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COMPARISON OF THE BACTERIAL STOOL MICROBIOTA IN ESTABLISHED PSORIATIC ARTHRITIS (PSA) AND PSORIASIS (PSC) - EXPLORATORY ANALYSIS OF PILOT DATA

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Background: Psoriatic arthritis (PsA) is a complex inflammatory condition with both genetic and environmental risk factors contributing to disease. A potential environmental risk factor, known to modify the immune system, is the intestinal microbiota. In PsA there is evidence of intestinal inflammation [a,b] and recently dysbiosis of the gut microbiota has been reported in treatment naïve PsA patients[c] . However, there is no information on the temporal stability of the microbiota over time in established PsA on treatment compared to matched PsC controls.

Objectives: To explore the temporal stability of gut microbiota composition and reveal associations with PsA compared to PsC while on stable on treatment with methotrexate.

Methods: Patients with PsA and PsC were recruited to the study if they had been on a stable dose of methotrexate for 6 months. Bacterial DNA was extracted and the V3-V4 hypervariable region of the 16S rRNA was amplified and sequenced on MiSeq. The resultant data was analysed using a bespoke bioinformatics pipeline and taxa were assigned using the Ribosomal Database Project classifier according to the SILVA119 database. The Wilcoxon rank sum test was used to assess alpha diversity indices, while permanova testing using Bray Curtis distance and DESeq2 values corrected for false-discovery rate (FDR) were used to compare beta diversity indices after removing low abundance (<0.5%) Operational Taxonomic Units (OTU). The ALDEx2 analysis package was used to assess effect size.

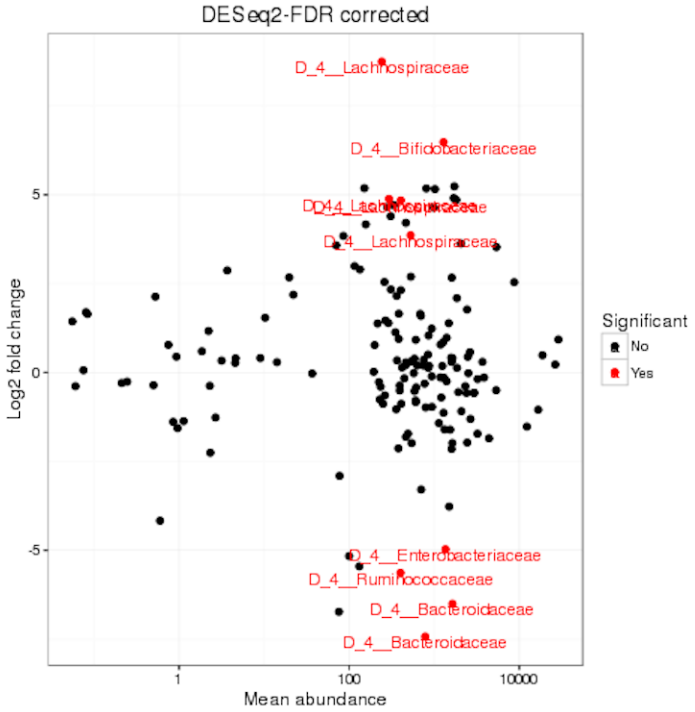
Results: Stool samples were available 9 PsA (n=13) and 6 PsC (n=12) individuals. Second stool samples were also obtained from the PsA (n=5) and PsC (n=4) groups.

Table Baseline Demographics		
Demographic variables	PsA (n=9)	PsC (n=6)
Age mean (range) yrs	56.8 (40-72)	58.5 (27-79)
Gender Female (%)	2 (22)	4 (67)
Duration of Psoriasis mean (median) yrs	23.7 (26)	26.7 (30)
Type 1 Psorasis (Age at onset <40yrs) (%)	7 (77.8)	3 (50)

No significant difference in the alpha diversity indices was observed between PsA and PsC. The beta diversity index showed no significant difference between the two conditions using permanova test. However, using the DESeq2-FDR analysis, 8 OTUs were identified which had significantly ($p < 0.01$) different abundances in PsA compared to PsC. The taxa (Lachnospiraceae & Ruminococcaeceae) predominantly belonged to the Firmicutes phylum, family Lachnospiraceae and Actinobacteria phylum, family Bifidobacteriaceae (Bifidobacteriaceae). The significant OTUs with DESEq2 had an effect size > 1 using ALDEx2 but the BH p-

value was not significant ($p<0.01$), which may be due to the small sample size. There were no significant differences in the diversity measures over time.

Image/graph:



Conclusions: These results suggest that a gut enterotype with predominant Firmicutes/Actinobacteria composition is associated with stable/well controlled disease and is stable over time. This requires replication in a larger cohort.

References: a.Lindqvist, 2006 b.Scarpa,2000 c.Scher,2015

Disclosure of Interest: None declared