

Analysis of differentially expressed serum proteins in patients with allergic rhinitis at the initial stage of rush allergen-specific immunotherapy

yinli jiang¹, siyi tang¹, Xinhua Zhu¹, shuhong wu¹, yuehui liu¹, zhaokun wu¹, qinqin liu¹, and haishen peng¹

¹Nanchang University Second Affiliated Hospital

May 26, 2020

Abstract

Objective: To analyze the differential expression of related serum proteins was detected in patients with AR who were sensitized to dust mites pre- and 6-day post-RIT. **Methods:** Serum samples were collected from 15 AR, 15 6-day post-RIT and 10 healthy control patients. This analysis was performed using iTRAQ technique and was coupled with 2-dimensional gel electrophoresis and mass spectrometry. To determine the intimacy of the screened related differential proteins, a hierarchical analysis was performed with Cluster 3.0 software, and the results were visualized using Java TreeView software. Last, an ELISA was employed to validate the selected CRP, CTHRC1 and WDR89 protein expression data. **Results:** Compared with the healthy control group, the most upregulated protein in the AR group and the most downregulated proteins in the 6-day post-RIT group were CTHRC1 and WDR89. Compared with the healthy control group, the most downregulated protein in the AR group and the most upregulated protein of the 6-day post-RIT group was CRP. The serum protein levels of CRP, CTHRC1 and WDR89 proteins were determined by ELISA. It was found that the differential expression of CTHRC1 and WDR89 in the AR and 6-day post-RIT groups were statistically significant ($P < 0.05$), whereas no statistically significant difference ($P > 0.05$) was found in the differential expression of serum CRP in the AR and 6-day post-RIT groups. **Conclusions:** We found that CTHRC1 and WDR89 might be associated with the pathogenesis of AR, and they may play a regulatory role in the RIT.

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