A multi-center study on the incidence and clinical profile and outcome is recommended to obtain a better picture of the acute pancreatitis in Filipino children to help clinicians in recognizing and decreasing the morbidity and mortality of this disease.

**IDDF2019-ABS-0113**  
**FGF14 IS A FUNCTIONAL TUMOR SUPPRESSOR THROUGH INHIBITING PI3K/AKT/MTOR PATHWAY IN COLORECTAL CANCER**  
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**Background**  
Colorectal cancer (CRC) is one of the most common malignancies worldwide. Emerging evidence indicates that promoter methylation of genes associated with gene silencing plays an important role in the development and progression of CRC. In this study, we aimed to investigate the epigenetic regulation, biological function and molecular mechanism of FGF14 in CRC.

**Methods**  
The expression of FGF14 in CRC cell lines, CRC tissues and paired adjacent normal tissues was detected by PCR and Western blot. The biological function of FGF14 in CRC was interrogated by cell viability assay, colony formation, flow cytometry, cell invasion and migration assay, as well as in vivo study.

**Results**  
We found FGF14 was downregulated or silenced in all (10/10) CRC cell lines, while it was expressed in normal colonic tissues. The expression of FGF14 was lower in primary CRCs as compared to their adjacent normal tissues. Significant higher methylation of FGF14 was observed in CRCs than that in normal tissues based on the data from TCGA database. The loss of FGF14 gene expression was restored by treatment with DNA methyltransferase inhibitor 5-Aza. Re-expression of FGF14 in CRC cell lines inhibited cell viability and colony formation, and induced cell apoptosis. In xenograft mouse model, overexpression of FGF14 significantly reduced tumor growth (P<0.001). FGF14 induced mitochondrial apoptosis and inhibited PI3K/AKT/mTOR pathway.

**Conclusions**  
In conclusion, FGF14 is a novel tumor suppressor, which suppresses cell proliferation and induces cell apoptosis via mediating PI3K/AKT/mTOR pathway.

**IDDF2019-ABS-0120**  
**PAN-CANCER STUDY OF PROGRESSIVE PROTEIN SIGNATURES FOR DIGESTIVE CANCERS**  
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**Background**  
As functional executors, protein signatures will be more sensitive than gene signatures in characterizing biological systems. The direct study of the functional proteome is capable to complement and extend omics analysis. Especially, combining cancer research with proteome analysis can identify protein biomarkers to distinguish disease types or subtypes.

**Methods**  
The progressive signatures during dynamical biological processes are attracting more and more attention. As an