Frequency of DNA Damage in Metaplasia and Adenocarcinoma of the stomach and esophagus and its correlated with Expression of Glycerolipid Metabolism Genes

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Gastroesophageal adenocarcinomas are frequently preceded by chronic inflammation, that leads to replacement of normal mucosa by a columnar tissue (intestinal metaplasia). Although malignant transformation of intestinal metaplasia is rare, most patients with adenocarcinomas of either organ frequently have a history of intestinal metaplasia. Hence, whereas the former can not be defined as a precursor lesion, it can be considered a risk factor. Earlier, we demonstrated, by cDNA microarray, that alterations in metabolic pathways related to citokynes and glycerolipid metabolism could be functionally associated with malignancy. A total of nine differentially expressed genes were validated by RT PCR (IL1R2, CCL20, INHBA, IL4R, IFNAR2, AKR1B10, ALDH3A2, ADH1B and CDS1) and our hypothesis is that these differences might increase the rate of DNA damage due to higher production of aldehydes generated by ROS produced during chronic inflammation. Here we present the protein levels of three markers of DNA and protein damage (8-OH-dG, malondyaldehyde and ?-H2AX) using tissue microarray and western blot in a universe of 582 samples. All markes showed a similar profile, being all significantly more present in inflammatory, metaplasic and malignant tissues compared to normal tissues. Collectively, the expression of these markers showed a profile compatible with that of cDNA array and with the notion that, in patients with adenocarcinomas, a reduced expression of genes involved in aldehyde metabolism might be indeed associated to malignant transformation.

Key words: *DNA Damage, Gastric Cancer, Glycerolipid Metabolism, Reactive Oxygen Species*

Supported by CAPES