

R Spiller,¹ C Swan,² E Campbell,¹ M Hastings,³ G Dukes,⁴ P Whorwell,³ I Hall², N Duroudier* ¹NIHR BRU NDDC, University of Nottingham, Nottingham, UK; ²Department of Therapeutics and Molecular Medicine, University of Nottingham, Nottingham, UK; ³Neurogastroenterology, Wythenshawe Hospital, Manchester, UK; ⁴Academic DPU, GlaxoSmithKline, Harlow, UK

Introduction The heritability of irritable bowel syndrome (IBS) has been estimated at approximately 50–60%. An important subgroup (18%) of all IBS patients develop symptoms after gastrointestinal infection (postinfective IBS, PI-IBS). PI-IBS develops in 10% of *Campylobacter jejuni* infection, 2/3 of which are of the IBS with diarrhoea subtype (IBS-D).

Aims To use changes in rectal mucosal gene expression following *C jejuni* infection which were also seen in irritable bowel syndrome as a guide to identify and test candidate genes in IBS.

Methods Study 1: 31 patients with documented *C. jejuni* infection, 37 IBS with diarrhoea and 25 healthy volunteers provided blood and rectal biopsies for mRNA assessment using an Affymetrix array. Genes showing >1.5-fold change in both Group 1 and 2 compared with HV were validated by qPCR. Polymorphisms of these candidate gene were assessed in 168 IBS-D, 132 IBS with constipation (IBS-C) and 153 healthy volunteers (HV).

Results As previously reported¹ the following proinflammatory genes were increased in rectal biopsies following *C jejuni* infections and in IBS-D: *CCL11*, *CCL13*, *TNFSF15*, *Calpain* and *GABRE* while *NR1D1* and *GPR161* were depressed. We found no difference in the distribution of genetic polymorphisms of the *CCL11*, *CCL13*, genes between HV and IBS. We found an increased frequency of the T allele in the *TNFSF15* SNP rs6478108 in IBS-D (72% versus 62% in HV, $p=0.007$) but not IBS-C, in keeping with the T allele being associated with an increased risk of Crohn's disease. Similarly we found increased frequency of the proinflammatory C allele from the *TNFSF15* SNP rs7848647 and the G allele from *TNFSF15* SNP rs6478109 in D-IBS ($p=0.007$ and $p=0.015$ respectively). Although owing to small numbers we found a non-significant difference in *TNFSF15* gene expression associated with the risk alleles ($p=0.1$) there was a linear test for trend for the CC genotype of rs6478108 to have a lower *TNFSF15* expression.

Conclusion We have identified a proinflammatory genetic tendency for increased *TNFSF15* expression which may predispose to the development of IBS with diarrhoea.

Competing interests R. Spiller Grant/Research Support from: Norgene, Consultant for: Boehringer, Alberio, Conflict with: Study supported by grant from GSK, C. Swan: None Declared, E. Campbell: None Declared, M. Hastings: None Declared, G. Dukes Employee of: GSK, P. Whorwell: None Declared, I. Hall: None Declared.

Keywords genetics, Inflammation, Irritable Bowel Syndrome.

REFERENCE

1. Spiller *et al.* *Gut* 2009;58(Suppl 1):A30.