Letters to the Editor

AURKA and Breast Cancer in *BRCA1/2* Mutation Carriers

To the Editors: A recent article reported, ''the *F31I* polymorphism in *AURKA* is not associated with a modified risk of breast cancer found in 3,884 breast cancer *BRCA1* and *BRCA2* carrier cases compared to unaffected *BRCA1/2* mutation carriers'' (1). This agrees with our previously published results where no association of increased breast cancer risk was found in 107 *BRCA1* and *BRCA2* breast cancer carrier cases compared with 653 unaffected wild-type *BRCA1/2* controls (2), which Couch et al. did not cite. We also found strong association with homozygous *31I* in 652 sporadic breast cancer cases compared with unaffected controls. In addition, we compared the *F31I* polymorphism in the 107 *BRCA1/2*-mutated breast cancer cases with 40 unaffected *BRCA2* mutation carriers. We found that the unaffected *BRCA2* mutation carriers had clearly higher *31I* allele frequency of 27.5% compared with 21.0% in *BRCA1/2* breast cancer cases, which indicates that the 31I isoform might be protecting against breast tumor development in *BRCA2* mutation carriers. Our results, and those of Couch et al., about *BRCA1/2* mutation carrier cases agree with recent studies on familial or high-risk breast cancer cases that did not find association between the *F31I* polymorphism and breast cancer risk. On the other hand, increased sporadic breast cancer risk is associated with the *F31I* polymorphism as discussed before (2). It is therefore clearly important when looking for low-penetrance cancer susceptibility genes to acknowledge the influence of major cancer genes, such as *BRCA1* and *BRCA2*.

Couch et al. (1) state both in abstract and introduction, ''amplification of *AURKA* has been detected at higher frequency in tumors from *BRCA1* and *BRCA2* mutation carriers than in sporadic breast tumors, suggesting that overexpression of AURKA and inactivation of BRCA1 and BRCA2 cooperate during tumor development and progression.'' No citations were given for this statement and, to our knowledge, there are no published data showing association between *AURKA* amplification and BRCA1 inactivation. On the other hand, we recently reported a strong association between *AURKA* (*Aurora-A*) amplification and *BRCA2* mutation in breast tumors (3). In this study, we analyzed 61 breast tumor tissue sections for *AURKA* amplification by fluorescence *in situ* hybridization, where 20 had *BRCA2* mutation. Other studies based on comparative genomic hybridization of *BRCA1/2*-mutated breast tumors agree with our results where chromosome region 20q13, the location of the *AURKA* gene, is more often amplified in *BRCA2*-mutated tumors compared with sporadic and *BRCA1*-mutated breast tumors (4-6).

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