Conclusions: These data show a strong correlation of inflammatory responses between the colitis and radiation-induced models of GI injury, with a common TNF-mediated, neutrophilic component in the colon and jejunum, respectively. Further studies will investigate time course and tissue differences. The efficacy of AVX-470m in both models highlights the central role of TNF in GI tract inflammation, and supports the therapeutic potential of an oral anti-TNF antibody in GI inflammatory disease.

This project has been funded in part by the Biomedical Advanced Research and Development Authority (BARDA), Department of Health and Human Services, under Contract No. HHSO100201100027C. This project has also been supported in part by NIH grant 2R44DK083810-02.

P042 Microbiota stability in vivo and in vitro

F.T. Hegge1*, H. Vebø1, E. Ciemniejewska1, C. Føyland1, S. Kreso1, M. Sekelja 1, A. Røseth 2, C. Casen 1. Genetic Analysis AS, Oslo, Norway, 2Lovisenberg Diakonale Hugler, Unger-Vetlesens Institute, Oslo, Norway

Background: Genetic Analysis AS (Oslo, Norway) has developed a proprietary technology for analysis of gut microbiota in humans. The technology enable simultaneous detection of >100 bacteria using a DNA probe methodology that utilizes common and variable DNA sequences within the 16s rRNA gene. The technology is currently being commercialized as an IBS dysbiosis test. As faecal samples for commercial testing most often are collected at home by the patient, the sample has to be transported from the collection site to the analysis laboratory. This transportation might take several days, in which the sample is stored in a sample collection tube. During this period the microbial growth and DNA degradation can occur, altering the 16s rRNA gene composition of the sample. GA has investigated how the gut microbiota develops over time in a sample collection tube without any stabilizing buffer. In addition, a person’s microbiota is expected to exhibit natural variation over time. This variation occur even without the influence of travel, diet or medication (antibiotics). GA has investigated the normal variation (intra-person variation) in microbiota over multiple sampling points over several months.

Methods: For the storage/transport testing, eight healthy persons donated samples. A further analysis included 10 dysbiotic samples. For the intra-person testing five volunteers have been collecting samples regularly over a period of 12 weeks. The volunteers have been living “normal” lives. All samples were analysed using the GA-map™ IBS Dysbiosis test.

Results: Using the GA-map™ IBS Dysbiosis Test no difference in bacterial composition was seen after 8 days at room temperature. Furthermore, using the GA-map™ IBS Dysbiosis Test it has been demonstrated that each person’s microbiota vary less over time than variation between healthy persons. I.e. each person’s microbiota is unique and stable over 12 weeks. It is important to remember that these studies are performed using the GA-map™ IBS Dysbiosis Test and limited to the bacterial sub-population detected by this test.

Conclusions: The sampling of feces for use in the GA-map™ IBS Dysbiosis Test can be performed up to five days prior to freezing at –20°C until further analysis. The natural variation occurring in persons living “normal” lives do not influence the results of the GA-map™ IBS Dysbiosis Test. (i.e. the inter-person variations dominate the intra-person variations). The microbial fingerprint of each individual is recognizable and specific over time.

P043 Microbial balances altered by restriction of dietary iron ameliorated immune-mediated colitis

1Kansai Medical University, Department of Gastroenterology and Hepatology, Osaka, Japan, 2Kyoto University Hospital, Department of Gastroenterology and Hepatology, Kyoto, Japan

Background: Inflammatory bowel disease (IBD) is a chronic and relapsing remitting inflammatory disorder characterized by recurrent intestinal inflammation. In addition to the excessive immune responses to commensal enteric bacteria, environmental factors are involved in the pathogenesis of IBD. Generally, iron is essential for the growth and virulence of most bacterial species. Previous epidemiologic studies reported the significant association between high content of iron in water supply and an increased incidence of IBD, and that oral, but not intravenous, iron supplementation increased disease activity in IBD. Taken together, dietary iron could be one of the potential candidates for environmental factors in IBD. The aim of this study is to investigate the effect of dietary iron on intestinal inflammation and enteric microbiota using a murine experimental colitis model.

Methods: IL-10 knockout mice were fed with iron-deprived (<3.2 mg/kg) or iron-supplemented (200 mg/kg) diets immediately after weaning (n = 7 in each group, 4 weeks of age). Mice were housed in specific pathogen free conditions, and then sacrificed at 4 and 8 weeks after feeding these refined diets. We evaluated intestinal inflammation by blinded histologic scores, measured TNF-α and IL-12p40 secretion by colonic explant culture, and quantified IL-17 and IFN-γ secretion from unseparated mesenteric lymph node (MLN) cells stimulated with cecal bacterial lysate by enzyme-linked immune-sorbent assay (ELISA). In addition, we analyzed the compositional changes of enteric microbiota by terminal restriction fragment length polymorphisms (T-RFLPs), using cecal contents obtained from both groups at 8 weeks after feeding refined diets.

Results: Histologic scores were significantly lower in the iron-deprived diet group compared with in the iron-supplemented diet group (2.7±0.5 vs. 10.0±3.7 at 8 weeks, p<0.05). Colonic TNF-α and IL-12p40 secretion were significantly lower in the iron-deprived diet group compared with in the iron-supplemented diet group (IL-12p40; 16.0±7.5 vs. 52.9±17.0 ng/mL at 8 weeks, p<0.05). Both of IL-17 and IFN-γ secretion from MLN cells were lower in the iron-deprived diet group than in the iron-supplemented diet group. Cluster analysis of T-RFLPs showed distinct differences in the profiles of enteric microbiota between the iron-deprived and -supplemented diet groups.

Conclusions: Restriction of dietary iron attenuates colonic inflammation in IL-10 KO mouse with a compositional alteration of enteric microbiota.