

Abstract

Introduction: At our post-genomic era the studies of epigenetic regulation constitutes one of the tools for understanding the function of genes. Epigenetic regulation can directly control the temporal and spatial gene activity or silencing. The molecular basis of these regulations are DNA bases modifications, chromatin remodeling and RNA interference. At the same time, these mechanisms have a special way of transferring genetic information to subsequent generations called epigenetic inheritance. It has been proven epigenetic deregulation of certain genes as cause for many disease. For this reason, the study of epigenome HLA genes seems particularly important because these genes play a fundamental role in regulating the immune system.

Aims: The aim of this work is to create a description of epigenetic modifications within families. It is an analysis of histone modifications and DNA methylation in the promoter region of the gene *HLA DQA1*. The aim was also to compare the differences in epigenetic modifications between alleles and compared the differences in these modifications between generations. The results will be compared with the analysis of the level of expression of the gene *HLA DQA1*.

Methods: From collected peripheral blood of donors were isolated DNA, RNA, and leukocytes. DNA was used for genotyping. Another part of the DNA samples were converted by bisulfite method, and then sequenced. The collected data were analyzed for DNA methylation. The isolated RNA was subjected to reverse transcription followed by quantitative PCR for analysis of expression levels. Leukocytes were used for chromatin immunoprecipitation and subsequently for quantitative PCR to assess the extent of trimethylation and acetylation of histone H3.

Results: Within the modifications was a statistically significant difference in acetylation between alleles *01 and *05 wherein acetylation of *01 was significantly higher. Trimethylation analysis did not provide statistically significant results. Statistically insignificant results are also in comparing of the state of histone modifications between generations. DNA methylation analysis revealed statistically significant differences between alleles *01 and *03 and *05, wherein the DNA methylation of *01 higher than that of alleles *03 and *05. Comparison of DNA methylation differences between generations showed significant differences between the first generation, less methylated as compared to the third generation. By comparing the expression and modification there was no statistically significant relationship.

Keywords: epigenetics, DNA methylation, histone modifications, HLA class II, DQA1, mRNA expression