

Expressions of Spectrum of Inflammation-related and Clotting-related Genes in Hemorrhagic Stroke Patients with Stagnated Heat Syndrome

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ABSTRACT **Objective** To explore the correlation between stagnated heat syndrome and clotting, inflammation in hemorrhagic stroke patients. **Methods** Hemorrhagic stroke patients with stagnated heat syndrome and non-stagnated heat syndrome were selected and divided into stagnated heat group and non-stagnated heat group, with 9 patients in each group. The blood samples of both groups were collected to extract lymphocytes. High-throughput sequencing was applied to detect gene expressions. The functions and pathways of the differentially expressed genes were analyzed. **Results** There was significant difference in gene expression spectrum of both groups. Compared with the non-stasis heat group, there were 2867 genes whose expression was up-regulated ≥ 2 times, and 1877 genes whose expression was down-regulated ≥ 2 times. The pathways that related to differentially expressed genes were coagulation-related pathways, inflammatory immune-related pathways, vascular endothelial pathways, apoptosis, and cell cycle related pathways. Real-time PCR was used to verify the expression of tumor necrosis factor receptor superfamily 18 (TNFRSF18), matrix metalloproteinase 23B (MMP23B), DNAJ homologous B subfamily 14 (DNAJB14), interleukin 2 receptor α (IL2RA), C1Q tumor necrosis factor 3 (C1QTNF3), platelet-derived growth factor (PDGFRB), blood coagulation factor VIII (F8) and blood coagulation factor II (F2), and the results were consistent with the gene chip. **Conclusion** The essential feature of hemorrhagic stroke of stagnated heat syndrome is related to clotting and inflammation. Stasis elicited by stagnation of blood and heat caused by inflammatory reaction might be the nature of hemorrhagic stroke with stagnated heat syndrome.

Keywords hemorrhagic stroke; inflammation; phlegm-heat syndrome; clotting; gene expression spectrum

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