EP-0021 (PE-0592) The long-term metabolic profile and microbiota status are altered after right hemicolectomy in patients with colorectal cancer

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Background and Aim: The long-term effect of gut microbiota and subsequent metabolic profiles in colectomy patients is limited. We evaluated and compared long-term effects of metabolic profiles and microbiota status in early colorectal cancer (CRC) patients receiving curative colectomy to the controls. ***Methods:*** In this cross-sectional study, we analyzed metabolic syndrome (MS) occurrence in 165 patients after curative partial colectomy with right hemicolectomy (RH) or low anterior resection (LAR) and 333 age-sex matched controls. Fecal samples from some of those with RH, LAR, and controls were analyzed by next-generation sequencing method. ***Results:*** MS occurrences were significantly higher in patients after RH, but not LAR, when compared with the controls over the long-term (> 5 years) follow up (P = 0.020) (Table 1). Compared with control group, RH group showed lower bacterial diversity (P = 0.007), whereas LAR group showed significantly higher bacterial diversity at the genera level (P = 0.016). Compared with the control group, the principal component analysis revealed significant differences in bacterial genera abundance after RH and LAR ($P < 0.001$). *Firmicutes* to *Bacteroidetes* ratio was significantly lower in the RH group than the control group (22.0% versus 49.4%, $P < 0.05$). ***Conclusion:*** Early CRC patients after RH but not LAR had a higher occurrence of MS than the controls during long-term follow up. In parallel with the metabolic profile, gut microbial diversity also significantly decreased after RH. This study suggests that patients after curative RH due to CRC should receive not only standard surveillance including colonoscopy but also standard regular metabolic screening.

Keywords: metabolic syndrome, gut microbiota, colorectal cancer, right hemicolectomy

Table 1 Anthropometric and laboratory data between patiens with right hemicolectomy and patients without GI tract surgery.

	Patients with RH	Control subjects	p value
	N= 53	N= 333	
Age y/o	70.2 ± 9.8	69.8 ± 7.0	0.225
Sex, M (%)	23 (43.4%)	191 (57.4%)	0.074
body mass index	23.8 ± 3.6	24.5 ± 3.1	0.187
waist (cm)	86.0 ± 8.8	86.4 ± 10.8	0.909
systolic BP (mm Hg)	131 ± 16	126 ± 18	0.113
diastolic BP (mm Hg)	76 ± 10	75 ± 11	0.704
HDL-cholesterol (mg/dL)	55 ± 13	51 ± 13	0.117
Total cholesterol (mg/dL)	187 ± 34	203 ± 38	0.023
Triglyceride (mg/dL)	123 ± 68	120 ± 60	0.797
Serum glucose (mg/dL)	110 ± 24	100 ± 22	0.029
Metabolic syndrome + (%)	30 (56.6%)	104 (31.2%)	0.020

Abbreviations: GI, gastrointestinal; BP, blood pressure; HDL, high density lipoprotein; RH, right hemicolectomy.

OE-0426 (PE-0593) Determining the specific gut microbiota patterns associated with colorectal cancer

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Background and Aim: The role of gut microbiome in the etiology of colorectal cancer (CRC) is emerging, and the type of microbiota patterns in South Asian populations has not been studied. Hence, we set out to study the gut microbiota patterns in patients with CRC, diabetes (DM), and healthy individuals to find the specific gut microbiota patterns associated with CRC. ***Methods:*** The relative abundance of 45 types of gut microbiota was determined in stool samples in patients with CRC (n = 24), DM (n = 20), and healthy individuals (n = 44), using a PCR array. Data were analyzed using a specific software for analysis. ***Results:*** *Bacteroides fragilis* was expressed 23.88-fold higher in patients with CRC, and 77.09-fold higher in patients with DM when compared to healthy individuals. *Aeromonas* species were the predominant microbes, in patients with DM (226.64-fold higher), followed by *Enterococcus faesium* (183.1-fold higher), *Shigella dysentriae* and *Streptococcus agalactiae* compared to healthy individuals. *Akkermansia muciniphila*, *Bacteroides vulgatus*, and *Bacteroides thetaiotaomicron* were 5.87, 2.12, and 8.03-fold higher in CRC patients, while expression of most bacterial species of the genus *Enterobacteriaceae* were lower (Fig. 1). ***Conclusion:*** Bacteria of the genus *Enterobacteriaceae* were most abundant type of gut bacteria patients with DM, while their abundance was lower in patients with CRC. *Bacteroides fragilis* was equally highly expressed in patients with DM and CRC. Since DM is known to be a risk factor for the development of CRC, the role of *Bacteroides fragilis* in the pathogenesis of CRC should be further investigated.

Keywords: colorectal cancer, gut microbiota, Sri Lanka

Figure 1 (A) The $\log_{10}$ of the fold change for the CRC patients relative to the Healthy individuals. (B): The $\log_{10}$ of the fold change for the DM patients relative to the Healthy individuals.