Global transcriptomic analysis of dormancy within *Staphylococcus epidermidis* biofilms

V. Carvalhais[1,2,3], A. França [1,3], R. Vitorino[2], G. Pier [3], M. Vilanova [4] and N. Cerca[1*]

[1] Institute of Biotechnology and Bioengineering - CEB-IBB - University of Minho, Braga, Portugal
[2] QOPNA, Mass Spectrometry Center, Department of Chemistry, University of Aveiro, Aveiro, Portugal
[3] Division of Infectious diseases, Brigham and Women´s Hospital, Harvard Medical School, Boston, MA, USA
[4] ICBAS – Institute of Biomedical Sciences Abel Salazar, University of Porto, Porto, Portugal.
* Corresponding author: nunocerca@ceb.uminho.pt

Dormant bacteria are cells in a non-replicate state which can lead to the development of recalcitrant infections [1,2]. Dormancy improves long-term bacterial survival and facilitates their pathogenesis [3] by increasing their tolerance to antibiotics [4] and evasion of the host immune system [5,6]. Generally, dormant bacterial cells have a low-metabolism, allowing them to survive and resist in harsh microenvironments. Due to their important role in the establishment of disease, an *in vitro* model to induce dormancy within *S. epidermidis* biofilms was developed based on growth modulation by glucose and magnesium [6]. Our aim was to identify the major transcriptomic differences between *S. epidermidis* biofilms with induced and inhibited dormancy, assessing biological triplicates from *S. epidermidis* biofilms by RNA-seq technology.

A global comparison showed significant differences in the expression of 147 genes ($p < 0.05$). Among the differentially expressed genes, major differences were identified in biological processes such as oxidation-reduction and acetyl-CoA metabolism. Moreover, gene interaction network analysis revealed that the translation process is involved in the inhibition of dormancy within *S. epidermidis* biofilm. Conversely, oxidation-reduction processes were increased during dormancy.

General transcriptomic differences caused by dormancy within *S. epidermidis* biofilms were identified. The global changes found in this work give information obtained from the bulk of the biofilm which includes some non-dormant bacterial cells.

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References

1. Fauvart M, De Groote VN, Michiels J. 2011; 60: 699-709.
2. Lewis K. 2007; 5: 48-56.
3. Dworkin J, Shah IM. 2010; 8: 890-896.
4. Shapiro JA, Nguyen VL, Chamberlain NR. 2011; 60: 950-960.
5. Zandri G, Pasquaroli S, Vignaroli C, Talevi S, Manso E, Donelli G, Biavasco F. 2012; 18: E259-E261.
6. Cerca F, Andrade F, Franca A, Andrade EB, Ribeiro A, Almeida AA, Cerca N, Pier G, Azeredo J, Vilanova M. 2011; 60: 1717-1724.