



Cancer Genomics: Chapter 15. Genomics of Colorectal Cancer

Daniel Gaston, Carman Giacomantonio

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Colorectal cancer (CRC) is the third most common form of cancer and a leading cause of cancer-related mortality in both men and women, particularly in Western and developed nations. The high mortality rate has been attributed to the fact that colon cancer is often diagnosed at a late stage. Three primary subtypes of CRC have been described based on their molecular pathology and their underlying genetics: chromosomal instability (CIN), microsatellite instability (MSI), and CpG island hypermethylation. Over the last 30 years, molecular and genetic studies have determined a number of key genetic pathways that are subverted in CRC, including those involving APC, KRAS, and the p53 tumor suppressor. More recently, high-throughput, genome-wide studies have begun to characterize the broader genomic features of CRC. These high-throughput studies provide an ever expanding, and increasingly complex view of the molecular underpinnings of CRC. The chief goal of these studies being the identification of new therapeutic targets, as well as the definition of prognostic and diagnostic biological markers of CRC. Here, we highlight the key genetic and molecular pathways underlying CRC, as well as more recent insights into this disease uncovered by genomic studies.

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