

Description for the general public

The main goal of the project is to gain additional knowledge regarding functioning of the dioecious plants. In dioecious species female and male flowers grow on separate plants. Dioecy is relatively rare in angiosperm plants, but much more frequent in gymnosperm, where it is observed in more than a half of species. It was demonstrated in numerous studies that female individuals bear higher costs of reproduction, because they have to produce, not only flowers, but also seeds and related structures (like cones and fruits). Higher reproductive effort of females is also related to slower growth compared to males. It is likely that this is a reason why female individuals cope less efficiently with unfavourable environmental conditions. Necessity of supplying generative organs (seeds, flowers or fruits) cause that female invest less than male in growth and development. Despite of the fact, that relationships between genders, described above, are commonly observed, molecular basis of this differences are not clear. The implementation of different strategies of resource allocation could be the cause of different tolerance to stress factors among male and female individuals and those differences most likely will be reflected at molecular (genome) level.

The key to understand mechanisms of male and female individuals functioning in stress conditions could be found at the level of information located in their genomes. In our study we plan to describe differences among genders at the level of: 1) reading information from their genomes (on mRNA level); 2) proteins (enzymatic analysis); 3) chemical elements and compounds concentration in needles.

Our study will be conducted on common juniper. It can be used as a model for dioecious tree species, since it is representative for long-living dioecious plants. It means differences in growth rate between genders and greater sensitivity of females on climatic factors. Since, in whole Europe, it is observed, that common juniper populations decline and one of the main reason could be gender related differences in response to global environmental changes.

Proposed studies will be conducted on mature individuals with known gender, growing in pot experiment, exposed to two treatments: fertilization and lack of fertilization. In order to verify our hypothesis we plan to use, inter alia Next Generation Sequencing (NGS), namely, modern method, which allows to obtain data related to functioning of all genes very quickly. We expect that different genders will show different enzymatic activity, differences in gene expression and chemical concentration and that those differences will be greater in the case of individuals growing in low nutrient treatment.