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The coding potential of *Pseudomonas aeruginosa*: Gene discovery across strains by computational comparative genomics and ribosome profiling

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*P*seudomonas aeruginosa is an opportunistic pathogen of growing relevance for hospitalized patients and in particular in the development of cystic fibrosis. Complete genome sequences of several strains of *P. aeruginosa* have been sequenced in an effort to identify the genetic basis of the differences in virulence observed among strains. Interpretations of the results of comparative genomics rely on accurate and comparable annotations of genomic features across strains. To compare as accurately as possible the coding potential of different *P. aeruginosa* strains, we used a hybrid approach combining computational and experimental analyses. Potential coding regions were identified in all strains combining the results of four popular computational gene prediction methods with evolutionary conservation analysis and our recently-developed approach for computational "frame-analysis", based on the identification of sequence segments with statistically significant 3-base compositional periodicity indicative of the presence of codon structures. Furthermore, we experimentally identified on a transcriptomic scale coding regions actively undergoing translation in the reference strain *P. aeruginosa* PAO1, using the recently developed technique of ribosome profiling. This analysis was repeated in control growth and in conditions of oxidative stress, which is relevant to the infection of the cystic fibrotic lung. These analyses allowed us to identify several genes whose distribution across strains was not reflected by published annotations. By ribosome profiling in *P. aeruginosa* PAO1 we also identified genes that could not be predicted computationally and precisely defined the position of the start-of-translation of several genes. Furthermore, we characterized changes in patterns of translation related to oxidative stress. Our analyses significantly enhance our understanding of the coding potential of the different strains of *P. aeruginosa* and provide for the first time information on the regulation of translation in environmental conditions relevant to the interaction with the human host.

Biography

Luciano Brocchieri has completed his PhD in theoretical population genetics from the University of Parma, Italy, and Postdoctoral studies at Stanford University, Department of Mathematics. He was Senior Scientist at Stanford University, Department of Mathematics and is now Assistant Professor at the University of Florida, Department of Medicine. His research is focused on the analysis of the evolution of gene families and on the development of bioinformatics methods for the identification and analysis of gene sequences. He is the author of several papers, reviews and commentaries published in international reputed scientific journals.

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