Analyzing Differential Expression of p53, BCL2, and BAX in T-Cell Acute Lymphoblastic Leukemia

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Introduction

Acute Lymphoblastic Leukemia is a severe blood disease and it is one of the most common type of childhood leukemia. T-cell Acute Lymphoblastic Leukemia occurs in the malignant transformation of T-cells in the thymus and approximately 15-18% of childhood Acute Lymphoblastic Leukemia patients belong to T-Cell Acute Lymphoblastic Leukemia. Several genes which are involved in T-cell development have been demonstrated to have important roles in leukemogenesis. Here, we studied 30 T-ALL childhood patients for their expression levels of *p53*, *BAX*, and *BCL2* by quantitative real time PCR. *p53*, is a tumor suppressor gene, and *BAX* are pro-apoptotic genes while *BCL2* inhibits apoptosis. *p53* was found to be significantly upregulated in patient samples when compared with control thymocytes. Upregulation of *p53* might lead the cells to malignant transformation.

Materials and Methods

Differential gene expressions were detecting by quantitative real time PCR.

- T-ALL Patient Samples (n=30)
- Healthy Thymocytes and Thymus
- RNA Isolation
- cDNA Synthesis
- Quantitative Real Time PCR (qRT-PCR) (Figure 1)

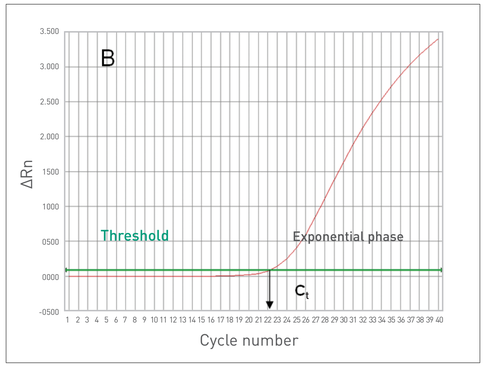
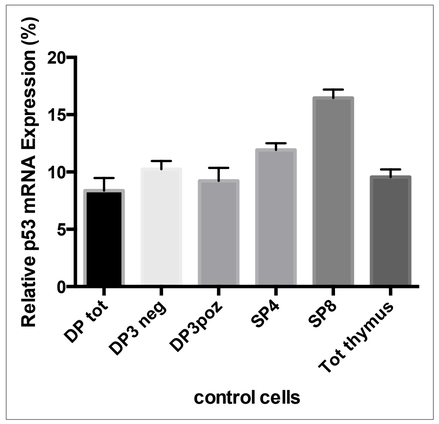
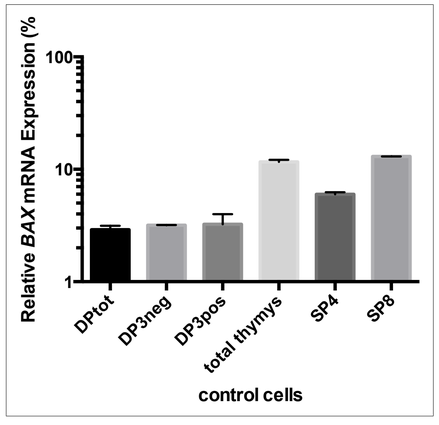


Figure 1: Ct (threshold cycle) for qRT-PCR

Relative quantification by $\triangle Ctmethod(Ct_{targetgene} - Ct_{housekeepinggene})$.

Results





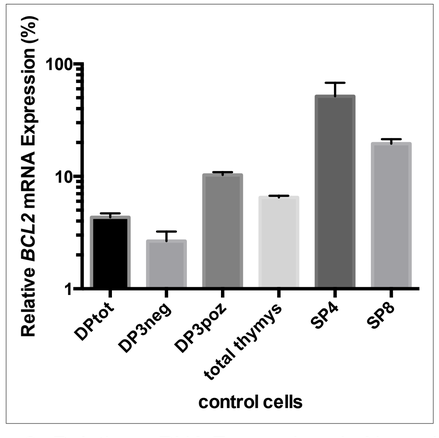
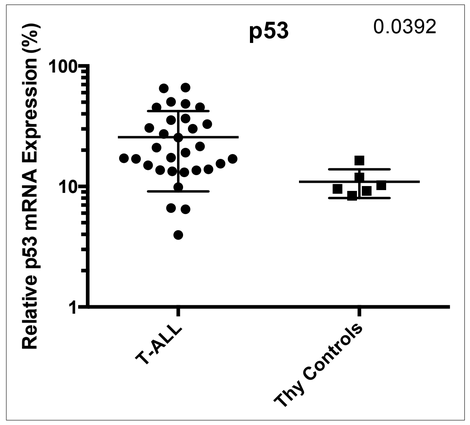
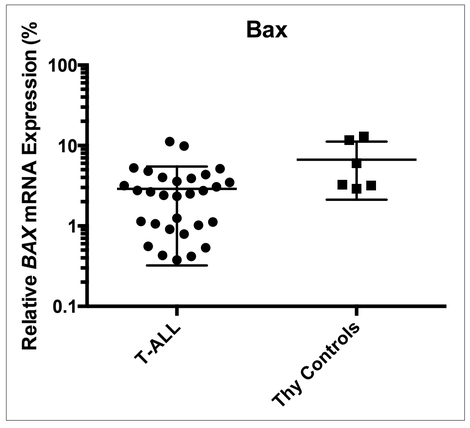


Figure 2: Relative mRNA Expressions in Normal Thymocytes





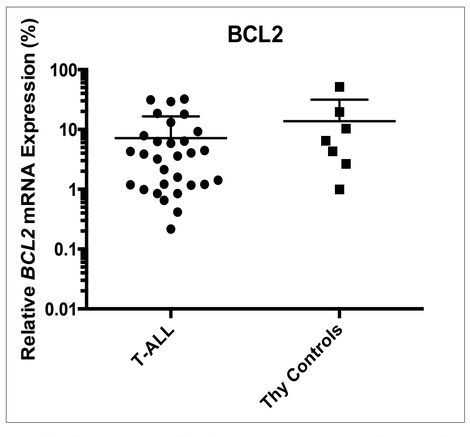


Figure 3: Relative mRNA expressions in T-ALL Patient Samples

Conclusions

Here in this project, the differential expression of *p53*, *BAX*, and *BCL2* genes were studied. *p53* expression is significantly upregulated in T-ALL patient samples when compared with healthy samples (p=0.0392). The lowest expression level for *p53* is observed in double positive (DP) stage among normal thymocytes samples and it is upregulated during T-cell development. Expression of —*BAX* gene is regulated by *p53*. However there is no significant difference in the expression of *BAX* observed by q-RT-PCR data. Significant expression difference for *BCL2* in T-ALL patients is also not observed. In the T-cell development stages expression of all three genes reaches maximum level in SP stage, last stage of the development. Analyzing other members of the apoptosis pathway, whole genome analysis with more patient samples, detecting protein products of our target genes by immunohistochemistry or western blot, studying epigenetic mechanisms that control gene expression can be as a future aim of the project.

References

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- Dik WA, Pike-Overzet K, Weerkamp F, de Ridder D, de Haas EF, and Baert MR et al. New insight on human t cell development by quantitative t cell receptor gene rearrangement studies and gene expression profiling. J Exp Med., 201:1715–1723, 2005.

Acknowledgments

I wish to express my sicere thanks to Asst. Prof. Yuk Yin NG, thesis supervisor, for all his supports and the continuos encouragement. I am also grateful to Dr. Ozden Hatirnaz NG for her supervision, support and knowledge. I am thankful to Istanbul University Institute of Experimental Medicine to provide me all the necessary materials for the research.

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