Genetic variation in the major mitotic checkpoint genes does not affect familial breast cancer risk.

Abstract:
Aneuploidy, an aberrant number of chromosomes, is a very common characteristic of many types of cancers, including tumors of the breast. There is increasing evidence that defects in the spindle assembly checkpoint, which controls correct chromosome segregation between two daughter cells, might contribute to tumorigenesis. In the present study we examined the effect of promoter and coding single nucleotide polymorphisms (SNPs) in six major spindle checkpoint genes (BUB1B, BUB3, CENPE, MAD2L1, MAD2L2, TTK) on familial breast cancer (BC) risk. A case-control study was carried out with a total of nine SNPs using 441 German, familial BC cases and 552 controls matched by age, ethnicity and geographical region. Neither the individual SNPs in the studied genes nor the haplotypes in the BUB1B, CENPE and TTK genes caused any significant effect on the risk of BC. We used the multifactor-dimensionality reduction method in order to identify gene-gene interactions among the six mitotic checkpoint genes, but no association was detected. Therefore, our results indicate that the investigated SNPs in the mitotic checkpoint genes do not affect the risk of familial BC.