From marine natural products to original synthetic antibiofilm leads: toward greener antifouling solutions

Yves Blache*, Olivier Bottzeck, Annie Praud-Tabariès
Université de Toulon, laboratoire MAPEM, EA 4323, 83957 La Garde, France

Biofouling (growth of marine sedentary organisms) causes notable damage to ship-hull, harbour structures, industrial cooling and filtration systems. The growth of macrofouling organisms on hard surfaces is generally preceded by the formation bacterial biofilms which are agglomerates of bacteria on a surface that is surrounded or held together by extracellular polymeric substances. Bacteria produce these, in part, to help them attach to surfaces and bind to one another. Subsequently, biofilms are reported to facilitate the attachment of larvae of macrofouling organisms and thus the formation of a biofouling community itself. Therefore, an environmentally acceptable method targeting the reduction of the formation of biofilms becomes highly desirable in view of manufacturing some original antifouling coatings. Although eradication of planktonic bacteria communities has been largely controlled, it has been estimated that bacteria within a biofilm can display up to 1000-fold increased resistance to antibiotic or biocide treatment. In this context, some of the anti-biofilm techniques that are tested today are aimed to the discovery of new potential anti-biofilm compounds from marine organisms such as sponges, soft corals or algae. In this field, our group purified series of marine natural products as potential antibiofilm leads and initiated a program aimed to establish structure-activity relationships of such natural products as potential antifouling compounds. For this purpose “click chemistry” methodologies were retained as interesting high through processes. Results showed that some compounds exhibited non-toxic specific anti-biofilm activities against marine bacterial biofilms in vitro and finally appear to be good candidates as potential green biocides for use in antifouling coatings.

Keywords: biofilm, click chemistry, 1,2,3-triazoles, marine bacteria

References

Global transcriptomic analysis of dormancy within Staphylococcus epidermidis biofilms

V. Carvalhais1,2, A. França1,3, R. Vitorino2, G. Pier1, M. Vilanova4 and N. Cerca1*

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: munocerca@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 St. 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.

This work was funded by Fundação para a Ciência e a Tecnologia (The Foundation for Science and Technology: FCT) and COMPETE (Programa Operacional Factores de Competitividade) grants PTDC/BIH-MIC/113450/2009 and FCOMP-01-0124-FEDER-014309. AF and VC were funded by FCT fellowship SFRH/BD/62359/2009 and SFRH/BD/78235/2011, respectively.

Keywords: dormancy; RNA-seq; S. epidermidis biofilm

References