**SMARCA5 methylation and expression in gastric cancer**

Gigek, CO¹; Lisboa, LCF¹; Leal, MF¹; Silva, PNO¹; Lima, EM²; Assumpção, PP³; Burbano, RR⁴; Smith, MAC¹

¹ Disciplina de Genética, Departamento de Morfologia e Genética, Universidade Federal de São Paulo, SP, Brasil.
² Departamento de Biologia, Campus Ministro Reis Veloso/Parnaíba, Universidade Federal do Piauí, PI, Brasil.
³ Serviço de Cirurgia, Hospital Universitário João de Barros Barreto, Universidade Federal do Pará, PA, Brasil.
⁴ Laboratório de Citogenética Humana e Genética Toxicológica, Instituto de Ciências Biológicas, Universidade Federal do Pará, PA, Brasil. carolina.gigek@unifesp.br

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Gastric cancer is the fourth most prevalent cancer in the world. However, due to its poor prognosis, gastric cancer is the second most common cause of death from cancer. The early detection of gastric cancer is very important for a good prognosis. DNA methylation is the most common epigenetic alteration and is associated with gene silencing. SMARCA5, is a member of SWI/SNF chromatin remodelling family of proteins, which has a helicase and ATPase activity. This protein is important for gene expression, DNA replication, DNA repair and maintenance of chromatin structure. SMARCA5 promoter and exon 1 have a 1 kb Cpg island with CG content up to 60%. This Cpg island contains binding sites of methylation-sensitive transcription factors, as Sp1, Myb, CREB, AP1 and MZF1. These data suggest that SMARCA5 expression may be regulated by DNA methylation. Here we evaluated SMARCA5 expression and promoter methylation in gastric carcinogenesis. Immunohistochemistry was analyzed in 54 gastric cancer and 18 normal gastric mucosa samples. 92 gastric cancer and 47 normal mucosa samples were investigated through methylation specific PCR. This is the first study evaluating SMARCA5 expression and promoter methylation status in gastric carcinogenesis. We observed higher immunoreactivity of SMARCA5 in gastric cancer samples than in normal mucosa. Moreover, SMARCA5 promoter methylation was associated with absence of protein expression. In conclusion, our data suggest that SMARCA5 immunoreactivity, as a potential marker of proliferation and malignization, may be used to help diagnosis in gastric cancer or could be an interesting therapeutic target.

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