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Title: Dynamic changes of serum sTREM-1 and its gene polymorphisms associated with sepsis prognosis

Dr. Longxiang 8077 Su slx77@163.com [1,2], Prof. Dr Lixin 8078 Xie xielx@263.net MD [1,2], Dr. Zhaoxu 8079 Jiang shanyuan1101@sina.com [1,2], Dr. Xin 8080 Zhang zx115@foxmail.com [1,2] and Prof. Dan 8081 Feng fddd@163.net [3]. [1] Department of Respiratory Medicine, Hainan Branch of Chinese PLA General Hospital, Sanya, Hainan, China, 572013 ; [2] Department of Respiratory Medicine, Chinese PLA General Hospital, Beijing, China, 100853 and [3] Department of Medical Statistics, Chinese PLA General Hospital, Beijing, China, 100853 .

Body: Introduction:More and more studies have confirmed that sepsis is an acquired genetic disease. Objectives:To explore how sepsis prognosis is associated with the dynamic changes of serum sTREM-1, as well as with gene polymorphisms. Methods: 80 subjects were selected from inpatients in the RICU,SICU,and EICU. 80 healthy volunteers acted as control. To detect the dynamic changes of serum sTREM-1 over a 14-day observation, ELISA was performed. Four exons of TREM-1 gene were sequenced on ABI3730. Results: The nonsurvivors'sTREM-1 levels remain significantly higher than the survivors' over period of 14 days($P<0.01$). The curves show that the nonsurvivors register higher sTREM-1 levels at the initial stage, which steadily go up with the passage of time. In contrast, the survivors'sTREM-1 levels are on the decline all the time. Three TREM-1 SNPs (rs144672509,rs2234237 and rs2234246) are detected from four exons. In three inherited models, rs2234237 is clearly related to sepsis prognosis($P<0.05$). The log-rank test shows that patients with the rs2234237 genetic variation stand a greater probability of a 28-day death($P<0.05$). However, no relationship is spotted between TREM-1 gene polymorphism and the dynamic concentrations of serum sTREM-1. Logistic regression analysis shows that sTREM-1,APACHE II score,and TREM-1 rs2234237 genetic variation are risk factors affecting the prognosis. Conclusions: Dynamic changes in serum sTREM-1 may be more accurate and valuable for sepsis monitoring and for dynamic assessments of prognosis. It is proved that TREM-1 rs2234237 polymorphism is associated with high 28-day mortality among sepsis patients, constituting a risk factor affecting prognosis.