Isolation of salt exposure-sensitive genes in human small intestine cells: A new approach for the molecular evaluation of the role of salt exposure in upper gastrointestinal carcinogenesis in humans

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Summary

Upper gastrointestinal cancer (UGIC) is one of the most common malignant tumors in Japan. A large number of studies have indicated that salted, smoked, pickled, and preserved foods (rich in salt, nitrite, and preformed N-nitroso compounds) and *Helicobacter pylori* infection are associated with an increased risk of UGIC. In contrast, strong evidence has been provided that high consumption of fresh fruit and raw vegetables and a high intake of antioxidants are associated with a reduced risk of UGIC. These factors may vary in effect between populations and individuals but, if active, may affect the cell genome which may further influence the course and progression of chronic inflammations, and can finally result in overt UGI neoplasia. The molecular biology of gastric cancer has revealed a spectrum of gene errors which vary in type and extent between different histological types of cancer, and between individual cases. There is evidence that the intestinal metaplasia or the gastric epithelium in atrophic gastritis reveal signs of abnormal expression of various regulatory genes well before the appearance of gastric neoplasia. It is possible that the mechanisms leading to genetic aberrations in epithelial cells are triggered very early in the gastritis cascade, and that atrophic gastritis and intestinal metaplasia result from these processes.

In the present study we hypothesized that there may be differential expression of genes in the UGI epithelial cells that are cultured in high salt-concentration and the cells cultured in a normal condition. Therefore RNA expression in human small intestine epithelial cells that were cultured in high salt medium (HSI-HS+) was studied using a cDNA microarray method. Four genes were differentially expressed: three were increased and another gene was suppressed in HIS-HS+. cDNA microarray will allow the isolation of salt-sensitive genes and may help develop a molecular profile of gastrointestinal disorders which have close relationship with salt exposure.