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**Novel transcriptomic panel identifies histologically active eosinophilic oesophagitis**

Gueguen E, Morsy Y, Mamie C, et al. [Novel transcriptomic panel identifies histologically active eosinophilic oesophagitis.](https://gut.bmj.com/content/73/7/1076) Gut 2024; 73: 1076-1086. doi: 10.1136/gutjnl-2023-331743

Eosinophilic oesophagitis (EoE) is a chronic inflammatory disorder characterised by eosinophilic infiltration of the oesophagus. Diagnosis requires ≥15 eosinophils per high-power field and exclusion of other conditions that may mimic EoE. Recent work has identified three variations from conventional EoE (EoE-like oesophagitis, lymphocytic oesophagitis, non-specific oesophagitis).

Gueguen et al., aimed to identify a diagnostic genetic panel to differentiate between conventional EoE with and without active inflammation, and these variants. Oesophageal tissue and clinical data were obtained from a concurrently running cohort study, and grouped by presence/absence of inflammation and fibrosis. Data included symptom severity, endoscopic activity and histological activity. RNA sequencing and differential gene expression analysis was then performed.

Differently expressed genes from each subgroup were compared in order to identify genes only associated with inflammatory activity but not with fibrosis. A novel set of 53 dysregulated genes closely associated with inflammatory activity in EoE was identified (Histologically Active EoE Diagnostic Panel [HAEDP]). The HAEDP was able to separate out and detect histologically active EoE regardless of fibrosis, and identify disease severity in patients with active inflammation. Seventeen genes were common to the HAEDP and previously identified diagnostic panels, and combining these, facilitated differentiation of patients with conventional EoE from variants (from a publicly available dataset). All findings were achieved from single-level biopsies.

Gueguen et al., acknowledged low patient numbers and the lack of a comprehensive sampling strategy, but concluded that their work has identified a unique panel to accurately reflect the inflammatory activity of EoE and accurately differentiate variants.