

GENETICS

The help of epigenetics in differential diagnosis

Epigenetic changes, such as DNA methylation, have an important role in cancer by regulating gene expression and determining which genes are 'turned on' or 'off'. In fact, in colon cancer, several genes have been described to be activated by hypermethylation of their promoters.

Shu Wang and collaborators were interested in describing the cumulative effect that the methylation of different candidate genes might have on tumour development and progression. "The cumulative analysis of promoter methylation gives more-accurate diagnostic results than the analysis of single promoters," explains Wang, "in this project, we quantitatively analysed DNA methylation levels of seven critical genes in tumour and noncancerous samples."

Using a cationic conjugated polymer (CCP)-based fluorescence resonance energy transfer (FRET) method they had previously developed, the authors measured the methylation

levels of colon-cancer-related genes in 50 carcinoma and 50 adenoma cases, and in 50 controls. They also compared the sensitivity of the method in detecting cumulative methylation with single-gene methylation.

A combination of two to three genes allowed a correct-classification rate of 86.3% of patients with colon adenoma and precancerous carcinoma. Moreover, carcinoma cases could be distinguished from adenoma cases with an accuracy of 97.5%.

Wang hopes that these results might lead to the development of more-accurate methods of differential diagnosis of colon cancer.

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Original article Yang, Q. *et al.* Detection and differential diagnosis of colon cancer by a cumulative analysis of promoter methylation. *Nat. Commun.* doi:10.1038/ncomms2209