IDDF2019-ABS-0315 **FAMILIAL ADENOMATOUS POLYPOSIS AND ITS ASSOCIATIONS : EXPERIENCE FROM TERTIARY REFERRAL CENTRE IN INDIA**

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Background Familial Adenomatous Polyps (FAP) is an autosomal dominant rare condition characterised by more than 100 adenomatous polyps with a high risk of colonic carcinoma. It can be also associated with extracolonic neoplasms. Herein we present with 4 cases of FAP associated with upper and lower GI tumours within a period of 6 months.

Our aim was to study the association of FAP with various neoplasms

Methods Indian data on FAP and its variants is scarce and is limited to case reports due to its low incidence. We report our experience of 4 cases of FAP in a duration of 6 months (July 2018- December 2018) with its associated manifestations.

Results The first patient was a 41-year-old female who presented with bleeding PR, mucus in stools and abdominal pain. She was a known case of FAP with restorative proctocolectomy and ileoanal anastomosis done. After 10 years of the initial surgery ulceroproliferative perianipillary growth was identified which was diagnosed as moderately differentiated adenocarcinoma. Another case was a 58-year-old female who presented with complaints of bleeding PR with palpable rectal mass. She was diagnosed as attenuated FAP with tubular and tubulo-villous adenomas on histology. There was a rectal growth showing features of synchronous adenocarcinoma. Remaining 2 cases of FAP (46-year male, 13-year female) presented with bleeding PR and abdominal pain. Follow up upper gastrointestinal endoscopy revealed fundic gland polyps in the stomach. One of which also showed the presence of gastric adenoma in the antrum.

Conclusions FAP can present with a variety of intestinal and extraintestinal manifestations. This case series highlights the need for upper gastrointestinal scopy in patients with FAP. It also focuses on the need for increased awareness of the syndrome and its variants while treating patients with polyposis related conditions.

IDDF2019-ABS-0316 **LONG NON-CODING RNA CRCAL-2 PROMOTES GASTRIC CANCER METASTASIS BY ACTIVATING WNT/BETA-CATENIN PATHWAY VIA STABILIZING THE NUCLEAR TRANSPORT PROTEIN RAN**

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Background Long non-coding RNAs (lncRNAs) are emerging as key molecules in gastric cancer (GC), yet their potential molecular mechanisms are not well understood. The aim of our study is to identify lncRNAs that are up-regulated in gastric cancer tissues and explore their function in gastric cancer metastasis.

Methods RNA sequencing of 48 paired gastric tumor and non-tumor tissues in SYSUCC was conducted. The upregulated

lncRNAs were selected and overlapped with those in TCGA database. A siRNA library was established using the top 50 lncRNAs highly expressed in GC and used to identify lncRNAs that significantly affected cell migration based on transwell assays. The expression of our focused lncRNA CRCAL-2(ColoRectal Cancer Associated lncRNA-2) was measured using quantitative reverse transcription PCR assays and lncRNA in situ hybridization. In vivo, cell-based and patient-derived xenograft (PDX) models were used to further explore roles of CRCAL-2 in GC metastasis. Then, RNA pull-down, mass spectrometry analyses, western blot and RNA-binding protein immunoprecipitation (RIP) were performed to identify interaction proteins and related mechanisms of CRCAL-2.

Results lncRNA CRCAL-2, significantly overexpressed in the tumor tissues, was identified as the key regulator of GC metastasis. Upregulated CRCAL-2 in GC correlated with poor overall survival. Knockdown of CRCAL-2 significantly reduced GC cells migration, invasion, and metastasis of xenograft tumors in nude mice. Mechanistically, CRCAL-2 promoted GC metastasis by directly interacting with and stabilizing the nuclear transport protein RAN, resulting in increasement of nuclear import of beta-catenin and ultimately, activation of downstream targeted EMT(Epithelial-Mesenchymal Transition) genes. Additionally, the transcription factor YY1 could bind to the promoter of CRCAL-2 to upregulate its expression.

Conclusions Our results suggest that YY1/CRCAL2/beta-catenin axis play a crucial role in GC metastasis, and the newly identified lncRNA CRCAL-2 might be developed as a biomarker and potential therapeutic target of GC in patients.

IDDF2019-ABS-0317 **INCIDENCE OF HELICOBACTER PYLORI ANTIBIOTIC RESISTANCE A SINGLE CENTER CROSS-SECTIONAL STUDY**

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Background Helicobacter pylori infection has become increasingly resistant to traditional first-line treatment regimens because of emerging antibiotic resistance coupled with poor patient compliance with completing the treatment course. There is limited data regarding the incidence of H. pylori treatment resistance in the Philippines. This study aims to guide physicians in deciding the choice of the treatment regimen for both treatment-naïve and treatment-resistant organisms.

Methods This is a prospective, cohort study in St. Luke's Medical Center. We currently enrolled 73 patients positive for H. pylori infection based on rapid urease test, and gastroscopy, biopsy of the antrum, incisura and corpus and subsequent H. pylori culture and sensitivity against amoxicillin, clarithromycin, metronidazole, tetracycline, and levofloxacin were done.

Results Thirty-eight percent (38%) or 28 out of 73 patients enrolled are H. pylori culture positive and we were able to isolate and do sensitivity analysis in 42 samples. The incidence rate of Helicobacter treatment-resistant infection is high at 66.7% or 28 out of 42 isolates. Among the medications used,

no resistance was noted for amoxicillin and tetracycline, while the resistance rates are as follows for other antibiotics: clarithromycin 28.6% (12/42), metronidazole 40.5% (17/42) and levofloxacin 61.9% (26/42).

Conclusions The rates of resistance to clarithromycin, metronidazole and levofloxacin are high in Filipino *H. pylori* strains. This is in contrast to the earlier antibiotic susceptibility study by Destura *et. al* in 2004 in which all isolated strains were sensitive to tested antibiotics. This new pattern of resistance indicates the decreased usefulness of the first line therapy in the Philippines and the need for other treatment regimens is emerging.

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IDENTIFICATION OF GUT MICROBIOTA AND METABOLITE SIGNATURE IN PATIENTS WITH IRRITABLE BOWEL SYNDROME

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Background Irritable bowel syndrome (IBS) is the most common gastrointestinal disorder with a prevalence of 10%~15%. The underlying mechanism of IBS is largely unknown. This study aimed to determine whether fecal metabolite and microbiota profiles could act as biomarkers for IBS and to uncover the possible gut microbe-metabolite associations.

Methods By using a gas chromatography coupled to time-of-flight mass spectrometer (GC-TOFMS) and 16S rDNA amplicon sequencing, fecal metabolites and microbiota of 15 healthy volunteers (normal control =NC) and 15 adult IBS patients were measured.

Results The IBS patients had a significantly differential metabolite profile as compared to NC group, 4 clusters with 31 metabolites were significantly up-regulated in the IBS group as compared to the NC group. Compared with the NC group, 19 microbes were significantly up-regulated and 12 microbes were down-regulated in the IBS group. The correlation matrices between IBS clinical traits and differential abundant metabolites (DAMts) or microbes (DAMbs) indicated that partial DAMts clusters were positively associated with age, the frequency of abdominal pain/abdominal discomfort and the number of bowel movements; part of DAMbs clusters was also positively associated with those above-mentioned symptoms. By correlating metabolite levels with the amount of microbial genera, a network and correlation matrix was generated to identify two DAMts/DAMbs core panels for IBS and NC groups.

Conclusions The finding of this study puts a global perspective on metabolomics and microbiota profiling in IBS patients and provides a theoretical basis for future research on the pathophysiology of IBS.

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RELATIONSHIP BETWEEN AUTISM AND GUT MICROBIOME: CURRENT STATUS AND UPDATE

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Background Recently, many reports indicated the role of the gut microbiome in the development of autism in young children. Microbes are capable of synthesizing small molecules like fatty acids and sugars which act as signalling molecules to activate/deactivate nervous system or even trigger an inflammatory response. Thus, the current review aims to explore the role of microbes in the development of autism, summarizing data from animal models and human studies.

Methods Referring to the preferred reporting items for systematic reviews and meta-analyses (PRISMA) guidelines, searches were performed in three databases (PubMed, ScienceDirect, Web of knowledge and; database inception to 31/12/2018) using ‘microbiome’ OR ‘microbiota’ combined with ‘autism’ as MeSH terms. All the titles and abstracts retrieved were screened based on the inclusion and exclusion criteria. Studies reporting gut microbiome data in relation to the development of autism were included. Studies without gut microbiome data and/or reports on the evaluation on autism were excluded, along with reviews, conference abstracts, case studies, and comments.

Results Out of the 2237 articles were accessed, seven studies were eligible for the qualitative analysis according to the inclusion criteria. Two studies described the murine model of autism, while the remaining five studies focused on children. One study revealed that there are no significant differences in gut microbiome among the three groups—severe, mild and healthy children, while three studies indicated that there is a higher abundance of *Proteobacteria* and *Bacteroides* in autistic children, with a reduced population of *Firmicutes* and *Actinobacteria* (figure 1). One study highlighted that higher *Clostridiaceae* species present in autistic children which explain for the development of autism in children as these species could produce toxic metabolic products (e.g., phenols, p-cresol, indole derivatives). Similar results were also observed in autistic animal models - there is increase abundance of *Bacteroides*, *Parabacteroides*, *Sutterella*, *Dehalobacterium* and *Oscillospira* genera.

Conclusions Altogether, these results revealed a positive correlation between dysbiosis and autism. Microbiome alterations may contribute to the development of autism, particularly via the production of toxic bacterial metabolites and alteration in immune function. By keeping the ‘healthy’ gut bacteria in