Association of a let-7 *KRAS* rs712 polymorphism with the risk of breast cancer

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ABSTRACT. Breast cancer (BC) is a common malignancy affecting women, with increasing incidences of this disease in China every year. Recent studies have extensively investigated a single nucleotide polymorphism in the let-7 miRNA binding site of the 3'-untranslated region of *KRAS* mRNA. The aim of this study was to determine the genotype frequency of the *KRAS* rs712 polymorphism, and evaluate its effect on BC risk. This hospital-based case-control study comprised 228 patients with histologically confirmed BC and 251 healthy controls. The let-7a *KRAS* rs712 polymorphism was analyzed by polymerase chain reaction-restriction fragment length polymorphism. We observed no statistically significant association between BC risk and the let-7a *KRAS* rs712 polymorphism (GT *vs* GG, OR = 0.98, 95%CI = 0.66-1.46; TT *vs* GG, OR = 0.78, 95%CI =

0.28-2.21). However, the rs712 polymorphism was significantly associated with the N status of BC patients (GG *vs* GT/TT, OR = 0.52, 95%CI = 0.30-0.92; G allele *vs* T allele, OR = 0.60, 95%CI = 0.37-0.97). We found no association between the let-7 rs712 polymorphism and BC risk. However, the let-7 rs712 G/T polymorphism was discovered to play a potential role in BC tumor metastasis; therefore, it may be employed as a new biomarker or therapy targeted towards resistant tumor metastasis.

Key words: let-7; *KRAS*; Polymorphism; Breast cancer

