gutflix
GI learning, personalised

Summary

TRANSCRIPTOMIC PROFILING OF LYMPHOCYTIC COLITIS HIGHLIGHTS DISTINCT DIARRHOEAL PATHOMECHANISMS COMPARED TO OTHER INFLAMMATORY BOWEL DISEASES

Julia Montague

UEG Week Copenhagen 2023 | Poster

IBD

October 15, 2023

Bulk RNA-sequencing of lymphocytic colitis mucosa reveals a dampened immune response against microbiota, distinct induction of regulatory non-coding RNAs, and decreased water channel and cell adhesion molecule expression compared to collagenous colitis and classic inflammatory bowel disease.

KEY POINTS

- Whole mucosa bulk RNA-sequencing was performed on lymphocytic colitis, collagenous colitis (active disease), and healthy control samples (n=4-10 per cohort), with comparison to ulcerative colitis and Crohn's disease samples (n=4 per group).
- The lymphocytic colitis transcriptome showed a limited mucosal immune response against microbiota compared to collagenous colitis and classic inflammatory bowel disease, despite massive mucosal immune cell infiltration.
- A distinct induction of regulatory non-coding RNA species was observed in lymphocytic colitis samples.
- Compared to collagenous colitis, lymphocytic colitis showed decreased water channel and cell adhesion molecule gene expression, associated with reduced intestinal epithelial cell proliferation.
- The authors conclude that regulatory micro-RNAs may represent a disease-specific feature potentially amenable to therapeutic intervention.

VIEW THIS CONTENT ON GUTFLIX

https://gutflix.eu/search/d/0248f2b8-743c-11ee-80ea-0242ac140004

AI-generated summary

This summary was generated by an AI large language model based on the content transcript. It is for informational purposes only and should not be considered a substitute for clinical judgment. Always rely on your professional expertise and the full clinical context when making clinical decisions.