Molecular diagnosis of colorectal tumors by expression profiles of 50genes expressed differentially in adenoma and carcinomas

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摘要

Abstract

Most colon cancers are thought to develop through the 'adenoma-to-carcinoma sequence' model. To elucidate the mechanisms underlying this pathway, we analysed gene-expression profiles of 20 colorectal tumors (nine adenomas and 11 differentiated adenocarcinomas) by means of a cDNA microarray representing 23 040 genes coupled with laser-capture microdissection. A two-dimensional hierarchical clustering analysis of expression profiles of the 20 tumors correctly separated the carcinoma group from the adenoma group. Furthermore we identified 51 genes whose expression was commonly up-regulated, 376 that were commonly down-regulated in both types of tumors as opposed to normal colonic epithelium and 50 whose expression levels were significantly different between adenomas and carcinomas. On the basis of expression profiles of the 50 discriminating genes, we established a scoring system to separate adenomas from carcinomas. Application of this scoring system for evaluating five additional colorectal tumors correctly predicted their histological features. The genome-wide information reported here should contribute to a more profound understanding of colorectal tumorigenesis, particularly of adenoma-carcinoma progression, and provide indicators for developing novel strategies to diagnose, treat, and ultimately prevent colorectal carcinomas

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