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Battling antimicrobial resistance where it counts: An extended proteome research of five bacterial species

Gilberto Igrejas[1,2], Tiago Santos[1], Catarina Marinho[1] and Patrícia Poeta[2]
[1]University of Trás-os-Montes, Portugal
[2]Universidade Nova de Lisboa, Portugal

Proteomics is the large-scale study of proteins and it is often considered the next step in the study of biological systems. Unlike the genome, the proteome is dynamic: It varies according to cell type and its functional state and the evaluation of protein profiles in response to various stress mechanisms, such as sensitivity to antibiotics or modifications related to antimicrobial resistance which represents a valid and integrating approach for the development of new therapeutic strategies. Antimicrobial resistance presents a significant challenge to scientists in the field of infectious diseases. The identification of protein determinants for resistance not only provides biomarkers for resistance to a particular drug but also aids in the understanding of the mechanisms of antibiotic function and resistance. The full knowledge of how antibiotics resistance evolves and is transmitted between potential hosts of different ecosystems takes on great importance. The functional genomics and proteomics unit based at the University of Trás-os-Montes and Alto Douro (UTAD) in Vila Real, Portugal, has recently completed 10 years of proteomic research related to antimicrobial resistance. During this time, five different bacterial species and 32 bacterial strains were studied, isolated from clinical and wildlife samples, 2770 protein spots were characterized through 2-DE and MALDI-TOF MS, and 392 proteins identified by shotgun proteomics (LC-MS/MS). The group has accomplished the evaluation of ESBL-producing *Escherichia coli* strain protein profiles, proteome comparison of vancomycin-resistant *Enterococcus* spp. strains compared to the proteome of the same strain without antimicrobial stress, whole proteome analysis of quinolone-resistant *Salmonella* strains, a sub-proteome analysis of a methicillin-resistant *Staphylococcus* aureus strain and several other proteomic approaches which we intend to overview in this review with the intention of connecting the dots between this large protein database and other antimicrobial resistance published results and determining a metabolic pathway which results in antimicrobial behavior.

gigrejas@utad.pt