《上一篇/Previous Article|本期目录/Table of Contents|下一篇/Next Article》

[1]李文英,余鸿,陈兴书,等.人Sox10基因启动子区高甲基化的预测和验证[J].第三军医大学学报,2013,35(20):2168-2171.

Li Wenying, Yu Hong, Chen Xingshu, et al. Prediction and analysis on methylation of human Sox10 gene promoter[J]. J Third Mil Med Univ, 2013, 35(20): 2168-2171.

点击复制

人Sox10基因启动子区高甲基化的预测和验证(PDF)分

导航/NAVIGATE

本期目录/Table of Contents

下一篇/Next Article

上一篇/Previous Article

《第三军医大学学报》[ISSN:1000-5404/CN:51-1095/R] 卷: 35 期数: 2013年第20期 页码: 2168-2171 栏目: 论著 出版日期: 2013-10-30

Title: Prediction and analysis on methylation of human Sox10 gene

promoter

作者: 李文英; 余鸿; 陈兴书; 肖岚

第三军医大学基础医学部组织学与胚胎学教研室,重庆市神经科学研究所; 泸州医学院

基础医学院组织学与胚胎学教研室; 自贡市第三人民医院病理科

Author(s): Li Wenying; Yu Hong; Chen Xingshu; Xiao Lan

Department of Histology and Embryology, Chongqing Institute of Neuroscience, College of Basic Medical Sciences, Third Military Medical University, Chongqing, 400038, Department of Histology and Embryology, Luzhou Medical College, Lu zhou, Sichuan Province, 646000, Department of Pathology, Zigong Third Peoples'

Hospital, Zigong, Sichuan Province, 643020, China

关键词: 人Sox10基因启动子区甲基化; 生物信息学分析; MSP; BSP; 人多形性胶质母细胞瘤

Keywords: methylation of human Sox10 gene promoter; bioinformatics analysis; methylation

specific PCR; bisulfite sequencing PCR; glioblastoma multiforme

分类号: R394-33, R394.3

文献标志码: A

Abstract:

摘要: 目的 运用生物信息学方法预测人Sox10基因启动子区甲基化情况并进行实验验

证。 方法 从GenBank获取人Sox10 基因序列,利用 Methyprimer 11.0 软件、Li lab、CpG Island Searcher预测其启动子区CpG岛。进一步运用甲基化特异性PCR(methylation specific PCR,MSP)和重亚硫酸盐测序(bisulfite sequencing PCR,BSP)方法检测人Sox10基因启动子区CpG岛在多形性胶质母细胞瘤和瘤周组织中的甲基化情况。 结果 经过生物信息学分析发现,人Sox10基因启动子区存在2个CpG岛,分别为165(1 241~1 405)bp和105(1 478~1 582)bp。针对这两个CpG岛设计引物行MSP和BSP实验,研究发现,在人多形性胶质母细胞瘤和瘤周组织中Sox10基因启动子区CpG岛均出现部分甲基化,其中在多形性胶质母细胞瘤中的甲基化率为90.5%,在瘤周组织中的甲基化率为28.5%。 结论 本研究证实了人Sox10基因启动子区CpG

岛在多形性胶质母细胞瘤中出现高甲基化,提示其表达下调可能受甲基化调节。

Objective To investigate the methylation of human Sox10 gene promoter by bioinformatics and exprimental vertification. Methods Human Sox10 gene sequence was obtained from GenBank. CpG island methylation in human Sox10

工具/TOOLS

引用本文的文章/References

下载 PDF/Download PDF(1106KB)

立即打印本文/Print Now

查看/发表评论/Comments

导出

统计/STATISTICS

摘要浏览/Viewed 113

全文下载/Downloads 67

评论/Comments

RSS XML

gene promoter was predicted by Methyprimer software 11.0, Li lab and CpG Island Searcher. Then CpG island methylation status of Sox10 gene promoter was detected in glioblastoma multiforme and adjacent noncancerous tissues by methylation specific PCR (MSP) and bisulfite sequencing PCR (BSP).

Results Two CpG islands, 165 bp (1 241-1 405) and 105 bp (1 478-1 582), were found in human Sox10 gene promoter according to bioinformatics analysis. CpG islands of human Sox10 gene promoter were partially methylated in the adjacent noncancerous tissues and glioblastoma multiforme, indicated by MSP results. BSP results showed that the percentage of methylation was 90.5% in glioblastoma multiform and 28.5% in the adjacent noncancerous tissues. Conclusion CpG islands of human Sox10 gene promoter are hypermethylated in glioblastoma multiforme. The down-regulation of human Sox10 gene might be mediated by the methylation as compared with adjacent noncancerous tissues.

参考文献/REFERENCES:

李文英, 余鸿, 陈兴书, 等. 人Sox10基因启动子区高甲基化的预测和验证[J].第三军医大学学报,2013,35(20):2168-2171. 相似文献/REFERENCES:

[1]李继元,李洪,杨天德.人低温离体灌注心脏心肌缺血损伤早期蛋白组学研究[J].第三军医大学学报,2011,33(03):225. Li Jiyuan,Li Hong,Yang Tiande.Proteomics in early myocardial ischemic injury of isolated human heart during hypothermia-perfusion[J].J Third Mil Med Univ,2011,33(20):225.