

Decreased risk of developing lung cancer in subjects carrying the *CLPTM1L* rs401681 (G>A) polymorphism: evidence from a meta-analysis

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ABSTRACT. A genome-wide association study revealed that a single nucleotide polymorphism, *CLPTM1L* - rs401681 (G>A), located at the 5p15.33 locus was significantly associated with increased risk of various cancers; however, its association with lung cancer is currently inconclusive. In order to explore the relationship between this polymorphism and lung cancer risk more precisely, we performed a meta-analysis of eight eligible studies involving 9935 cases and 11,261 controls. The pooled odds ratio (OR) and the 95% confidence interval (CI) were calculated using a fixed- or random-effect models. Results indicated that this polymorphism was significantly associated with lung cancer risk in all genetic models (*GA* vs *GG*: OR = 0.88, 95%CI = 0.83-0.94; *AA* vs *GG*: OR = 0.81, 95%CI = 0.70-0.93; *AA/GA* vs *GG*: OR = 0.86, 95%CI = 0.81-0.91; *AA* vs *GA/GG*:

OR = 0.86, 95%CI = 0.76-0.99). An analysis stratified by ethnicity and source of controls revealed a significantly decreased risk among European groups and population-based studies in all genetic models, and among Asian populations only in the dominant model comparison. Additionally, in a subgroup analysis by histology type, the *CLPTMIL* rs401681 polymorphism was found to significantly decrease the risks of both adenocarcinoma and squamous cell carcinoma of the lung in all genetic models. In conclusion, our study indicated that the *CLPTMIL* - rs401681 (G>A) polymorphism was significantly associated with decreased lung cancer risk, especially among European populations. Due to some minor limitations, our findings should be confirmed in further studies.

Key words: Genetic polymorphism; *TERT-CLPTMIL*; rs401681 (G>A); Lung cancer; Meta-analysis