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Summary

MULTI-OMIC PROFILING REVEALS ROSEOMONAS MUCOSA AS A MICROBIAL MODULATOR OF INTESTINAL FIBROSIS IN CROHN'S DISEASE

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Meta-analysis of RNA-seq data from Crohn's disease patients identifies enrichment of the bacterium Roseomonas mucosa in fibrotic tissue, with experimental evidence that its lysates increase fibrosis marker expression in mucosal fibroblasts.

KEY POINTS

- Over 50% of Crohn's disease patients develop intestinal fibrosis, often resulting in strictures, and fibrotic complications remain a major unmet clinical challenge despite improved anti-inflammatory therapies.
- Microbial profiling revealed consistent enrichment of Roseomonas mucosa in CD samples across fibroblasts, epithelial, endothelial, and immune cell compartments.
- Fibroblasts stimulated with R. mucosa lysates showed increased expression of fibrosis markers (α-SMA, vimentin, FAP) compared to controls.
- Gene ontology analysis revealed enrichment of antimicrobial immune responses during fibrosis progression, and the authors suggest that Roseomonas mucosa or its components may influence mucosal cell transcriptional programming and contribute to fibrosis development.
- This research may inform scientists and clinicians investigating microbiota-driven mechanisms of intestinal fibrosis in inflammatory bowel disease.

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