Abstract OWE-010 Figure 4  NMDS weighted UniFrac (bacteria–biopsies – disease distribution) \(R^2=0.17\) \(p=0.001\)

The mucosal bacterial community was dysbiotic and influenced by subject, disease distribution (figure 4) and diagnosis (figure 5). In terms of mycobiome, fewer viable reads were obtained, due to limited template. \textit{Saccharomyces} was the most abundant fungi, but it was absent in some samples, other relevant genera were \textit{Malassezia}, \textit{Cladosporium}, \textit{Aspergillus} and \textit{Candida}. The last was found more often in controls.

Conclusions CD patients' bacterial community is dysbiotic but fungi are not. \textit{Saccharomyces} dominated most of faecal samples, but not biopsies. This implies it may not be a permanent resident of the mucosae. Fungi may arise from food: it is possible drug-related acute respiratory illness.

Results 1601 (49% male, median age 33 years \([IQR 23-47]\)) eligible patients were recruited from 118 sites. Patients were treated with IFX (751 [47%]: REM, 200 [12%] CT-P13) or ADL (650 [41%]). Baseline characteristics included: median disease duration 3 years \([IQR 1-10]\); steroids 27%, azathioprine 44%, mercaptopurine 8%, methotrexate 5%; median CRP in IFX 9 mg/L \([IQR CI 3-24]\) and 6 mg/L \([IQR 2-14]\) in ADL. PNR at week 12-14 was 21%, 21% and 26% in the REM, CT-P13 and ADL treated patients respectively. PNR was associated with older age \((p=0.0004)\), higher BMI \((p=0.03)\) and low DL \((p<0.0001)\) for IFX and ADL. Week 54 remission rate was 40%, 40% and 34% of the REM, CT-P13 and ADL treated patients. At wk 54, the immunogenicity rate for REM, CT-P13 and ADL was 26%, 28% and 11% rising to 42%, 38% and 23% by 3 years respectively \((IFX vs. ADL p<0.0001, REM vs. CT-P13 p=0.25)\). Immunogenicity was associated with non-remission at wk 54 \((p<0.001)\) for both IFX and ADL). Immunomodulator use reduced the risk of immunogenicity for both IFX \((HR=0.37, p<0.0001)\) and ADL \((HR=0.34, p<0.0001)\). 140 patients (9%) withdrew drug for SAEs including 5 who died, 3 from CD and 2 from possibly drug-related acute respiratory illness.

Conclusions This is the largest prospective real-life study of anti-TNF therapy in IBD. We report the clinical effectiveness, safety and immunogenicity of REM, CT-P13, and ADL. This cohort provides a unique bioresource for multi-omic studies investigating personalised approaches to anti-TNF therapy.

Abstract OWE-010 Figure 5  NMDS weighted UniFrac (bacteria-all biopsies – diagnosis) \(R^2=0.11\) \(p=0.001\)

The mucosal bacterial community was dysbiotic and influenced by subject, disease distribution (figure 4) and diagnosis (figure 5). In terms of mycobiome, fewer viable reads were obtained, due to limited template. \textit{Saccharomyces} was the most abundant fungi, but it was absent in some samples, other relevant genera were \textit{Malassezia}, \textit{Cladosporium}, \textit{Aspergillus} and \textit{Candida}. The last was found more often in controls.

Conclusions CD patients' bacterial community is dysbiotic but fungi are not. \textit{Saccharomyces} dominated most of faecal samples, but not biopsies. This implies it may not be a permanent resident of the mucosae. Fungi may arise from food: it is hard to discriminate what comes from food and what is active in the gut. The concept of a resident, symbiotic mycobiome needs further exploration.