DISTINCT TISSUE AND BLOOD PROTEOMIC SIGNATURES ARE ASSOCIATED WITH FIBROSTENOTIC CROHN'S DISEASE

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UEG Week Barcelona 2026 | Presentation

Mechanisms & Personalised Medicine | IBD

October 19, 2026

Proteomic profiling of full-thickness intestinal tissue and longitudinal serum from 62 fibrostenotic Crohn's disease patients identified 91 proteins associated with stricturing disease, including extracellular matrix proteins THBS2, SPON2, and RSPO1 that declined after surgical resection but remained elevated compared to luminal disease controls.

KEY POINTS

- Out of 5,400 proteins analyzed, 1,349 were differentially expressed in stenotic tissue compared to resection margins, and 276 were differentially expressed in serum comparing fibrostenotic to luminal disease patients, with 91 proteins overlapping between tissue and serum.
- Extracellular matrix proteins THBS2, SPON2, and RSPO1 were consistently elevated in both stenotic tissue and serum at baseline, showed significant reduction following surgical resection, but remained elevated compared to luminal Crohn's disease throughout 12 months of follow-up.
- Protein signatures correlated with tissue fibrosis severity and were more enriched with higher degrees of fibrosis on pathology scoring.
- No significant differences in THBS2, SPON2, and RSPO1 were observed between macroscopically normal proximal and distal resection margins, providing internal control validation.
- The findings demonstrate a coordinated signature of matrix remodeling, immune activation, and dysregulated tissue repair with potential as fibrostenotic Crohn's disease phenotype-specific biomarkers.

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