Long non-coding RNAs (lncRNAs) have received increased research interest owing to their participation via distinct mechanisms in the biological processes of Clinically Non-Functioning Pituitary Neuroendocrine Tumors. However, changes in the expression of lncRNAs in gonadotropin secreting pituitary neuroendocrine tumor, which is the most common nonfunctional pituitary neuroendocrine tumors, have not yet been reported. In this study, we performed a genome-wide analysis of lncRNAs and mRNAs obtained from gonadotrophin adenoma patients' samples and normal pituitary tissues using RNA-seq. The differentially expressed lncRNAs and mRNAs were identified using fold-change filtering. We identified 839 lncRNAs and 1015 mRNAs as differentially expressed. Gene Ontology analysis indicated that the biological functions of differentially expressed mRNAs were related to transcription regulator activity and basic metabolic processes. Ingenuity Pathway Analysis was performed to identify 64 canonical pathways that were significantly enriched in the tumor samples. Furthermore, to investigate the potential regulatory roles of the differentially expressed lncRNAs on the mRNAs, we constructed general co-expression networks for 100 coding and 577 non-coding genes that showed significantly correlated expression patterns in tumor cohort. In particular, we built a special sub-network of co-expression involving 186 lncRNAs interacting with 15 key coding genes of the mTOR pathway, which might promote the pathogenesis of gonadotrophin tumor. This is the first study to explore the patterns of genome-wide lncRNAs expression and co-expression with mRNAs, which might contribute to the molecular pathogenesis of gonadotrophin adenoma [1].

---

[1] Li J, Li C, Wang J, Song G, Zhao Z, Wang H, Wang W, Li H, Li Z, Miao Y, Li G, Zhang Y. Genome-wide analysis of differentially expressed lncRNAs and mRNAs in primary gonadotrophin adenomas by RNA-seq. Oncotarget. 2016 Dec 15. doi: 10.18632/oncotarget.13948. [Epub ahead of print] PubMed PMID: 27992366.