

GeneRose: Genetic evaluation of European rose resources for conservation and horticultural use

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Genetic Diversity

This EU-project focuses on the conservation and use of natural resources in the species *Rosa*. Attempts to preserve rose gene pools without sufficient knowledge about the genetic background may counter-act efforts to increase biodiversity, compromise the maintenance of (rare) indigenous species in landscaping and make it difficult to (re)introduce autochthonous plant material in the wild. Given that genetic authenticity is an important feature in nature conservancy; the use of molecular tools to perform an in-depth investigation of genetic variability and relatedness is of utmost importance. The project will gather information on inter- and intraspecific relationships as well as on population structure by the use of AFLP and microsatellite DNA markers. The phylogeny of the wild species will be analyzed using AFLP and DNA sequencing, and the ancestral species of the modern cultivars will be determined.



Ornamental Value

Many of the wild species harbor attractive or useful features (esthetical value of flowers and hips, as well as the rambling growth habit that make them useful as a natural fence) and can therefore replace cultivated varieties in forestation and restoration of small elements in landscapes (hedges, wooded banks). However, the use of indigenous and autochthonous plant material for these purposes requires that such material can be properly identified and propagated.

Disease resistance

Disease resistance is a very important feature in modern sustainable agriculture, which aims at a low environmental impact. In roses fungal diseases like blackspot, powdery and downy mildew, and rust infect the leaves and decrease both the growth and the esthetical value of the plants. Both in garden roses and for cut flowers fungicides are used to an ever-increasing extent. Wild roses constitute a promising source for fungal disease resistance. Therefore more knowledge on the sources of resistance, the existence of different physiological races of the pathogens, and standardized disease screening methods are needed. This project will develop practical tools for breeders to enable efficient screening of breeding stock material and offspring, and will generate knowledge on the segregation of disease resistance and its inheritance.



Crossing Techniques

Introduction of germplasm from wild species is a prerequisite for improving disease resistance in modern rose cultivars. For enlargement of the relatively small gene pool in rose cultivars, wild rose species must be characterized and problems due to crossing barriers between these species and modern cultivars must be solved. At present, interspecific hybridization between wild species and modern cultivars is hampered by a ploidy barrier: the large majority of modern rose cultivars are tetraploids; wild species are mostly diploid, although some are tetraploid and species in the section *Caninae* are usually pentaploid (but still produce haploid pollen through the aberrant *canina*-meiosis). This project aims to focus on crossing barriers that are caused by different ploidy levels. Besides classical techniques like chemically induced chromosome doubling or dihaploidization, modern techniques like pollen sorting will be used.

