

## POPULARIZED ABSTRACT

In the era of global warming caused by CO<sub>2</sub> accumulation, it is extremely important to gain knowledge about the basic processes occurring in plants. Particularly important is the reproduction aspect of crop plants and this is directly associated with sex determination. Flower formation is influenced by various genetic-dependent processes but also by the environment, which as a result of climate change can significantly affect yield. Biological progress in agriculture is a consequence of knowing and understanding the mechanisms of growth, development, and reproduction in various species. The explanation of how the morphogenesis processes are determined is the cognitive goal of the work carried out in many species. However, until now, there is no full picture of the genetic regulation of these processes.

In this project, we intend to identify molecular networks and elements of their regulation in developing cucumber flowers of different sexes. Cucumber (*Cucumis sativus* L.) is one of the model plants in the studies on such issues because it produces female, male and hermaphroditic flowers. Buds of 1-2 mm cucumber have primordia of male and female organs. At the next stage of development - stage of 3-5 mm, the bud is already sexually differentiated. Primordia of pistils and stamens or one of them continue the development, while the others are inhibited.

With a properly selected collection of cucumber mutants, differing in gender, we want to study the development of flowers through the analysis of different stages - from the formation of floral growth tips, through developing flower buds of size: 1-2 mm, 3-5 mm and 6-8 mm, as well as leaves. We intend to perform NGS sequencing of genomes and miRNA profiles, and then bioinformatic results, verified by experimental analyzes (PCR, Sanger sequencing, stem-loop RT-qPCR, target RT-qPCR) merge with the profiles of transcriptomes and metabolomes (from previous projects), creating maps of interaction and regulation between molecules affecting the development of flowers (experimentally verified by Y2H assay, PCR, Sanger sequencing). Subsequently check how the high temperature and low watering influence (mimicking the climate changes) on the expression of genes encoded central nodes in multi-omic interaction maps.

Considering the current state of knowledge, we hypothesized that there is a connection between miRNA and differentially expressed genes which are an important element in regulating the development of protein-protein interaction network (PPI) influencing sex differentiation.

Important achievements in the project will be: 1) obtaining the knowledge of the genomes of plants presenting different sexes and conducting comparative genomics work to analyze variability related to sex determination, 2) cognition of miRNA profiles of leaves and generative tissues (flower buds at various stages of development) which will allow to identify the known and novel miRNA molecules, to determine their expression level and indicate those miRNAs that are specific for the development of a specific sex, as well as to trace of potential target molecules, 3) correlation and construction of multidimensional molecular networks, including regulatory elements such as ethylene (the main sex regulation hormone); and 4) checking how the increase in temperature and water deficiency affects the key genes responsible for flower sex formation .

Thanks to the creation of such multidimensional networks, we will obtain information on the system of sex determination, while understanding the mechanisms of plant reproduction leading to genetic diversity is of great importance for modern breeding as well as biological sciences concerning development and differentiation. In agricultural practice, it is often preferable to obtain or increase the share of plants with flowers of a specific gender. For example, in cucumbers, fruit as a commercial product arises from a female flower, so from an economic point of view, the grower will prefer plants with flowers most of this sex. At the same time, pollen from male flowers is needed for pollination and development of the fruit. In plant breeding, it is the sexual phenotype that determines the choice of breeding method and the way in which a given plant will be grown. Further analysis of the molecular basis of flower morphogenesis and plant sex determination will open up new breeding opportunities in agriculture and horticulture, such as change of flower structure, as well as anatomical features of fruit, more efficient seeding, new markers for breeders, creation of new varieties of cultivated species and ornamental plants and plants intended for biofuel industry, more efficient food production, control of the flowering term, which can contribute to adaptation to other climatic conditions.