TARGETED DEEP DNA METHYLATION ANALYSIS IN GaSTRIC CANCER TISSUES USING SEMICONDUCTOR SEQUENCING

OBJECTIVO:
Epigenetic control using inhibitors of DNA methylation, such as Decitabine (5-AZA), may offer new possibilities in gastric cancer therapy. Our research group previously identified 86 differentially expressed genes by microarray analysis comparing Decitabine-treated and nontreated gastric cancer cell lines. Among the upregulated genes identified by this methodology, LRRC37A2 and SNORD42B were selected for further analyzes. This study aimed to evaluate and correlate LRRC37A2 and SNORD42B methylation and mRNA levels in gastric cancer tissues.

MÉTODOS:
Gastric cancer and adjacent nontumor samples from 40 patients with primary gastric adenocarcinoma were studied. The mRNA level was assessed by quantitative reverse transcription PCR and DNA methylation analysis was evaluated using Ion TorrentTM PGM sequencer.

RESULTADOS:
Gastric tumors presented reduced LRRC37A2 and SNORD42B expression than nontumor samples. Higher LRRC37A2 promoter methylation was associated with tumors of patients with lymph node metastasis, whereas SNORD42B did not show methylation for target regions. Our preliminary results detected no correlation between LRRC37A2 mRNA and methylation levels.

DISCUSSÃO:
LRRC37A2 and SNORD42B are possible tumor suppressor genes in gastric cancer. LRRC37A2 methylation may play an important role in advanced gastric tumors.

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