



E-002

## Spatial Transcriptomics For Perihilar Cholangiocarcinoma: What Happened In The Resection Margin?

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**Background** : Spatial heterogeneity of tumor microenvironment is a well-known cause of therapeutic resistance and poor prognosis in pancreaticobiliary cancers. Recently, new emerging technology, especially spatial transcriptomics platform, has emerged in cancer research to reveal complex tumor biology harboring in situ pathologic information of tumor microenvironment. This study is to aim the identification of inter and intra-heterogeneity of peri-hilar cholangiocarcinoma using the spatial transcriptomic technique with spatially different patient samples including primary tumor with lymph nodes.

**Methods** : This study enrolled two patient samples from surgical resection with peri-hilar cholangiocarcinoma with formalin-fixed paraffin-embedded (FFPE) blocks. Four areas of interest with a 5mm size were selected, and the RNA sample for tumor, stroma, and tumor-infiltrating lymphocytes (TILs) from each AOI was sequenced using the MERSCOPE spatial transcriptome platform (Vizgen Technologies, Inc., USA).

**Results** : Spatial transcriptome data were obtained from one primary tumor site and one metastatic lymph node tissue from two patients, respectively. In both patients, there were significant differences in the gene expression patterns of cancer cells between the primary tumor and the lymph node metastasis site. In particular, the peri-hilar primary site showed remarkable transcript expression patterns and immune cell infiltration patterns depending on the tumor site, and a characteristic submucosal infiltration trend was observed in the invasive front area close to the tumor resection margin. Around the resection margin, the distribution of CD8 T cells tended to be relatively small, and co-localization of cancer cells and fibroblasts was frequently observed.

**Conclusions** : Using the spatial transcriptomics for perihilar cholangiocarcinoma, not only tumor heterogeneity according to the location of the TME, which can be confirmed by pathological findings, but also the mutation pattern of the transcriptome itself was confirmed. It is necessary to confirm whether this pattern appears in more samples, and it is believed that deep consideration of tumor biology is necessary when considering surgical treatment for peri-hilar cholangiocarcinoma.

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