1. Research project objectives/ Research hypothesis

Bronchial asthma and allergic rhinitis are classified as chronic airway diseases, responsible for many medical and socioeconomic problems. Numerous studies highlight the frequent co-occurrence of both diseases, suggesting similarities in their pathomechanisms. Therefore, allergic inflammation in upper and lower airways may by regulated by common genes and biological pathways. Nowadays, diagnostic methods has many deficiencies such as poor specificity and invasiveness. Therefore, new non-invasive tests, allowing fast and accurate diagnosis, as well as monitoring the effects of treatment, are required. For this purpose, small non-coding RNA may be used. Due to limited availability of clinical material, rat model of induced bronchial asthma and allergic rhinitis will be used. The main hypothesis of this project is that during allergic inflammation there are significant changes in miRNAs expression, both in nasal epithelium and lungs. Moreover, these changes may also be present in peripheral blood. Intercellular transport of miRNA, using exocrine follicles, may be involved in this process. The major aim of this project is identification of miRNA genes showing similar expression profile in sensitized rats, thus directly involved in allergic inflammation of the airways.

2. Research project methodology

In this project we will use Brown Norway rat strain, considered to be the best *in vivo* model to study inflammation in the airways, will be used in this project. Rats (n=20) will be purchased from a certified producer and subjected to three-week sensitization procedure, using house dust mites extract (treated group, n = 10) or 0,9% saline (control group, n = 10). The blood of the animals will be drawn up intravitally, to determine the concentration of anti-HDM antibody, IL-4 and IFN-γ. When the inflammation is confirmed, rats will be sacrificed. Tissues from lungs, nose, and peripheral blood will be collected for RNA isolation. Additionally, samples obtained from the nose and lungs will be used for microscopic staining (to confirm inflammation) and miRNAs genes profiling (384 different miRNA genes). Unsensitised rats will constitute biological control for this experiment. For selected genes, exhibiting significantly altered expression profile in tissues, collected from sensitized animals, real- time PCR will be performed. At this stage, cDNA obtained from peripheral blood, will be additionally used in miRNAs profiling. For selected miRNAs, exhibiting similar expression profile in all analyzed tissues, immunohistochemical staining, using a fluorescently-labeled probes, will be performed. This enables the semi-quantitative determination of miRNAs expression directly in animals tissues. For selected miRNA, *in silico* analysis will be done, to determine their target genes.

3. Expected impact of the research project on the development of science, civilization and society

Our studies will contribute to better understanding of mechanisms involved in airway inflamation. In future, it may be useful for developing new therapeutic targets for bronchial asthma and allergic rhinitis.