Association between \textit{RASSF1A} promoter methylation and renal cell cancer susceptibility: a meta-analysis

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ABSTRACT. Epigenetic inactivation of Ras-associated domain family 1A (\textit{RASSF1A}) by hyper-methylation of its promoter region has been identified in various cancers. However, the role of \textit{RASSF1A} in renal cancer has neither been thoroughly investigated nor reviewed. In this study, we reviewed and performed a meta-analysis of 13 published studies reporting correlations between methylation frequency of the \textit{RASSF1A} promoter region and renal cancer risk. The odds ratios (ORs) of eligible studies and their corresponding 95\% confidence intervals (95\%CIs) were used to correlate \textit{RASSF1A} promoter methylation with renal cell cancer risk and clinical or pathological variables, respectively.
RASSF1A promoter methylation was significantly associated with the risk of renal cell cancer (OR = 19.35, 95%CI = 9.57-39.13). RASSF1A promoter methylation was significantly associated with pathological tumor grade (OR = 3.32, 95%CI = 1.55-7.12), and a possible positive correlation between RASSF1A promoter methylation status and tumor stage was noted (OR = 1.89, 95%CI = 1.00-3.56, P = 0.051). Overall, this meta-analysis demonstrated that RASSF1A promoter methylation is significantly associated with increased risk of renal cell cancer. RASSF1A promoter methylation frequency was positively correlated with pathological tumor grade, but not the clinical stage. This study showed that RASSF1A promoter methylation could be utilized to predict renal cell cancer prognosis.

Key words: RASSF1A; Promoter; Methylation; Renal cell cancer; Meta-analysis