PRELIMINARY RESULTS

AFA MIC assays

A/C cluster representative strain (ICE25) is more susceptible to lauric (C12:0), linoleic (C18:2Δ9,12) and palmitoleic (C16:Δ9) acids than the B cluster representative strain (19N), as shown in Figure 1 and Table 1.

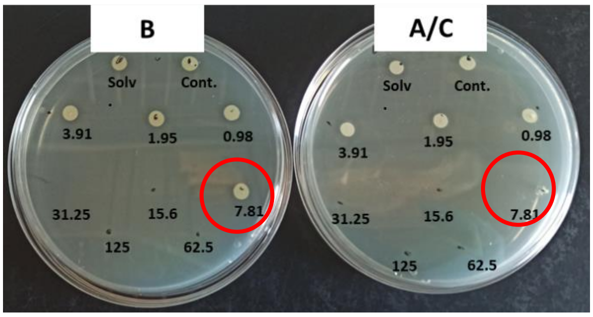

Figure 1 – *S. epidermidis* growth in the presence of lauric acid (concentrations in µg/mL). After 20 h of growth with different lauric acid concentrations, a culture aliquot was plated in TSA and was incubated at 37°C for 24 hours. At 7.81 µg/mL, bacterial growth was only observed for the strain belonging to the B lineage (surrounded by the red circle).

Table 1 - Minimum inhibitory concentrations (MIC) and minimum bactericidal concentrations (MBC) in µg/mL of lauric, linoleic and palmitoleic acids for *S. epidermidis* representative strains of B and A/C lineages.

Fatty acid	MIC		MBC	
	19N	**ICE25**	**19N**	**ICE25**
Lauric acid (C12:0)	15.6	7.8	15.6	7.8
Linoleic acid (C18:2Δ9,12)	>4000	250*	>4000	>4000
Palmitoleic acid (C16:Δ9)	>500	31.2	-	-

*Values for 60% growth inhibition

3D-reconstructed skin cytotoxicity assays

Lauric, linoleic and palmitoleic acids (AFA) do not show cytotoxicity on the 3D reconstructed skin model at the respective MIC concentrations determined for the SE pathogenic strain.

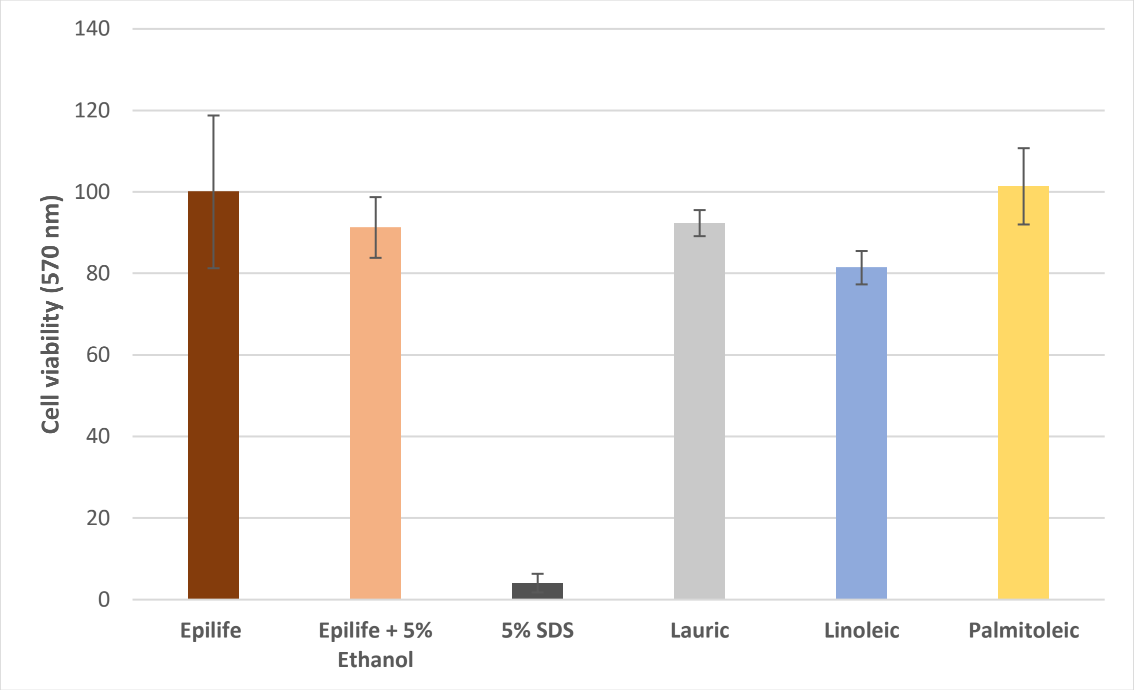

Figure 2 - Cell viability on the 3D RHE model considering Epilife medium as 100% cell viability. Epilife+5% ethanol and 5% SDS were used as negative and positive controls, respectively.

Table 2. S. epidermidis ICE25 and 19N strains genome comparison. Comparison of *S. epidermidis* ICE25 (A/C cluster) against 19N (B cluster) genome using *S. epidermidis* RP62a as the reference genome. Highlighted in grey are the parameters for the individual comparison of 19N and ICE25 genomes against *S. epidermidis* RP62A reference genome. Percentages between brackets are relative to the reference.

Number of genes	***S. epidermidis* RP62A**	
In reference	2494	
	ICE25	**19N**
In strain	2258	2508
Strain-specific	73	55
Matching genes	2156 (86%)	2172 (87%)
Equal to reference	913	69
New in strain*	102	336

*New in strain = In strain - Matching genes

Table 3 *S. epidermidis* ICE25 and 19N strains proteome comparison. Number of proteins differentially abundant between both strains per metabolic/biological process.

Metabolic/Cellular Process	**Number of proteins more abundant in**	
	ICE25	**19N**
Central Metabolism	22	14
Cell wall composition	3	4
Stress response and regulation	0	20
Virulence	3	0
pH homeostasis	2	5
Proteolytic activity	10	5
Recombination and replication	0	3
Aminoacyl-tRNA biosynthesis	1	5
Glycine, THF & IMP biosynthesis	0	9
Translation	4	4