



## ***Hymenoptera* venom immunotherapy is associated with changes in serum proteomic profiles**

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Hymenoptera venom allergy is one of the main causes of anaphylaxis. The basic treatment of sensitized patients is venom immunotherapy (VIT).

In this study we aimed to investigate changes in serum protein/peptide profiles in *Hymenoptera* venom allergic patients undergoing VIT. The analytical-bioinformatic strategy was proposed.

Serum samples were collected from 23 venom allergic patients one day before starting VIT and on the 90th and 180th day of treatment. As a control group were venom allergic patients but not qualified to immunotherapy. Samples were analyzed using MALDI-TOF/TOF mass spectrometer. For the processing of the obtained MS data, "R" software environment was applied and for statistical analysis "Metaboanalyst" and "ClinProTools" software were used.

VIT was associated with significant increase of IgG4 level in desensitized patients. Comparison of profiles characteristic to patients the day before and 180th day of immunotherapy by parametric statistical methods allowed to select nine peaks distinguishing between these two groups. Among these peaks the following proteins were identified: fibrinogen alpha chain, mucin 3A, complement C3. Non-parametric (ANOVA) analysis confirmed relations in protein/peptide level changes in time. Profiles of control group obtained in two-time points showed no significant differences. As a result of multivariate analysis for profiles characteristic to patients on the day before and 180th day of VIT obtained average cross-validation (CV)=68.87%, recognition capability (RC)=79,94%. Comparison between patients on the 180th day of VIT and control allowed to obtain CV=84,78% and RC=100%.

VIT is associated with significant changes in protein/peptide profiles in Hymenoptera venom allergic patients.