Association between the 8q24 rs6983267 T/G polymorphism and prostate cancer risk: a meta-analysis


1Clinical Laboratory, East Suzhou Municipal Hospital, Nanjing Medical University, Gusu District, Suzhou, Jiangsu Province, China
2Department of Radiotherapy, East Suzhou Municipal Hospital, Nanjing Medical University, Gusu District, Suzhou, Jiangsu Province, China

*These authors contributed equally to this study.

Corresponding author: H.S. Zhu
E-mail: xintaozhangxintao@163.com

Received August 17, 2015
Accepted October 2, 2015
Published December 29, 2015
DOI http://dx.doi.org/10.4238/2015.December.29.43

ABSTRACT. Recent studies have indicated that single nucleotide polymorphisms (SNPs) within the 8q24 region may be a risk factor for prostate cancer (PCa). Here, we performed a meta-analysis to evaluate the association between the 8q24 rs6983267 T/G polymorphism and PCa risk. A systematic literature search was carried out in multiple electronic databases independently by two investigators. Pooled odds ratios (ORs) and 95% confidence intervals for 8q24 rs6983267 T/G and PCa were calculated using a fixed-effect model (the Mantel-Haenszel method). In total, 24 case-control studies from 19 articles were included in our meta-analysis. Our analysis indicated that there is a significant PCa risk associated with the rs6983267 polymorphism in a dominant model (GG vs GT+TT, pooled OR = 1.298, P < 0.001); recessive model (GG+GT vs TT, pooled OR = 1.302, P < 0.001); and homozygote comparison (GG vs TT, pooled OR = 1.494, P < 0.001). Similarly, in a subgroup analysis of European and Asian descent, our results revealed that there are associations between
rs6983267 T/G polymorphism and PCa susceptibility with the dominant model (GG vs GT+TT), recessive model (GG+GT vs TT), and homozygote comparison (GG vs TT). To investigate the association between rs6983267 and risk of PCa under different clinical conditions, further analyses were conducted regarding different clinical characteristics including the Gleason score, tumor stage, and PSA level to provide a more comprehensive view of PCa risk and this SNP. Publication bias was assessed using the Begg test and the Egger test, and none was detected.

Key words: Prostate cancer; Meta-analysis; Polymorphism