Transcriptional regulation of C4 metabolism in maize

The need to increase productivity of our major cereal crops is well known. The world population is growing fast, over the next 50 years it is expected to increase by 50% and, at the same time, climate change will probably result in more extreme variations in weather and cause adverse effects on crop production. In addition, the increasing demand for biofuels will generate competition between grain for food and grain for fuel. It has been suggested that crop yield increases to match the population growth can only be achieved by increasing the photosynthetic efficiency. Given that crops using the C4 photosynthetic pathway show increased photosynthetic efficiency, many attempts have been made in order to introduce the C4 pathway into C3 crop plants, such as rice and potato. Several C4 related genes (single or combined) have been transformed into C3 crops, however, although some advances have been made, we are still far from having C3 plants performing as C4. One of the reasons is probably the lack of proper gene regulation when C4 genes are expressed in a C3 plant. It is also likely that the key genes (e.g. master regulators controlling the C4 photosynthetic pathway) have not yet been transformed in C3 crops. Actually, little is known concerning the regulation of C4 related genes, particularly the transcription factors (TF) involved. Major TFs are known to regulate different genes acting in the same metabolic pathway and, therefore, they may play a key role controlling C4 metabolism. This project will focus on the transcriptional regulation of *PEPC*, a cell type-specific gene that encodes a key enzyme in the C4 photosynthesis pathway and is highly induced by light. However, if necessary, we may use other key C4 genes, such as *NADP-ME* or *PPDK*, that are also highly regulated at the transcriptional level. Hence, this project will address the following objectives: a) Identify novel TFs binding to the promoter of *PEPC* in maize and b) To analyze the expression profile (cell-specificity and light-induction), in vivo localization, and transcriptional activity of the TFs identified.

Initially, we will construct a light-induced cDNA expression library, which will be screened (Yeast One-Hybrid system) to identify novel TF binding to the promoters of *ZmPEPC*. After TF identification, we will investigate their cell-specific, mesophyll (M) vs bundle sheath (BS) and light-induced gene expression. These studies together with other available data will allow selecting the TFs that will be further analyzed for cellular localization and transcriptional activity.

Supervisor: Nelson Saibo
Email: saibo@itqb.unl.pt
Genomics of Plant Stress Laboratory
Tel: 214469644