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Meta-analysis of promoter methylation in eight tumor-suppressor genes and its association with the risk of thyroid cancer

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Promoter methylation in a number of Tumor-Suppressor Genes (TSGs) can play crucial roles in the development of thyroid carcinogenesis. The focus of the current meta-analysis was to determine the impact of promoter methylation of eight selected candidate TSGs on thyroid cancer and to identify the most important molecules in this carcinogenesis pathway. A comprehensive search was performed using Pub Med, Scopus and ISI Web of Knowledge databases and eligible studies were included. The methodological quality of the included studies was evaluated according to the Newcastle Ottawa scale table and pooled Odds Ratios (ORs); 95% Confidence Intervals (CIs) were used to estimate the strength of the associations with Stata 12.0 software. Egger's and Begg's tests were applied to detect publication bias, in addition to the Metatrim method. A total of 55 articles were selected and 135 genes with altered promoter methylation were found. Finally, we included eight TSGs that were found in more than four studies (RASSF1, TSHR, PTEN, SLC5A, DAPK, P16, RARβ2 and CDH1). The order of the pooled ORs for these eight TSGs from more to less significant was CDH1 (OR=6.73), SLC5 (OR=6.15), RASSF1 (OR=4.16), PTEN (OR=3.61), DAPK (OR=3.51), P16 (OR=3.31), TSHR (OR=2.93) and RARβ2 (OR=1.50). Analyses of publication bias and sensitivity confirmed that there was very little bias. Thus, our findings showed that CDH1 and SCL5A8 genes were associated with the risk of thyroid tumor genesis.

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