

Abstract P87 Table 1

	2016/17		2017/18		2018/19	
<b>Prescriptions</b>	666		883		607	
1. Prednisolone	519	77.9%	749	84.8%	521	85.8%
- Budesonide**	147	22.1%	134	15.2%	86	14.2%
<b>Age, mean (SD)</b>	40	19	39	19	39	20
<b>Gender</b>						
<b>Male, n (%)</b>	360	54.1%	470	53.2%	325	53.5%
<b>Diagnosis, n (%)</b>						
- Crohn's disease	315	47.3%	362	41.0%	237	39.0%
- IBD-U	43	6.5%	44	5.0%	34	5.6%
- Ulcerative colitis	308	46.2%	477	54.0%	336	55.4%
<b>Steroid courses</b>						
Duration, mean (sd)	13.02*	14.00	9.90*	9.40	8.40*	7.10
≤ 8 weeks, n(%)	355	53.3%	573	64.9%	386	63.6%
> 8 weeks, n(%)	311	46.7%	310	35.1%	221	36.4%

\*  $p < 0.01$ , ANOVA \*\* 78% of budesonide prescriptions were for CD

steroid exposure. The Registry has established an infrastructure capable of serving as a platform for future nationwide prospective steroid audit.

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#### THE IMPACT OF NOD2 DEFICIENCY ON THE GUT MYCOBIOTA IN CROHN'S DISEASE PATIENTS IN REMISSION

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**Introduction** Crohn's disease (CD) is strongly associated with risk variants in *Nod2* and an imbalanced gut microbiome. Historical and emerging data indicate that gut fungi play an important role in CD pathogenesis, however a causal link between fungi and dysregulated immunity remains obscure. A recent study has shown that NOD2 acts beyond peptidoglycan sensing and is activated via a fungal chitin-dependent pathway to induce anti-inflammatory cytokine responses. Currently it is unknown what impact *Nod2* deficiency may have on the gut mycobiota in CD.

**Methods** CD patients of known *Nod2* genotype were identified from the UK IBD genetics consortium. Patients in remission were selected if they carried 2 of the common *Nod2* variants (homozygotes or compound heterozygotes). Each *Nod2* mutant patient was matched to a *Nod2* wild-type patient. Participants without CD and of a known *Nod2* genotype were recruited from the Cambridge BioResource. DNA was extracted from stool samples using the DNeasy PowerLyzer PowerSoil kit. The ITS1 region of the eukaryotic ribosomal cluster was amplified and sequenced using the illumina MiSeq. Sequence data was processed using Mothur and reads were assigned taxonomy using the UNITE database (v8). 16S rRNA gene sequences of participants were used from a previous study.<sup>1</sup>

**Results** 81/109 individuals were included in the analysis (34 CD patients [53% *Nod2* mutant] and 47 non-CD individuals [39% *Nod2* mutant]. No differences were found in  $\alpha$  diversity metrics (OTU richness and Shannon diversity) in samples from CD patients *vs.* non-CD or *Nod2* wild type *vs.* mutant individuals. The phylum *Ascomycota* was the most abundant in CD *vs.* non-CD (FDR-Adj.  $P = 0.00096$ ), whereas *Basidiomycota* was the most abundant phylum in non-CD *vs.* CD (FDR-Adj.  $P = 0.019$ ). An inverse relationship was found between bacterial and fungal Shannon diversity metrics in *Nod2* wild type individuals that was independent of CD ( $r = -0.349$ ;  $P = 0.029$ ). Principal coordinates analysis using weighted Bray-Curtis dissimilarities of fungal taxa showed separation in fungal community composition between CD and non-CD individuals ( $R^2 = 0.021$ ;  $P = 0.01$ ; PERMANOVA). The genus *Candida* showed the greatest effect on fungal community composition in CD, whereas in non-CD individuals, the genus *Cryptococcus* exerted the greatest effect on the mycobiota composition.

**Conclusions** This study confirms previously identified compositional changes in the enteric mycobiota in CD patients. However, no differences were observed in the fungal community when stratified by *Nod2* genotype (wild type *vs.* mutant).

#### REFERENCE

1. Kennedy NA, Lamb CA, Bery SH, et al. *Inflamm Bowel Dis* 2018;**24**(3):583–92.

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#### PATIENT PERCEPTIONS AND CONCERNS REGARDING PREGNANCY AND FERTILITY IN INFLAMMATORY BOWEL DISEASE

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**Introduction** Voluntary childlessness is recognised in Inflammatory Bowel Disease (IBD) patients, despite fertility being comparable to the general population. This may be due to misconceptions of medication safety and the impact on pregnancy. We aimed to:

1. Identify patients' specific concerns regarding IBD and having children

- Quantify the need for more information
- Determine a preferred information format
- Evaluate patient confidence in different clinicians' knowledge of IBD and pregnancy/fertility

**Method** A medical student led Quality Improvement Project over 11 consecutive weeks (Oct-Dec 2019). IBD patients attending outpatient clinics completed a self-administered survey, tailored to men (M), parous (P) or nulliparous (NP) women.

**Results** 156 participants completed the survey: 67 males (=37 yrs, range 17–65) and 89 females (=37 yrs, range 17–66, 43P, 46NP). The disease distribution was Crohn's Disease 36%, Ulcerative Colitis 50%, Indeterminate Colitis 3% and 11% were unsure. The mean disease duration was 109.5 months (5–540 months). 71% felt their disease was in remission.

66.2% felt they did not have enough information regarding the impact of IBD on raising a family, specifically fertility and pregnancy, including 63% of the male patients. 42.3% of