

Micro Biotec'13

PORTUGUESE CONGRESS OF
MICROBIOLOGY AND BIOTECHNOLOGY

6th - 8th December | Aveiro Portugal

Abstracts Book



Systems Biology

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AN ECOSYSTEM WITHIN OUR MOUTH

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The oral cavity is an ecosystem in which hundreds of microorganisms establish themselves mainly as biofilm communities. The different oral biofilms have been studied for a while and the amount of information on these communities has increased greatly especially after the revolution in the molecular microbial identification techniques. However, it is still challenging to answer questions such as: what is typical community of a healthy mouth? What species appear or disappear as oral or systemic diseases evolve? Can we associate a health or disease status to a community? What is the role of the microbial community in the normal or pathological pathways?

Large scale studies, such as the Human Microbiome Project, have produced data which facilitated the answer to these questions (1). Smaller scale studies also exist providing results from molecular identification of microorganisms from the different microhabitats in the mouth. However not only are these results scattered through the literature but also provide snapshots of what is present in that particular environment, under those particular conditions. The Computational Biology group at Institute of Health Sciences in Viseu is focused on creating resources which integrate the data produced by the different projects and studies to allow a true systems analysis of the oral cavity (2,3).

Our work has been centered on the analysis of proteomics results and the identification of the proteins (human and microbial) present in the oral cavity which resulted in a database with over 10 000 proteins (OralOme) along with an associated interface (ORALCARD) which allows the exploration of that information. The ongoing work aims at the inclusion of the genomic information from 16S studies in order to allow the analysis of the oral microbial communities' composition both in health and disease. An extension of this work, currently being improved by our group, is the study of the protein-protein interactions (PPIs) present in this ecosystem. The tool OralInt explores the data present in the OralOme database to predict PPIs between human and microbial proteins. These predictions have obvious impact on the understanding of the Oral Ecosystem and are crucial for diagnosis and therapeutics of oral and possibly systemic diseases.

The work so far has led to the following conclusions: the amount of information present in the literature for human proteins is much greater than for microbial ones; the species identified as present in the oral cavity by proteomics data are much less than those identified by 16S data, which reveals the limitations of microbial protein identification in oral samples; the human mouth has very diverse communities both in health and in disease depending on the specific habitat which is colonized.

The main conclusion is that the complexity and variability of this ecosystem requires new bioinformatics and visualization tools and strategies in order to convert the large amount of data from studies providing snapshots of the system, into a true whole system level platform which allows the understanding of pathways and processes (the Oral Physiome).

References:[1] The Human Microbiome Project Consortium. (2012) Nature 486, 207–214 (14 June 2012) doi:10.1038. [2] Rosa, Nuno; Correia, Maria J; Arrais, Joel P; Lopes, Pedro; Melo, José; Oliveira, José L; Barros, Marlene. 2012, Archives of Oral Biology 57, 7: 853 – 864. [3] Arrais, Joel P; Rosa, Nuno; Melo, José; Coelho, Edgar D; Amaral, Diana; Correia, Maria J; Barros, Marlene; Oliveira, José L. 2013, Archives of Oral Biology 58, 7: 762 – 772.