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.

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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 ascendency 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 EpiSolumeter 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**

i. 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).

ii. Among commensal gut microbiota, the highest number of resistance phenotypes (n=12) and AMR encoding functions were detected in Faecalibacterium prausnitzii.

iii. Among pathogens, Vibrio cholera and Klebsiella pneumoniae showed maximum resistance phenotypes (n=22).

iv. 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.

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**Activity 1**

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

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**Background** The emergence of extensive drug-resistant pathogens is a major public health concern. The growing prevalence of antimicrobial resistance (AMR) has led to the urgent need for novel approaches to combat this global challenge. Commensal gut microbiota play a crucial role in maintaining gut health, but their impact on the emergence of drug-resistant pathogens remains largely unexplored.

**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. 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.

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**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.