

THE EFFECT OF COMMONLY PRESCRIBED MEDICATIONS ON THE TRANSCRIPTOME OF PATIENTS SUFFERING FROM IBD AND OTHER CHRONIC INFLAMMATORY DISEASES

Bimba Hoyer

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Poster

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RNA sequencing of 625 chronic inflammatory disease patients reveals that prednisolone, azathioprine, and anti-TNF biologics produce distinct transcriptomic signatures that contribute substantially to overall gene expression variation and should be considered in molecular studies.

KEY POINTS

- Prednisolone in low disease activity patients was associated with 224 downregulated genes (including adaptive immune response, immunoglobulin production, B cell proliferation pathways) and 602 upregulated genes (acute inflammation, innate immune response, NF-κB regulation) among top varying genes
- Azathioprine analysis of 24 IBD patients showed 144 downregulated genes related to cytokine production, cell proliferation, and T, B, and NK cell activity, with more than 80% of differentially expressed genes under epigenetic regulation
- Anti-TNF biologics were associated with upregulated immunoglobulin genes (75% of shared differentially expressed genes), with higher expression in anti-TNF patients compared to both healthy controls and no-biologics patients
- Azathioprine was the driver of at least 25% of variation in 151 genes, 70 of which were among the top 2000 varying genes across all patients
- The authors suggest these medication effects should be considered as potential confounders when performing transcriptomic analyses on blood samples from chronic inflammatory disease patients

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