Reduced frequency of two activating KIR genes in patients with sepsis

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OBJECTIVES: Natural killer (NK) cell activity is regulated by activating and inhibitory signals transduced by killer cell immunoglobulin-like receptors (KIR). Diversity in KIR gene repertoire among individuals may affect disease outcome. We examined sixteen KIR genes in a cohort of critical care patients aiming to identify patterns that could be associated with sepsis.

METHODS: Male and female patients (ages range between 14 and 94 years old) were included. DNA samples from 211 patients with sepsis and 60 critical care patients with no sepsis (controls) collected in the period between 2004 and 2010 were included and genotyped for KIR genes using the polymerase chain reaction method with sequence-specific oligonucleotide (PCR-SSO).

RESULTS: There were significantly lower frequencies of activating KIR2DS1 and KIR3DS1 in sepsis patients than in controls (41.23% *versus* 55.00%, and 36.49% *versus* 51.67%; p = 0.041 and 0.025, respectively). Statistical analysis found no association between individual KIR genes and clinical outcomes, such as organ dysfunction, hospital and ICU stay and/or mortality, or even patient gravity, measured through SOFA-1 and APACHE II.

CONCLUSIONS: These results provide evidence that activating KIR genes 2DS1 and 3DS1 are more prevalent in critical patients without sepsis than in patients with sepsis, suggesting a potential protective role of activating KIR genes in sepsis.