



Rosa

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Presently, about 100–250 species are usually recognized in the genus *Rosa*. The low levels of DNA sequence divergence found across the genus suggest that it is a young genus with much speciation taking place after the last glaciation. Poor phylogenetic resolution and commonly occurring contradictions between chloroplast and nuclear gene phylogenies suggest that hybridization has been a strong driving force in the evolution of roses, often accompanied by polyploidization. In addition, extensive anthropogenic impact has led to the development of many new semi-wild and/or cultivated rose varieties. Some wild species have become invasive.

Résumé en
anglais

This chapter describes the taxonomy of roses. It presents examples of interesting traits in wild species that may be valuable to broaden the genetic base of cultivated roses, such as thornlessness, winter hardiness, drought resistance, and improved shelf-life. Also fragrance and compounds with possible health effects are discussed. The highest priority in rose breeding research is the development of disease resistant roses. Different resistance mechanisms have been found for black spot and powdery mildew in various wild rose species. We describe how resistance genes are being mapped using crosses between wild, diploid rose species, and how other genes for traits of interest are being identified.

We proceed with a discussion of various ways to overcome the taxonomic and ploidy level barriers for introgression of traits into cultivated hybrid rose or garden rose germplasm, including dihaploidization, polyploidization, and transgenics. Even so, breeding programs with wild species are usually time-consuming. For garden roses, the genetic and morphological distance between modern cultivars and the wild species is smaller, which makes the use of wild species easier than in the case of cut roses.

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