Identify and characterize the cancer stemness role of maelstrom in hepatocellular carcinoma

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Hepatocellular carcinoma (HCC) is the fourth most common type of cancer in Hong Kong SAR and ranks as third leading mortality rate of cancer type worldwide. A wise strategy for better understanding the enrolled molecular mechanisms in HCC progression, which is needed to discover novel diagnostic markers and therapeutic targets. According to analysis our RNA sequence data of three paired HCC and non-tumor tissue samples, human maelstrom (MAEL) gene was chosen to study. Our preliminary data suggested that MAEL frequently upregulated in HCC patients, associated with tumor size, adjacent organ invasion, tumor recurrence and worse overall survival rate. Previous study demonstrated that MAEL promoted HCC cells proliferation and metastasis as well as upregulating several stemness related genes expression in mRNA level through AKT/GSK3β/Snail signaling pathways. However, the cancer stemness regulating ability and downstream targets of MAEL are still not well studied. Therefore, this project would focus on revealing novel targets of MAEL and further investigate the unique role in regulating cancer stemness. We analyzed MAEL expression and survival data in TCGA LIHC cohort, the results were consistent with our previous findings. We found that overexpress MAEL could not only promote the ability of HCC cell proliferation and mobility in vitro, but also increase the proportion of CD133+ cells, self-renew and sorafenib resistant ability. Moreover, knockout MAEL showed reverse results in PLC8024 cell line inhibited these functions. We applied next generation sequencing (NGS) technology to compare with vector group and MAEL transfected group cells which revealed that MAEL enrolled in extracellular matrix (ECM) receptor interaction pathways mediated cancer stem cell marker CD44 expression. This finding confirmed by Q-PCR, western blots and flow cytometry. Taken together, these data suggest MAEL could promote HCC cells proliferation, metastasis as well as increasing stem cell features

Biography

Shi Chaoran was graduated from Capital Medical University in 2015 as the major of Medical Laboratory Tests (MLT). After finished the internship in Beijing Anzhen Hospital, he joined in Department of Clinical Oncology, HKU as research in October 2015. In September 2017, he began his postgraduate study in the same laboratory with supervision of Prof. Dora Kwong and Prof. XY Guan. Their laboratory focuses on discovering novel cancer related genes and mir-RNAs in gastric cancer (GC), hepatocellular carcinomas (HCC), esophageal carcinomas (ESCC) and nasopharyngeal carcinoma (NPC). His current study is supported by Health and Medical Research Fund (No.04150826).

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