gutflix
GI learning, personalised

Summary

# CD4+ T CELL TRANSCRIPTOMIC, EPIGENETIC AND CLONAL PROFILES IN MONOZYGOTIC TWINS REFLECT SHARED HOST IMPRINTING RATHER THAN CROHN'S DISEASE STATUS

Femke van Wijk

UEG Week Barcelona 2026 | Presentation

Histopathology | Surgery | Radiology & Imaging | Mechanisms & Personalised Medicine | Immunology | IBD

October 20, 2026

**Single-cell analysis of monozygotic twins with Crohn's disease reveals that CD4+ T cell transcriptomes, epigenomes, and TCR repertoires are shaped primarily by shared genetics and early-life environment rather than by disease status.**

## KEY POINTS

- Both affected and unaffected monozygotic co-twins displayed highly similar CD4+ T cell transcriptional, epigenetic, and TCR clonal profiles regardless of disease concordance, yet both groups differed from unrelated healthy controls.
- Pro-inflammatory pathways were upregulated in both Crohn's disease twins and their healthy co-twins compared to unrelated controls.
- TCR repertoires showed greater overlap in paired αβ CDR3 sequences within twin pairs compared to unrelated individuals, with no expanded clones detected.
- Disease concordance had limited impact on transcriptional, epigenetic, and clonal profiles of naive and gut-homing memory CD4+ T cells.
- The study used single-cell RNA sequencing with paired TCR profiling on CD-concordant (n=4) and CD-discordant (n=4) monozygotic twin pairs plus unrelated healthy controls (n=4), and DNA methylation profiling on larger cohorts (CD-concordant n=2, CD-discordant n=9, controls n=11).

VIEW THIS CONTENT ON GUTFLIX

https://gutflix.eu/search/d/9f098ae4-d12d-11f1-80d9-daaa6dbee0a2

**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.