

## UEG Week 2015 - Abstract Submission

*Topic area: 1. Advances in GI science using omic technologies*

*Topic: 1.7. Other*

UEG15-ABS-5251

### **EFFECT OF CO-MORBIDITIES ON URINARY METABOLIC PROFILING IN THE CHARACTERISATION OF PATIENTS WITH INFLAMMATORY BOWEL DISEASE.**

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**Has this abstract previously been presented?:** Yes

**Please specify where the abstract has been presented before:** This work has been presented at a national meeting

**Has this abstract been previously published?:** No

**Please select "Yes" in case your abstract should be considered as "Translational/Basic Science".:** Yes

**This abstract should be taken into consideration for the "Today's science; tomorrow's medicine" sessions.:** Yes

**Does the presenting author fulfil the criteria and want to apply for the travel grant?:** Yes

**Travel grant selection:** Clinical Science travel grant

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**Introduction:** Several studies have successfully used metabolic profiling (metabonomics) of urine to distinguish patients with IBD from healthy controls (1); many discriminatory metabolites identified relate to microbial or host-microbial cometabolism, supporting the concept of gut dysbiosis in IBD pathogenesis. An individual's metabolic phenotype may be influenced by factors including comorbidities such as diabetes mellitus, and previous studies have been restricted to IBD patients with no significant comorbidities which does not accurately reflect clinical practice. In order to assess the potential of metabonomics in a clinically relevant population, this study analysed urinary metabolic profiles of IBD patients with and without comorbidities.

**Aims & Methods:** Nuclear magnetic resonance spectroscopy was used to acquire urinary metabolic data from 51 IBD patients with at least one significant comorbidity (including diabetes mellitus, asthma and ischaemic heart disease), 46 patients with IBD alone, and 54 healthy controls. Groups were matched for age, sex, race, BMI and IBD diagnosis. As a preliminary analysis, resonances specific for metabolites influenced by gut microbes based on prior observations were integrated and analysed using appropriate univariate statistics.

**Results:** Univariate analysis showed that hippurate excretion was significantly lower in patients with IBD and comorbidities compared to healthy controls ( $p=0.01$ ), as well as patients with IBD alone ( $p=0.04$ ) confirming results of other published studies. In addition, trimethylamine (TMA) levels were relatively increased in patients with IBD and comorbidities ( $p=0.03$ ) and IBD alone ( $p=0.07$ ) compared to healthy controls, although trimethylamine-N-oxide (TMAO) levels showed no significant difference due to IBD or comorbid status.

**Conclusion:** In this study urinary hippurate was significantly lower in IBD patients, regardless of other comorbid diagnoses or treatments, which is consistent with previous studies. Hippurate is not a specific marker for IBD but rather related to gut microbiome metabolic dysfunction as it has also been observed when comparing the urine metabolic profile of lean and obese people and in intestinal parasitic infections. The relative increase in TMA has not been previously reported in humans, but correlates with a study that shows increasing TMA with progression of IBD in the IL10 knock-out mouse model (2). Future work will include multivariate analysis of this dataset to elucidate metabolic phenotypes associated with complex comorbidities in IBD.

**References:** (1) Williams HR et al. Am J Gastroenterol. 2009;104(7):1894

(2) Murdoch T et al. Anal. Chem. 2008, 80, 5524–5531

**I confirm having declared any potential Conflict of Interest for ALL authors listed on this abstract:** Yes

**Disclosure of Interest:** None Declared

**Keywords:** Inflammatory bowel disease, metabonomics