

AB 2017/061

Determining the role of the gut microbiome in the aetiology of colorectal cancer**A.G.P.S Gamage¹, B. D. Gamage¹ and G. N. Malavige²**¹Department of Surgery, Faculty of Medical Sciences, University of Sri Jayewardanepura, Sri Lanka.²Department of Microbiology, Faculty of Medical Sciences, University of Sri Jayewardanepura, Sri Lanka.**Objective**

The role of the gut microbiome in the aetiology of CRC is emerging. Therefore, we set out to determine the gut microbiota pattern in patients with colorectal cancer (CRC) to determine specific microbiota associated with CRC.

Methods

Bacterial DNA was extracted from fresh stool samples from 10 patients with CRC and 10 healthy individuals. The pattern of the gut microbiome and quantification was carried out using quantitative real time PCR for 45 types of gut microbiota using a PCR array. Data was analysed using the specific software for analysis of bacterial DNA quantification.

Results: Marked differences in the gut microbiome pattern was seen in patients with CRC when compared to healthy individuals. *Bacteroides fragilis* was expressed as log 10 fold in patients with CRC when compared to healthy individuals, whereas, *Aeromonas enteropelogenes*, *Aeromonas hydrophila*, *Aeromonas punctata*, *Aeromonas media*, *Akkermansia muciniphila*, *Anaerotruncus colihominis*, *Bacteroides fragilis*, *Bacteroides thetaiotaomicron*, *Citrobacter freundii* and *Bacteroides vulgatus* species, were several fold higher in healthy individuals. *Akkermansia muciniphila*, *Bacteroides thetaiotaomicron* and *Bacteroides vulgatus* were also several fold more abundant in those with CRC

Conclusion

The gut microbiome patterns appear to be markedly different in those with CRC, specifically with high abundance of *Bacteroides fragilis*, which suggests a possible role of this bacteria in the pathogenesis of CRC.