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Genetic Polymorphisms and Bacterial Infections in Neonates

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Abstract

© 2016, Springer Science+Business Media New York.Identifying single nucleotide polymorphisms (SNPs) in the genes involved in sepsis may help to clarify the pathophysiology of neonatal sepsis. The aim of this study was to evaluate the relationships between different forms of bacterial infections in neonates and genes potentially involved in the response to invasion by infectious agents. The study involved 20 neonates with a diagnosis of sepsis, 25 neonates with localized bacterial infections, and otherwise healthy neonates born during the study period. A total of eight SNPs in four candidate genes including Toll-like receptors (TLR2, TLR4) and pro-inflammatory cytokines (IL-1, Il-6) were genotyped. Genotypes CT and TT of IL-1β C3953T were associated with a significantly increased risk of developing sepsis (OR = 9.3; p = 0.02). The percentage of heterozygotes for the mutant allele was 65 %, while homozygotes—5 %. Among the patients with localized bacterial infections, TLR4 Asp299Gly, genotypes CT and TT IL-1β C3953T, and genotypes GC and CC IL-1β G-1473C showed the association with an increased risk of developing diseases (p = 0.05, p = 0.04, p = 0,04, respectively). These results show that genetic variability seems to play a role in sepsis and localized bacterial infections in neonates by influencing susceptibility to the disease.

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Keywords

Cytokines, Genetic polymorphisms, Innate immunity, Neonatal sepsis

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