



Profiling of pathogenic bacteria by colony morphology – identification of potential biofilm resistance and virulence determinants

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Colony morphology changes may be an indicator of the phenotypic variations associated to pathogenecity, virulence and antimicrobial resistance of infection-causing microorganisms. Particularly, phenotypic changes derived from biofilm growth and in response to environmental stressors. For instance, in patients with cystic fibrosis, P. aeruginosa colony morphology undergoes a conversion from non- to mucoid form augmenting bacteria resistance to antibiotics considerably. However, the specific correlation between some colony traits and the biological impact is unknown.

This study was thus designed to inspect the colony associated phenotypic alterations, particularly the putative virulence determinants of biofilm-colonies, via morphological observation and whole cell MALDI MS proteomics. The annotation of colony morphology features was supported by a novel, in-house developed ontology, named colony morphology ontology (CMO), and annotations are available at the MorphoColDB framework [1]. The considerable diversity of the morphotypes observed within and across species, with diferente biofilm-forming abilities and susceptibilities [2], led to the application of this method in support of the identification of virulent morphotypes as primary therapeutic candidates. Further results on the protein expression of P. aeruginosa and S. aureus colonies confirmed important differences between intra-species morphotypes and has promoted investigation of the role of stress-regulated proteins.

Although preliminary, these results confirm the potential of using a combination of highthroughput screening of pathogenic bacteria proteome with susceptibility tests and expert inputs to reach a comprehensive understanding of the persistence and antimicrobial resistance of pathogenic bacteria, as well as to design new therapeutic strategies.

References

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