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Identification of a minimal overlapping amplified region at 19q13.1-q13.2 in four ovarian cancer cell lines. *T.C.M. Tang, J.S.T. Sham, X.Y. Guan.* Department of Clinical Oncology, The University of Hong Kong, Hong Kong, People's Republic of China.

High-level amplification of DNA sequence at 19q13.1-q13.2 in ovarian cancer has been frequently detected by using chromosome microdissection and comparative genomic hybridization (CGH). This strongly suggests that 19q13.1-q13.2 contains a putative oncogene(s) which plays an important role in the development or progression of ovarian cancer. In order to narrow down the amplified region at 19q13.1-q13.2 (about 39cM), four ovarian cancer cell lines which have been confirmed containing amplicon at 19q13.1-q13.2 were studied for identifying a minimal overlapping amplified region (MAR). Fluorescence in situ hybridization (FISH) with cosmid clones and Southern blot analysis with cDNA probes in average genomic distance at 1 cM (from D19S425 to D19S418) were performed. At least two MARs have been identified at 19q13.12 (about 200 kb) and 19q13.13 (about 1.2 Mb), respectively. Amplification and overexpression of several candidate oncogenes within the two amplicons have been studied by Southern and Northern blot analysis in four ovarian cancer cell lines. Further study of genes within these two amplicons may lead to the isolation of the oncogene(s) which is the biological target of amplification events in ovarian cancer.