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DNA methylation of microRNA genes in gastric carcinoma and its clinicopathological association

Ho Gun Kim
Chonnam National University, South Korea

Background & Aim: To explore the role of epigenetic mechanisms in the down-regulation of miRNA genes, we examined the presence of DNA methylation-associated silencing of miRNAs in gastric carcinoma and observed that aberrant methylation of these miRNAs is associated with expression of target gene products.

Materials & Methods: The extent of promoter methylation of *has-miR-9-1, has-miR-9-3, has-miR-129-2 and has-miR-137* was assessed using methylation-specific polymerase chain reaction in 100 gastric carcinoma tissues and corresponding non-tumor tissues. The potential target gene products of miRNAs were studied by immunohistochemistry and the relationship between methylation profiles of miRNAs.

Results: Methylation of the *has-miR-9-3* and *has-miR-137* CpG island was frequently observed in tumor tissues (89% and 86%, respectively) and non-tumor tissues in 100 gastric carcinoma patients (70% and 78%). However, methylation level of the *has-miR-129-2* did not shown significant difference in tumor tissues (97%) compared with non-tumor tissues (90%) and normal gastric tissues (90%). Expression of NF-κB and SOX4 protein, which are *has-miR-9 and has-miR-129-2* potential target respectively, were inversely correlated with methylation level of miRNAs.

Conclusion: The results suggest that specific miRNAs methylation in gastric carcinoma could be an important molecular mechanism causing loss of control of its target and it may be correlated with the high transcriptional activity of target gene. Epigenetic silencing of some miRNAs may involve in the early stage of gastric carcinogenesis.

Biography

Ho Gun Kim is a Professor in the Department of Surgery and Pathology at Chonnam National University Medical School, Gwangju, South Korea.

dockim@jnu.ac.kr

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