Gut Microbiota and their Metabolites In Colorectal Cancer: A Systematic Review

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Colorectal cancer (CRC) is a worldwide health concern which requires efficient therapeutic strategies. The evaluation of human microbiota can be critical in this regard, since the disruption of the normal community of gut bacteria is an important issue in the development of CRC.

The current study provides a detailed overview of the most critical gut bacteria DNA detected in the standard sample types of CRC. Therefore, several databases, Medline, Scopus, and Embase, Cochrane library for English published articles were evaluated. In addition, the importance of metabolites derived from gut bacteria and their relationship with the microbiota have been evaluated.

Several studies compare the evaluation of microbiota derived from tissue and stool samples of CRC patients and healthy controls. The incidence risk of CRC is higher in developed countries than in developing ones, which is highly related to dietary differences. Moreover, it is currently unclear how dysbiosis could progress CRC. Some of the crucial gut bacterial mechanisms involved in CRC progression have been related to *Escherichia*, *Streptococcus*, *Bacteroides*, *Enterococcus*, *Fusobacterium*, *Salmonella*, *Helicobacter* and *Clostridium*. On the other hand, some positive impacts on CRC prevention have been similarly related to the mechanisms of *Bifidobacterium* and *Lactobacillus*. In addition, there are plenty of data describing the role of short-chain fatty acids (SCFAs) and phenolic compounds in cancer prevention. Nevertheless, the nitrogen metabolites, reactive oxygen species (ROS), phytochemicals, uracil, bile acids and some amino acids which can produce potentially harmful compounds such as ammonia, p-cresol, hydrogen sulfide, and some amines during fermentation, may potentially promote CRC.

Given existing evidence of dysbiosis in CRC, the link between gut bacteria and CRC development has become an urgent topic for future biomedical research. Ultimately, the combined use of microbiota and metabolites analyses can be very significant for reaching a targeted therapeutics and innovative precision strategy for CRC.