Análise do Perfil de Expressão Gênica em Tumores Humanos através de cDNA Microarray

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A common feature in the pathogenesis of gastric and esophageal adenocarcinoma is chronic inflammation, manifested as gastritis associated to *Helicobacter pylori* infection and esophagitis. However, not all individuals with these symptoms develop cancer, suggesting that other factors are critical in determining whether an individual is at risk for neoplastic progression. Using cDNA microarrays, we determined the expression profile of esophagus and stomach samples, representing normal mucosa, intestinal metaplasia and adenocarcinoma. Based on the expression profile of 4600 genes, grouped according to the Kyoto Encyclopedia of Genes and Genomes, we determined functional modules that are differentially active in the various sample groups. We found that the cytokine-cytokine receptor interaction and the glycerolipid metabolism modules showed interesting profile considering the number and kind of tissue that they were active or repressed. The cluster analysis by *K*-means algorithm was performed and the best result was obtained with *K*=3 and, for both modules, a clear separation between squamous tissue samples (normal esophagus mucosa and esophagitis mucosa); malignant columnar samples (gastric and esophagic carcinomas) and non-malignant columnar samples (intestinal metaplasia of the esophagus and stomach and normal gastric mucosa) was observed. The genes which contribute to the significant expression of the cytokine-cytokine receptor interaction module were IL1R2, CCL20, CCL18, INHBA, IL4R and IFNAR2 and for the glycerolipid metabolism module were AKR1B10, ALDH3A2, ADH1B, CDS1, and DGKQ. Also, using the concept of relevance networks, we determined the linear correlation for all pair of genes within the cytokine and glycerolipid modules and a statistically significant change in the linear correlation between genes belonging to each functional module could be observed when intestinal metaplasia and adenocarcinomas of the stomach or Barrett´s mucosa and adenocarcinomas of the esophagus or esophagogastric junction. The role of lipid metabolism and inflammation might be relevant to better understand the process of chronic inflammatory response associated to intestinal metaplasia of the stomach and esophagus and its subsequent progression to adenocarcinoma.