Genetic diversity and genetic similarities between Iranian rose species

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SUMMARY
Wild rose species were collected from different regions of Iran for a rose breeding programme. They included accessions from Rosa persica, R. foetida, R. pimpinellifolia, R. hemisphaerica, R. canina, R. iberica, R. damascena, R. beggeriana, and R. orientalis. Ten microsatellite (simple sequence repeat; SSR) markers were used to analyse the genetic variation among these rose species. The SSR markers amplified alleles in all species, even if they were from different sections within the genus. An unweighted pair group method cluster analysis (UPGMA) based on similarity values revealed five main groups. The data showed no support for any distinction between different sections within the genus. The phylogenetic analysis when these markers are amplified in all species of a genus.

Rosa species are distributed throughout the temperate and sub-tropical regions of the northern hemisphere. Rehder (1940) divided the genus into four sub-genera, three of which contain only one or two species: Hulthemia, Platyrhodon, and Hesperhodos. The fourth sub-genus, Rosa, contained about 95% of all 200 species and was subdivided into ten sections: Pimpinellifoliae, Rosa (Gallicanae), Caninae, Carolinae, Cinnamomeae, Synstylae, Banksianae, Laevigatae, Bracteatae, and Indicate. This classification of the genus Rosa was based on morphology; however, due to the absence of any clear differences between many of the species, a wide range of inter-specific hybridisations, and the ability of rose species to cross relatively easily, understanding genetic relationships in the genus Rosa has been difficult (Koopman et al., 2008). It becomes even more complicated in the section Caninae (dogrose) due to heterogamic meiosis, the ability of dogroses to hybridise between sections and subsections, and predominantly matroclinal inheritance (Nybom et al., 2004).

Several attempts have been made to use molecular markers to obtain a deeper insight into genetic relationships in the genus Rosa. Phenetic or phylogenetic relationships within wild rose species have been studied using non-coding regions of chloroplast DNA (Bruneau et al., 2007), intergenic spacer sequences of the nuclear genome (Wissemann and Ritz, 2005), and RAPD (Millan et al., 1996) and AFLP (Koopman et al., 2008) markers. However, sequencing did not resolve all the taxonomic relationships between species due to a lack of polymorphism. Microsatellite markers (simple sequence repeats; SSRs) are ideal tools with which to study genetic relationships and the diversity of plants in breeding programmes, and for conservation purposes. SSRs are genetically-defined PCR-based markers, typically co-dominant and multi-allelic. They can also be used to align and integrate diploid and tetraploid genetic maps (Debener and Linde, 2009). As they are transferable across related species, SSR markers may also be useful for establishing species relationships, as was done in diverse groups of species ranging from tomato (Alvarez et al., 2001) to Darwin’s finches (Petren et al., 1999), and the Western Canary Island lizard (Rochard and Thorpe, 2001).

SSR markers have been developed in rose (Esselink et al., 2003; Zhang et al., 2006; Hibrand-Saint Oyant et al., 2008) and have been used to estimate genetic variation between hybrid tea rose and rootstock varieties (Esselink et al., 2003), among several hundred hybrid tea