Introduction

Proteasomes are the large multienzyme complexes, that provide degradation of regulatory, damage or misfolded proteins, development of CD8+ T-cells during positive selection in thymus and generation of antigenic peptides binding to MHC class I antigen-presenting molecules [Tsymokha A., 2010].

The catalytic part of proteasome represents by 20S core is a cylindrical particle, consists of highly regulated group of proteins - α and β subunits, arranged in a stack of four ring [Tsymokha A., 2013].

Proteasome maturation protein (POMP) is a chaperone that directly associated with immature proteasomes. POMP coordinates process of β subunits incorporation into hemiproteasome and further maturation of proteasome. Finally, POMP is destroyed by newly formed proteasome as its first substrate [Ferrington D, 2012, Burri L, 2000]. POMP is required for 20S biogenesis, silencing of POMP expression impairs recruitment of β5 and β5i subunits in proteasome and as a consequence lead to decreasing of proteasomal activity [Tanaka K, 2013, Ferrington D, 2012].

The proteasomes are involved into process of activation of different transcription factors that can initiate and maintain allergic inflammation. Among them Nuclear factor kappaB (NF-κB) – transcription factor, that coordinate expression of proinflammatory genes and production of cytokines, chemokines, including interleukin-4 (IL-4), IL-5, IL-13 [Hayashi T, 2000, Ferrington, 2012]. Another example is JunB – Th2- specific transcriptional factor. Due to this proteasome inhibition through inhibition of NF-κB and JunB reduces allergic inflammation and production of pro inflammatory cytokines [Weathington N, 2013].

Activation of transcription factors may require the involvement of signaling pathways mitogen-activating protein kinase (MAPK). MAPK family includes Jun amino-terminal kinase (JNK), cellular signal-regulating kinase (ERK) and p38 protein. Each of them involved in the implementation of allergic inflammation – activation of T cells, tissue infiltration of eosinophils and mast cells, production and release of cytokines and bronchial hyperreactivity in asthma [Pelaia G, 2005].

Endogenous specific MAPK phosphatases (DUSPs or RTOs) have inhibitory effect on pro-inflammatory cascade of MAPK. MRK-1 inhibits MAPK-dependent airways remodulation, Degradation of endogenous MRK-1 occurs via the ubiquitin-proteasomal proteolysis.

The proteasomes also have a crucial role in the differentiation of keratinocytes and hydration of the horny layer [Dahlqvist, 2010]. Failure of these processes can lead to manifestation of atopic dermatitis, sensibilisation and atopic march development.
**Purpose**

The aim of this study was to investigate the association of single nucleotide polymorphism (SNP) in *POMP* gene with atopic disease in children.

To test this hypothesis, the differences in the frequency of polymorphisms rs4769628 in *POMP* gene in children without allergic disease (control group) and children with manifestation of atopic march were investigated.

**Methods**

Genotyping of polymorphism were performed in the following populations: patients with atopic diseases and control group, using Real-time PCR.

**Results**

In this study, the association of polymorphism rs4769628 in *POMP* gene and atopic diseases in children were demonstrated. 62.26% of patients and 53.06% of control group had major allele of rs4769628 in *POMP*. 33.67% and 37.76%, respectively, had heterozygous allele. Minor genotype GG was not detected in children with atopic diseases, 9.18% of healthy children are carriers of minor allele (p < 0.05). Minor variant of rs4769628 in *POMP* gene is associated with reduced risk of developing atopic diseases in children.

The association of polymorphism rs4769628 in *POMP* gene with the severity of bronchial asthma and atopic dermatitis in children were investigated. There was no statistical significance in the frequency of polymorphisms depending on severity of diseases. These diseases are multifactorial, so their clinical course depends on a combination of genetic factors and unfavorable factors of the environment.

**Conclusion**

The single-nucleotide polymorphism in *POMP* gene is associated with reduced risk of developing atopic diseases in children. The polymorphism rs4769628 in *POMP* gene can be used as an prognostic marker for the development of atopic diseases in children.