The Gut Microbiome: Potential Risk Factor for Colorectal Cancer

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Colorectal cancer (CRC) is one of the world's leading causes of cancer death. Changes in gut microbiota composition and metabolism have been accepted as major contributors to colorectal carcinogenesis. The aim of this study is to assess if two genotoxic bacterial genes (pks and usp) are present in colonic mucosa tissue from individuals with and without colorectal neoplasia (CRN) in order to establish that pathogenic bacteria carrying these genes are in direct contact with the tissue, and to evaluate if these genes are potential risk factors for CRC. In addition, we compared results with concordant stool samples to determine agreement. The Puerto Rico Familiar CRC Registry provided fifteen colonic tissue samples from five healthy and ten CRN individuals. The detection of pks and usp genes was performed by qPCR and associations to CRC were assessed using odds ratios. The agreement between tissue and stool samples was calculated using kappa statistic. Both genotoxic bacterial genes were detected in colonic mucosa tissue samples. This is the first time usp has been detected in colonic tissue. Although no statistical significant associations between the presence of pks and usp genes in tissue samples were observed, these were more prevalent in CRN samples. When comparing tissue and stool samples profiles, the presence of toxic bacterial genes had an agreement of nearly 90%. Analysis with larger sample number is necessary to determine a more definite association between genotoxic bacterial genes with CRC and if they can be used for CRC risk-stratification and prevention in the future.

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