

Deaths from sepsis are the most common cause of death and rank among the leading causes of death. In these diseases caused by bacteria, the time for the detection of the bacteria causing the problems and their immediate treatment is important so as not to produce serious effects of sepsis and to avoid septic shock. But conventional methods such as blood culture, biochemical identification, immunological testing or PCR amplification only give us long-term resolution of a small fraction of bacteria.

According to the latest published studies on the metabolomic changes produced by infecting microorganisms in patients, they produce a type of biomarkers or biosignatures that are produced when these pathogens proliferate and grow. Trials have shown that using specific metabolomic biosignatures of plasma pathogens, these pathogens that cause sepsis could be detected in a much faster and more efficient way. The big problem with this novel idea is the small number of samples that are registered against the large number of characteristics that occur in different sepsis infections.

The solution of using the machine learning model has been seen to this problem, which could integrate a large amount of clinical information and through the use of predictive algorithms could give us a greater identification of pathogens.

A retrospective cohort study of some clinical cases of sepsis has been carried out, where the information of the 1152 patients with signs of the disease has been collected and 100 individuals with a resolved clinical case have been chosen and compared with 29 controls. Both Gram-negative and Gram-positive organisms have been analyzed, among them the most prominent *Streptococcus pneumoniae*, *Staphylococcus aureus* and *Escherichia coli*. The variables of the studies have been used the sensitivity, the specificity and the value of AUC of the clinical and metabolomic characteristics in the prediction of the diagnostic results.

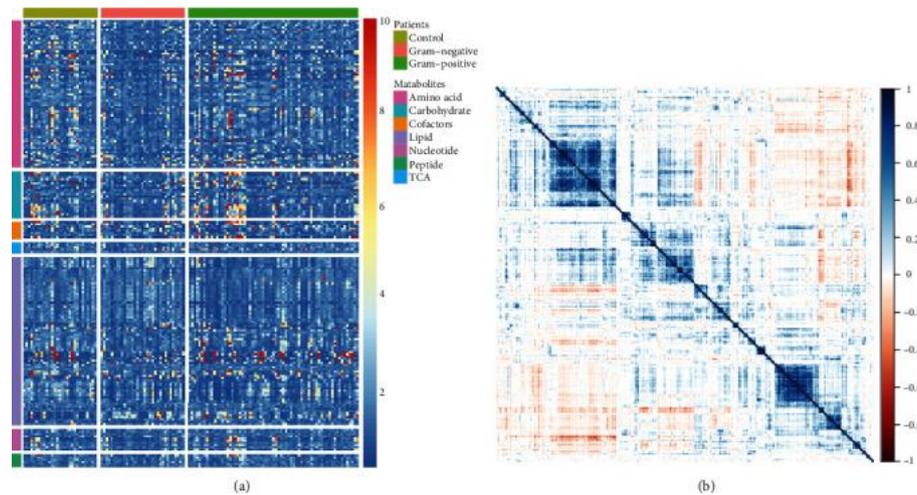


Figure 1: a) Characteristics of metabolomic biomarkers for septic patients. b) Identification of the 3 groups through the correlation of biomarkers.

We can conclude that the studies analysed by the machine learning model gave us abnormal nitrogen metabolism results, cellular respiratory disorders, and kidney or intestinal failure. These data are important in order to detect sepsis and discriminate against other possible common causes. This advance in septic diseases could help us to identify the causative pathogens in a much greater way and try to take advantage of more time in treating the disease. We can highlight the great advantage of the machine learning model of great information management and a great speed in searching for a common factor to a problem for its greater resolution and detection.

- (1): Zheng L, Lin F, Zhu C, et al. Machine Learning Algorithms Identify Pathogen-Specific Biomarkers of Clinical and Metabolomic Characteristics in Septic Patients with Bacterial Infections. *Biomed Res Int.* 2020;2020:6950576. Publicado 2020 Jul 27. doi:10.1155/2020/6950576