Association between genetic variants in DICER1 and cancer risk: An updated meta-analysis

Abstract

Dysfunctions in mechanisms of gene regulation based on RNA interference are recognized as a common feature of the molecular basis of cancer pathogenesis. Therefore, as one of the crucial components of the machinery involved in the biogenesis of both siRNAs and microRNA molecules, DICER was recognized as one of the candidates for the research in the field of carcinogenesis. Due to their potential functional properties, several genetic variants located within DICER1 gene were analyzed for their possible association with the susceptibility to cancer through case-control studies. In order to elucidate their effect on the overall cancer risk, we conducted an updated meta-analysis of all eligible association studies. The publications were selected based on PubMed database search, while OpenMeta-analyst and MetaGenyo software were used for quantitative data synthesis. Statistically significant results were found for the association of rs1057035 with the overall cancer risk under multiple genetic models ($P_{CT\ vs.\ TT} < 0.001$, $OR_{CT\ vs.\ TT} = 0.870$, 95% CI = 0.812-0.933; $P_{allelic} = 0.009$, $OR_{allelic} = 0.896$, 95% CI = 0.825-0.973; $P_{dom} < 0.001$, $OR_{dom} = 0.874$, 95% CI = 0.817-0.934; $P_{overdom} = 0.004$, $OR_{overdom} = 0.858$, 95% CI = 0.773-0.953). Other selected genetic variants within DICER1, rs13078, rs1209904 and rs3742330, did not show the association with the overall susceptibility to malignant diseases. We conclude that rs1057035 may represent a potential biomarker associated with the risk of developing cancer, which requires a confirmation in a larger set of studies.