Centro: Saúde

Curso: Medicina

Titulo: **Evaluation of sepsis prognosis using mass spectrometry**

Autor(es) Afonso José Celente Soares

E-mail para contato: afonsocelente@gmail.com IES: HFAG

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RESUMO

Using mass spectrometry, we aim to identify protein profiles that can be used to evaluate the prognosis of sepsis. Plasma samples were collected from ten patients with sepsis (five survivors (SS-I-V) and five non-survivors (SNS-I-V)) at three distinct phases (I, II and III) after diagnosis. Samples were also collected from five controls (C-I-V). In total, 100 µg of protein were subjected to trypsin digestion. Peptides were fractionated and analyzed using a nano-LC coupled to an LTQ-Orbitrap. After processing and "label-free" quantitation, MS/MS spectra were confronted with the NextProt database. The STRING 9.1 was used for interactions and functional annotation The average number of proteins identified in each condition studied was 298. The areas of the SS and SNS phases and C spectra were compared. Several proteins were identified as differential: haptoglobin, serum amyloid A protein, apolipoprotein A-II, fibrinogen, prothrombin, thrombospondin, fibronectin, kininogen, hemopexin, zinc finger protein, and complement C3 and C4. The quantification data of these proteins revealed differences in expression between the sepsis survivors and non-survivors as well as their phases and controls. The set of identified proteins was subjected to an interaction interface for the classification of biological processes related to these proteins, revealing a large number of pathways that are involved in sepsis. The methodology employed the digestion of plasma protein in solution with trypsin and isoelectric focusing followed by the separation of peptides by LC MSMS in Orbitrap. This protocol allowed for the identification of a large number of proteins in each patient plasma sample, revealing differences in expression among SS and SNS patients at various phases and C controls. It is quite likely that biochemical pathways and nodes are activated differently in patients who survive and those who do not. Proteomics can reveal these differentially expressed proteins and aid in understanding the pathogenesis of sepsis.