Association between MIR499A rs3746444 polymorphism and breast cancer susceptibility: a meta-analysis

ABSTRACT

Numerous studies have investigated the association of MIR499A rs3746444 polymorphism with breast cancer susceptibility, but the results have been inconsistent. In this work, we performed a meta-analysis to obtain a more reliable estimate of the association between the polymorphism and susceptibility to breast cancer. A comprehensive literature search was conducted on PubMed, Scopus, Web of Science (WoS), China National Knowledge Infrastructure (CNKI), VIP and Wanfang databases up to January 2020. A total of 14 studies involving 6,797 cases and 8,534 controls were included for analysis under five genetic models: homozygous (GG vs. AA), heterozygous (AG vs. AA), dominant (AG + GG vs. AA), recessive (GG vs. AA + AG) and allele (G vs. A). A statistically significant association was observed between the polymorphism and an increased breast cancer susceptibility under all genetic models (homozygous, OR = 1.33, 95% CI = 1.03–1.71, P = 0.03; heterozygous, OR = 1.08, 95% CI = 1.00–1.16, P = 0.04; dominant, OR = 1.15, 95% CI = 1.02–1.30; P = 0.03; recessive, OR = 1.35, 95% CI = 1.06–1.72, P = 0.01; allele, OR = 1.12, 95% CI = 1.00–1.26, P = 0.04). Subgroup analysis based on ethnicity suggested that significant association was present only among Asians, but not Caucasians. In conclusion, MIR499A rs3746444 polymorphism was significantly associated with breast cancer susceptibility among Asians, suggesting its potential use as a genetic risk marker in this population.