but when they present with significant complication, surgery is warranted. Cholecystocolonic fistulas are uncommon and when present is usually associated with significant biliary disease. This paper aims to present an evenly atypical manifestation of this variant and much more that it presents in a very rare manner in the form of lower GI Bleeding.

Methods We present a case of a 61-year-old male with Acute Myelogenous Leukaemia with no established biliary disease. He was post-appendectomy with loop ileostomy. He complained of recurrent abdominal pain with hematochezia.

Results Plain film of the abdomen revealed gas distended bowel loops in the disorganised pattern. Initial colonoscopy prior to the contemplated takedown of ileostomy was done revealing an ascending colon stricture and colitis. Anaemia and infection were addressed. The abdominal pain persisted, and he had massive hematochezia, 2nd look colonoscopy revealed an ulcerated area oozing with blood and bile flowing into the ascending colon hence a fistula was suspected. The patient did not respond to conservative management of the bleeding hence he underwent Right hemicolectomy and cholecystectomy with adhesiolysis and takedown of ileostomy which confirmed the diagnosis of cholecystocolonic fistula and was further supported by the histopathologic findings.

The patient improved post-operatively and was discharged subsequently.

Conclusions Be prudent in handling atypical scenarios in a morbid and complicated patient. A stepwise approach and a high index of suspicion especially in unusual situations can often lead us to the correct diagnosis.

IDDF2018-ABS-0255 IMPACT OF COMMENSAL HUMAN GUT MICROBIOTA IN THE EMERGENCE OF EXTENSIVE DRUG-RESISTANT PATHOGENS

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Background Antimicrobial resistance (AMR) in human health associated bacterial pathogens is a serious concern across the globe. Human gastrointestinal tract (GIT) is populated with trillions of microbial species that contribute to nutrient assimilation, host and microbial cell signalling, pathogenesis and antimicrobial resistance (AMR). Indiscriminate usages of antimicrobial in healthcare, livestock, and agriculture provide an evolutionary advantage to the resistant variants. The ascendancy of resistant variants threatens the efficacy of most, if not all, of the antimicrobial drugs commonly used to prevent or cure microbial infections. The aim of this current study was to understand the impact of commensal gut microbiota in the emergence of extensively drug-resistant (XDR) enteric pathogens.

Methods Commensal anaerobic gut microbiota was isolated from the healthy Indians without a history of hospitalisation and antibiotic intake in last one year. AMR phenotypes were characterised in an anaerobic workstation using commercially avail Epsilometer test (E-test) strip. Genome of all the isolates was sequenced in GS-FLX +pyrosequencer. Genome assembly was done in GS *de novo* assembler. Genome annotation and analysis of resistance genes were done using Rapid Annotations using Subsystems Technology (RAST) platform.

Results

- AMR traits in enteric bacteria, both in commensals and pathogens, are physically linked with mobile genetic elements (MGEs) and could rapidly disseminate to the bacterial species through horizontal gene transfer (HGT).
- Among commensal gut microbiota, the highest number of resistance phenotypes (n=12) and AMR encoding functions were detected in *Faecalibacterium prausnitzii*.
- Among pathogens, *Vibrio cholerae* and *Klebsiella pneumoniae* showed maximum resistance phenotypes (n=22).
- Genes encoding antibiotic resistance in commensal and pathogenic bacteria are physically linked with MGEs and could disseminate vertically to the progeny and laterally to the distantly related microbial species.

Conclusions XDR pathogenic and commensal enteric bacteria are isolated from healthy Indian subjects without a significant history of hospitalisation or antibiotic consumption. Consequently, the transmissible AMR genes present in the genome of gut commensals could be a potential source of resistance functions for the enteric pathogens.

IDDF2018-ABS-0264 PREVALENCE OF ANXIETY, DEPRESSION AND QUALITY OF LIFE IN AMONG SCHOOL GOING ADOLESCENT WITH IRRITABLE BOWEL SYNDROME

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Background Irritable bowel syndrome (IBS) is the most prevalent functional gastrointestinal disorders (FGIDs) that affects different aspects of life and patients experienced depression and anxiety more than others. There have been few Asian studies regarding anxiety and depression associated IBS. The aim of this study was to evaluate the frequency, magnitude and importance of anxiety and depression in among school going adolescent with IBS in Jaipur city, India.

Methods A Cross-sectional survey of students of four classes from 9th to 12th studying in government schools in Jaipur city, India. Ten government schools in Jaipur were randomly selected through lottery method. In each school, for each of the four classes, a section was randomly selected again by the lottery method. Forty students were selected from each school reaching a sample size of 470. This clinical trial study was done in IBS patients (with mild-to-moderate symptoms) divided into two case and control groups. All participants were asked to complete self-administered questionnaires: one addressing symptom severity and the hospital anxiety and depression scale (HADS). The patients were also asked to complete the IBS-specific quality of life (IBS-QOL) questionnaire.

Results Anxiety and depression were observed in 32.1% and 34.5% of IBS patients, respectively, and in 26.6% and 17.2% of healthy subjects, respectively ($p < 0.05$ for both) in school adolescent. Both anxiety and depression were associated with self-reported symptom severity ($p < 0.05$ and $p < 0.05$, respectively). As determined by multivariate analysis, symptom severity was the most important factor in the prediction of anxiety and depression. Self-reported symptom severity and