P15 Identification of novel long non-coding R.N.A based biomarkers in prostate cancer

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Introduction & Objectives: While many prostate cancers (PCa) are indolent, in around 20 % of all the PCas, an originally hormone-sensitive PCa will progress to a lethal and non-curable castration-resistant prostate cancer (CRPC). Thus, there is a critical need to identify biomarkers that can distinguish indolent from aggressive disease. Accumulating evidence suggests that long non-coding RNAs (lncRNAs) play a considerable role in tumorigenesis by being involved in key processes in cancer cells such as proliferation, invasion, and metastasis. In the current study, the aim is to identify lncRNAs with strong differential expression between localized primary PCa and metastatic PCa as novel biomarkers.

Materials & Methods: We performed a comprehensive gene expression analysis using RNA sequencing data consisting of 105 samples, collected from 34 PCa patients. The samples include 7 primary tumors and 98 metastatic PCa samples from the liver, adrenal, bone, and lymph node. Moreover, in our analysis, we needed normal samples from the liver, adrenal, bone, and lymph node to be used as a control for tissue-specific expression. We had already collected normal tissue of the liver and adrenal from our PCa patients, but for bone and lymph node, we used publicly available RNA-seq data. For differential expression analysis, DESeq2 Bioconductor package was used. Currently, we are studying transcription factors such as AR and ERG, that potentially regulate the differentially expressed lncRNAs, using previously published ChIP-seq data.

Results: Our results indicate that patient-to-patient variability is large in our lncRNA dataset, and the samples mainly clustered by patient IDs. We also identified tissue-specific expression patterns. After correcting for the effect of the patients and tissue types, we found a total of 61 lncRNAs that were differentially expressed in metastatic lesions compared to the primary PCa tumors. Of the 61 lncRNAs, 14 lncRNAs were up-regulated and 47 lncRNAs were down-regulated in metastatic PCa.

Conclusions: Taken together, we identified prostate cancer metastasis-specific lncRNAs that may play a role in the progression of PCa. Further experiments will be performed to evaluate the potential value of the candidate lncRNAs as PCa biomarkers.