

## Runx3 基因甲基化与胃癌发生和转移的关系

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### Relationship between Hypermethylation of Runx3 Gene in Promoter Region and Cogeneration, Metastasis of Gastric Carcinoma

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**摘要** 目的 探讨Runx3基因启动子甲基化与胃癌发生发展过程的关系。方法 采用逆转录-聚合酶链反应(RT-PCR)检测80例胃癌组织及肿瘤周围粘膜组织中Runx3mRNA的表达,同时用甲基化特异性PCR(MSP)方法检测Runx3基因启动子甲基化情况。结果 80例胃癌组织标本中Runx3基因的表达( $0.5971 \pm 0.1013$ )较肿瘤周围组织中表达明显下调( $0.8297 \pm 0.2912$ ),差异有统计学意义( $P < 0.05$ )。正常粘膜组织中未发现Runx3基因启动子的甲基化,80例胃癌组织中有43例检测到Runx3基因启动子的甲基化,胃癌组织Runx3基因启动子甲基化率显著增高( $P < 0.05$ )。胃癌标本中Runx3 mRNA的表达与其病理临床特征密切相关,在低分化和有淋巴结转移胃癌组织标本中Runx3mRNA的表达显著下调( $P < 0.05$ )。结论 Runx3基因启动子甲基化是导致Runx3基因失活的主要原因之一并且与胃癌的发生、发展密切相关。

**关键词:** 胃癌 Runx3 基因 RT-PCR DNA 甲基化

**Abstract:** Objective To investigate the relationship of methylation of human runt-related transcription factor 3 (Runx3) gene on metastasis and oncogenesis of gastric carcinoma. Methods Using RT-PCR technique, specimens from 80 gastric cancer patients (tumor tissues, adjacent tissues) were detected for their expression of the Runx3 gene. Meanwhile, Methylation-specific PCR was used to detect methylation of Runx3 promoter region. Results The expression of Runx3 gene mRNA detected in gastric carcinoma ( $0.5971 \pm 0.1013$ ) was lower than that in adjacent tissues samples ( $0.8297 \pm 0.2912$ ) ( $t = 6.7480, P < 0.05$ ). No methylation of Runx3 promoter was found in adjacent tissues samples. But it was found in 43 cases in 80 gastric carcinoma specimens. The rate of methylation of Runx3 promoter in gastric carcinoma was higher than that in adjacent tissues ( $P < 0.05$ ). The Runx3 mRNA were down-regulated in lymphnode metastasis or poorly differentiated groups, but the Runx3 promoter methylation were detected in those groups markedly. A significant difference was noted between two groups ( $P < 0.05$ ). Conclusion Hypermethylation was one of reasons which induced Runx3 gene inactivation in human gastric carcinoma. Methylation of Runx3 promoter maybe correlated to on cogeneration, metastasis of gastric carcinoma.

**Key words:** Gastric carcinoma Runx3 gene RT-PCR DNA methylation

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