

Treatment of Macrophages with Gram-Negative and -Positive Bacterial Secretomes Induce Distinct Metabolic Signatures

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ABSTRACT

Infectious diseases represent major health and economic challenges globally. Emergence of multiple drug-resistant bacteria in the community and hospital has become a worldwide concern that requires novel approaches for rapid diagnosis and treatment. Metabolomics approach is a powerful tool providing important chemical information about the cellular phenotype of living systems, and the changes in their metabolic pathways in response to various perturbations. Metabolomics has become an important tool to study host-pathogen interactions and to discover potential novel therapeutic targets. In this study, untargeted LC-MS metabolic profiling was applied to differentiate between the impact of the secretome of the Gram-positive *S. aureus* SH1000 and Gram-negative *P. aeruginosa* PAO1 bacterial pathogens on THP-1 macrophages. The results showed that *S. aureus* and *P. aeruginosa* secretome affected alanine, aspartate and glutamate metabolism; sphingolipid metabolism; glycine and serine metabolism; GL metabolism; and tryptophan metabolism with different trends in THP-1 macrophages. However, the impact of both bacterial secretome on arginine and proline metabolism was similar. These data could contribute to a better understanding of pathogenesis and resistance of these bacteria and could pave the way for developing new therapeutics that selectively targeting Gram-positive or Gram-negative bacteria.