeb_dowo r=0.65). The seed yield and phosphorus utilization efficiency (PERgen) were positively correlated only in optimal condition (Wiatrowo, r=0.58).

Soil treatment effects (E) were significant for all characters, although genotype-treatment (G-E) interactions were significant only for nitrogen content in seeds (%Ngen). Noteworthy, relationships between GY and nitrogen efficiency were stronger in nitrogen-limited conditions (optimal conditions r=0.31, stress conditions: Wi, r=0.50, P, r=0.65).

The results indicate that the importance of components of physiological efficiency for pea yielding increases in the sub-optimal conditions. Broad variability of all physiological traits gives a high probability of QTL mapping with success.

P149 – S18

Understanding the molecular mechanisms underlying the differential response to water deficit of *Medicago truncatula* expressing AtTPS1 gene

Branco D.[1], Almeida, A. M.[2], Alcântara A.[3,4], Silva J.M.[3,4], Silva A. B.[3,4], Coelho A.[5], Fevereiro P.[1,4], Araújo S.[1,6]

1 - Plant Cell Biotechnology Laboratory, ITQB -NOVA. saraujo@itqb.unl.pt

2 - Ross University, School of Veterinary Medicine, P.O. Box 334, Basseterre, Saint Kitts and Nevis

3 - Biosystems and Integrative Sciences Institute (BioISI), Faculdade de Ciências, Universidade de Lisboa, Campo Grande, 1749-016 Lisbon, Portugal.

4 - Departamento de Biologia Vegetal, Faculdade de Ciências, Universidade de Lisboa, Campo Grande, 1749-016 Lisbon, Portugal.

5 - Proteomics of Non-Model Organisms Laboratory, Instituto de Tecnologia Química e Biológica António Xavier (ITQB), Universidade Nova de Lisboa (UNL), 2780-157 Oeiras, Portugal.

6 - Plant Biotechnology Laboratory, Department of Biology and Biotechnology 'L. Spallanzani', Università degli Studi di Pavia, via Ferrata 1, 27100 Pavia, Italy.

The manipulation of trehalose metabolism is a promising approach to improve abiotic stress tolerance in plants. We have shown that *Medicago truncatula* plants engineered with trehalose-6-phosphate synthase 1 (AtTPS1) from Arabidopsis have improved response to water deficit (WD).

This work aims to unveil the molecular mechanisms underlying the differential response of AtTPS1 expressing plants. The transcriptome and proteome changes were studied in roots and leaves of wild type (M9-10a) and transgenic (TPS+) plants grown under well watered (WW), WD and WD recovery (WDR) conditions.

Differentially expressed transcripts encoding for transcription factors (TFs) were extracted from Illumina-based MACE data. Hierarchical clustering evidenced TFs with contrasting expression profile between lines that may likely be involved in the improved WD response of TPS+ plants.

Differentially accumulated proteins (DAPs) were identified from 2D-DIGE coupled to MALDI TOF/TOF analysis. The number of DAPs belonging to each MapMan functional category depends on the line /organ studied. Hierarchical clustering revealed that M910a and TPS+ have different protein accumulation profiles upon WD and WDR in response to applied treatments.

The integration of physiological, proteomic and transcriptomic data will enhance our knowledge on metabolic pathways activated with the manipulation of trehalose metabolism. This knowledge can be used in the design and selection of legumes with improved WD response.

P150 – S18

Genetic and genomic mapping of genes conferring resistance to four anthracnose races in common bean genotype BAT93

Murube E., Campa A., Ferreira, J.J.
Plant genetic group, SERIDA, Asturias, Spain

Anthracnose, caused by the fungus *Colletotrichum lindemuthianum* (Sacc. & Magnus) Lamb.-Scrib. is one of the most destructive diseases of common bean (*Phaseolus vulgaris* L.). Resistance to anthracnose in common bean generally follows a qualitative and race-specific mode of inheritance. In this work, using forward genetic analysis, we investigate the physical location in the bean genome of genes conferring resistance to anthracnose races 6, 38, 39 and 357 in a RIL population (140 lines) derived from the cross Xana × BAT93 (Susceptible x Resistant). Resistance to four races fitted to that expected for one resistance gene. Co-segregation in pairs was observed between response to races 6 – 357 and 38 – 39. One recombinant line resistant for races 38 and 39 and susceptible for races 6 and 357 was observed suggesting that two closely linked genes are involved in the resistance. A dense genetic linkage map was developed in this RIL population through Genotyping by Sequencing (GbS). A total of 7156 SNPs were obtained although 1566 were not considered due to its distorted segregation. Resistance genes were mapped on linkage group Pv04 between markers SNP04_031 (physical position 1.61 Mb) and SSR4_1.743.4 (1.74 Mb). *In silico* exploration in the bean reference genome revealed 8 genes that codify proteins with LRR domains, normally involved in the response to pathogens thus being candidates to be controlling this resistance.

P151 – S18

Genetic resistance to powdery mildew in common bean: recent advances.

Ferreira J.J., Murube E., Campa A.
Plant Genetic Group, SERIDA, Asturias, Spain

Powdery mildew (PM) is a serious disease in many legume species including common bean (*Phaseolus vulgaris* L.). In this work, the species causing PM in the bean local crops was identified as *Erysiphe polygoni* through molecular analysis of the internal transcribed spacer region. Under controlled conditions in seedling tests, 16 of 288 tested materials showed a complete resistance without visible symptoms. Inheritance of resistance was studied in the Xana/Cornell RIL population, and in five F2:3 segregating populations involving the resistance sources G122, Porrillo Sintético, BGE003161, Belneb and G19833. Results revealed a qualitative mode of inheritance for PM resistance being identified two independent resistance genes located on linkage groups (LG) Pv04 and Pv11. These genes show a dominant epistatic relationship, the gene conferring total resistance response masking the effect of the gene conferring partial resistance. The gene governing total resistance was mapped on LG Pv04 in cultivars Porrillo Sintetico, BGE003161, and Belneb, while in Cornell 49242 was mapped on LG Pv11. The gene conferring partial resistance was mapped on LGs Pv11 and Pv04 in cultivars X2776 and Cornell 49242, respectively. Interestingly, both resistance genes were mapped in regions with many genes codifying to typical R proteins. This information will be relevant for the implementation of breeding programs focused on the development of cultivars carrying genetic resistance to PM.

P152 – S18

The pursuit for resistance sources to biotic stresses in *Lathyrus sativus*

<u>Almeida N.F.</u>[1], Gonçalves L.[1], Lourenço M.[2], Julião N.[3], Aznar-Fernández T.[4], Rubiales D.[4], Vaz Patto M.C.[1]

1 - Instituto de Tecnologia Química e Biológica António Xavier, Universidade Nova de Lisboa, Av. da República, 2780-157 Oeiras, Portugal.
2 - Câmara Municipal de Alvaiázere, Praça do Município, 3250-100 Alvaiázere, Portugal.
3 Simões & Ramos Lda, Estrada Nacional 110, 3250-404 Rego da Murta, Portugal.
4 - Institute for Sustainable Agriculture, CSIC, Apdo. 4084, E-14080 Córdoba, Spain.

The need for more sustainable and environmentally safe agriculture has reinforced interest in legume cultivation in Europe. These species have the unique capacity for symbiotic nitrogen fixation, highlighting their importance in both natural and agricultural ecosystems. In addition, genotypes that are naturally resistant to pathogens are useful for reducing pesticide application. Grass pea (*Lathyrus sativus*) is a feed, food and fodder crop, with great adaptability to inauspicious environments, high protein content and resistance to serious diseases. It is one of the most promising sources of calories and protein for the drought-prone and marginal areas of Asia and Africa, being an alternative to marginal soils and for cropping systems diversification in Europe.

As part of the European LEGATO and the Portuguese QUALATY projects, we focus on the search for resistance sources to weevils and fungal diseases on a collection of hundred grass pea genotypes from diverse origins, including Europe, Africa and Asia. Along with the phenotypic observations (resistance level) on field and controlled conditions, we used DArT-seq and E-SSRs to access the genetic diversity within and among grass pea accessions. This will allow identifying any relationship between genetic diversity and resistance level. The acquired data will reveal valuable diverse sources of resistance for the development of modern grass pea cultivars, improving the attractiveness of this underused but promising crop.

P153 – S18

Variability of N_2 fixation in cowpea under phosphorus deficiency is related to phosphorus use efficiency.

Lazali M.[1,3]**, Brahimi S.**[1]**, Ounane S.M.**[2]**, Drevon J.J.**[3]

1 - Département d'Agronomie, Faculté des sciences de la nature et de la vie et des sciences de la terre. Université Djilali Bounaama Khemis Miliana. Route Thniet El Had, Soufay 44225 Khemis Miliana, Algérie.

2 - Département de Productions Végétales. Ecole Nationale Supérieure Agronomique (ENSA). Avenue Hassan Badi 16200 Alger, Algérie.

3 - Institut National de la Recherche Agronomique, UMR Ecologie Fonctionnelle & Biogéochimie des Sols et Agroécosystèmes, INRA-IRD-CIRAD-SupAgro. Place Pierre Viala, 34060 Montpellier, France.

Low availability of phosphorus (P) is a major constraint to legume production, and efforts are being made to identify legume genotypes with tolerance to low P and greater P use efficiency (PUE). Cowpea (*Vigna unguiculata* L.) genotypes vary in their adaptation to low-P soils. In order to investigate to what extent this variation may be related to PUE for symbiotic nitrogen fixation (SNF), five genotypes, Adrar, El Kala, Djenet, Tizi Ouzou and Bejaia, were grown in semi-hydroponic culture with sufficient versus deficient P supply. At the flowering stage, the biomass of plants and nodules and their P contents was determined after measuring the quantity of N_2 fixed. The results showed that nodule and shoot biomass were less when P was deficient. The genotypes that presented the maximum growth during the experiment presented a high efficiency in use of the rhizobial symbiosis calculated as the slope of plant biomass regression as a function of nodulation. Under P-deficiency, efficiency in use of P for SNF was significantly increased in the genotypes El Kala, Djenet and Adrar and accompanied with an increase of the efficiency in use of the rhizobial symbiosis. Hence the large differences show that traits for more P uptake-efficient plants exist in the tested cowpea genotypes. This opens the possibility to breed for more P uptake-efficient varieties as a way to bring more sparingly soluble soil P into cycling in crop production and obtain capitalisation of soil P reserves.

P154 – S18

Soil microbial community diversity increases resilience of pea plant after drought

Sorin C., Maron P.A., Girodet S., Nowak V., Duc G., Prudent M.
Institut Nacional de la recherche agronomique, INRA, UMR1347 Agroécologie, F-21065 Dijon cedex, France

We hypothesized that the stability (resistance and resilience) of pea production under drought may be enhanced with increasing the diversity of soil microbial communities. An experiment was conducted under greenhouse conditions where pea plants were grown during three months under three levels of soil microbial community diversity, obtained by a dilution approach. For half of them, a water stress was applied during two weeks at vegetative stage followed by a rewatering until the end of the growth cycle, while the other plants were well watered throughout the experiment. We measured traits reflecting plant development and growth, plant resource acquisition and allocation among compartments and seed production (i) after drought to evaluate the resistance of the plant, and (ii) at physiological maturity to evaluate the resilience of the plant. Our results show that the plant biomass depletion due to drought did not vary with the level of microbial diversity. Adaptation of root system and plant transpiration was dependent on the level of microbial diversity: under low diversity level, root traits and stomatal conductance were less affected by drought than under high diversity level. After rewatering, plants in interaction with a higher diversity level had a higher biomass, indicating a better resilience. Seed production was also enhanced by the higher microbial diversity level.

P155 – S18

Marker-assisted Backcross Selection of Virus Resistance in Pea (*Pisum sativum L*)

Scegura A., McPhee K.
North Dakota State University, USA

Viruses are a destructive plant pathogen resulting in significant yield loss and reduced grain quality. Pea seed-borne mosaic virus (PSbMV) is an economically important viral disease in pea (*Pisum sativum L.*) and has recently been detected in the Northern Great Plains with significant impact on the industry. PSbMV is aphid-transmitted from plant to plant and can be seed-borne. It causes malformed leaves, discolored or split seed and reduced size and number of seed. Marker assisted backcross breeding will be used to transfer the single recessive resistance allele for PSbMV (sbm-1) located on LG VI into locally adapted breeding lines. Parental breeding lines were hybridized with cv. Lifter in the fall of 2015 to develop F1 progeny. F1 plants were selfed or backcrossed to the adapted breeding line as the recurrent parent in the greenhouse in the spring of 2016. F2 and BC1 seed will be planted in the field and individual plants possessing sbm-1 identified using the 4Egenomic primers previously developed. Individual plants containing sbm-1 will be allowed to self-pollinate to produce BC1F2 seed or will be backcrossed to the recurrent parent. F5, BC1F4 and BC2F3 populations will be evaluated for disease resistance against the PSbMV strain present in the Northern Great Plains and for agronomic adaptation including yield performance.

P156 – S18

A transcriptomic approach identifies candidate genes for drought tolerance during the reproductive phase in pea.

Vernoud V.[1], Rossin N.[1], Prudent M. [1], Le Signor C. [1], Sanchez, M. [1], Pateyron S. [2], Balzergues S. [2], Aubert G.[1], Burstin J. [1], Gallardo K. [1], Thompson R. [1].

1 - Agroécologie, AgroSup Dijon, CNRS, INRA, Univ. Bourgogne Franche-Comté, F-21000 Dijon, France.

2 - POPS Transcriptomic Platform, IPS2, CNRS, INRA, Univ 12 Paris Sud, Univ Evry, Univ Paris-Diderot, Sorbonne Paris-Cite, Univ Paris-Saclay, 91405 Orsay, France

Drought is a major environmental factor limiting the productivity of crop plants. In pea drought stress occurring during the reproductive phase can greatly affect seed yield and quality. We investigated the response of pea plants (var. Caméor) subjected to water stress during the seed filling period, a phase when massive remobilization from the vegetative organs occurs to sustain seed high-nitrogen demand. Pea plants were subjected to drought stress at the beginning of the seed-filling period of the first two nodes for 8 days. Total and one-seed biomass decreased by 35% and 20% respectively by this limited water stress. Nitrogen allocation to the different plant compartments was also affected, with an increased N allocation to the leaves from the vegetative nodes and a decrease to the root and seed compartments. Transcriptomic changes in water-stressed leaves from the vegetative nodes were analysed by hybridization of a 40k pea micro-array: 178 genes were at least two fold up-regulated in water-stressed samples compared to well-watered samples, whereas 55 genes were down-regulated. Among the most strongly up-regulated genes were those encoding a glutamine amidotransferase, a sucrose transporter from the SWEET family, a phosphoenolpyruvate carboxykinase and a carotenoid cleavage dioxygenase involved in strigolactone biosynthesis.

Acknowledgement: this project was supported by the Burgundy Region (AGRALE6, FABER program) and the FP7 LEGATO project.

P157 – S18

The use of microsatellites markers and bioinformatics tools to locate the genomic region related to rust resistance in chickpea (*Cicer arietinum* L.).

Caballo C.[1], Flores A.[2], Gil J.[2], Madrid E.[3], Rubio J.[1] and Millan T.[2]

1 - Área de Mejora y Biotecnología. IFAPA. Apdo 3092. 14080 Córdoba, Spain.

2 - Dept. of Genetics, University of Córdoba, Campus Rabanales Ed. C-5, 14071 Córdoba, Spain.

3 - Max Planck Institute for Plant Breeding Research Department of Plant Developmental Biology. Carl-von-Linne Weg 10, D-50829 Cologne, Germany

Chickpea rust is caused by *Uromyces ciceris-arietini.* In previous studies a gene that controls resistance to chickpea rust was identified in the linkage group 7 (LG7) of the chickpea genetic map. However the physical position of this gene is still unknown. In order to compare the genetic and physical maps a group of microsatellites distributed across the chromosome 7 were selected following according to chickpea database (cicarmisatdb.icrisat.org). A recombinant inbred line (RIL) population derived from an interspecific cross between *Cicer arietinum* (ILC72) x *Cicer reticulatum* (Cr5-10), susceptible and resistant to rust, respectively, were used for linkage analysis.

Six out of twenty microsatellites were positioned in LG7. These results allow us to narrow the area related to the resistance. Nevertheless, additional markers should be included in this region in order to develop fine mapping in this area.

These findings could be the starting point for a Marker-Assisted Selection (MAS) programme for rust resistance in chickpea and identify candidate gene.

Acknowledgement: this work has been supported by the INIA project contract RTA2013-00025, co-financed by the European Union through the ERDF 2014-2020 “Programa Operativo de Crecimiento Inteligente”

P158 – S18

Overexpression of a phytocystatin leads to delayed senescence and enhanced drought tolerance in soybean

Makgopa M. E.[1,3], **Quain M. D.**[1,2], **Marquez-Garcia B.**[1,4], **Kunert K.J.**[1,3], **Foyer C. H.**[1]

1 - Centre for Plant Sciences, Faculty of Biology, University of Leeds, Leeds, LS2 9JT, UK.
2 - CSIR, Crops Research Institute, Kumasi, Ghana.
3 - Department of Plant Sciences, University of Pretoria, Pretoria 0002, South Africa.
4 - VIB Department of Plant Systems Biology, Ghent University, 9052 Gent, Belgium.

Cysteine proteinases and their naturally occurring inhibitors, cystatins, have many functions that remain poorly characterised, particularly in crop plants. Senescence is characterised by increases in proteolytic enzymes involved in various processes in the plant's responses to stress. Transgenic soybean plants over-expressing a cysteine protease inhibitor (OC-I) were successfully generated and characterized. Plants of transgenic lines had differential transgene expression. Transgenic lines had lower protease activity determined by an in-gel assay using SDS-PAGE. Transgenic lines retained more chlorophyll than controls at later stages of development. Under drought stress, transgenic lines performed better CO2 assimilation (photosynthesis) and instantaneous water-use efficiencies (IWUE) than wild-type plants. Results obtained in this study have shown an important role of cysteine proteases in plant growth and development and plant stress. Future work will focus on identifying these OC-I sensitive proteases and investigating their individual function in plant growth and development and stress.

P159 – S18

Interactions between soil water content, stomatal conductance and abscisic acid content of field pea cultivars submitted to drought stress

Petrović G.[1], Stikić R.[2], Živanović T.[2], Vucelić-Radović B.[2], Šurlan-Momirović G.[2], Đorđević V.[1], Petrović I.[2]

1 - Institute of Field and Vegetable Crops, Novi Sad, Serbia.

2 - Faculty of Agriculture, University of Belgrade, Belgrade, Serbia.

Drought is one of the main abiotic stresses limiting agricultural production of many important crops. Plants respond to drought stress by closing their stomata and reducing transpiration water loss. The drought stress experiment was conducted on seven selected cultivars of field pea in control conditions (phytotron chamber). The plants were irrigated at the optimal soil water content until the third pair of leaves began emergence, after which soil drought was induced by termination of irrigation up to 18% (moderate drought), and 9% substrate water content (severe drought). Control plants were irrigated at the optimal level of soil water regime (36% substrate water content). A measurement of stomatal conductance and ABA concentration was performed. The stomatal reactions differed between cultivars, but only under moderate drought conditions, while all cultivars reacted by the faster stomatal closure under severe drought. The correlation between ABA in leaves and changes in stomatal conductance revealed that stomatal conductance in cultivar Dukat was most affected by the accumulation of ABA in leaves (10 x increase) and that this reaction could be explained by "chemical signals" of drought. Contrary to the previous, the lowest stomatal sensitivity to increased concentration of ABA (2.5 x increase) in cultivar Javor indicates the "hydraulic signals" of drought.

P160 – S18

Use of MACE technology to identify positional and expressional candidate genes for resistance to *Didymella pinodes* in pea

Winter P.[1], Rubiales D.[2], Fondevilla S.[2]

1 - GenXPro GmbH, Altenhöferallee 3, 60438, Frankfurt am Main, Germany. pwinter@genxpro.de

2 - Institute for Sustainable Agriculture-CSIC, Avd. Menendez Pidal s/n, 14004, Cordoba, Spain.

MACE (Massive Analysis of cDNA Ends) allows ultra-deep transcription profiling without PCR introduced bias by combining second-generation sequencing and the TrueQuant technology. In MACE each cDNA molecule is represented by one sequence (the tag) of 94 bp, originating from a region around 100–500 bp from the 3’ (poly-A) end of the transcript. High-throughput sequencing of tags provides numerical gene expression values and allows the identification of SNPs and INDELS from the 3’ends of the genes. In the frame of “LEGATO” project, we are using MACE to identify positional and expressional candidate genes for resistance to *Didymella pinodes* in pea. MACE has been used to perform a detailed transcriptomic study to identify genes differentially expressed in a resistant reaction (accession P665) compared to a susceptible one (cv. Messire). The resulting sequences will be used to identify SNPs between P665 and Messire for these differentially expressed genes. These SNPs will be further genotyped in the RIL population P665 x Messire in a high throughput way by sequencing MACE libraries from 94 RIL families. This will allow the mapping of these differentially expressed genes in the P665 x Messire genetic map and the study of their possible co-localization with the QTLs associated with resistance to *D. pinodes* that have been already identified in this population.

This research is funded by the European Community (FP7/2007-2013) grant agreement FP7-613551, LEGATO.

P161 – S18

An update on host plant resistance and race scenario of *Fusarium oxysporum* f. sp. *ciceris*, Fusarium wilt pathogen of chickpea (*Cicer arietinum* L.) in India

Sharma M.
ICRISAT, India

The severity & yield losses of Fusarium wilt (F. oxysporum f. sp. ciceris (Foc) differ from place to place owing to existence of G×E interactions & physiological races. Attempts have been made to identify stable sources of resistance through multi-location testing & to assess current race scenario of Foc. Chickpea wilt nursery, consisting of 27 highly resistant lines to wilt, was tested through multi-location/multi-year evaluation at hot spot locations. ANOVA indicated variability in wilt incidence due to genotypes, environments, & G×E. GGE biplot identified stable genotypes/discriminating environments for FW. Complete resistance to genotypes across the locations was not found; 4 lines (ICCV05527, ICCV05528, ICCV96818, ICC11322) with stable resistance were found. Foc isolates (110) collected from diverse geographical locations in India were characterized using standard host differentials. DArT markers were developed & their utility in genotyping of 110 isolates were demonstrated. DArT arrays revealed total 1,813 polymorphic markers. Cluster analysis/ PCA/population structure indicated that isolates of Foc were partially classified based on geographical location. DArT markers were able to group the isolates in consistent with phenotypic grouping. Race-specific unique/rare alleles were detected. Study generated significant information & can be used further for development & deployment of region-specific resistant cultivars of chickpea.

P162 – S18

Morphological and molecular characterizations of Ascochyta blight caused by *Ascochyta rabiei* in *Cicer anatolicum*

Sari D.[1], **Berger J.**[2], **Kahraman A.**[3], **Aydogan A.**[4], **Can C.**[5], **Bukun B.**[6], **Penmetsa R.V.**[7], **von Wettberg E. J.**[8], **Toker C.**[9]

1 - Akdeniz University, Faculty of Agriculture, Department of Field Crops, Antalya, Turkey duygusari@akdeniz.edu.tr
2 - CSIRO, Plant Ind. Wembley, Australia
3 - Harran University, Faculty of Agriculture, Department of Field Crops, Sanliurfa, Turkey
4- Field Crops Central Research Institute, Ankara, Turkey
5 - Gaziantep University, Faculty of Art and Science, Department of Biology, Gaziantep, Turkey
6 - Dicle University, Faculty of Agriculture, Department of Plant Protection, Diyarbakir, Turkey
7 - University of California, Department of Plant Pathology, Davis, USA
8 - Florida International University, Department of Biological Sciences and International Center for Tropical Botany, Miami, Florida, USA
9 - University, Faculty of Agriculture, Department of Field Crops, Antalya

Chickpea (*Cicer arietinum* L.), the only cultivated species in the genus *Cicer* L., is individually the most important pulse crop of the world. Cultivated chickpea is susceptible to Ascochyta blight caused by *Ascochyta rabiei* (Pass.) Lab. This is one of the major biotic stresses causing yield losses of up to 100% and having a global distribution. Ascochyta blight affects negatively all aerial parts of both domesticated chickpea and its wild relatives. Characteristic Ascochyta blight lesions were observed on *Cicer anatolicum* ALEF., which is one of the perennial wild relatives of chickpea, growing in the South Eastern Anatolia Region, Turkey. Plants showed leaves, petioles, stems, and pods with brown lesions. Symptoms on leaves, stems, pods and seeds were evaluated morphologically to identify the blight disease. Infected samples were collected and taken to the laboratory for the molecular characterization. Firstly, samples were incubated to potato dextrose agar (PDA) plates for understanding the morphological characteristics typical of *A. rabiei*. DNA was extracted from small pieces of fungus isolates using CTAB method. For the fungus characterization, internal transcribed spacer (ITS) regions (ITS-1, 5.8S rDNA subunit, ITS-2) were amplified. The ITS sequence had ≥99% nucleotide identity with the corresponding sequence in GeneBank for *A. rabiei*. The sequence was deposited in GenBank (Accession No. KU879335). As a result, it is the effective method for identification of the fungus.

P163 – S18

An intersubspecific genetic map in lentil: QTL identification for Ascochyta resistance, and seed traits.

Neyra C. D., Rey-Baños R., Miliani A. S., García-López, M., Sáenz de Miera L. E., Pérez de la Vega, M., García P.
Dept. Genetics, University of Leon, Spain

An intersubspecific genetic map has been developed analyzing 94 F7 recombinant inbred lines obtained from a cross between *Lens culinaris* subsp. *culinaris* cv. Lupa and *L. c.* subsp. *orientalis* (BG 16880) using the single seed descent method. A total of 417 genetic markers of several types, based in gene sequences, retrotransposons, transposons and anonymnous sequences, showed the expected mendelian segregation (1:1) and were used in the map construction.

The genetic map showed seven large linkage groups that seem to correspond with the seven chromosomes of lentil than and been identified due to the previous studies on synteny between Lens and Medicago. Besides the 7 main linkage groups, several small ones appear, mainly including anonymous and/or retrotransposon based markers.

The genetic map has been used to identify QTL for several traits of economical importance in lentil such as resistance to Ascochyta, and seed size and weight. A small number of QTL were detected for each trait (3 for Ascochyta resistance, 2 for seed weight and 3 for seed size).

P164 – S18

Evaluation of yield and morphological characters of registered chickpea varieties in different ecological conditions of Turkey

Mart D.
Eastern Mediterranean Research Institute, Adana, Turkey

Registered chickpea varieties were tested in two different ecological conditions to evaluate their yield and adaptation parameters. The experiments were conducted in Cukurova-Adana located in the Mediterranean region for winter planting and in Erzurum located in the Eastern Anatolia region for summer planting, during 2014-2016. A total of 34 registered chickpea varieties and 17 genotypes were evaluated. The highest and the lowest grain yield values were 17.1- 508.5 kg/da and 7.2 -441.8 kg/da for Experiment I and Experiment II in the Cukurova-Adana location, respectively. Similarly the highest and the lowest grain yield values were 157.1- 131.5 kg/da and 129.6-136.8 kg/da for Experiment I and for Experiment II respectively, in the Erzurum location.

This study was supported by The Scientific and Technological Research Council of Turkey (TUBITAK) with project number 113O070.

P165 – S18

Cytological and molecular responses of PsAPY1-silenced pea to the host-adapted fungal pathogen

Miki M.[1], Yamasaki S.[1], Yao S.[1], Matsui H.[1], Noutoshi Y.[1], Yamamoto M.[1], Ichinose Y.[1], Shiraishi T.[1,2], Toyoda K.[1]

1 - Okayama University, Japan
2 - Research Institute of Biological Sciences, Okayama, Japan

Our research focusing on the plant cell wall where most pathogenic fungi first make contact with host cells have discovered the ecto-type ATP-hydrolyzing enzyme (apyrase; EC3.6.1.15) as a key player of extracellular defense. In response to elicitor from *Mycosphaerela pinodes*, the catalytic activity in extracts from the cell walls of pea is enhanced in vitro, with the consequent increase of O2- generation by peroxidase(s). By contrast, the supprescins A and B, virulence factors secreted by the same fungus, inhibit the apyrase as well as the peroxidase-catalyzed O2- generation in a host-specific manner. These results indicate that plant cell wall is capable of recognizing and responding to incoming elicitor molecules and that the ecto-ATPase spatially regulates the apoplastic oxidative burst. Here we silenced PsAPY1 gene encodings the ecto-ATPase in pea, using an Apple latent spherical virus-based virus-induced gene silencing. The PsAPY1-silenced peas (_PsAPY1) exhibited enhanced disease susceptibility phenotype against infection by pycnospores of *M. pinodes*. Indeed, the peroxidase-catalyzed O2- generation as well as expression of PR10-mRNA was impaired when PsAPY1-silenced pea was exposed to chitosan elicitor. On the basis of these results, it is likely that PsAPY1 spatially regulates the apoplastic oxidative burst as well as the downstream signaling that leads to expression of defense-related genes in pea.

P166 – S18

Extracellular apyrase PsAPY1 in pea required for resistance to fungal and bacterial pathogens

Yamasaki S.[1], Miki M.[1], Yao S.[1], Matsui H.[1], Noutoshi Y.[1], Yamamoto M.[1], Ichinose Y.[1], Shiraishi T.[1,2], Toyoda K.[1]

1 - Okayama University, Japan

2 - Research Institute of Biological Sciences, Okayama, Japan

The suppressors from Mycosphaerella pinodes inhibit the ecto-ATPase activity of host cell wall as well as the peroxidase-catalyzed O2- generation, temporarily reducing the ability of the host cells to defend itself. Here we silenced PsAPY1 gene that encodes the ecto-ATPase in pea, using an Apple latent spherical virus-based gene silencing. The PsAPY1-silenced peas (DPsAPY1) exhibited enhanced disease susceptibility even against infection by a non-adapted fungal pathogen, Colletotrichum higginsianum. Notably, on the surface of PsAPY1-silenced pea, a hyphal tip-based entry (HTE), a recently discovered way to enter the plant cells without appressorial formation, significantly increased, eventually causing necrotic spots. A similar result was also observed with Pseudomonas syringae pv. glycinea (non-pathogenic to pea), that the bacteria were able to propagate in the apoplatic space of PsAPY1-silenced pea. In our separate study we showed reduced responsibility of DPsAPY1 to chitosan and lipopolysaccharides (LPS), which is derived from fungal cell wall and glycolipid components of the outer membrane of the Gram-negative bacteria, respectively. Indeed, the chitosan-induced O2- generation as well as expression of PR10-mRNA was impaired in PsAPY1-silenced pea. It is thus likely that PsAPY1 spatially regulates the apoplastic oxidative burst as well as the downstream signaling leading to expression of defense-related genes in pea.

P167 – S18

Fusarium redolens a new causal agent of fusarium yellowing on chickpea in Tunisia

Bouhadida M.*[1], **Jendoubi W.***[1,2], **Gargouri S.**[3], **Beji M.**[1,4], **Kharrat M.**[1], **Chen W.**[5]

*** Authors contribute equally**

1 - Field Crops Laboratory, University of Carthage, INRAT, Rue Hedi Karray, 2080 Ariana, Tunisia. mariembouhadida@gmail.com

2 - National Agronomic Institute of Tunisia, 43 Av Charles Nicolle, 1082 Tunis, Tunisia

3 - Crop Protection Laboratory, University of Carthage, INRAT, Rue Hedi Karray, 2080 Ariana, Tunisia

4 - University of Tunis El Manar, Faculty of Sciences of Tunis, Campus University, El Manar, Tunis, Tunisia

5 - USDA-ARS, Washington State University, Pullman, WA 99164, USA

One of the most important biotic stresses contributing to the instability in chickpea yields is Fusarium wilt, caused by the soil-born fungus Fusarium oxysporum f. sp. ciceris (Foc). This disease has been reported in most chickpea growing areas in Tunisia and over the world causing significant annual yield losses under favorable conditions (Sharma and Muehlbauer 2007). There are eight races of the pathogen. A disease survey was conducted in order to determine the races present and their distribution in Tunisia. Chickpea plants showing typical wilt symptoms in Tunisia were collected from different chickpea growing areas in 2013. Sequencing of the translation elongation factor 1α (TEF-1α) gene and PCR protocols of the collected Fusarium isolates allowed quick and precise differentiation of F. oxysporum, F. redolens and F. oxysporum f. sp. ciceris. The association of F. redolens with wilting-like symptoms in chickpea in Tunisia is noticed for the first time. Pathogenicity assays using 3 chickpea genotypes (ILC482, JG62 and cv. Beja 1) and isolates from different geographic origins indicated that F. redolens is highly virulent on chickpea. Fusarium redolens induces a disease syndrome similar to that caused by the yellowing pathotype of Foc. Studies focusing on identification of sources of resistance and genes/QTLs involved in the resistance to this new pathogen on chickpea will be undertaken.

P168 – S18

Effects of salt stress on growth, nodulation and nitrogen fixation of Faba bean (*Vicia faba* L. minor) cultivated in Algeria

Chaker-Haddadj A.[1], **Nabi F.** [2], **Lazali M.**[2], **Sadji H.**[1], **Ounane S. M.**[2]

1 - Laboratoire de Biologie et de Physiologie des Organismes, Equipe de Biologie du Sol, Faculté des Sciences Biologiques, Université des Sciences et de la Technologie Houari Boumediène, BP 32, El Alia, Bab Ezzouar, 16111 Alger, Algérie

2 - Département de Phytotechnie, Ecole Nationale Sciences Agronomiques, El-Harrach 16200 Alger, Algérie

The two major environmental factors that currently reduce plant productivity are drought and salinity. Salinity in soil or water is one of the major stresses especially in arid and semi-arid regions, and it could severely limit crop production. In Algeria, more than 20% of irrigated lands are affected by salinity.

The aim of this study was to evaluate the effects of 50 and 100 mM NaCl concentrations on growth, nodulation, nitrogen fixation and accumulation of proline of four faba bean (*Vicia faba* L. *minor*) cultivars growing symbiotically with *Rhizobium leguminosarum* bv *viciae*. The response to salt stress depended on the cultivar and the level salt. Thus, 100mM NaCl caused a great reduction in dry weight of shoot and root. Number, dry weight of nodules per plant and nitrogen fixation were reduced with increasing salinity for all cultivars. However, proline content was increased in leaves of all cultivars tested. Sidi Aich and Espresso were less affected by salt than the sensitive cultivars Castel and Maya. Our results suggest that the NaCl tolerance of the Sidi Aich and Espresso cultivars is supported by better growth, the less N2 fixation inhibition and a higher osmotic adjustment.

P169 – S18

Interactive exploration of the Medicago stress response through time-series analysis in the MetaboClust software package

Rusilowicz M.[1,2], **Dickinson M.**[3], **Charlton A.**[3], **O'Keefe S.**[1,2], **Wilson J.**[1,4]

1 - York Centre for Complex Systems Analysis, University of York
2 - Department of Computer Science, University of York
3 - Fera Science Ltd.
4 - Departments of Mathematics and Chemistry, University of York

As omics technologies such as LC-MS have increased their throughput capabilities, this has allowed the acquisition of sample sizes sufficient for meaningful time series analysis. Large scale plant breeding programs such as ABSTRESS, an international project into biotic and abiotic plant stress, generate many mega-variate datasets. Whilst a number of statistical tools and methodologies are available to analyse such data, it is not always apparent a priori which methods and parameters will produce desirable results. This is especially true of large scale, non-targeted studies.

Here we introduce a novel software solution called MetaboClust for the purposes of analysing data from such studies. We demonstrate this by analysing the effects of combined biotic and abiotic stress in *Medicago truncatula*, a model legume.

The non-targeted dataset comprises just under 2900 variables for 4 experimental groups over 13 time-points, representing LC-MS spectra obtained from processed leaf samples for stressed and non-stressed plants over two weeks. The software assists the user in selecting appropriate parameters through visual and interactive feedback. We use this to select a suitable smoothing function from which we can cluster the time-profiles. The software allows these clusters to be compared with known metabolic pathways for Medicago, obtained from MedicCyc, with an aim to identify pathways potentially affected by the experimental conditions. Two such pathways are presented.

P170 – S18

Genetic diversity of *Vicia faba* L. landraces in Morocco: a reservoir for the enhancement of the competitive ability to weed stress

Ghaouti L.[1], Aqtbouz N.[1], Belqadi L.[1], Link W.[2]

1 - Département de Production, Protection et Biotechnologies Végétales, Institut Agronomique et Vétérinaire Hassan II, Rabat, Morroco

2 - Department of Crop Sciences, Georg-August Universität, Göttingen, Germany

Faba bean, the major legume crop in Morocco, is an ancient crop with a large extent of genetic diversity. Over 90% of the farmers are cropping landraces using traditional farming practices with very low inputs.

The yield loss attributed to weeds in faba bean can amount 60-70%. Mechanical and chemical weeding is very rarely used. The high level of genetic diversity of Moroccan faba bean landraces constitutes an option for farmers to cope with weed stress.

No study exists so far on the competitiveness of the Moroccan landraces to weeds. The objective of this study is (1) to assess the genetic diversity of the Moroccan populations and (2) to evaluate their competitive ability to weeds.

A set of 60 Moroccan local populations, and 2 checks (Aguadulce; Defez) which are commonly used cultivars, were (1) analyzed molecularly through AFLP to assess their genetic diversity and (2) tested under field conditions in 4 environments to assess their competitive ability toward weeds. A split-plot design was used with 2 treatments (with / without weeds). The white mustard was used as a model weed.

AFLP analysis revealed a large diversity within (82%) and between (18%) the local populations.

The analysis of variance showed that the differences between genotypes and treatments as well as their interactions were significant for maturity, yield and yield components.

P171 – S18

Potential of arbuscular mycorrhizal fungi and nitrogen fixing bacteria for improving the production of grain legumes under water stress

Carvalho P.[1], Rocha I.[2], Ma Y.[2], Nunes M.[1], Marques G.[3], Látr A.[4], Vosátka M.[5], Freitas H.[2], Oliveira R.S.[1,2]

1 - Department of Environmental Health, Research Centre on Health and Environment, School of Allied Health Sciences, Polytechnic Institute of Porto, Vila Nova de Gaia, Portugal.

2 - Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, Coimbra, Portugal.

3 - CITAB - University of Trás-os-Montes and Alto Douro (UTAD), Department of Agronomy, Vila Real, Portugal.

4 - Symbiom Ltd., Lanskroun, Czech Republic. 5 Institute of Botany, Academy of Sciences of the Czech Republic, Pr_honice, Czech Republic.

Grain legumes are widely cropped plants with significant economic, social and environmental importance. Arbuscular mycorrhizal fungi (AMF) and nitrogen fixing bacteria (NFB) can improve plant nutrition and increase drought tolerance. The study aimed at assessing the effect of AMF and NFB inoculation in promoting the growth and yield of a grain legume as a sustainable agricultural practice. Cowpea [*Vigna unguiculata* (L.) Walp.] was inoculated with AMF and NFB and subjected to three levels of water stress: no stress, moderate stress or severe stress. Inoculated plants had improved grain yield under water stress when compared with non-inoculated controls. Plant growth was also significantly increased in inoculated plants. Inoculation with AMF and NFB can improve the productivity of grain legumes. These microbial inoculants can contribute for sustainable production of heathy food under adverse environmental conditions.

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P172– S18

Effect of pea seed-borne mosaic virus (PSbMV) Pathotype 4 on field pea

Pasche J.
North Dakota State University, USA

Pea seed-borne mosaic virus (PSbMV; family Potyviridae) causes large yield and seed quality losses in field pea (*Pisum sativum*). The incidence and severity of damage caused by the virus varies across cultivars and is influenced by pathotype, among other things. The objective of this research was to evaluate infection frequency of PSbMV pathotype 4 (P4) and the effect of the virus on seed transmission, symptoms, weight, and number per pod in 20 cultivars. PSbMV isolate ND14-1, 99% identical in nucleotide sequence to P4, was obtained from infected field pea seed grown in North Dakota, USA in 2014. The isolate was mechanically inoculated onto field pea cultivars 5 weeks after planting (WAP) and infection frequency was evaluated using enzyme-linked immunosorbent assay (ELISA) at 8 and 11 WAP. Of the cultivars evaluated, two were resistant (presumably containing sbm1 allele), one was moderately susceptible (25% infection frequency), and all others were susceptible (50-80% infection frequency) to PSbMV P4. Yield reductions up to 52% observed in PSbMV infected plants 15 WAP were mainly attributed to reduced seed size. In many cultivars, seed and pod number increased due to delayed plant maturity. Daughter seeds from infected plants were sorted by symptoms and tested for PSbMV 5 WAP. No difference in seed transmission was observed between symptomatic and asymptomatic seed, confirming that seed symptoms do not predict virus presence. Seed transmission of PSbMV P4 ranged from 0-52%.

P173 – S18

Development of a freezing test in controlled conditions for *Pisum sativum*.

Hascoët E.[1], Devaux C.[2], Beji S.[3], Jaminon O.[1], Dufayet V.[4], Lecomte C.[4], Delbreil B.[3], Lejeune-Hénaut I.[1]

1 - USC ICV-AFP, INRA, 80203, Péronne, France
2 - USC ICV-AFP, Terres Univia, 80203, Péronne, France
3 - USC ICV-AFP, Université Lille1, 59655, Villeneuve d'Ascq, France
4 - UMR Agroécologie, INRA, 21065, Dijon, France

Freezing is a major environmental limitation to crop productivity for a number of species including legumes. In the context of global climate change, winter crops will experiment milder autumn temperatures that could be detrimental to the achievement of cold acclimation, which is the ability for plants to increase their level of frost tolerance (FT) in response to low but non-freezing temperatures. For the pea crop, a modelling approach has shown that climate warming will increase the occurrence of freezing damage events, even if these latter will be less severe (Castel et al., 2014). Thus, breeding for frost tolerant winter peas requires not only to improve their FT threshold, but also to raise their cold acclimation rate. In order to evaluate the genetic variability of both traits, we are adjusting a protocol in controlled conditions, which provides an indirect evaluation of FT by the measurement of tissues’electrolyte leakage (EL). Pea stem samples have been collected after variable durations of cold acclimation at 4°C day/2°C night in a climatic chamber. They have been then progressively cooled at 2°C h-1 in a programmable temperature-test chamber to reach test temperatures ranging from +4°C to -36°C. After 14 days of cold acclimation, EL evaluation enabled the same ranking of genotypes according to their FT threshold as obtained in the Chaux-des-Prés field platform. Improvements of the protocol are however still needed to use it as a routine ranking test.

P174 – S18

Nested Association Mapping for resistance to *Aphanomyces* root rot of pea in *Medicago truncatula*

Tollenaere R.[1], Hajri A.[1], Bonhomme M.[2], Boutet G.[1], Young N.[3], Baranger A.[1], Jacquet C.[2], Pilet-Nayel M.-L.[1]
1 - INRA, UMR1349 IGEPP, PISOM, UMT INRA/Terres Inovia, Le Rheu F-35653, France
2 - UPS-CNRS, LRSV, F-31326 Castanet-Tolosan, France
3 - University of Minnesota, Saint Paul, MN-55108, USA

Pea is an important food crop worldwide, providing more than 17Mt in the year 2013-2014 (FAOSTAT, 2016). It is the most widely grown legume crop in the European Union. The high nutritional content of peas, in particular, their protein content makes them a desirable food source for both humans and livestock.

A major disease of this legume is *Aphanomyces* root rot caused by the soilborne oomycete pathogen, Aphanomyces euteiches Drechs. There are few methods known to effectively control this disease, which impacts greatly on productivity. The search for resistance traits in pea is imperative for increasing yield.

Medicago truncatula is used to study the legume/Aphanomyces pathosystem as it is easily manipulated, there is a high quality genome available and it is a natural host of Aphanomyces. We used nested association mapping analysis of connected RIL populations of Medicago truncatula in order to investigate the diversity of loci and candidate genes underlying quantitative resistance to Aphanomyces root rot, by comparison with previous QTL or genome-wide association studies. Results will provide new data to analyse the genomic conservation of resistance loci between M. truncatula and pea and to identify candidate genes underlying resistance QTL in pea using translational genomics.

P175 – S18

Characterization of low-strigolactone germplasm in pea (*Pisum sativum* L.) resistant to crenate broomrape (*Orobanche crenata* Forsk.)

Pavan S.[1], Schiavulli A.[2], Marcotrigiano A.R.[1], Bardaro N.[1], Bracuto V.[1], Ricciardi F.[2], Charnikhova T.[3], Lotti C.[2], Bouwmeester H.[3], Ricciardi L.[1];

1 - Department of Plant, Soil and Food Science, Section of Genetics and Plant Breeding, University of Bari, via Amendola 165/A, 70126 Bari, Italy

2 - Department of Agriculture, Food and Environmental Science, University of Foggia, via Napoli 25, 71100 Foggia, Italy;

3 - Laboratory of Plant Physiology, Wageningen University, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands

Crenate broomrape (*Orobanche crenata* Forsk.) is a devastating parasitic weed threatening the cultivation of legumes around the Mediterranean and in the Middle East. So far, only moderate levels of resistance were reported to occur in pea (*Pisum sativum* L.) natural germplasm, and most commercial cultivars are prone to severe infestation. Here, we describe the selection of a pea line highly resistant to O. crenata, following the screening of local genetic resources. Time series observations show that delayed emergence of the parasite is an important parameter associated with broomrape resistance. High performance liquid chromatography connected to tandem mass spectrometry (LC-MS/MS) analysis and in vitro broomrape germination bioassays suggest that the resistance mechanism might involve the reduced secretion of strigolactones, plant hormones exuded by roots and acting as signalling molecules for the germination of parasitic weeds. Two years replicated trials in non-infested fields indicate that the resistance is devoid of pleiotropic effects on yield, in contrast to pea experimental mutants impaired in strigolactone biosynthesis, and thus is suitable for use in breeding programs.

P176 - S18

Flower abscission rates of early-maturing soybean varieties

<u>Aper J.</u>[1], Haezebrouck J.[2], Bral L.[2], Reheul D.[2], Baert J.[1]

1 - Plant Unit, Institute for Agricultural and Fisheries Research, Belgium,
2 - Faculty of Bioscience Engineering, Ghent University, Belgium

North western Europe could decrease its heavy dependency on imported protein crops by a local production of soybean. *Unfortunately*, the region's short and cold growing season is a serious limitation for high soybean yields. When the flowering time of early-maturing soybean varieties would start earlier, the potential yield could be improved, but then cold tolerance during flowering becomes more important. Therefore, the flower abscission rates during the flowering period were evaluated in an observation trial with 8 MG000 soybean varieties in 2014 and 2015 at an early and late sowing date in Merelbeke (Belgium) and in 2014 at a normal sowing date in Elsenborn (Belgium). We determined flowering time and counted the number of buds, young flowers, old flowers and pods on a weekly basis on nodes 4 to 9 during the beginning of flowering (R1) till the beginning seed stage (R5). These observations allowed us to calculate the abscission rates of the reproductive organs. When the abscission rates of old flowers were plotted over time, there was a clear response to the cold peaks that happened between two moments of observation. After cold events, more than 80% of the old flowers were lost. Cold events were not restricted to the beginning of the flowering period and returned frequently. The results of this study indicate that breeders should focus on cold tolerance during flowering to increase the potential yield level of soybean in north western Europe.

P177 – S18

Exploiting public SNP markers for mapping disease resistance QTL in Faba bean (*Vicia faba*)

Gostkiewicz K., Webb A., Thomas J., Wood T.
NIAB, Dept. Field Crops Research, Cambridge UK

Faba bean (*Vicia faba*) has suffered from less investment in selective improvement compared to other major arable crops. There has been limited development in marker-assisted breeding strategies and a lack of basic genomic information confounds fundamental investigations. Using a public set of faba KASP SNP markers (Webb et al., 2015) and germplasm developed through the DEFRA Pulse Crop Genetic Improvement Network (PCGIN) we have created genetic mapping populations to identify markers linked to quantitative trait loci (QTL) contributing to resistance against Peronospora viciae f sp fabae, *Ascochyta fabae* and *Botrytis fabae*. Linked genetic markers could be exploited by plant breeders, to track important regions of the genome to efficiently introgress resistance into new, improved varieties. F2:F3 populations segregating respectively for downy mildew and Ascochyta resistance have been genotyped using a selection of SNP markers. This information has been used to construct genetic maps on which QTL will be located; inoculated screens in controlled environments have been used to phenotype F3 faba seedlings in order to identify resistance QTL and provide plant breeders with genetic markers with utility for enhancing disease resistance.

P178 – S18

Microbial associations with legume plant trigger systemic resistance against *Didymella pinodes* infection

Desalegn G.
BOKU, Vienna

Species of ascochyta blight such as *Didymella pinodes* is one of the most damaging aerial pathogen of field pea (*Pisum sativum*. L) (Fondevilla et al., 2011; Tivoli and Banniza, 2007). It sometimes results in the loss of the entire crop, especially in monoculture and whenever there is a favourable environmental condition for its infection and further development. In a pot experiment, with and without D. pinodes infection tests were conducted to study the effects of three symbionts (Rhizobium, arbuscular mycorrhiza fungi and co-inoculation of the two) and non-symbiotic control treatments on pea in a completely randomized design with four replicates. After infection with this pathogen, leaf metabolites and proteome, disease severity and shoot biomass and green areas were analysed. We found significantly highest biomass and green areas in pea plants inoculated with Rhizobium. Furthermore, the overall regulation of the citric acid cycle, amino acid and secondary metabolism including the pisatin pathway were most pronounced in rhizobia associated plants which had also the lowest infection rate and the slowest disease progression. The co-inoculation increased the synthesis of stress related proteins, while mycorrhizal treatments were involved in metal ion homeostasis and dampening of reactive oxygen species. Overall, we conclude that microbial associations, Rhizobium bacteria in particular, modify the interaction between host plant and the aerial pathogen.

P179 – S18

Development of differential sets to identify *Uromyces viciae-fabae* pathotypes in Australia

Ijaz U., Adhikari K., Bansal U., Bariana H., Trethowan R.
Plant Breeding Institute, The University of Sydney

Faba bean rust (*Uromyces viciae-fabae*) is an important disease in sub-tropical region of Australia and pathogen variability of this fungus is unknown. Pathotypes (races, strains) are the unique variants of a pathogen that differ in their ability to overcome the resistance in one or more hosts of the same species. The ability or inability of rust pathogen to infect a group of host genotypes allows the pathotype to be detected. These genotypes are known as differentials. The differential development work has been designed and performed at Cereal Rust Testing Laboratory, Plant Breeding Institute, Cobbitty. The pure rust urediospores suspended in light mineral oil (Isopar) were misted on the set of resistant plants using ultra low volume applicator (Microfit, Micron sprayer, UK). After inoculation, plants were kept for incubation in dark room with 100% relative humidity for 24 h. After incubation, plants were moved in microclimate room at 24±2 oC and seedlings were rated (0-4) for disease resistance. Seven seedling rust resistant genes were detected in cultivar Doza selections # 12034 & 14916, collected accession Ac1655, Ac1227#14908, Ac1257#14904 and some advanced lines IX114#15033 and 585c/1-11 in Australia. These seven genotypes showed significant distinct virulence/avirulence pattern against the collected rust isolates from three major faba bean growing states (NSW, Qld and SA) in Australia. The observed vir/avr pattern can be used to identify the current pathogen variables.

P180 – S18

Phenotyping for iron deficiency chlorosis in soybean plants at morphological, biochemical and multispectral level

Santos C.S.[1], **Araújo D.**[1,2], **Carvalho S.M.P.**[1,2,3], **Hajirezaei M.-R.**[4], **Giehl R.**[4], **von Wirén N.**[4], **Vasconcelos M.W.**[1]

1 - Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Universidade Católica Portuguesa, Porto, Portugal.

2 - GreenUP/CITAB-UP & DGAOT, Faculty of Sciences, University of Porto, Campus Agrário de Vairão, Rua Padre Armando Quintas, 7. 4485-661 Vairão, Portugal.

3 - Department of Plant Sciences, Horticulture and Product Physiology Group, Wageningen Univ., Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands.

4 - Molecular Plant Nutrition, Department of Physiology & Cell Biology, Leibniz-Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany.

Iron (Fe) is an essential mineral nutrient for plant growth. Albeit present in the soil in high concentrations, it is often deficient for uptake in calcareous conditions, because it is mostly present in an oxidized state. Like most crops, soybean (*Glycine max*. L) is prone to developing Iron Deficiency Chlorosis (IDC), a condition that severely affects plant growth. Phenotyping plants at a whole-plant, organ and cellular levels is essential to understand the mechanisms underlying Fe uptake, trafficking and homeostasis and this integrated view is essential in order to prevent IDC. We conducted a phenotyping experiment, under the scope of an STSM, where we grew a subset of soybean lines under Fe limitation and Fe sufficiency, collected and concentrated their root exudates and subjected them to analysis for organic acids and Fe mobilization capacity. We were able to classify the lines in terms of their Fe efficiency and the main factor contributing for their behaviour. Regarding these results, we selected an Fe efficient line and conducted another experiment where plants were germinated and grown for seven days under hydroponic conditions with Fe supply and then, in a time course trial, they were transferred for Fe deficiency and grown for 2, 4, 6 and 8 days under Fe deficiency. Plant growth was 25, 31, 46 and 15 % lower in Fe deficient plants (fresh weight) and total chlorophylls were also decreased in more than double when compared to the control conditions. Also, at each time point, multispectral measurements were performed using a XpeCAM X01 camera, the reflectance of the main trifoliate leaf was analysed in a wavelength range of 450 to 950 nm and the correlations of these measurements and SPAD values (which correspond to the visual symptoms) were established.

P181 – S18

Identification of pea accessions with combined resistance to Fusarium wilt and drought

Rispail N.[1], Bani M.[1,2], Rubiales D.[1]

1 - Institute for Sustainable Agriculture, CSIC, Avda. Menéndez Pidal s/n, 14004 Cordoba, Spain

2 - Ecole Nationale Supérieure de Biotechnologie, ville universitaire Ali Mendjeli, 25100 Constantine, Algérie

Pea, *Pisum sativum* L. is one of the major legume crops worldwide. However, its yield remains relatively low mainly due to its high susceptibility to stresses. Pea is particularly susceptible to drought and to *Fusarium* wilt caused by the soilborne fungal pathogen *Fusarium oxysporum*, whose damage is favored by by warm temperatures and dry weather. Loses caused by this pathogens are thus expected to be more severe and widespread in future due to climate changes that also predicted an increase of drought prone areas. The use of resistant cultivars is currently the most efficient control approach. However, the existing resistance level introduced in legume cultivar is still insufficient to control the disease. It is thus crucial to identify and exploit new sources of resistance to F. oxysporum and drought. In the frame of the EU project, ABSTRESS, we initially established an optimum inoculation method suitable to study legume response to fusarium wilt and its interaction with drought stress using the model legume Medicago truncatula. This methodology was then applied to screen a large Pisum collection to identify pea accessions resistant to *F. oxysporum*. Twenty pea accessions were found highly resistant to F. oxysporum. The response of these resistant sources to combined fusarium wilt and drought stresses were then tested under controlled condition allowing identification of several accessions with high level of resistance to fusarium wilt and tolerant to drought. These sources of resistance would be very valuable to introgress resistance to both stresses in pea cultivar.

P192 – S18

Efficiency of different traits for phenotyping soybean drought tolerance in an automated platform when estimated under different basis.

Peirone L., Irujo, G. P., Aguirrezábal, L.A.N.
Laboratorio de Fisiología Vegetal, Unidad Integrada Balcarce (INTA-FCA, UNMdP), Argentina, Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET).
laguirre@mdp.edu.ar

An automated platform was used to assess the efficiency of different traits for phenotyping drought tolerance, taking into account only one basis, i.e. heritability. The aim of this work was to compare the efficiency of different traits for phenotyping when estimated under different basis. Seven soybean genotypes were studied under well watered and water deficit treatment (WD). WD started at 33 days after emergence (DAE), and finished at 57 DAE. 34 traits were measured before and after the onset of the WD measured in the Glyph platform, a low-cost automatic automated platform developed for soybean, which allows the evaluation of genotypes under precisely controlled water deficit condition. The efficiency of these traits for phenotyping were estimated for the basis time from emergence to phenotyping ii) coefficient of genetic determination (CGD), sample size, measurement time and measurement cost. Traits with a high efficiency on time from emergence (Transpiration efficiency estimated at 13, 20, 27, 33 and 38 DAE, Leaf Area Ratio and Shoot Dry Weight at 38 DAE) were also efficient when estimated on basis cost, measurement time, and sample size. They showed intermediate values of CGD. The framework applied in this work for a joint analysis of efficiency of several traits under different basis could be helpful for selecting those more efficient for phenotyping given the bottleneck of each specific case (e.g. capacity of the phenotyping platform, available sensors, budget).

P191 - S18

Determination of peas genotypes for yield and yield Components in Cukurova region

Türkeri M., Mart D., Yücel D., Karaköy T.
East Mediterranean Agricultural Research Institute, Andana, Turkey

This research was carried out to determine the seed yield and yield components of some pea genotypes under Çukurova ecological conditions during 2014-2015 at East Mediterranean Agricultural Research Institute Doğankent Location. Genotypes and cultivars from ICARDA and Menemen Gene Bank were used as trial material. According to the results of the observation at genotypes, were examinate plant height, flowering number of day, seed yield, 100 seed weight. According to the results of the analyses; the highest and lowest seed yield values 376.8–91.7 kg/da, flowering number of day values 101.0-72.0 day, plant height values151.6-48.3 cm, 100 seed weight 24.5-15.5 gr were obtained from genotypes. These results provide an initial step toward the identification of (*Pisum sativum* L.) that may be useful for the development of breeding *Pisum sativum* L.

P193 – S18

Drought stress responses of Portuguese cowpea accessions

Carvalho M.[1], Lino-Neto T.[2], Matos M.[3,4], Castro I.[1,3] and Carnide V.[1,3]

1 - Centre for Research and Technology of Agro-Environment and Biological Sciences (CITAB), University of Trás-os-Montes and Alto Douro (UTAD), 5000-801 Vila Real, Portugal.

2 - Biosystems & Integrative Sciences Institute (BioISI), Plant Functional Biology Center (CBFP), University of Minho, Campus de Gualtar, 4710-057 Braga, Portugal.

3 - Department of Genetics and Biotechnology, University of Trás-os-Montes and Alto Douro (UTAD), 5000-801 Vila Real, Portugal.

4 - Biosystems & Integrative Sciences Institute (BioISI), Sciences Faculty, University of Lisbon, Campo Grande, 1749-016 Lisbon, Portugal.

Cowpea (*Vigna unguiculata* L. Walp.) is pointed as one of the most tolerant grain legume crops to drought. As a result, this crop has been considered as an ideal model to study the molecular mechanisms of drought tolerance. To evaluate and determine the tolerance level of two Portuguese cowpea accessions (Fradel and Pinhel), several biochemical and production parameters were determined in plants submitted to three water treatments (25%, 50% and 75% of field capacity, FC) during 15 days. As control, a drought-sensitive (CB46) genotype was used.

As expected, plants subjected to 25% of FC treatment always presented higher stress levels. However, the Portuguese accessions seem to present a reduced inducible drought response than CB46 genotype, as evaluated by biochemical parameters. The high constitutive levels of proline present in both Portuguese accessions may have resulted in reduced drought stress levels, detected by H2O2 quantification and lipid peroxidation, or by anthocyanin levels, as compared to susceptible control. The number of cowpea pods and seeds weight in drought conditions was much more affected in Fradel than in CB46. In contrast, Pinhel was the genotype that presented higher tolerance to drought concerning the same production parameters. Although the evaluation of biochemical parameters has revealed a weak inducible drought response of both Portuguese cowpea genotypes, they both differed in production parameters in relation to the susceptible control.

List of Participants

Last name	First Name	Affiliation	Email Address	Poster nº
Abdelguerfi	Aissa	ENSA ALGIERS	aabdelguerfi@yahoo.fr	P40 – S4
Abugaliyeva	Aigul	LLP "Kazakh Research Institute of Agriculture and Plant Growing"	kiz_abugalieva@mail.ru	P117 – S13
Acikgoz	Esvet	Uludag University	esvet@uludag.edu.tr	P106 – S13
Adam	Eveline	Saatzucht Gleisdorf GmbH	eveline.adam@gmx.at	P107 – S13
Adeniyi Micheal	Adefisan	University of Ibadan, Nigeria	adefisanadeniyi@hotmail.com	
Adeosun	Isaiah Ademola	University of Ibadan,Nigeria	vickolat@gmail.com	
Aguirrezabal	Luis	Universidad Nacional de Mar del Plata - CONICET, Argentina	luisaguirrezabal@gmail.com	P90 – S11
Ahmad	Salman	University of Sargodha, Sargodha	salmanahmad@uos.edu.pk	
Ainouche	Abdelkader	Université de Rennes1, UMR CNRS Ecobio	kader.ainouche@univ-rennes1.fr	P190 – S3
Akindele	Samuel Tope	Olarok & Co	olarokco@gmail.com	
Akogor	Ukpor Friday	Elan League International Limited	engrfrifun@gmail.com	
Al Masmoudi	Yassine	Inra	yassine.almasmoudi@gmail.com	P7 – S2
Alalade	Clement	Oyo state ministry of Agriculture	oyoagric@gmail.com	
Alizadeh	Khoshnood	Dryland Agricultural Research Institute	khoshnod2000@yahoo.com	P45 – S7
Almeida	Nuno	ITQB NOVA	nalmeida@itqb.unl.pt	P152 – S18
Alsina	Ina	Latvia University of Agriculture	Ina.Alsina@llu.lv	
Amokrane	Yanis	ENSA Alger / ECOLAB CNRS/INPT/UPS	yanisamokrane@yahoo.fr	P14 – S2
Anay	Ayse	East Mediterranean Agricultural Research Institute	ayseanay@hotmail.com	
Annicchiarico	Paolo	CREA - Centre for Fodder Crops and Dairy Productions	paolo.annicchiarico@crea.gov.it	Oral – S8

Aper	Jonas	ILVO	jonas.aper@ilvo.vlaanderen.be	P176 – S18
Araújo	Susana	ITQB NOVA	saraujo@itqb.unl.pt	P149 – S18
Arlauskienė	Aušra	Joniškėlis Experimental Station of the Lithuanian Research Centre for Agriculture and Forestry	arlauskiene.ausra@gmail.com	P137 – S14
Arribas Martinez	Claudia	INIA	arribas.claudia@inia.es	P51 – S7
Atienza	Sergio	IAS-CSIC	sgatienza@ias.csic.es	P67 – S8
Aubert	Gregoire	INRA	gregoire.aubert@dijon.inra.fr	
Aulrich	Karen	Thünen Institute of Organic Farming, Federal Res. Institute for Rural Areas, Forestry and Fisheries	karen.aulrich@thuenen.de	P47 – S7
Babatunde	Moruff Abiodun	Fetches International	fetchesinter@gmail.com	
Bahceci	Hakan	International Pulse Trade and Industries Confederation	tuba.durgun@hakanfoods.com	KeyLect -1
Balliu	Astrit	Agricultural University of Tirana	aballiu@ubt.edu.al	P127 – S14
Baranger	Alain	INRA	Alain.Baranger@rennes.inra.fr	Oral – S12
Barata	Ana Maria	BPGV/INIAV	ana.barata@iniav.pt	P34 – S4
Barcelos	Carina	INIAV	carina.barcelos@iniav.pt	P36 – S4
Barradas	Ana	Fertiprado	abarradas@fertiprado.com	
Bedoussac	Laurent	ENFA/INRA	laurent.bedoussac@toulouse.inra.fr	Oral – S5
Beji	Sana	University Lille1	sana.beji@ed.univ-lille1.fr	Oral – S18
Ben	Cecile	ECOLAB CNRS/INPT/UPS	ben@ensat.fr	P39 – S4
Benezit	Maud	INRA	Maud.Benezit@grignon.inra.fr	P123 – S13
Bentaibi	Abderrahim	Institut National de la Recherche Agronomique, Morroco	abentaibi@yahoo.fr	Oral –S5
Bianco	Carmen	IBBR - CNR	carmen.bianco@ibbr.cnr.it	P189 – S3

Biarnes	Veronique	Terres Inovia	v.biarnes@terresinovia.fr	P125 – S13
Bing	Dengjin	Agriculture and Agri-Food Canada	dengjin.bing@agr.gc.ca	P105 – S13
Blake	Sara	South Australian Research and Development Institute (SARDI)	sara.blake@sa.gov.au	
Bobille	Hélène	UR LEVA-ESA, UMR SESAN-IRHS, Univ. Angers	h.bobille@groupe-esa.com	P88 – S11
Böhm	Herwart	Thünen-Institute of Organic Farming	herwart.boehm@thuenen.de	P130 – S14
Boros	Lech	Plant Breeding & Acclimatization Institute-NRI	l.boros@ihar.edu.pl	P73 – S8
Bouhadida	Mariem	Crops Laboratory, University of Carthage, INRAT, Tunisia.	mariembouhadida@gmail.com	P167 – S18
Bourion	Virginie	INRA	virginie.bourion@dijon.inra.fr	Oral – S3
Boutet	Gilles	INRA	gilles.boutet@rennes.inra.fr	Oral – S8
Bowness	Robyne	Alberta Agriculture and Forestry	robyne.bowness@gov.ab.ca	P136 – S14
Bozoğlu	Hatice	Ondokuz Mayıs Unıversity		
Bronze	Maria	ITQB/IBET	mbronze@itqb.unl.pt	Oral - S7
Brünjes	Lisa	University Göttingen, Germany	Lbruenj@uni-goettingen.de	Oral – S15
Burstin	Judith	INRA, France	judith.burstin@dijon.inra.fr	KeyLec - 8
Buurman	Milika	Limagrain UK Ltd	milika.buurman@limagrain.co.uk	
Caballo Linares	Cristina	IFAPA	cristinacaballolinares@gmail.com	P157 – S18
Cabello-Hurtado	Francisco	University of Rennes 1	francisco.cabello@univ-rennes1.fr	
Campa	Ana	SERIDA	acampa@serida.org	Oral – S10
Campos	Felisbela	Syngenta | Seed Care	felisbela.campos@syngenta.com	
Can	Canan	University	can@gantep.edu.tr	

Caré	Rita	CiB - Centro de Informação de Biotecnologia	gabcom@cibpt.org	
Carlsson	Georg	Swedish University of Agricultural Sciences	georg.carlsson@slu.se	Oral – S14
Carović-Stanko	Klaudija	University of Zagreb, Faculty of Agriculture, Department of Seed Science and Technology	kcarovic@agr.hr	P22 – S4
Carton	Nicolas	UR LEVA-ESA	n.carton@groupe-esa.com	Oral – S16
Carvalho	Márcia	CITAB, University of Trás-os-Montes and Alto Douro, 5000-801 Vila Real, Portugal	marciac@utad.pt	Oral – S4
Castro	Isaura	CITAB, University of Trás-os-Montes and Alto Douro, 5000-801 Vila Real, Portugal	icastro@utad.pt	P193 – S18
Ćeran	Marina	Institute of Field and Vegetable Crops	marina_tomicic@yahoo.com	P112 – S13
Chaker-Haddadj	Assia	Université des Sciences et de la Technologie Houari Boumedienne, Algérie	assiachaker@yahoo.fr	P168 – S18
Charlton	Adrian	Fera Science Limited	adrian.charlton@fera.co.uk	Oral – S13
Chatterton	Syama	Agriculture and Agri-food Canada	syama.chatterton@agr.gc.ca	Oral – S6
Chen	Weidong	USDA ARS	weidong.chen@ars.usda.gov	Oral – S12
Cimmino	Alessio	University of Naples Federico II (UNINA)	alessio.cimmino@unina.it	P98 – S12
Clemente	Alfonso	Estacion Experimental del Zaidin (CSIC)	alfonso.clemente@eez.csic.es	Oral – S9
Cnops	Gerda	ILVO	gerda.cnops@ilvo.vlaanderen.be	P108 – S13
Collado	Elena	Universidad Politecnica De Cartagena	elenacolladomarin@hotmail.com	P146 – S18
Corre-Hellou	Guenaelle	ESA	g.hellou@groupe-esa.com	Oral – S16
Costa	Sara	ITQB NOVA	smcosta@itqb.unl.pt	P81 – S8
Coyne	Clarice	USDA ARS	clarice.coyne@ars.usda.gov	Oral – S6
Cupina	Branko	University of Novi Sad, Faculty of Agriculture	cupinab@polj.uns.ac.rs	Oral – S2
Dadu	Rama	University of Melbourne	rdadu@student.unimelb.edu.au	

Davidson	Jenny	SARDI	jenny.davidson@sa.gov.au	
Deokar	Amit	University of Saskatchewan, Canada	aadeokar@gmail.com	P71 – S8
Desalegn	Getinet	BOKU, Vienna	getinet.desalegn@boku.ac.at	P178 – S18
Dickinson	Michael	Fera Science Limited	michael.dickinson@fera.co.uk	Oral – S18
Djordjevic	Vuk	Institute of filed and vegetable crops	vuk.djordjevic@ifvcns.ns.ac.rs	P111 – S13
Dobránszki	Judit	Research Institute of Nyíregyháza University of Debrecen	dobranszki@freemail.hu	
Domoney	Claire	John Innes Centre	claire.domoney@jic.ac.uk	Oral – S7
Dostálová	Radmila	AGRITEC, Research, Breeding and Services, Ltd.	dostalova@agritec.cz	P120 – S13
Duarte	Isabel	INIAV	isabel.duarte@iniav.pt	P118 – S13
Dubois	Gaëtan	European Commission - DG AGRI	gaetan.dubois@ec.europa.eu	Oral – S1
Duc	Gérard	INRA	gerard.duc@dijon.inra.fr	
Duckworth	Randall	Global Pulse Confederation (CICILS/IPTIC)	r.duckworth@cicilsiptic.org	
Duque	Ana Sofia	ITQB NOVA	sduque@itqb.unl.pt	P61 – S7
Ellis	Noel		thnoelellis@gmail.com	KeyLec - 4
Emmrich	Peter	John Innes Centre	peter.emmrich@jic.ac.uk	P80 – S8
Evidente	Antonio	University of Naples Federico II (UNINA)	evidente@unina.it	P99 – S12
Ezekwe	Innocent	University of Ibadan,Nigeria	vickolat@gmail.com	
Farkas	Rita	AMBIS Ltd.	farkas.ritadiana@gmail.com	
Feinstein	Alina	NRGene	alina@nrgene.com	
Fernandes	Hortense	UTAD-Departamento de Agronomia	hortenseafernandes@gmail.com	
Fernández	Juan A	Universidad Politécnica de Cartagena	juan.fernandez@upct.es	P20 – S4

Ferrándiz	Cristina	IBMCP, CSIC-UPV, Valencia, Spain	cferrandiz@ibmcp.upv.es	P84 – S8
Ferreira	Juan	SERIDA	jjferreira@serida.org	P151 – S18
Fevereiro	Pedro	ITQB Nova	psalema@itqb.unl.pt	
Fierro	Marco	Università degli Studi del Molise	marco.fierro@studenti.unimol.it	P23 – S4
Fischer	Kristin	Julius Kühn-Institut, Institute for Breeding Research on Agricultural Crops	kristin.fischer@julius-kuehn.de	Oral – S4
Fondevilla	Sara	Institute for Sustainable Agriculture-CSIC	sfondevilla@ias.csic.es	P140 – S18
Francis	Stephen	PGRO / Fen Peas	Stephen@fenpeas.com	
Frazoa	Sofia	Soul Trails	sofia.frazoa@gmail.com	
Füchtbauer	Winnie	Sejet Plant Breeding	wsf@sejet.com	
Fülöp	Katalin	Bonafarm Bóly Zrt.	Jozsefne.Fulop@boly.bonafarm.hu	
Fustec	Joelle	Ecole Supérieure d'Agriculture, UR LEVA, Angers, France	j.fustec@groupe-esa.com	P187 – S3
Gaad	Djouher	National High School of Agriculture	gaad_djouher@yahoo.fr	P18 – S4
Galoburda	Ruta	Latvia University of Agriculture	galoburda@yahoo.com	P58 – S7
Ganci	Patrizia	European Commission	patrizia.ganci@ec.europa.eu	
Garcia	Pedro	Dept. Genetics, University of Leon	pgarg@unileon.es	P163 – S18
Gawłowska	Magdalena	Institute of Plant Genetics, Polish Aademy of Sciences	mgaw@igr.poznan.pl	P148 – S18
Gentzbittel	Laurent	ECOLAB CNRS/INPT/UPS	gentz@ensat.fr	Oral – S6
Ghaouti	Lamiae	Institut Agronomique et Vétérinaire Hassan II	lamiaeghaouti@hotmail.com	P170 – S18
Ghislain Ludovic	Mbemba	Cooperative Agriculteur Maty	cooperativeagriculteurmaty@gmail.com	
Ghoulam	Cherki	Faculty of sciences and Techniques, Cadi Ayyad University	c.ghoulam@uca.ma	P185 – S3

Godinho	Bruno	Fertiprado	bgodinho@fertiprado.com	
Gomez di Marco	Perla	Universidad Politecnica De Cartagena	perla.gomez@upct.es	P43 – S7
Gonçalves	Letice	ITQB NOVA	letice.let@gmail.com	P25 – S4
Gragera-Facundo	Juan	CICYTEX-La Orden, Junta de Extremadura, Spain	juan.gragera@gobex.es	P133 – S14
Guillamon	Eva	INIA	guillamon.eva@inia.es	P52 – S7
Guindon	María	IICAR-CONICET (Instituto de Investigaciones en Ciencias Agrarias de Rosario)	ferguindon@gmail.com	P121 – S13
Guinet	Maé	AgroSup Dijon	mae.guinet@@dijon.inra.fr	Oral – S16
Gupta	Soma	Indian Agricultural Research Institute, New Delhi, India	somugupta24@gmail.com	P115 – S13
Gutierrez Leiva	Natalia	ZAYINTEC-IFAPA	natalia.gutierrez@zayintec.com	
Guy	Stephen	Washington State University	sguy@wsu.edu	Oral – S16
Hamwieh	Aladdin	ICARDA	a.hamwieh@cgiar.org	
Harzic	Nathalie	Jouffray-Drillaud	nharzic@jouffray-drillaud.fr	
Hascoët	Emilie	INRA	Emilie.Hascoet@mons.inra.fr	P173 – S18
Hassissene	Nadia	University of Bejaia, Algerie	nadhassi1@gmail.com	P63 – S7
Heshmati	Sara	Georg-August-Universität Göttingen	sarah.heshmati@agr.uni-goettingen.de	P11 –
Hingane	Anupama	International Crops Research Institute for Semi-Arid Tropics	h.anupama@cgiar.org	P126 – S13
Holdt	Courtney	North Dakota State University	courtney.holdt@ndsu.edu	P6 – S2
Hu	Jinguo	USDA/ARS	jinguo.hu@ars.usda.gov	
Hunady	Igor	AGRITEC PLANT RESEARCH Ltd.	hunady@agritec.cz	P62 – S7
Hybl	Miroslav	Crop Research Institute	hybl@genobanka.cz	P9 – S2

Iannetta	Pietro	The James Hutton Institute	pete.iannetta@hutton.ac.uk	Oral – S1
Ijaz	Usman	The University of Sydney, Australia.	usman.ijaz@sydney.edu.au	P179 – S18
Infantino	Alessandro	CREA - Centro di ricerca per la patologia vegetale	alessandro.infantino@crea.gov.it	
Ishola	Alabi	Animal Science Department,University of Ibadan,Nigeria	vickolat@gmail.com	
Jackson	Scott	Center for Applied Genetic Technologies, USA / University of Georgia	sjackson@uga.edu	KeyLec - 13
Jallow	Assiatou	PHARMACUETICAL	spaceworld.technology@yahoo.com	
Jallow	Momodou	University of the Gambia	technical.alasana.sos@gmail.com	
Jensen	Erik Steen	Swedish University of Agricultural Sciences	erik.steen.jensen@slu.se	Oral – S17
Jeuffroy	Marie-Hélène	INRA, France	jeuffroy@grignon.inra.fr	KeyLec - 2
Jha	Ambuj	University of Saskatchewan	ambuj.jha@usask.ca	Oral – S9
Jhajj	Kuldeep r	Punjab Agricultural University, Ludhiana, Punjab (India)	kuldeepjhajj89@gmail.com	P12 – S2
Jimenez-Lopez	Jose C.	CSIC, Estacion Experimental del Zaidin; Department of Biochemistry, Cell and Molecular Biology of Plants	josecarlos.jimenez@eez.csic.es	Oral – S7
Journet	Etienne-Pascal	INRA - CNRS	etienne-pascal.journet@toulouse.inra.fr	Oral – S16
Julier	Bernadette	INRA	bernadette.julier@lusignan.inra.fr	Oral – S13
Justes	Eric	INRA, France	Eric.Justes@toulouse.inra.fr	KeyLec - 14
Kadziuliene	Zydre	Lithuanian Research Centre for Agriculture and Forestry	zkadziul@lzi.lt	P65 – S7
Kafadar	Feyza	University of Gaziantep	incik@gantep.edu.tr	
Kalo	Peter	NARIC Abricultural Biotechnology Institute	kalo@abc.hu	P79 – S8
kamara	Sewa	rokupr food development project	gibrillaff02@gmail.com	

Karayel	Reyhan	Black Sea Agriculture Research Institute	reyhank55@hotmail.com	P60 – S7
Karki	Nar	Chitawan Eco Agro Pvt. Ltd.	chitwan.ecoagro1@gmail.com	
Katanski	Snežana	IFVCNS, Institute of Field and Vegetable Crops, Novi Sad	snezana.katanski@nsseme.com	P57 – S7
Kaur	Sukhjiwan	AgriBio, Agriculture Victoria, DEDJTR	sukhjiwan.kaur@ecodev.vic.gov.au	Oral – S8
Keller	Jean	University of Rennes 1	jean.keller@univ-rennes1.fr	Oral – S3
Kemal	Seid	ICARDA	s.a.kemal@cgiar.org	KeyLec - 12
Khahlu	Tshepang	University of Pretoria	tkhahlu@gmail.com	P87 – S11
Khamassi	Khalil	Institut National deRecherche Agronomique	khkobe@hotmail.com	P78 – S8
Kimber	Rohan	SARDI	rohan.kimber@sa.gov.au	
Kisha	Theodore	USDA-ARS	theodore.kisha@ars.usda.gov	P29 – S4
Kiss	Gyorgy	AMBIS Ltd.	kiss.gyorgybotond@gmail.com	P107 – S13
Knotova	Daniela	Agricultural Research, Ltd.	knotova@vupt.cz	P48 – S7
Knudsen	Jens	Nordic Seed	jeno@nordicseed.com	
Konosonoka	Inara	Latvia University of Agriculture	inara.konosonoka@gmail.com	P49 – S7
Kritzinger	Quenton	University of Pretoria	quenton.kritzinger@up.ac.za	P8 – S2
Kroc	Magdalena	Institute of Plant Genetics, Polish Academy of Sciences, Poznan, Poland	mkro@igr.poznan.pl	P139 – S14
Kron	Roberto	AGRIFUTUR	RKM@Agrifutur.com	
Kronberga	Arta	Institute of Agricultural Resources end Economics	Arta.Kronberga@arei.lv	P21 – S4
Książkiewicz	Michał	Institute of Plant Genetics of the Polish Academy of Sciences	mksi@igr.poznan.pl	P72 – S8
Kuoppala	Kaisa	Natural Resources Institute Finland (Luke)	kaisa.kuoppala@luke.fi	P46 – S7

Kushwah	Ashutosh	Punjab Agricultural University, Ludhiana, Punjab, India	anshu.kushwah24@gmail.com	P114 – S13
Kwateng	George	Swedish university of agricultural science	jean_kwatson@yahoo.co.uk	P3 – S2
Laouar	Meriem	ENSA ALGIERS	laouar_m@yahoo.fr	P122 – S13
Lazali	Mohamed	University of Khemis Miliana	m.lazali@yahoo.fr	P153 – S18
Lazarević	Boris	Faculty of Agriculture, University of Zagreb	blazarevic@agr.hr	
Le May	Christophe	Agrocampus, INRA	lemay@agrocampus-ouest.fr	P96 –S12
Le Signor	Christine	INRA	clesignor@dijon.inra.fr	Oral - S10
Leitão	Susana	ITQB NOVA	sleitao@itqb.unl.pt	P147 – S18
Lejeune-Henaut	Isabelle	INRA	Isabelle.Lejeune@mons.inra.fr	
Lemken	Dominic	University Göttingen	dlemken@gwdg.de	Oral – S5
Lepetit	Marc	INRA LSTM	lepetit@supagro.inra.fr	Oral – S3
Lepse	Liga	Pūre Horticultural Research Centre, Latvia	liga.lepse@puresdis.lv	P19 – S4
Lesné	Angélique	INRA	angelique.lesne@rennes.inra.fr	P113 – S13
Lingner	Annika	University of Goettingen, Germany	alingne@agr.uni-goettingen.de	Oral – S14
Link	Wolfgang	Georg-August-Universität Göttingen	wlink@gwdg.de	
Lopera-Cardona	Seneida	University of Antioquia	seneida.lopera@yahoo.com	P53 – S7
Lotti	Concetta	University of Foggia	concetta.lotti@unifg.it	P38 – S4
Louarn	Gaëtan	INRA	gaetan.louarn@lusignan.inra.fr	Oral – S11
Lund	Bente	Norddeutsche Pflanzenzucht Hans-Georg Lembke KG	b.schaper@npz.de	
Madhavan	Ramakrishnan	World Vegetable Center	ramakrishnan.nair@worldveg.org	Oral – S15
Madueño	Francisco	IBMCP, CSIC-UPV, Valencia, Spain	madueno@ibmcp.upv.es	

Magrini	Marie	INRA	mbmagrini@toulouse.inra.fr	Oral – S5
Makgopa	Eugene	University of Pretoria	eugene.makgopa@up.ac.za	P158 – S18
Marais	Julie	INRA	julie.marais@dijon.inra.fr	P56 – S7
Marciniak	Katarzyna	Centre for Modern Interdisciplinary Technologies, Nicolaus Copernicus University in Torun, Poland	marciniak@umk.pl	P91 – S11
Mariam	Yusufu	University of Ibadan, Nigeria	adefisanadeniyi@hotmail.com	
Marie	Siwo Foko	SHUMAS CAMEROON	gci_cameroon@yahoo.com	
Markell	Samuel	Department of Plant Pathology North Dakota State University Fargo, ND 58102 U.S.A	samuel.markell@ndsu.edu	P103 – S12
Marques	Guilhermina	Universidade de Trás-os-Montes e Alto Douro	gmarques@utad.pt	P183 – S3
Marshall	Athole	Aberystwyth University	thm@aber.ac.uk	
Marsolais	Frédéric	Agriculture and Agri-Food Canada	Frederic.Marsolais@agr.gc.ca	KeyLec - 7
Mart	Durdane	East Mediterranean Agricultural Research Institute	durdanemart@yahoo.com	P164 – S18
Martin-Pedrosa	Mercedes	INIA	mmartin@inia.es	P50 – S7
Martos Fuentes	Marina Marta	Universidad Politécnica de Cartagena	marina.fuentes@upct.es	P68 – S8
Mascarenhas	Lisette	Saskatchewan Pulse Crop Development Board	lmascarenhas@saskpulse.com	
Mavis Nyoh	Mowoh	SHUMAS CAMEROON	sshumascameroon@yahoo.com	
Maya-Blanco	Valentin	CICYTEX-La Orden, Junta de Extremadura, Spain	valentin.maya@gobex.es	P31 – S4
Mayerne Nemere	Vera	Bonafarm - Bóly Zrt.	Vera.MayerneNemere@Boly.bonafar.hu	
McClean	Phillip	North Dakota State University	phil.mcclean@gmail.com	
McPhee	Kevin	North Dakota State University	kevin.mcphee@ndsu.edu	Oral – S17
Mecha	Elsa	ITQB NOVA	emecha@itqb.unl.pt	Oral – S9

Medard	Wamba	Cooperative Agricultor of Maty	cooperativeagriculteurmaty@gmail.co	
Mediene	Safia	INRA	safia.mediene@grignon.inra.fr	Oral – S17
Mehmood	Yasir	Nathan Campus, Griffith University, Australia	yasir.mehmood@griffithuni.edu.au	Oral – S12
Mejia	Maria del Mar	Universidad de Antioquia	seneida.lopera@yahoo.com	
Melis	Rita	CNR-ISPAAM	rita.melis@ispaam.cnr.it	
Memud	Afees	MUSADEM TRADING PTY	larryola78@gmail.com	
Mendler-Drienyovszki	Nóra	Research Institute of Nyíregyháza University of Debrecen	mendlernedn@gmail.com	P110 – S13
Mentag	Rachid	National Institute of Agricultural Research of Morocco (INRA)	rachidmentag@yahoo.ca	P100 – S12
Metzner	Ralf	Institute for Plant Sciences, Forschungszentrum Jülich GmbH, Germany	r.metzner@fz-juelich.de	Oral – S11
Miki	Momiji	Okayama University	pdl11qj7@s.okayama-u.ac.jp	P165 – S18
Mikić	Aleksandar	Institute of Field and Vegetable Crops	aleksandar.m.mikich@gmail.com	P116 – S13
Millan	Teresa	University of Cordoba	teresa.millan@uco.es	
Milošević	Branko	IFVCNS/Institute of Field and Vegetable Crops, Novi Sad	branko.milosevic@nsseme.com	P54 - S7
Monnet	Anne-Flore	INRA	anne-flore.monnet@agroparistech.fr	Oral – S7
Moussart	Anne	Terres Inovia	a.moussart@terresinovia.fr	P97 –S12
Muel	Frédéric	Terres Inovia	f.muel@terresinovia.fr	Oral- S1
Mullineaux	Phil	University of Essex, UK	mullin@essex.ac.uk	KeyLec - 11
Murube Torcida	Ester	SERIDA	emurube@serida.org	P150 – S18

Mustapha	Adetayo	preserve college	temtechnology@gmail.com	
Narits	Lea	Estonian Crop Research Institute	lea.narits@etki.ee	P44 – S7
Nayyar	Harsh	Panjab University, Chandigarh, INDIA	nayarbot@pu.ac.in	P16 – S2
Nazzicari	nelson	CREA - Centre for Fodder Crops and Dairy Productions	nelson.nazzicari@crea.gov.it	P30 - S4
Nelson	Matthew	Royal Botanic Gardens Kew	m.nelson@kew.org	Oral – S4
Odewunmi	Adetola	KKS GLOBAL INVESTMENT NIGERIA LIMITED	kksglobalinvestment@yahoo.com	
Oladipo	Solomon	solomon oladipo enterprise	oladipoakins@yahoo.com	
Oliveira	Miguel	UTAD Centre for Functional Ecology, Department of Life Sciences,	miguelp.oliv@gmail.com	P13 – S2
Oliveira	Rui	University of Coimbra, Polytechnic Institute of Porto	rsoliveira@uc.pt	P171 – S18
Olle	Margit	Estonian Crop Research Institute	margit.olle@gmail.com	P92 - S12
Oluwakayode	Arirejogun	University of Ibadan, Nigeria	adefisanadeniyi@hotmail.com	
Omondia	Emionwele	Omad Concept Nig Limited	omadconcept@yahoo.co.uk	
Omri	Noura	INRATunisia	noura.mori@gmail.com	
Ortiz	Rodomiro	Swedish University of Agricultural Sciences	rodomiro.ortiz@slu.se	
Osorno	Juan	North Dakota State University	juan.osorno@ndsu.edu	Oral – S18
Ouji	Ali	Institution of Agricultural Research and Higher Education. Northwest Semi-Arid Region, El Kef.	ali_ouji@yahoo.fr	
Özkan	Hakan	Çukurova University	hozkan@cu.edu.tr	P42 – S4
Paiva	Jorge Almiro	Institute of Plant Genetics Polish Academy of Sciences	jpai@igr.poznan.pl	P77 – S8
Paknejad	Farzad	Karaj Branch,Islamic Azad University,Karaj, Iran	farzadpaknejad@yahoo.com	P86 – S11
Papa	Roberto	Università Politecnica delle Marche, Italy	r.papa@univpm.it	P75 – S8

Parreira	José	ITQB NOVA	jsalvado@itqb.unl.pt	P70 – S8
Pasche	Julie	North Dakota State University	julie.pasche@ndsu.edu	P172 – S18
Pavan	Stefano	University of Bari	stefano.pavan@uniba.it	P175 – S18
Pazos Navarro	Maria	University of Western Australia	maria.pazosnavarro@uwa.edu.au	Oral – S13
Pecetti	Luciano	CREA - Center for Fodder Crops and Dairy Productions	luciano.pecetti@crea.gov.it	Oral – S15
Pelzer	Elise	INRA	pelzer@grignon.inra.fr	Oral – S14
Penmetsa	R. Varma	University of California at Davis	rvpenmetsa@ucdavis.edu	P76 – S8
Pereira	Graça	INIAV	graca.pereira@iniav.pt	P37 – S4
Pérez de la Vega	Marcelino	Universidad de León	m.perez.delavega@unileon.es	P144 – S18
Peric	Vesna	Maize Research Institute "Zemun Polje"	vesnaperic@yahoo.com	P32 – S4
Petrović	Gordana	Institute of Field and Vegetable Crops, Novi Sad	gordana.petrovic@nsseme.com	P159 – S18
Petrović	Kristina	Institute of Field and Vegetable Crops	kristina.petrovic@ifvcns.ns.ac.rs	P95 - S12
Pilet-Nayel	Marie-Laure	INRA	marie-laure.pilet@rennes.inra.fr	Oral – S6
Pilorgé	Etienne	Terres Inovia	e.pilorge@terresinovia.fr	
Polanco	Carlos	Universidad de León	carlos.polanco@unileon.es	P145 – S18
Pooryousef	Mahmoud	Mahabad branch, Islamic Azad University	dr.pooryoosef@gmail.com	P129 – S14
Porqueddu	Claudio	CNR-ISPAAM	c.porqueddu@cspm.ss.cnr.it	Oral – S14
Proskina	Liga	Latvia University of Agriculture	liigaproskina@inbox.lv	Oral – S9
Prudent	Marion	INRA	Marion.Prudent@dijon.inra.fr	P154 – S18
Puspitasari	Winda	Georg-August-University of Goettingen	winda.puspita@gmail.com	P119 – S13
Quillévéré-Hamard	Anne	INRA-IGEPP	anne.quillevere@rennes.inra.fr	P101 – S12

Ravnskov	Sabine	Aarhus University	Sabine.Ravnskov@agro.au.dk	
Rebola Lichtenberg	Jessica	Georg-August- University of Göttingen	jessica.rebola-lichtenberg@forst.uni-goettingen.de	P59 – S7
Rewald	Boris	University of Natural Resources and Life Sciences, Vienr	boris.rewald@boku.ac.at	Oral – S15
Ribeiro	Carlos	Universidade de Trás os Montes e Alto Douro	cribeiro@utad.pt	P27 – S4
Rispail	Nicolas	Instituto de Agricultura Sostenible - CSIC	nrispail@ias.csic.es	P181 – S18
Robles-Bolivar	Paula	CSIC, Estacion Experimental del Zaidin; Department of Biochemistry, Cell and Molecular Biology of Plants	paurrobo@gmail.com	P85 – S11
Rocha	Inês	Centre for Functional Ecology, Department of Life Sciences, University of Coimbra	ines.sousa.rocha@uc.pt	P17 – S3
Ronen	Gil	NRGene	gil@nrgene.com	
Rosa	Eduardo	UTAD	erosa@utad.pt	
Rosewarne	Garry	Agriculture Victoria, Australia	garry.rosewarne@ecodev.vic.gov.au	P124 – S13
Rubiales	Diego	CSIC, Cordoba, Spain	diego.rubiales@ias.csic.es	Oral – S18
Rubio	Josefa	IFAPA	josefam.rubio@juntadeandalucia.es	
Ruge-Wehling	Brigitte	Julius Kuehn-Institut	brigitte.ruge-wehling@julius-kehn.de	Oral – S18
Ruland	Michael	Georg-August-Universität Göttingen	mruland@gwdg.de	P33 – S4
Rusilowicz	Martin	Fera Science Limited	mjr129@york.ac.uk	P169 – S18
Rybiński	Wojciech	Institute of Plant Genetics Polish Academy of Sciences	wryb@igr.poznan.pl	P24 –S4
Sakiroglu	Muhammet	Kafkas University	msakiroglu@kafkas.edu.tr	P69 – S8
Salawu	Olakunle	Olarok &Co	olarokco@gmail.com	
Sallaku	Glenda	Agricultural University of Tirana	gsallaku@ubt.edu.al	P128 – S14
Salon	Christophe	Inra	christophe.salon@dijon.inra.fr	

Sánchez Navarro	Virginia	Universidad Politécnica de Cartagena	virginia.sanchez@upct.es	Oral –S17
Santalla	Marta	CSIC	msantalla@mbg.csic.es	Oral – S10
Santos	Carla	CBQF - Centre for Biotecnology and Fine Chemistry of Universidade Católica Portuguesa	carla.sancho.santos@gmail.com	P180 – S18
Sari	Duygu	Akdeniz University	duygusari@akdeniz.edu.tr	P162 – S18
Sarkar	Abhimanyu	The John Innes Centre, Norwich, U.K.	abhimanyu.sarkar@jic.ac.uk	P74 – S8
Sarker	Ashutosh	ICARDA	a.sarker@cgiar.org	Oral – S13
Sarpong	Bernard	RUGZIL LTD	allenmorris0112@gmail.com	
Savvas	Dimitrios	Agricultural University of Athens	dsavvas@aua.gr	Oral – S17
Scegura	Amy	North Dakota State University	amy.scegura@ndsu.edu	P155 – S18
Schneider	Anne	Terres Inovia	a.schneider@terresinovia.com	P15 – S2
Scrimshaw	Jim	PGRO	jim@pgro.org	
Seabra Pinto	Alexandra	INIAV	alexandra.pinto@iniav.pt	P1 – S1
Seidenglanz	Marek	AGRITEC L.t.d.	seidenglanz@agritec.cz	P102 – S12
Seljåsen	Randi	NIBIO Norwegian Institute of Bioeconomy Research	randi.seljasen@nibio.no	P135 – S14
Senberga	Alise	Latvia University of Agriculture	alisesenberga@gmail.com	P184 – S3
Serrano	Maria do Carmo	INIAV, I.P.	carmo.serrano@iniav.pt	Oral – S9
Severinsen	Annegrethe	Psykolog Praksis	psykologen@mail.dk	
Sharma	Mamta	ICRISAT	mamta.sharma@cgiar.org	P161 – S18
Shtienberg	Dani	ARO, the Volcani Center	danish@volcani.agri.gov.il	
Siebrecht	Daniel	Georg-August-Universität Göttingen, Department of Crop Siences, Division of Plant Breeding	daniel.siebrecht@agr.uni-goettingen.de	P109 – S13

Sivasankar	Sobhana	CGIAR Research Program on Dryland Cereals; CGIAR Research Program on Grain Legumes; ICRISAT	s.sivasankar@cgiar.org	
Smykal	Petr	Palacky University in Olomouc	petr.smykal@upol.cz	Oral – S10
Sousa	Manuel	Frescura Sublime Unipessoal Lda.	sousamaf@gmail.com	P132 – S14
Stoddard	Fred	University of Helsinki	frederick.stoddard@helsinki.fi	
Stougaard	Jens	Aarhus University, Denmark	stougaard@mbg.au.dk	KeyLec – S3
Streit	Juliane	Georg-August-University Goettingen| Department for Crop Sciences | Devision of Agronomy	juliane.streit@agr.uni-goettingen.de	Oral – S16
Sutton	Tim	South Australian Research and Development Institute	tim.sutton@sa.gov.au	
Svabova	Lenka	Agritec Plant Research, Ltd.	svabova@agritec.cz	P82 – S8
Szabó	Zoltan	NAIK	szabo.zoltan@abc.naik.hu	
Tampakaki	Anastasia	Agricultural University Of Athens	tampakaki@aua.gr	P28 – S4
Taran	Bunyamin	University of Saskatchewan	bunyamin.taran@usask.ca	Oral – S15
Thami-Alami	Imane	INRA Morocco	thamialami_ma@yahoo.fr	P186 – S3
Thompson	Richard	INRA UMR Agroecologie	thompson@dijon.inra.fr	
Tobar Pinon	Maria Gabriela	North Dakota State University	gabriela.tobarpinon@ndsu.edu	P35 – S4
Toklu	Faruk	Çukurova UniversityY	fapet@cu.edu.tr	P41 – S4
Tollenaere	Reece	INRA	reece.tollenaere@rennes.inra.fr	P174 – S18
Toom	Merili	Estonian Crop Research Institute	merili.toom@etki.ee	P182 – S3
Tormo	Elodie	TERRES UNIVIA	e.tormo@terresunivia.fr	Oral – S9
Torres	Ana Maria	IFAPA	anam.torres.romero@juntadeandalucia.es	Oral – S10
Toyoda	Kazuhiro	Okayama University	pisatin@okayama-u.ac.jp	Oral – S18

Turkeri	Meltem	East Mediterranean Agricultural Research Institute - ADANA	irmakturk@hotmail.com	P191 – S18
Upadhyaya	Hari Deo	ICRISAT	h.upadhyaya@cgiar.org	
Vågen	Ingunn	NIBIO - Norwegian Institute of Bioeconomy Research	ingunn.vaagen@nibio.no	
Vaz Patto	Maria Carlota	ITQB NOVA	cpatto@itqb.unl.pt	Oral – S10
Verma	Praveen	National Institute of Plant Genome Research	pkv@nipgr.ac.in	P83 – S8
Vernoud	Vanessa	INRA	vanessa.vernoud@dijon.inra.fr	P156 – S18
Verret	Valentin	INRA	valentin.verret@grignon.inra.fr	Oral – S17
Vickers	Roger	PGRO	Roger@pgro.org	
Videira e Castro	Isabel	INIAV, I.P.	isabel.castro@iniav.pt	P188 – S3
Villegas-Fernández	Ángel	Spanish National Research Council	amvf@cica.es	P94- S12
Vogt-Kaute	Werner	Naturland Fachberatung	w.vogt-kaute@naturland- ratung.de	P2 – S1
Voisin	Anne-Sophie	INRA Dijon	anne-sophie.voisin@dijon.inra.fr	
von Wettberg	Eric	Florida International University - Main Campus	eric.vonwettberg@fiu.edu	Oral – S4
Vorster	Juan	University of Pretoria	juan.vorster@up.ac.za	Oral - S11
Vosatka	Miroslav	Symbiom	vosatka@ibot.cas.cz	Oral – S3
Vujic	Svetlana	University of Novi Sad, Faculty of Agriculture	antanasovic.svetlana@polj.uns.ac.rs	P5 – S2
Vymyslicky	Tomas	Agricultural Research, Ltd.	vymyslicky@vupt.cz	P4 – S2
Wan	Ping	Beijing University of Agriculture	pingwan3@163.com	Oral – S8
Ward	Rebecca	Processors and Growers Research organisation	becky@pgro.org	P93- S12
Warkentin	Tom	University of Saskatchewan	tom.warkentin@usask.ca	Oral – S15

Watson	Christine	SLU/SRUC	christine.watson@slu.se	Oral – S2
Wiesel	Lea	Processors and Growers Research Organisation	lea@pgro.org	P142 – S18
Winter	Peter	GenXPro GmbH	pwinter@genxpro.de	P160 – S18
Witten	Stephanie	Thünen Institute of Organic Farming - Federal Res. Institute for Rural Areas, Forestry and Fisheries	stephanie.witten@thuenen.de	P131 – S14
Wood	Thomas	NIAB	tom.wood@niab.com	P177 – S18
Yamasaki	Shiori	Okayama University	pdcx1ose@s.okayama-u.ac.jp	P166 – S18
Yucel	Derya	Agricultural Ministry	deryayucel01@gmail.com	P141 – S18
Zaidi	Farid	University of Bejaia, Algerie	idiazdiraf@yahoo.fr	P64 – S7
Zeipina	Solvita	Pūre Hortcultural Research Centre	solvita.zeipina@gmail.com	P66 – S7
Živanov	Dalibor	IFVCNS/Institute of Field and Vegetable Crops, Novi Sad	dalibor.zivanov@nsseme.com	P55 - S7

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