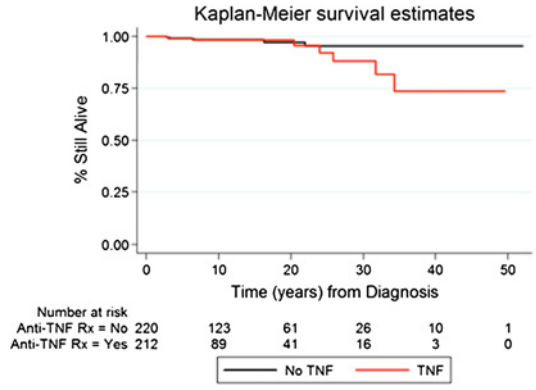
software. Proportional hazard regression model was used to assess mortality. Other SAE and OI were studied using logistic regression, t-test, and χ^2 with Fishers exact.

Results Cohort 1: 137 (64.5%) CD patients. 170 (80%) received Infliximab (IFX) as their only anti-TNF treatment, 34 (16%) IFX and Adalimumab (ADA) and 8 (4%) ADA only. Cohort 2: 220 patients comprising 88 (40%) CD. The mean age at drug initiation was 35.3 (SD 16.1) yrs in cohort 1, 45.7 (SD 15.9) yrs in cohort 2 ($p<0.0001$). Median follow-up after drug initiation in cohort 1 was 2.7 years (0—11.0), total 714.9 yrs, in cohort 2 6.4 (0—30.8) yrs, total 1524 yrs. There were 8 (4%) deaths in cohort 1 (1 cardiovascular (CVS), 3 sepsis, 3 solid organ malignancies, 1 haematological malignancy) and 5 (2%) deaths in cohort 2 (2 CVS, 2 sepsis, 1 haematological malignancy). Cohort 1 patients had a higher mortality when corrected for age at diagnosis (HR 3.4 95% CI 1.1 to 10.5) Abstract PWE-233 figure 1. In cohort 1 there were two cases of demyelination (1 suspected), 1 TB reactivation, 40 in-patient treated infections, 8 malignancies, seven cases of *Clostridium difficile* and no drug induced lupus. Hospital recorded SAE did not differ between cohorts 1 and 2 and no risk factors were identified. The mean number of primary care recorded OI was 5.8 (SD 5.8) in cohort 1 and 4.5 (SD 4.2) in cohort 2.



Abstract PWE-233 Figure 1

Conclusion The age at diagnosis adjusted mortality of IBD patients treat with anti-TNF is significantly greater than patients treated with thiopurines alone. Causality is unclear and may reflect underlying disease severity. Anti-TNF treated patients have similar rates of other SAE and primary care OI compared to patients treated with thiopurines alone.

Competing interests None declared.

PWE-234 OPTIMISING THE RESPONSE TO THIOPURINE THERAPY: A SEARCH FOR NOVEL EXPLANATIONS FOR THIOPURINE HYPERMETHYLATION

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Introduction Thiopurines are not effective in up to 1/3 of patients with inflammatory bowel disease (IBD) and 1/5 have to discontinue therapy due to side effects. An important cause of these problems is thiopurine hypermethylation. This is a catabolic process leading to an unfavourable thiopurine metabolite profile (high methylmercaptopurine (MeMP) to low thioguanine nucleotide (TGN) ratio; >11:1), which cannot be predicted by measurement of thiopurine-*S*-methyltransferase (TPMT) activity. Importantly thiopurine hypermethylation can be circumvented with the use allopurinol in combination with a low dose thiopurine. The aim of this study is to establish the mechanism of thiopurine hypermethylation and identify predictive genetic markers to allow early combination therapy. We hypothesised that thiopurine hypermethylation occurs as a result of genetic factors that affect methylation flux and the cellular transport of methylated metabolites.

Methods 168 age and dose-matched patients prescribed AZA/6-MP were identified. Genomic DNA was extracted from EDTA blood samples of 76 patients demonstrating thiopurine hypermethylation and 92 patients with normal methylation profiles. Polymorphic sequence variants in genes predicted to affect thiopurine methylation flux and cellular metabolite transport were identified from single nucleotide polymorphism (SNP) databases and genotyped by Taqman assay. Associations were tested using Fisher's Exact test.

Results We found a significant association between the haplotype of rs9332377 T and rs4646316 C, which encodes a low-activity synonymous Catechol-O-methyltransferase (COMT) variant, and protection from thiopurine hypermethylation (rs9332377 T, $p=0.0178$, rs4646316 C, $p=0.03$). A polymorphism in the nucleobase transporter, ABCB5, was significantly associated with thiopurine hypermethylation (rs2031641 G/G, $p=0.0098$). The association was strengthened when patients with MeMP levels >5000 pmol/l vs MeMP <5000 pmol/l were compared ($p=0.0065$).

Conclusion Changes in methylation flux due to the activity of methyltransferases other than TPMT affect the formation of thiopurine methylated metabolites, likely through direct competition for the essential co-factor S-adenosylmethionine. Furthermore, polymorphism in the ABCB5 gene, which affects the nucleotide-binding domain of this transporter, is associated with thiopurine hypermethylation, suggesting reduced cellular efflux of methylated metabolites. Further studies are now indicated to establish the role of these genetic markers in clinical practice.

Competing interests None declared.

PWE-235 SCREENING USING THE EUROPEAN CROHN'S AND COLITIS ORGANISATION (ECCO) GUIDELINES DEMONSTRATES HIGH STRONGYLOIDES SERO-PREVALENCE IN MIGRANTS WITH INFLAMMATORY BOWEL DISEASE

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Introduction Strongyloidiasis can persist and cause hyperinfection years after acquisition when host immunity is impaired. European Crohn's and Colitis Organisation guidelines[1] on opportunisitc infections recommend that Inflammatory Bowel Disease (IBD) patients returning from endemic areas be screened. However, prevalence of intestinal helminths in migrant IBD patients is unknown. We investigated the sero-prevalence of Strongyloidiasis and factors associated with infection.

Methods Migrant patients attending IBD clinic over a 10-month period, with a diagnosis of Crohn's disease (CD) or Ulcerative colitis (UC), were tested for Strongyloides serology. Eosinophil count and inflammatory markers were measured. Ethnicity was used as a proxy for migrant status. Sero-positive patients were followed-up with a Strongyloides charcoal culture before treatment with Ivermectin. Repeat eosinophil count and inflammatory markers were performed 3 months later. T test and χ^2 analysis ($p<0.05$) were performed using SPSS for Windows.

Results 97 migrant patients (54 CD vs 43 UC) were tested. 13/97 patients were sero-positive. In both groups, over 70% of patients were from Asia. Mean eosinophil counts ($\times 10^9$/l) were not different between the two groups (0.29 vs 0.22, $p>0.05$). No significant