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Screening of differentially expressed genes between multiple trauma patients with and without sepsis

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ABSTRACT. The purpose of this study was to identify critical genes associated with septic multiple trauma by comparing peripheral whole blood samples from multiple trauma patients with and without sepsis. A microarray data set was downloaded from the Gene Expression Omnibus (GEO) database. This data set included 70 samples, 36 from multiple trauma patients with sepsis and 34 from multiple trauma patients without sepsis (as a control set). The data were preprocessed, and differentially expressed genes (DEGs) were then screened for using packages of the R language. Functional analysis of DEGs was performed with DAVID. Interaction networks were then established for the most up- and down-regulated genes using HitPredict. Pathway-enrichment analysis was conducted for genes in the networks using WebGestalt. Fifty-eight DEGs were identified. The expression levels of *PLAU* (down-regulated) and *MMP8* (up-regulated) presented the largest fold-changes, and interaction networks were established for these genes. Further analysis revealed that PLAT (plasminogen activator, tissue) and SERPINF2 (serpin peptidase inhibitor, clade F, member 2), which interact with PLAU, play important roles in the pathway of the component and coagulation cascade. We

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hypothesize that PLAU is a major regulator of the component and coagulation cascade, and down-regulation of *PLAU* results in dysfunction of the pathway, causing sepsis.

Key words: Sepsis; Multiple trauma; Differentially expressed genes; Interaction network; Functional enrichment analysis; Pathway analysis

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