

PIK3C Agene mutations in breast carcinoma in Malaysian patients

ABSTRACT

Somatic mutations of phosphoinositide-3-kinase, catalytic, α ; PIK3CAgene have been reported in several types of human cancers. The majority of the PIK3CAmutations map to the three “hot spots” — E542 K and E545 K in the helical (exon 9) and H1047R in the kinase (exon 20) domains of the p110 α . These hot spot mutations lead to a gain of function in PI3 K signaling. We aimed to determine the frequency of PIK3CAmutations in the three most common Malaysian cancers. In this study, we assessed the genetic alterations in the PIK3CAgene in a series of 20 breastcarcinomas, 24 colorectal carcinomas, 27 nasopharyngeal carcinomas (NPC), and 5 NPC cell lines. We performed mutation analysis of the PIK3CAgene by genomic polymerase chain reaction (PCR) and followed by DNA direct sequencing in exons 9 and 20. No mutations were detected in any of the 24 colorectal and 27 NPC samples, but one hot spot mutation located at exon 20 was found in a NPC cell line, SUNE1. Interestingly, PIK3CA somatic mutations were present in 6/20 (30%) breast carcinomas. Two of the six mutations, H1047R, have been reported previously as a hot spot mutation. Only one out of three hot spot mutations were identified in breast tumor samples. The remaining four mutations were novel. Our data showed that a higher incidence rate of PIK3CAmutations was present in Malaysian breast cancers as compared to colorectal and nasopharyngeal tumor tissues. Our findings also indicate that PIK3CAmutations play a pivotal role in activation of the PI3 K signaling pathway in breast cancer, and specific inhibitors of PIK3CA could be useful for breast cancer treatment in Malaysia.