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Proteomic characterization of Vancomycin-resistant *Enterococci* clinical strains

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Enterococci have emerged as important nosocomial pathogens due to their multiple antibiotic resistances being *E. faecalis* and *E. faecium* considered the third and fourth most commonly isolated nosocomial pathogens worldwide causing up to 14% and 9.6% of hospital acquired infections in the US and Europe respectively. Vancomycin-resistant *enterococci* (VRE) were first identified as hospital-associated pathogens in Europe during the mid-1980s and have rapidly disseminated worldwide. VRE most frequently colonize the gastrointestinal tract and skin of humans and animals and are able to survive in the environment in extensive colonization periods which brings to light a current concern of transmission of these strains and its resistance characteristics. Protein expression of vancomycin-resistant *Enterococci* was analyzed using an extensive two-dimensional electrophoresis survey through Isoelectric Focusing (IEF)×Sodium Dodecyl Sulphate-Polyacrilamide Gel Electrophoresis (SDS-PAGE) in order to obtain an accurate protein separation from different sub-proteome extractions. Proteomic tools then allowed the simultaneous identification and comparison of protein expression in different subcellular locations using Matrix-Assisted Laser Desorption/Ionization-Time of Flight/Mass Spectrometry (MALDI-TOF/MS) analysis under 50 ppm mass tolerance bioinformatic database inquiries on UniProtKB/Swiss-Prot. Two VRE clinical strains (*E. faecium* C865 and *E. faecalis* C2620) were studied resulting on the obtainment of a total of 471 spots concerning the membrane and cytoplasm sub-proteomes for both strains. Trypsin digested spots led to the identification and characterization of 331 proteins related to several biological processes from glycolysis to oxidative stress and more concerning antibiotic resistance. The understanding of the biological processes related to the bacteria's resistance to antibiotics more specifically vancomycin in *Enterococci* is a valuable tool for the battle against this major public health concern.

Biography

Luis Pinto is currently a PhD student from the University of Trás-os-Montes and Alto Douro in collaboration with the Complutense University of Madrid and the Bioscope Group from the University of Nova de Lisboa, working on proteomics, mass spectrometry and antibiotic resistance. He has a degree in Biology and a MSc in molecular genetics, both from the University of Trás-os-Montes and Alto Douro. He has published 5 papers and co-authored 10 other papers in reputed journals, publishing also in scientific chapters and presented other communications in international conferences.

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