

Evolutionary relationships in the genus *Daucus*: cytogenetic and morpho-anatomical comparative analysis of wild relatives of carrot

The need for increasing production capacity of crop plants in order to feed the continuously growing human population has become a real challenge, especially since the diversity of the plant world is exposed to threats related to continuous climate change and human activities. An additional threat to agricultural crops are diseases and insect pests. The breeding programmes that have currently been implemented use new sources of genetic variation, thanks to which plant cultivars with increased adaptive properties may arise. In this process, wild relatives of crop species play a significant role, being a source of genes that are useful for plant improvement. Thus, better understanding of phylogenetic relationships between wild species may provide benefits for future breeding programmes.

The genus *Daucus* comprises about 40 wild species and the cultivated carrot (*D. carota* subsp. *sativus*). The latter one is the most important member of the family Apiaceae, and one of the most significant root vegetable in the world, being the main source of provitamin A in human diet. Morphologically and genetically, the *Daucus* species are very diverse, and despite many years of studies (morphological, anatomical, and molecular), the taxonomic and phylogenetic relationships between them are still not fully resolved. Thus, in order to better understand these relationships, the application of information based on cytogenetic (chromosomal) data may be of great usefulness.

Each species has its unique karyotype, *i.e.* a chromosome complement with definite number and morphology, which represents the highest level of structural and functional organization of the nuclear genome. By comparing the chromosomes of different species, much can be learned about the evolutionary directions of karyotypes and their significance for speciation and biodiversity. It has been confirmed that repetitive DNA sequences play an important role in the process of shaping karyotypes, since they are characterized by their rapid evolution, leading to the high variability in terms of their distribution and copy number. This, in turn, makes them extremely useful in comparative studies concerning evolutionary and phylogenetic relationships between species. Besides, the repetitive sequences tend to cluster, so that they can easily be detected by molecular cytogenetic methods.

For this research project, following objectives have been established:

- to determine the chromosomal distribution of the main repetitive sequence families (identified in the carrot genome) in genomes of selected wild *Daucus* species and their relatives using fluorescence *in situ* hybridization;
- to ascertain the feasibility of these repetitive sequences for identifying chromosomal rearrangements within the studied species;
- to assess the nuclear DNA content in the studied species using flow cytometry;
- to compare the selected morpho-anatomical characters of pollen and seeds in these species in relation to phylogeny and taxonomy of the genus *Daucus*.

The realization of these objectives and integration of obtained results will allow to better understand issues related to genome evolution and phylogeny of the genus *Daucus*, and in particular will bring us closer to the answers to these questions: (1) How have the evolutionary relationships within *Daucus* species been shaped on the chromosomal level? (2) What were the directions of evolutionary changes in their karyotypes? (3) How important was the role of the repetitive sequences in this process? (4) Are the morpho-anatomical data of pollen and seeds useful in inferring the evolutionary relationships between the *Daucus* species?

The obtained information on genomes of wild *Daucus* species in relation to the carrot genome may be utilized in future breeding programmes for development of new cultivars of this valuable crop.