Towards *S. epidermidis* biofilm dormancy characterization

Virginia Carvalhais[1,2,4], Rui Vitorino[2,3], Manuel Vilanova[4] and Nuno Cerca[1]

(1) CEB , LIBRO, University of Minho, Portugal.
(2) QOPNA, University of Aveiro, Portugal.
(3) iBiMED, Health Sciences Program, University of Aveiro, Portugal.
(4) ICBAS, University of Porto, Portugal.

Despite being a common colonizer of human skin and mucosae, *S. epidermidis* has a strong ability to adhere to biomaterial surfaces. Therefore, *S. epidermidis* is among the most common causative agents of biofilm-associated infections. Dormant bacteria may be found among the metabolic heterogeneous cells within biofilms. These cells present a low metabolic activity and contribute to tolerance to the host immune response and antibiotics. We performed an integrative analysis of dormancy within *S. epidermidis* biofilms, using an in vitro model previously described by our group [1]. We conducted a whole-transcriptome and proteome analysis of biofilms with higher number of dormant bacteria. Our data highlighted that: translation process was decreased in dormancy; transcripts involved in oxidation-reduction processes and proteins involved in catalytic activity and GTPase activity were up-regulated in dormancy; genes involved in the pyruvate metabolism were upregulated in dormancy. Additionally, in order to assess if dormant *S. epidermidis* biofilms influence the reactivity to host immune system, we evaluated the immunoreactivity pattern to human sera. Interestingly, CodY protein was only reactive to sera in dormant biofilms and ClpP protein only reactive when dormancy was prevented. The expression of CodY is increased when cells experience nutrient deprivation since it senses nutrient availability [2]. The ClpP deletion was previously associated with reduced ability to form *S. epidermidis* biofilms and with reduced virulence in a rat model of biofilm-associated infection [3]. Our results suggest that magnesium is important to prevent nutrient limitation in *in vitro S. epidermidis* biofilms. Overall, using a multiple combined strategy, we demonstrated that our established dormancy model may be characterized by a decrease of translation process and an enhancement of oxidation-reduction processes and pyruvate metabolism. The immunoreactive results are consistent with previous results, where the dormancy profile may alter the interaction with host immune response.

[1] F. Cerca, F. Andrade, A. França, E.B. Andrade, A. Ribeiro, A.A. Almeida, N. Cerca, G. Pier, J. Azeredo, M. Vilanova, Journal of Medical Microbiology 60(Pt 12), 2011, 1717
[2] A.L. Sonenshein, Current Opinion in Microbiology 8(2), 2005, 203
[3] C. Wang, M. Li, D. Dong, J. Wang, J. Ren, M. Otto, Q. Gao, Microbes and Infection 9(11), 2007, 1376