A SPECIFIC MICROBIOTA SIGNATURE IS ASSOCIATED TO IMMUNOTHERAPY-RELATED COLITIS AS ASSESSED BY A MACHINE LEARNING APPROACH – A COMPARATIVE STUDY WITH INFLAMMATORY BOWEL DISEASES AND HEALTHY CONTROLS

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A machine learning approach to 16S rRNA sequencing data identifies a distinct bacterial signature that differentiates immune checkpoint inhibitor-associated colitis from inflammatory bowel disease and healthy controls.

KEY POINTS

- Nineteen patients with ICIs-colitis, 40 with ulcerative colitis, 34 with Crohn's disease, and 36 healthy controls were enrolled in this prospective pilot study using 16S rRNA gene sequencing of stool samples.
- Alpha diversity did not differ significantly between ICIs-colitis and healthy controls (p=0.94) but was significantly different between IBD and healthy controls (p=0.02) and between IBD and ICIs-colitis (p=0.03).
- ICIs-colitis showed high levels of Proteobacteria at the phylum level and very high levels of Enhydrobacters at the genus level compared to IBD patients, while IBD showed high Actinobacteria levels and UC patients showed high Bifidobacterium longum levels.
- Sparse partial least squares discriminant analysis achieved perfect class prediction and group separation using the complete feature set, with minimal performance loss when using only 5% of features.
- The authors state that future research will clarify whether microbiota profiling is useful for prediction, early diagnosis, and management of ICIs-colitis.

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