UNDERSTANDING THE EFFICACY OF FAECAL MICROBIOTA TRANSPLANTATION IN CLOSTRIDIUM DIFFICILE INFECTION: RE-ESTABLISHMENT OF GUT MICROBIOTA WITH THE ABILITY TO DEGRADE BILE?


Division of Digestive Diseases, Imperial College London, London, United Kingdom

Does this abstract contain original data?: Yes
Will this abstract be published/presented prior to June 2016?: No
This abstract is: A basic science submission
Does your Endoscopy abstract include a video?: No
Preferred presentation type: Oral or Poster

Introduction: Faecal microbiota transplantation (FMT) has recently emerged as a highly-effective therapy for recurrent/refractory Clostridium difficile (recently re-named Peptoclostridium difficile) infection (CDI); however, the specific mechanisms underlying the efficacy of FMT remain largely unclear. Given that different bile salt metabolites differentially affect C. difficile's ability to germinate and grow both in vitro and in vivo, we hypothesised that CDI is characterised by perturbed bile acid metabolism, and that FMT may exert its efficacy through re-establishment of gut microbiota that restore this process to normal.

Methods: Stool samples were collected from healthy volunteer donors participating in an FMT programme, whilst serial stool samples were collected from a patient successfully treated with FMT for refractory CDI both pre- and post-transplantation. Samples were assayed for structure of the gut microbiota using 16S rRNA gene sequencing, and for bile acid profiling via liquid chromatography mass spectrometry (LC-MS). Presence of bile salt hydrolases (responsible for deconjugation of glycine- and taurine-conjugated primary bile acids within the gut) was assessed via PCR of bacterial DNA extracted from stool.

Results: A 61-year-old man with refractory CDI was treated with FMT. He demonstrated a modest improvement in diarrhoea after a first FMT, but an immediate, complete and sustained resolution of symptoms after a second FMT from a different donor (performed two weeks after the first). 16S rRNA gene sequencing demonstrated a pattern of faecal bacterial communities that closely resembled that of the healthy donors by one week after the second FMT. Faecal LC-MS analysis revealed the patient's gut bile acid profile pre-FMT to be enriched sixfold in taurocholic acid (a potent trigger for C. difficile spore germination in vitro). Post-FMT, the patient's gut bile acid profile resembled that of healthy donors, with loss of taurocholate and enrichment of secondary bile acids (which are recognised in vitro as inhibitors of C. difficile growth). PCR of bacterial DNA extracted from faeces displayed no detectable BSH genes in the recipient either pre-FMT or by one week following the first FMT, but BSH presence was confirmed in the recipient by one week following the second FMT, as well as in both donors.

Conclusion: FMT may restore bile-degrading members of the gut microbiota, and consequently restore a normal bile acid metabolism to the gut that protects against C. difficile germination.

Disclosure of Interest: None Declared