



Single-cell transcriptome profiling of bronchoalveolar cells identifies a Th17 signature in severe equine asthma

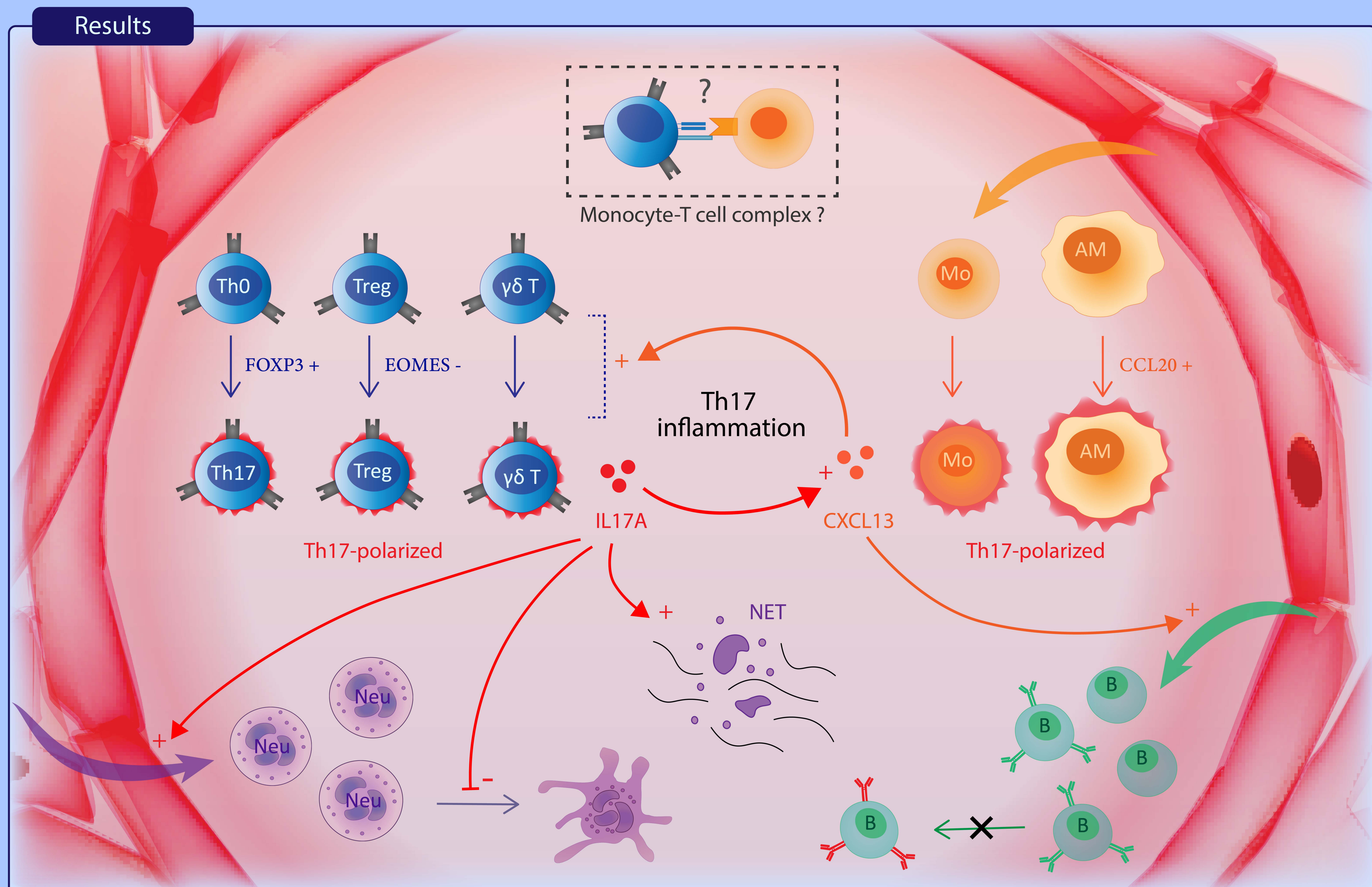
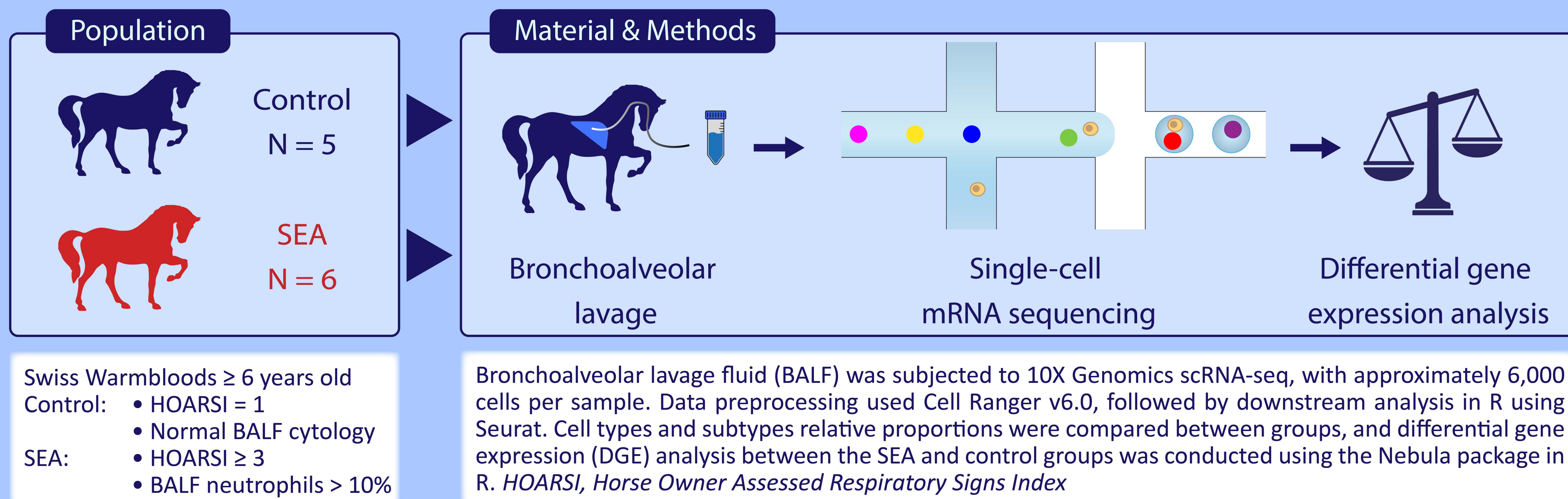
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Objective: identify the immune signature of severe equine asthma (SEA) using single-cell mRNA sequencing (scRNA-seq)



ScRNA-seq analysis of bronchoalveolar cells reveals a Th17-polarization of the pulmonary immune response in SEA. Th17-polarized T cells and monocyte-macrophages fuel an inflammation loop where activated monocytes release CXCL13, promoting Th17 polarization of T cells. IL17A, released by activated T cells, further induces CXCL13 release. Reciprocal activation of T cells and monocytes may also occur via direct cell-cell contact (monocyte-T cell complexes). IL17A and CXCL13 recruit B cells and neutrophils, respectively, from peripheral blood. IL17A influences neutrophils by decreasing apoptosis and enhancing their capacity for NETosis. In SEA, there is a reduced activation of non-switched plasma cells, resulting in a decreased pool of activated plasma cells necessary for a Th2 response. AM, alveolar macrophage; B, B cell; Mo, monocyte; Neu, neutrophil; NET, neutrophil extracellular trap; T, T cell; Th, T helper; Treg, regulatory T cell.

Key Points

- * In BALF from SEA-affected horses:
 - DGE analysis supports a Th17 response
 - B cells are more abundant
 - Activated plasma cells are decreased

- * Monocyte-lymphocyte complexes may be present in equine BALF