

# New evidence of lncRNA role in tumor progression and metastasis

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Intensive studies about non-coding RNAs (ncRNAs) in past decade show that ncRNAs are involved in many biological processes including development, differentiation and metabolism. ncRNAs are classified into small ncRNAs and long ncRNAs (lncRNAs). Small ncRNAs including siRNAs, piRNAs and miRNAs play roles in transcriptional gene silencing. Although the definition is crude, lncRNAs are defined as transcribed RNA molecules that are longer than 200 nucleotides (1,2). After the first recognition of lncRNA as having a transcriptional function in mouse by Okazaki *et al.*, there have been increasing numbers of articles regarding the roles and function of lncRNA in chromatin modification, transcriptional regulation post-transcriptional regulation, and human diseases (2-4). However much is still unknown regarding the functions of lncRNA in human diseases including cancer.

We now have two noteworthy findings in Yuan *et al.* regarding the roles of lncRNA in hepatocellular carcinoma (HCC). First they found that over-expression of an lncRNA termed MVIH (NCBI No.AK094613, Micro-Vascular Invasion in hepatocellular carcinoma) was associated with tumor progression, recurrence-free survival and overall survival of HCC patients. miRNAs, one of ncRNAs have been suggested in some reports to correlate with the outcome of HCC (5-7). Nevertheless this article would be the first report directly showing probability of lncRNA as a predictor for HCC patient survival.

Second the authors found that MVIH activated angiogenesis resulting in enhanced tumor growth and intrahepatic metastasis in mouse models. In additional experiments, they observed that MVIH inhibited secretion of phosphoglycerate 1 (PGK1) and that MVIH expression inversely correlated with the serum level of PKG1 in HCC patients. PKG1 has been reported to play a significant role

in angiogenesis (8,9). Although more studies providing detailed mechanisms are now required, this correlation between MVIH expression and PKG1 secretion provides a link for a molecular pathway between lncRNAs and tumor progression.

In spite of recent intensive investigation, lncRNAs are still mysterious in their functions and molecular consequences. So far only few results have been published regarding involvement of lncRNA in tumor progression and metastasis. Considering the large amount of lncRNA in organisms, we would not be surprised to find many more links to oncogenic expression to be unveiled in the future. We thus welcome the Yuan *et al.* report.

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