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Summary

TRANSCRIPTOMIC AND PROTEOMIC PROFILING OF COLONIC MUCOSA IN PATIENTS WITH IRRITABLE BOWEL SYNDROME WITH OR WITHOUT MENTAL/SOMATIC COMORBIDITIES: RESULTS FROM THE EUROPEAN MULTICENTER DISCOVERIE STUDY

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Mechanisms & Personalised Medicine | Immunology | Digestive Oncology | Colorectal

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Transcriptomic and proteomic profiling of colonic mucosa in 174 subjects (131 IBS patients, 43 healthy volunteers) reveals distinct molecular alterations in IBS patients that vary by comorbidity burden, with the most pronounced changes observed in patients with both mental and somatic comorbidities.

KEY POINTS

- Seven differentially expressed genes were identified between healthy volunteers and IBS patients with mental and somatic comorbidities (FDR<0.1), two of which related to barrier function and immune response were confirmed by qPCR (p=0.023 and p=0.083).
- Proteomic analysis identified 271 differentially expressed proteins in IBS patients with mental and somatic comorbidities compared with healthy volunteers, enriched in pathways related to DNA/RNA processing, extracellular matrix-receptor interaction, oxidative phosphorylation, and thermogenesis.
- Four proteins were consistently differentially expressed across all three IBS subgroups (IBS without comorbidities, IBS with anxiety/depression, IBS with mental and somatic comorbidities) when compared with healthy volunteers.
- Symptom severity scores for IBS, depression, anxiety, somatic symptoms, fibromyalgia, and fatigue increased progressively with the number of comorbidities (p<0.001).
- The study was conducted within the European DISCOvERIE project across five European centers using RNA sequencing (DESeq2 analysis, FDR<0.1) and LC-MS/MS proteomic analysis (limma package).

– Further validation studies are required to confirm potential diagnostic biomarkers identified in this analysis.

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