Long Non-coding RNA Signatures and Their Role in the Progression of Childhood T-cell Acute Lymphoblastic Leukemia

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Introduction

• Long non-coding RNAs are RNAs longer than 200 bps that do not encode any proteins and are able to alter gene expression.
• The expression levels of particular lncRNAs are correlated with the prognosis of pediatric patients with acute lymphoblastic leukaemia.

Aim of Study

• The aim of this study was to determine the potential roles of lncRNAs in the pathogenesis of childhood T-ALL.

Methods

• We used NGS approach to analyze the transcriptome of 25 childhood T-ALL in comparison with three healthy controls.
• FASTQ files were aligned with STAR, raw counts were obtained using HTSeq and differential expression analysis was performed using DESeq2.
• The result of RNA seq were validated using qPCR in a cohort of 50 other T-ALL patients.
• Functional enrichment analysis was performed using GO, Enrichr, gProfiler and lncRNA-mRNA co-relation was performed using R

Results

• A total of 672 differentially expressed lncRNAs were identified.
• The top 10 upregulated lncRNAs were selected and further assessed by RT-qPCR in vitro in the same samples and a different cohort.
• We found that lncRNAs LINC01221, LINC00977, RP11-472G21.2 and CTD-2291D10.4 were highly overexpressed (>10 fold) in the patients while PCAT18, CRNDE, and RP11-620J15.3 showed mild overexpression (2 to 5 fold increase).
• GSEA showed these lncRNAs are involved in regulating various genes involved in T-ALL progression

Conclusion

• Our work identified a lncRNA signature discriminating paediatric T-ALL from healthy subjects
• This study provides the keystone to future clinical studies determining the theragnostic value of the characterised long non coding transcriptome panorama in a clinical setting for childhood patient management.