



***AGER* genetic polymorphisms increase risks of breast and lung cancers**

N.C. Yin¹, X.P. Lang¹, X.D. Wang¹ and W. Liu²

¹Department of Thoracic Surgery, The First Affiliated Hospital of Liaoning Medical University, Jinzhou, China

²Department of Medical Oncology, The First Affiliated Hospital of Liaoning Medical University, Jinzhou, China

Corresponding author: W. Liu
E-mail: liuwei_lw1984@yeah.net

Genet. Mol. Res. 14 (4): 17776-17787 (2015)

Received September 14, 2015

Accepted November 15, 2015

Published December 22, 2015

DOI <http://dx.doi.org/10.4238/2015.December.22.2>

ABSTRACT. We evaluated the associations between three common polymorphisms in the *AGER* gene and the risks of breast (BC) and lung (LC) cancer using meta-analysis. A systematic electronic search of the literature was conducted to identify all potential correlation studies in Embase, Web of Science, Cochrane Library, CINAHL, PubMed, CISCOR, China BioMedicine (CBM), and China National Knowledge Infrastructure (CNKI) databases. Five case-control studies that investigated the correlation of *AGER* gene polymorphisms with BC and LC were included in the meta-analysis, representing 4337 subjects. An increased frequency of the *AGER* rs1800625 T>C polymorphism was observed in patients with either BC or LC. We found that the frequencies of *AGER* rs1800624 T>A and rs2070600 G>A variants were positively related to the risks of BC and LC under allelic models, but that these relationships were not detected under dominant models. Disease-stratified results under allelic models demonstrated that the frequencies of the *AGER* rs1800625 T>C and rs2070600 G>A polymorphisms were positively correlated with the susceptibility to LC, while the same correlations were not found in BC. Further subgroup analysis

by genotyping method indicated that the rs1800624 T>A variant was associated with increased risks of BC and LC under a dominant model in both non-polymerase chain reaction-restriction fragment length polymorphism (non-PCR-RFLP) and PCR-RFLP subgroups. In conclusion, these data indicated that common polymorphisms in the *AGER* gene might increase the risks of BC and LC.

Key words: *AGER*; Breast cancer; Lung cancer; Polymorphisms; Meta-analysis