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COMPARATIVE GENOMIC HYBRIDIZATION STUDIES ON CHOLANGIOCARCINOMA IN KOREA

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The elucidation of the genetic changes of cholangiocarcinoma is very important for understanding the molecular mechanism of carcinogenesis and progression of cholangiocarcinoma. In order to identify the gains or losses of the copy number of DNA sequence in cholangiocarcinoma, we used comparative genomic hybridization to study 33 cases of cholangiocarcinoma. The whole DNAs from each tumor tissue were labeled with different fluorochromes and then simultaneously hybridized to normal metaphase spread chromosomes. An image acquisition system was used to quantitate the signal intensities contributed by tumor and reference DNA along the entire length of each chromosome. Regions of amplification and deletion were demonstrated as quantitative alterations. The losses were prevalent on chromosome regions 11q, 16p, 17p, 17q, 19p, 19q ,20q, 21q and 22q, and the gains frequently occurred on 8q and 4q. The minimal regions of overlap for deletions were assigned to 1p36(TNFR2), 17p13.1(p53) and 9p13-22(p15, p16). Minimal overlapping amplified site was shown at 13q14.1-q34(RB1, RAP2A), 12q12-q14(CDK2, CDK4, MDM2), 1q21-24(PE1, TRK) and 4q21-q25(FGF5, EGF). Our study provides a comparative genomic hybridization-map of cholangiocarcinoma in detail that shows new genetic change as well as genetic divergence in this poorly understood group of cancer.