The aim of this project is to estimate DNA methylation in children of atopic mothers, and to evaluate the effect of the mother's atopy and diet on methylation profile and the risk for IgE-mediated food allergy and wheezing in the first year of life.

In recent decades there has been a substantial increase in the prevalence of allergic conditions. Environmental factors play a crucial role in this process. Even though genetic influence is equally important for phenotypic manifestation, it's unlikely that genes have changed in this relatively short period of time. The key question in recent epidemiologic studies is what happened in the environment and whether we can reverse these alterations to stop the allergy epidemic. Epigenetics connects the fundamental mechanisms of genetics and the environment to allergy development, with both genes and the environment mediating interaction on the molecular level.

The earliest manifestation of allergies in children is food allergies. The onset of food allergies early in life implies significant prenatal involvement in its development and makes this aspect especially relevant to the understanding of interactions between genes and the environment. The second most common allergic condition which manifests in early childhood is asthma. It is estimated that in 40% of cases, asthma begins in the first year of life.

A prospective cohort study of mothers and babies will be conducted. A homogeneous group of pregnant women will be selected, so as to limit the influence of factors other than diet and the presence of atopy. The population will consist of 200 pregnant women recruited from out-patient clinics in the 3rd trimester ≥28 Hbd, 20-35 years old, living in big city, with no exposure to tobacco smoke. The measurement of IgE specific for food and inhalant allergens together with total IgE, will be performed in each included pregnant woman. Additionally, all women will receive a questionnaire with queries about diet, supplementation of folic acid and vitamins, symptoms of allergic conditions like asthma, allergic rhinitis, atopic dermatitis, and IgE-mediated food allergy, medications and pets in the home. The methylation profile and gene expression of children from mothers in first phase will be analysed in cord blood taken at the time of delivery. Children will undergo allergy evaluations at 3, 6 and 12 mo of life. The children will also undergo a general developmental assessment. At 12 months of life blood will be taken for the allergeno-specific IgE. DNA methylation will be performed with HumanMethylation 450BeadChip. This microarray contains the information for 450,000 CpG sites at single-nucleotide resolution. Results achieved in methylation profiling will be used to choose specific genes for gene expression analysis.

Provided results will allow to estimate the association between mother's and child's atopy on the basis of epigenetic modification and will allow to identify genes related to allergy risk in the first year of child's life. Understanding the mechanisms which influence the development of allergy in the first year of life will allow for prevention by introduction of early interventions.