Updates of the microarray data in colorectal cancer analysis by using automated bioinformatic tools

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Colon tumorigenesis is considered a complex multistep process that occurs through a series of gene mutations, leading from precursor lesions to invasive and metastatic adenocarcinoma. The development and progression of cancer and the reversal of tumorigenicity are accompanied by complex changes in patterns of gene expression. Microarrays of cDNA provide a powerful tool for studying these complex phenomena.

The purpose of the present study was to determine differential gene expression in colon tumors as compared with normal tissue and to investigate the possible variability of gene expression among pools of microdissected colon tumors. We also developed an automated bioinformatic instrument in the programming language JAVA, for updating the data close to the database of UNIGENE (NCBI). Pools of colon and rectal tumors in different stages were analyzed using the system Gene Discovery Array Human system (Incyte Genomics) that consists of two nylon membranes in a double spotted pattern at a density of 36,864 per spots per filter or 18,376 individual cDNA clones. Our results showed several differentially expressed clones between normal and tumor tissue analyzed. That differential expression had been confirmed by RT-PCR semi-quantitative analysis in individual tumors. With the development of the bioinformatic tool, we efficiently

updated the data from 2001 to the present. We obtained some statistical data, for instance, in one of the analyses there were 432 clones with differential expression, in the updating analysis 319 became new genes and 113 remain ESTs or the same registration in the public database. With the development of this bioinformatic tools, the updating of the data was fast, efficient and safe, proving the great importance of computer science in the development of projects involving biology, and being essential in the discovery of new genes as well as the discovery of new current genes at the end of the sequencing of ESTs previously present in these analyses, with possible function in this tumorigenesis.

Key words: bioinformatics, JAVA, microarrays, DNA, RT-PCR, ESTs