

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

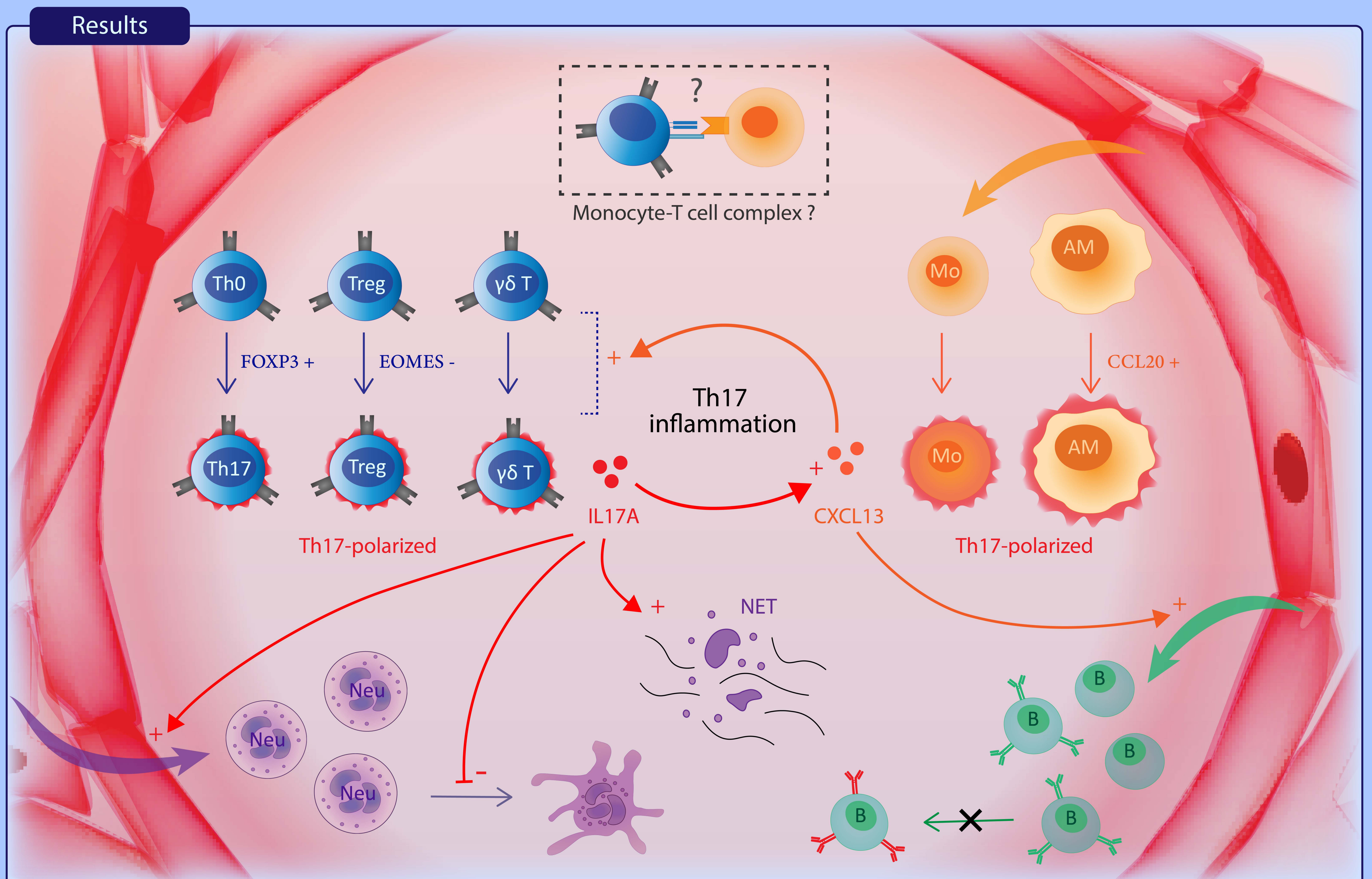
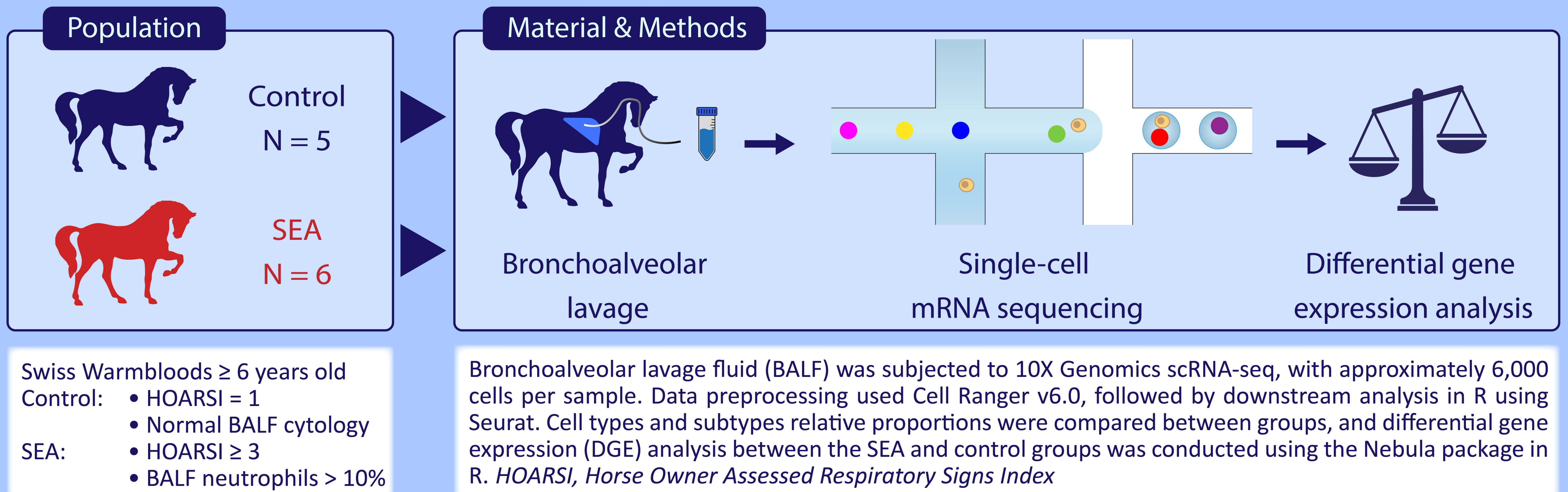
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**Objective:** identify the immune signature of severe equine asthma (SEA) using single-cell mRNA sequencing (scRNA-seq)



**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