The aim of the study is to identify the clinical, cytological, biochemical, immunological, and genetic markers responsible for the anti-IgE antibody treatment of patients with severe allergic asthma and hypersensitivity to aspirin (aspirin-induced asthma – AIA) compared to patients with aspirin-tolerant asthma (ATA), and compare the effects of aspirin desensitisation with anti-IgE treatment in patients with AIA.

The study group comprised adult patients with AIA (n=20) and adults with ATA (n=20) qualified for omalizumab therapy on the basis of the criteria of the Polish Programme for Treating Severe Allergic Asthma. The second group of patients will comprise patients with severe allergic AIA (n=30), who will undergo aspirin desensitisation. The study will be performed in two centres experienced in conducting such procedures (JU of Kraków and MU of Łódz). The patients will be subjected to clinical tests, cytological examinations of sputum and nasal lavage, as well as biochemical, immunological, and genetic tests when they are registered onto the project (baseline value) and after 16 (early response) and 52 (late response) weeks of treatment with both anti-IgE antibodies and aspirin desensitisation, i.e.:

1.the clinical evaluation will be based on an asthma control score and severity of nasal symptoms using validated scales - Asthma Quality of Life Questionnaire [AQLQ], Asthma Control Questionnaire [ACQ] and the visual analogue scale for nasal symptoms,

2. the cytological examination of cells from induced sputum and nasal lavage will be performed, with particular division into eosinophilic or non-eosinophilic phenotype,

3. it will identify the biochemical markers (concentrations of eicosanoids) and Th2 immune response markers (IL -5 , IL - 4, IL -13) in induced sputum supernatant (SPI) and nasal lavage fluid (PN). It will evaluate particular chemokines regulating the influx of eosinophils and Th2 lymphocytes in this material,

4. the project will identify the level of periostins, dipeptidyl peptidase-4 (DPP-4) and total and specific serum levels of IgE, SPI and PN,

5. it will evaluate the systemic (serum) and local (SPI and PN) production of lambda interferon,

6. an evaluation will be performed of the expression of 48 genes associated with allergic inflammation (eg.IL4-5-13) in cells from the sputum and nasal lavage,

7. it will determine the frequency of exacerbations in the year before treatment and after one year following treatment.

The obtained results will allow us to evaluate the relationships between clinical parameters and cytological, biochemical, immunological and genetic markers, and to identify specific markers of a good response to anti-IgE treatment (in the ATA and AIA groups), and the aspirin desensitisation (in only the AIA group). The reason for addressing these topics is the need for deeper understanding of the mechanisms behind the development of hypersensitivity to aspirin and the action of anti-IgE antibodies (omalizumab - OMA) in the AIA and ATA groups. AIA patients typically have a serious course of disease complicated by inflammation of the mucosa of the nose and sinuses with recurrent polyps. The only form of treatment available to this group of patients is aspirin desensitisation. However, for safety reasons and limited tolerance of the patients to chronic application of high doses of aspirin, this is not possible in all patients. Although the mechanism of action of AIA is independent of IgE, it has been confirmed to be associated with local and systemic eosinophilia, for which OMA is known to be an effective treatment. Therefore, comparing AIA and ATA patients with regard to the effectiveness of OMA treatment is justified, as is a comparison of the effects of aspirin desensitization. In addition, no such multidirectional (clinical, cytological, biochemical, immunological and genetic) evaluations of the effectiveness of anti-IgE therapy have yet been published. Predictors of good response to OMA are unknown, because the response does not depend on either the level of total or specific IgE in serum. The proposed analysis of the correlations between these varied parameters may lead to the identification of predictive markers allowing for the use of individualized therapy in specific phenotypes of asthma.