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[**Methylation of the polycomb group target genes is a possible biomarker for favorable prognosis in colorectal cancer.**](http://www.ncbi.nlm.nih.gov/pubmed/23010642)

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**Source**

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**Abstract**

**BACKGROUND:**

Colorectal cancer (CRC) is the second most common cancer in the Kingdom of Saudi Arabia with ever increasing incidence rates. DNA methylation is a common event in CRC where it is now considered an important phenomenon in CRC carcinogenesis and useful for the classification and prognosis of CRC.

**METHODS:**

To gain insight into the molecular mechanisms underpinning CRC in Saudi Arabian patients, we profiled the DNA methylation frequency of key genes (MLH1, MSH2, RASSF1A, SLIT2, HIC1, MGMT, SFRP1, MYOD1, APC, CDKN2A, as well as five CIMP markers) in 120 sporadic CRC cases. CRC tumors originating from the rectum, left, and right colons are represented in this cohort of formalin-fixed paraffin-embedded tissues.

**RESULTS:**

The most common methylation frequency was detected in the polycomb group target genes (PCGT) including SFRP1 (70%), MYOD1 (60.8%), HIC1 (61.7%), and SLIT2 (56.7%). In addition, MGMT methylation was detected at a high frequency (68.3%). RASSF1A, APC, and CDKN2A methylation frequencies were 42.5%, 25%, and 32.8%, respectively. K-means clustering analysis of the methylation events results in the clustering of the CRC samples into three groups depending on the level of methylation detected.

**CONCLUSION:**

Group II (PCGT methylation and CIMP-negative) methylation signature carried a favorable prognosis for male patients, whereas older patients with group I rare methylation signature have a potentially poorer clinical outcome. Impact: Methylation of the PCGT genes along with RASSF1A, APC, and MGMT can be potentially used as a new biomarker for the classification and prognosis of CRC tumors and independently of where the tumor has originated. Cancer Epidemiol Biomarkers Prev; 21(11); 2069-75. ©2012 AACR.

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