The role and mechanism study of lncRNAs involved in glucocorticoid resistance in paediatric acute lymphoblastic leukemia

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Introduction

Glucocorticoids (GCs) are key components in the treatment of childhood acute lymphoblastic leukemia (ALL) and most ALL therapeutic failures can be explained by cellular resistance to GCs. However, the mechanisms of GC resistance are poorly understood. LncRNAs are involved in normal hematopoiesis and leukemia development, whereas the roles of lncRNAs in GC resistance are still unknown. Our goal was to investigate the role of lncRNAs involved in glucocorticoid resistance in paediatric acute lymphoblastic leukemia, and also elucidate the mechanism preliminarily.

Materials and Methods

In this study, lncRNA microarray was performed on GC-resistant cell line CEM-C1 and GC-sensitive cell line CEM-C7 to screen the differential expression of lncRNAs. Five up-regulated and five down-regulated lncRNAs were randomly chosen for validation by Real-time PCR. GO-Pathway analysis was done to investigate potential signaling pathways regulated by the lncRNAs.

Results

In this study, lncRNA microarray was performed on GC-resistant cell line CEM-C1 and GC-sensitive cell line CEM-C7 to screen the differential expression of lncRNAs. Five up-regulated and five down-regulated lncRNAs were randomly chosen for validation by Real-time PCR. GO-Pathway analysis was done to investigate potential signaling pathways regulated by the lncRNAs.

Conclusions

Our study showed that lncRNA expression profile was altered in GC-sensitive and GC-resistant cells, indicating that differentially expressed lncRNAs may play important functional roles in GC resistance of ALL. And these lncRNAs may be involved in GC resistance by regulating signaling pathways associated with cell proliferation, differentiation and apoptosis. Our study provides new biological foundations for further mechanism study in GC resistance and also provides a new strategy for therapeutic development of ALL.