

**PREDISPOSITION TO SEPSIS, ACUTE TISSUE INFECTIONS AND DELAYED INFECTED WOUND HEALING MAY DEPEND ON THE SAME GENETIC POLYMORPHISMS AT TNF $\alpha$  G308A, TNF $\beta$  G252A, CCR2 G190A, CD14 C159T, TLR2 G2259A AND C2029T, TLR4 A1036G AND T1336C, AND TGF $\beta$  G25C**

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Most published studies on infections and genetic polymorphisms are dealing with sepsis.

**Aim:** We studied polymorphisms of selected allele of cytokines and TLRs at 9 polymorphic sites in patients with sepsis, acute tissue infections and prolonged wound suppuration as we hypothesize with same genetic predilection.

**Results:**

1) in entire group of patients with systemic and local infections, higher frequency of TNF $\alpha$ G308A GG, TNF $\beta$  G525A mutated homozygote AA, and CCR2 G190A mutated homozygote AA than in controls (all  $p < 0.0001$ ) was found. At TGF $\beta$  G25C site there was a low expression of GG compared with controls ( $p < 0.001$ ).

2) comparison of sepsis, acute tissue infections and delayed infected wound revealed more of CD14 C-159T CT, TLR1,2 C2259A GA and C2029T CT in sepsis than other infections but differences were not significant. There was lack of differences in subgroups in expression of TNF $\alpha$ G308A GG, TNF $\beta$  G525A heterozygote GA, CCR2 G190A AA, TLR4 1 A1036G AA and TLR4 2 C1336T CC.

**Conclusions:** Polymorphism of TNF $\alpha$  and  $\beta$ , CD14, TLR2,1, CCR2 and TGF $\beta$  genes at certain mutation points may be predisposing to surgical type of infections. No significant differences in investigated polymorphisms were found between sepsis, acute local tissue infections and delayed infected wound healing.