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Title: The preliminary proteomics analysis of bone marrow eosinophil progenitors in allergic asthmatic mice

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Body: Introduction: The early-stage airway inflammation of allergic asthma is associated with bone marrow (BM) progenitor cell commitment towards eosinophilic differentiation after allergen challenge. We sought to identify the differently expressed proteins by novel proteomic technology from the BM CD_{34}^{+} progenitor cells of asthmatic mice and analyzed their bioinformatics. Methods: The magnetic activated cell sorting separation coupled to fluorescence activated cell sorting separation strategy was used to harvest BM $CD34^{+}$ progenitor cells from naïve and ovalbumin-challenged asthmatic mice. Isobaric tags for relative and absolute quantitation combined with 2D nano LC-MS/MS technology was employed to profile proteome alterations in CD_{34}^{+} progenitor cells. The analysis of bioinformatics was performed finally. Results: Twenty-five proteins with 18 up-regulated and 7 down-regulated ones were identified. In the dysregulated proteins, 4 clusters of proteins were observed around collagen groups, ACTN1/Myosin groups, Mdh2 and Serpinh1, predominantly participating in pathways of focal adhesion, ECM-receptor interaction, tight junction and regulation of actin cytoskeleton. Conclusions: Collagen group and ACTN1 related focal adhesion, ECM-receptor interaction and regulation of actin cytoskeleton could be the key pathway in bone marrow response of asthma.