



<b>Title</b>	<b>Characterization of a Homogeneously Stain Region (HSR) in a new establishment hepatocellular carcinoma cell line</b>
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**Characterization of a Homogeneously Stain Region (HSR) in a new Establishment Hepatocellular carcinoma Cell Line.** *L. Hu<sup>1</sup>, J-M. Wen<sup>2</sup>, J-F. Huang<sup>3</sup>, J.S.T. Sham<sup>1</sup>, W-S. Wang<sup>3</sup>, M. Zhang<sup>2</sup>, D. Xie<sup>1</sup>, W-F. Zeng<sup>2</sup>, X-Y. Guan<sup>1</sup>.* 1) Clinical Oncology, The University of Hong Kong, Hong Kong, China; 2) Department of Pathology, Sun Yat-sen University of Medical Sciences, Guangzho, China; 3) Department of Sugery, Sun Yat-sen University of Medical Sciences, Guangzhou, China.

Hepatocellular carcinoma (HCC) is one of the most common malignancies worldwide and has a very poor prognosis. Recently, we established a HCC cell line from a metastatic tumor. GTG-banding analysis showed that this cell line is hypertriploid (71-78 chromosomes) with a large marker chromosome containing an HSR. A high-copy-number amplification at 11q13 was detected using comparative genomic hybridization. In order to characterize the amplicon, the HSR region was further studied by chromosome microdissection. The dissected DNA was directly PCR-amplified and then mapped to 11q13 by fluorescence in situ hybridization (FISH). DNA copy number of cathepsin F, a tumor invasion and metastasis-related gene at 11q13, has been studied by Southern blot analysis and no DNA amplification was detected. It suggests that the amplified region at 11q13 may harbor another cancer metastasis-related gene. Isolation of amplified transcriptions within the amplicon using microdissected DNA to select cDNA from the HCC cell line by hybrid selection is under the progress.