Abstract

Ras Genes in Human Breast Cancer

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The expression of ras mRNA levels in 27 human sporadic breast cancer specimens was examined, and compared to the corresponding adjacent normal tissue using the RT-PCR technique. Eighteen out of the 27 specimens (67%) exhibited two- to four-fold increased expression of ras mRNA levels, compared to corresponding normal tissue. The rates of augmented mRNA expression were similar among the three ras genes. A statistically significant correlation of overexpression of ras genes in specimens classified as Stage I disease was observed, compared to tumors in a more advanced stage (II or III). The incidence of codon 12 point mutations of the K-ras gene in fresh tissue samples was also assessed in 61 human sporadic breast cancer cases. Point mutations were detected in four (6.5%) out of the 61 cases examined; no correlation was found with any clinicopathological parameter. This is the first report to our knowledge of the differential expression of the ras family genes in breast carcinoma. Our findings indicate that the aberrant expression of ras genes may be an initial event in breast cancer oncogenesis and that K-ras point mutations are rarely involved in the development of mammary neoplasias.
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