

GENETIC POLYMORPHISMS INFLUENCING THE SUSCEPTIBILITY AND THERAPEUTIC RESPONSE IN SEPSIS

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The sepsis syndrome is determined by several factors, among them, difficulty of standardization of the therapeutic intervention and genetic variability. Genetic epidemiologic studies can improve the knowledge about susceptibility and response in the sepsis. In this work have been selected 13 polymorphisms located in the genes: tumor necrosis factor (TNF) alpha, TNF-beta, interleukin (IL)-1 receptor antagonist, IL-6, IL-10, heat shock protein (HSP) 70-2, cluster of differentiation (CD)-14, Toll-like receptor (TLR)-4 and TLR-2. The strategies adopted were Real-Time PCR, PCR and restriction enzyme. Patients included were those admitted to the Intensive Care Unit (ICU) of the Base's Hospital and classified as sepsis, severe sepsis and septic shock. The control samples were constituted from healthy volunteers. Our results showed increase of HSP70-2 GG genotype and of IL1ra 2 allele, and decrease of IL -6 (1753) CC and of IL-6 (174) G allele in severe sepsis with high mortality. These results reinforce the importance of genetic variation on the susceptibility and response in sepsis, as well as the idea to application of assays in the ICU for therapy based on genetic profile from patients.

Key words: heat shock protein; interleukin; outcome; polymorphism; septicemia; sepsis; tumor necrosis factor.

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