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Genetic variations in the IGF-IGFR-IGFBP axis confer susceptibility to lung and esophageal cancer

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ABSTRACT. Recent evidence suggests that genetic variations in the insulin-like growth factor (IGF)-IGF receptor (IGFR)-IGF binding proteins (IGFBP) axis may impact an individual's susceptibility to lung and esophageal cancer, but individually published results are inconclusive. Our meta-analysis aimed at providing a more precise estimation of these associations. An extensive literature search was conducted for appropriate articles published before May 15th, 2013. This meta-analysis was performed using the STATA 12.0 software. The crude odds ratios (ORs) with 95% confidence intervals (CIs) were calculated for each study and then pooled using a random effect model. Twelve case-control studies were included with a total of 2686 lung cancer patients, 771 esophageal cancer patients, and 5918 healthy controls. Our meta-analysis indicated that genetic variations in the IGF-IGFR-IGFBP axis may be associated with increased risk of lung and esophageal cancer, especially among Asian populations. Further subgroup analysis by gene type indicated that common polymorphisms in the IGF1/2, IGF-1R, and IGFBP-3/5 genes may be the main determinants for lung cancer risk, while IGF-1, IGF-1R, and IGFBP-1 genetic polymorphisms may increase the risk of esophageal

cancer. The current meta-analysis suggests that genetic variations in the IGF-IGFR-IGFBP axis confer susceptibility to lung and esophageal cancer, especially among Asian populations. Common polymorphisms in the IGF-IGFR-IGFBP axis may serve as useful biomarkers for predicting the risk of lung and esophageal cancer.

Key words: Lung cancer; Esophageal cancer; Polymorphism; Insulin-like growth factor; Meta-analysis

