Karyotype Analysis of Wild *Rosa* Species in Xinjiang, Northwestern China

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**Additional index words.** chromosome, ploidy, rose, taxonomy

**Abstract.** Wild *Rosa* species, which are highly variable and locally adapted, are widely distributed in the Xinjiang Uygur autonomous region of China. These species possess many important horticultural traits that are not found in the gene pool of modern cultivated roses. However, little is known about their cytological characteristics, because few of them have been karyologically analyzed. Karyological data of 13 samples of seven wild *Rosa* taxa, including *R. berberifolia*, two botanical varieties of *R. spinosissima*, *R. platycantha*, *R. beggeriana*, *R. acicularis*, and *R. laxa*, were investigated by means of squashes of shoot tips. The results showed that seven samples were diploid (2n = 2x = 14), whereas the other six samples were tetraploid (2n = 4x = 28). The karyotypes of all the test samples were composed of m and sm chromosomes, which include 1A, 2A, 1B, and 2B. There were differences in asymmetry index, centromere index, and distribution of relative lengths. The karyotype of the tetraploid *R. laxa* var. *laxa* sample from Aksu easily distinguished from the other *R. laxa* var. *laxa* samples tested in having the highest asymmetry index and the most evolved karyotype. This Aksu population merits recognition as a new botanical variety of *R. laxa*. The karyological data, most of which are first reports for their taxa, provide a comprehensive cytogenetic resource that can be used to better understand the taxonomy, evolution, and speciation in the genus *Rosa* and to identify candidate species for breeding programs.

The genus *Rosa* comprises ≈150 species that are widely distributed in diverse climates and habitats throughout the Northern Hemisphere (Quest-Ritson and Quest-Ritson, 2003; Rehder, 1940) from subtropical to cold-temperate regions. China’s 95 species (65 endemic) account for nearly half of the world’s *Rosa* species (Ku and Robertson, 2003). Therefore, China is a center of distribution of *Rosa* as it is with numerous other cultivated plants (Brichet, 2003), and China’s roses are a great genetic resource for rose improvement.

The Xinjiang Uygur autonomous region (hereafter referred to as Xinjiang) lies at the northwestern border of China (Fig. 1). The Tianshan Mountains transverse it centrally, dividing Xinjiang into southern and northern regions, which differ greatly from each other in climate. In regard to phytogeography, Xinjiang spans the junction of the Eurasian Forest subregion, the Eurasian Steppe subregion, and the Central Asiatic Desert subregion. Many of the wild *Rosa* species in Xinjiang are distributed widely (Fig. 2). Although 11 *Rosa* species and three botanical varieties were recorded from Xinjiang in *Flora of China* [Ku and Robertson, 2003 (Table 1)], further research has indicated that more than 20 species occur in Xinjiang with botanical varieties that exhibit all sorts of morphological characteristics (Bao, 1993; Liu, 1993; Liu and Cong, 2000; Ma and Chen, 1990, 1991; Yu et al., 1985, 2011). These botanical varieties have been described by different investigators and are notoriously difficult to distinguish, owing to the presence of intermediate forms (Han, 1995). In addition, nomenclatural synonyms and the selection and breeding of cultivars have added to the confusion (Macphail and Kevan, 2009).

There is much interest worldwide in the wild *Rosa* species from China, because they contributed much of the foundation of modern cultivated roses. Wild *Rosa* species with important traits, such as powdery mildew (*Podosphaera pannosa*) resistance, large flowers and hips, and cold and drought resistance are regarded as valuable breeding materials. Modern roses are primarily compose of eight to 11 *Rosa* species and only a few of the species have been involved. Those other species currently are not reported (Ma and Chen, 1992; Zlesak, 2006). Introggressing additional valuable genes from these species into modern rose germplasm is inevitably a long and difficult process (Zlesak et al., 2007), because of the long generation time and the frequent cross-incompatibility and hybrid sterility between parents of different ploidy levels. Therefore, there is interest in the variation of ploidy within and among wild *Rosa* species. Despite the
development of DNA sequence-based technology in recent years, cytological markers remain useful for plant identification, evaluation of biodiversity, and the study of plant evolution. It has long been known that some wild species, mainly diploids, represent potentially valuable genetic resources, especially for disease resistance. The wild Rosa species that have been reported are euploids with chromosome numbers ranging from $2n = 2x = 14$ to $2n = 10x = 70$ (Crane and Byrne, 2003; Darlington and Wylie, 1955; Jian et al., 2010a, 2012; Ma et al., 1997; Malecka et al., 1990; Malecka and Popek, 1984), and an accurate measurement of ploidy appears to be of enormous significance for cross-breeding. The various ploidy groups are not completely cut off from one another; however, the rose breeder who confines his or her hybridization to one ploidy group of species or botanical varieties will find his or her path smoothed and his or her aims more quickly achieved (Percy, 1964).

Karyotype analysis is a traditional cytogenetic first step in the comparison of genomes among related species (Crane and Byrne, 2003) under the usually correct presumption that karyotypic differences can affect meiotic chromosome pairing and hybrid fertility. Although the karyotypic variation within Rosa implies a rich genetic resource for rose breeding, it also frequently impedes breeding progress because of cross-incompatibility and hybrid sterility. Hence, elucidation of the karyotype and the physical structure of chromosomes can rationalize and accelerate the exploitation of genetic variation from wild relatives of crops (Baenziger et al., 2006). What is more, the results might be helpful in elucidation of some taxonomical problems and relations between particular species within this highly differentiated genus.

Therefore, a 3-year investigation on wild Rosa species in Xinjiang was conducted from 2009 to 2011 with two objectives:

Fig. 1. Location of study sites in Xinjiang, northwestern China (2009–11); ● wild Rosa species distributed in Xinjiang, including the 13 studied samples.

Table 1. Rosa taxa in Xinjiang, northwestern China, recorded in Flora of China (Ku and Robertson, 2003) and related cytological data.

| Subgenus | Section | Species               | Ploidy | Karyotype                  |
|----------|---------|-----------------------|--------|----------------------------|
| Hulthemia|         | R. berberifolia       | Diploid| No report                  |
| Rosa     | Pimpinellifolii | R. spinosissima var. spinosissima | Tetraploid | No report                  |
| Rosa     | Pimpinellifolii | R. spinosissima var. altaica | Tetraploid | No report                  |
| Rosa     | Pimpinellifolii | R. kokanica           | No report | No report                  |
| Rosa     | Pimpinellifolii | R. platycantha        | Diploid | No report                  |
| Rosa     | Pimpinellifolii | R. foetida            | No report | No report                  |
| Rosa     | Cinnamomeae   | R. beggeriana var. beggeriana | Diploid | $2n = 2x = 6m + 8sm$ (Yang et al., 2008) |
| Rosa     | Cinnamomeae   | R. beggeriana var. ilou | Diploid | No report                  |
| Rosa     | Cinnamomeae   | R. albertii           | No report | No report                  |
| Rosa     | Cinnamomeae   | R. acicularis         | Tetraploid | No report                  |
|          | Cinnamomeae   | R. oxyacantha        | No report | No report                  |
| Rosa     | Cinnamomeae   | R. laxa var. laxa     | Diploid, tetraploid | $2n = 4x = 12m + 16sm$ (Yang et al., 2008) |
| Rosa     | Cinnamomeae   | R. laxa var. mollis   | Diploid | No report                  |
| Rosa     | Cinnamomeae   | R. fedtschenkoana     | No report | No report                  |
Table 2. Locations of the tested wild *Rosa* samples in Xinjiang, northwestern China.

| Code | Species | Location | Latitude and longitude | Altitude (m) | Habitat | Remark |
|------|---------|----------|------------------------|--------------|---------|--------|
| 1    | *R. berberifolia* | Bagang Prefecture of Urumqi | 43°53.196’ N, 87°22.368’ E | 711 | Roadside, waste fields, barren land |
| 2    | *R. spinosissima* var. *spinosissima* | Chonghuer village of Buerjin Prefecture in Altai | 48°27.042’ N, 86°38.962’ E | 1688 | Grassy slopes | Flowers white or yellowish, 2–5 cm in diameter |
| 3    | *R. spinosissima* var. *altaica* | Wood farm of Haba river in Altai | 47°59.988’ N, 88°16.509’ E | 1311 | Scrub in forests | Flowers white, 5–7 cm in diameter |
| 4    | *R. platyacantha* | Bayingou in Dushanzi district of Karamay | 44°06.340’ N, 84°49.170’ E | 1678 | Forest margins |
| 5    | *R. beggeriana* var. *beggeriana* | Daxigou in Huocheng of Ili Kazak | 44°23.287’ N, 80°45.676’ E | 1015 | Slopes, river sides | Hip red |
| 6    | *R. beggeriana* var. *beggeriana* | Guozigou of Ili Kazak | 44°22.149’ N, 80°59.355’ E | 1241 | Side of miscellaneous and deciduous woods | Hip red |
| 7    | *R. beggeriana* var. *beggeriana* | Secondary forest in Nileke of Ili Kazak | 43°47.789’ N, 82°27.001’ E | 1056 | Secondary forests | Hip purple to dark brown |
| 8    | *R. acicularis* | Xiaodonggou in Altai | 47°58.598’ N, 87°07.573’ E | 982 | Roadside, bases of mountains |
| 9    | *R. laxa* var. *laxa* | Kuitun | 44°06.786’ N, 80°49.239’ E | 782 | Barren land | Papery leaflets, 3–6 flowers in a corymb |
| 10   | *R. laxa* var. *mollis* | Crane River of Altai | 47°54.404’ N, 88°07.174’ E | 969 | Bush woods on sunny slopes | Papery leaflets, 3–6 flowers in a corymb |
| 11   | *R. laxa* var. *laxa* | Guozigou of Ili Kazak | 44°22.672’ N, 80°59.765’ E | 1254 | Side of miscellaneous and deciduous woods | Papery leaflets, 3–6 flowers in a corymb |
| 12   | *R. laxa* var. *laxa* | Leat side in the area of fifth regiment of Agriculture First Division in Aksu | 41°28.756’ N, 80°46.795’ E | 1339 | Gobi desert and barren land | Leathery leaflets, 3–9 flowers in a corymb |
| 13   | *R. laxa* var. *laxa* | Tuomuerfeng natural preservation areas of Wensu in Aksu | 41°47.003’ N, 80°41.309’ E | 2112 | Rock patch in valleys and by the side of brooks | Paper leaflets, solitary flowers |

*Taxonomic names of the species are recorded in *Flora of China* (Ku and Robertson, 2003).*
1) to learn more details of the wild *Rosa* species and to compare species and botanical varieties on the basis of morphological and cytological characters; and 2) to exploit useful traits of wild *Rosa* species and identify candidate species for breeding strategies. In this article, the chromosome number and karyotype analysis are reported for 13 samples of seven wild *Rosa* taxa from different subregions of Xinjiang.

**Materials and Methods**

**Materials.** All the test samples were collected from the original sources in Xinjiang (Table 2), and the wild *Rosa* species were identified carefully according to the *Flora of China* (Ku and Robertson, 2003). Additional variants, recorded in the primary literature (Bao, 1993; Han, 1995; Liu, 1993; Liu and Cong, 2000; Ma and Chen, 1990; Yu et al., 1985, 2011), were surveyed and analyzed together. Table 2 lists the authorities for taxonomic names used in this article.

**Methods.** Shoot tips \( \approx 1 \text{ cm} \) long were collected from the vigorously growing plants \( \approx 0830 \text{ hr} \). The materials were treated first with \( 0.002 \text{ mol} \cdot \text{L}^{-1} \) 8-hydroxyquinoline for 50 min at \( 25 \text{ °C} \) and then fixed for 4 h in fresh Farmer’s fixative (1:3 glacial acetic acid/absolute alcohol) at \( 4 \text{ °C} \). Finally the shoot tips were softened with \( 1 \text{ M} \) hydrochloric acid at \( 55 \text{ °C} \) for 10 min and stained for 10 min with carbol-fuchsin before being squashed between a glass slide and a coverslip. The images were captured by a charge-coupled device (CCD) camera (ProgRes C5; Analytik Jena, Jena, Germany) attached to a microscope (Axio Scope, A1; Carl Zeiss, Oberkochen, Germany) and chromosome numbers were counted.

**Data Analysis.** For each genotype, at least 10 cells with good chromosomal dispersion were selected, counted, photographed, and analyzed. Images were processed with VideoTest-Karyo (Version 3.1; VideoTest, Saint-Petersburg, Russia), Image-Pro Plus (Version 6.0; Media Cybernetics, Rockville, MD) and Photoshop (Version CS2; Adobe, San Jose, CA). The centromeric position was classified as median (m), submedian (sm), or subterminal (st) according to Levan et al. (1964). The symmetry of karyotype was classified strictly according to the method of Stebbins (1971). The ratio of the sum of the length of...
Fig. 4. Chromosome karyotypes of studied *Rosa* species in Xinjiang, northwestern China (bar = 5 μm): (A) *R. berberifolia* (sample 1), (B) *R. spinosissima* var. *spinosissima* (sample 2), (C) *R. spinosissima* var. *altaica* (sample 3), (D) *R. platyacantha* (sample 4), (E–G) *R. beggeriana* var. *beggeriana* (samples 5, 6, 7), (H) *R. acicularis* (sample 8), (I) *R. laxa* var. *laxa* (sample 9), (J) *R. laxa* var. *mollis* (sample 10), (K–M) *R. laxa* var. *laxa* (samples 11, 12, 13).
the long arms of individual chromosomes to the total haploid length of the chromosome complement (AS.K%) was measured on the basis of Arano (1963), and index of relative length (IRL) and relative length composition of genome (RLC) were calculated in accordance with Kuo et al. (1972).

Results

Four spread metaphase of the studied Rosa taxa are shown in Fig. 3. Karyotypes of all studied Rosa species are shown in Fig. 4. Parameters of chromosomes of studied species are listed in Table 3. No aneuploidy and no odd ploidy were observed in this study.

Karyotype analysis of R. berberifolia. This morphologically distinctive species was diploid with a karyotype formula of 12 m + 2 sm. The genome was composed of all four types of chromosomes [i.e., long (L), medium long (M2), medium short (M1), and short (S)], which made the constitution of relative length 2n = 2L + 6M2 + 4M1 + 2S. The centromere index ranged from 35.43% to 46.16%, and the asymmetry index was 59.82%. The length ratio of longest to shortest chromosome (Lt/St) was 1.68. With none of the chromosomes' arm ratios larger than 2, the karyotype of R. berberifolia belonged to 1A.

Karyotype analysis of R. spinosissima. In all metaphase plates analyzed in R. spinosissima, a tetraploid chromosome number (2n = 4x = 28) was observed. However, chromosome morphology differed between R. spinosissima var. spinosissima and R. spinosissima var. altaica. All chromosomes of var. spinosissima were metacentric, and the constitution of relative length was 2n = 2L + 10M2 + 10M1 + 4S for R. spinosissima var. spinosissima and 2n = 2L + 6M2 + 16M1 + 2S for R. spinosissima var. altaica. In addition, R. spinosissima var. spinosissima had the largest Lt/St of 2.69, whereas R. laxa var. laxa (sample 10) had the smallest Lt/St of only 1.49. The asymmetry index of R. spinosissima var. spinosissima, 52.60%, was the smallest from all the studied species.

Karyotype analysis of R. platyantha. The chromosome number for R. platyantha was 2n = 4x = 28. The genome of this tetraploid species was composed of all four types of chromosomes, which made the constitution of relative length 2n = 4L + 10M2 + 12M1 + 2S. Although no satellites were observed in the genomes of most of the wild Rosa species in this study, for R. platyantha, the tenth chromosome pair had a pair of satellites.

Karyotype analysis of R. beggeriana var. beggeriana. All three tested samples were diploid with exclusively metacentric and submetacentric chromosomes. The constitutions of relative length of samples 5, 6, and 7 were 2n = 2L + 6M2 + 6M1, 2n = 2L + 2M2 + 10M1, and 2n = 2M2 + 10M1 + 2S, respectively. Besides, the asymmetry index of 63.77% from sample 5 was the largest among all the tested samples.

Karyotype analysis of R. acicularis. R. acicularis was tetraploid with 28 exclusively metacentric and submetacentric chromosomes (2n = 4x = 28). The genome was also composed of all four types of chromosomes, making the constitution of relative length 2n = 4L + 8M2 + 12M1 + 4S. The Lt/St ratio was 2.24. Therefore, with the arm ratio larger than two for one pair of chromosomes, the karyotype of this taxon was 2B.

Karyotype analysis of R. laxa. The five R. laxa samples were divided into diploids (2n = 2x = 14) and tetraploids (2n = 4x = 28) with values of the asymmetry index from 55.14% to 60.11%. The karyotypes of all five samples were made up of m and sm chromosomes, which included 1A, 2A, and 1B. The ideograms of the five tested samples for this species are illustrated in Figure 5.

Discussion

The basic chromosome number is relevant to the systematic position of a taxon at high taxonomic levels (Raven, 1975). Wild Rosa species comprise a polyploid complex with a base chromosome number of seven. Not surprisingly, the present investigations regarding the base chromosome number agree completely with previous reports.

As shown in Table 3, R. berberifolia and R. beggeriana var. beggeriana were found to be diploid, whereas R. spinosissima var. spinosissima, R. spinosissima var. altaica, R. platyantha, and R. acicularis were found to be tetraploid. Because previous chromosome counts of R. platyantha were diploid (Ku and Robertson, 2003), this species has two ploidy levels in its area of distribution. The aforementioned tetraploid species had more advanced karyotypes of 1B or 2B than the diploids had. There is no direct evolutionary relationship between the variations of the

Table 3. Parameters of chromosomes for 13 tested wild Rosa samples in Xinjiang, northwestern China.

| Code | Species                        | Chromosome no. | Karyotype formula | Arm ratio | Lt/St ratio | Asymmetry index (%) | Centromere index (%) | Karyotype group |
|------|--------------------------------|----------------|-------------------|-----------|-------------|---------------------|----------------------|-----------------|
| 1    | R. berberifolia                | 2n = 2x = 14   | 12 m + 2 sm       | 1.17–1.82 | 1.68        | 59.82               | 35.43–46.16          | 1A              |
| 2    | R. spinosissima var. spinosissima | 2n = 4x = 28  | 28 m              | 1.03–1.91 | 2.69        | 52.60               | 42.47–49.43          | 1B              |
| 3    | R. spinosissima var. altaica   | 2n = 4x = 28   | 28 m              | 1.09–1.68 | 2.05        | 57.90               | 37.33–47.88          | 1B              |
| 4    | R. platyantha                 | 2n = 4x = 28   | 28 m (2 sat, 10)  | 1.03–1.60 | 2.36        | 55.61               | 38.42–49.23          | 1B              |
| 5    | R. beggeriana var. beggeriana | 2n = 2x = 14   | 6 m + 8 sm        | 1.29–2.60 | 1.63        | 67.77               | 27.75–43.72          | 2A              |
| 6    | R. beggeriana var. beggeriana | 2n = 2x = 14   | 12 m + 2 sm       | 1.08–1.73 | 1.62        | 56.52               | 36.61–48.14          | 2A              |
| 7    | R. beggeriana var. beggeriana | 2n = 2x = 14   | 10 m + 4 sm       | 1.15–2.59 | 1.79        | 58.18               | 27.82–46.60          | 2A              |
| 8    | R. acicularis                 | 2n = 4x = 28   | 22 m + 6 sm       | 1.01–2.21 | 2.24        | 56.39               | 31.12–49.61          | 2B              |
| 9    | R. laxa var. laxa             | 2n = 4x = 28   | 28 m              | 1.12–1.51 | 1.86        | 57.20               | 39.82–47.15          | 1A              |
| 10   | R. laxa var. mollis           | 2n = 2x = 14   | 12 m + 2 sm       | 1.10–1.82 | 1.49        | 57.96               | 35.51–47.73          | 1A              |
| 11   | R. laxa var. laxa             | 2n = 2x = 14   | 14 m              | 1.03–1.43 | 1.74        | 55.14               | 41.07–49.23          | 1A              |
| 12   | R. laxa var. laxa             | 2n = 2x = 14   | 14 m              | 1.15–1.44 | 2.14        | 56.39               | 40.95–46.42          | 2A              |
| 13   | R. laxa var. laxa             | 2n = 4x = 28   | 20 m + 8 sm       | 1.22–1.82 | 2.51        | 60.11               | 35.45–44.96          | 1B              |

*Lt/St ratio = ratio of chromosome length, the longest chromosome to the shortest one.*

*The length of satellites is not included in the chromosome length.*
ploidy level and the species, as we can see from the tetraploid sample 9, which possessed a very symmetric karyotype. This phenomenon was also observed by Luo et al. (2009) in traditional Chinese rose cultivars. It is believed that wild *Rosa* species in China and Chinese traditional rose cultivars are all supposed to exhibit karyological diversity (Jian et al., 2010b, 2012; Luo et al., 2009; Yang, 2009; Yang et al., 2008), and our study confirmed those previous reports. However, in strong contrast to the present study, previous authors (Jian et al., 2012; Song and Li, 1989) have reported that only two types of karyotypes (1A, 2A) occur in the wild *Rosa* species, whereas four types of karyotypes (1A, 2A, 1B, 2B) were found in our research. However, among the studied samples, all of the karyotypes consisted of metacentric or metacentric with submetacentric chromosomes. Meanwhile, lack of satellites implies terminal position of the nucleolar organizer region, not absence of at least one nucleolar organizer region.

Many species occur at only one ploidy level, but a few form a polyploid series (Wissemann, 2003). Available results have divided *R. laxa* on the basis of ploidy (Cairns et al., 2000; Yang, 2009; Yang et al., 2008; Zhu, 2011). In this study, we found diploid and tetraploid *R. laxa* in different floristic regions. *R. laxa* is obviously variable in morphology. Guo (2010) studied the natural populations of *R. laxa* in the Tianshan Mountains and believed the genetic diversity of *R. laxa* was abundant both within populations and among populations. In this study, the tetraploid karyotype of sample 13 was distinct in having the highest asymmetry index and the most evolved arm.
that further, more detailed karyotype analysis will change the understanding of their evolutionary history. However, it is unlikely that populations, investigating their genetic relationships and better point of view, the chromosome morphology or karyotype could and can be used in its taxonomy (Ghanbari et al., n.d.). From our varieties. The chromosome counts of genus *Rosa* are always complicated and often present problems in the precise 

2002; Stebbins, 1971). In *Plant Speciation*, Grant (1981) devoted five chapters (15% of the total text) to polyploidy, reflecting the importance of the topic both to the author and to plant biologists. Alpine and arctic floras have been regarded to have high frequencies of polyploidy (Brochmann et al., 2004; Ohba, 1988). Species in these restricted areas had to face harsh environmental conditions that led to the creation of new adaptive traits. The Tomur National Nature Reserve lies on the southern flank of the Tianshan Mountains (lat. 41°40’ N to 42°02’ N, long. 80°07’ E to 80°52’ E) in Wensu County, which is one of the biggest alpine nature reserves in China. The mean elevation of the reserve is 4000 m and its climate is cold and arid with a mean annual rainfall 600 to 700 mm. *R. laxa* in Tomur exhibits tetraploidy, in accordance with the aforementioned generalization that extreme habitats promote the evolution of polyploidy.

Unfortunately, there is little information in the literature focused on the use of wild *Rosa* species in Xinjiang, although these species were found to have many desirable traits (Chen, 1997; Muller et al., 2008), partly because of their complex genetic background. This information gap should be addressed as early as possible. Although not discussed in this article, attention must be given to the relationship between the ploidy difference and the success of distant hybridization. Detailed analysis of the *Solanum* polyploid series, where the endosperm behavior has been mapped out over numerous species in the primary and secondary gene pools of potato (Carpoto et al., 2003), suggests that the same evolutionary path may account for the origin and evolution of polyploidy taxa in *Rosa*. We infer from the text and our hybridization data (unpublished) that *Rosa* has an endosperm balance requirement of two maternal genomes to one paternal genome for successful growth of the endosperm early in seed development. Further research in the likely existence of endosperm balance numbers in *Rosa* should also be conducted.

The cytological data would supply chromosomal proofs not only for the taxonomy and evolution of genus *Rosa*, but also facilitate the exploitation of useful traits of wild *Rosa* species in breeding strategies. As we know, polyploids are often associated with particular characteristics such as increased heterozygosity and gene redundancy, proportional increases in gene expression, increase in cell and body size, changes in stomata size, and environmental stress tolerance (Coughlan, 2012; Levin, 1983).

Different ploidy levels among the *R. laxa* var. *laxa* (samples 9, 10, 11) and the botanical varieties with desirable traits (samples 12, 13) could provide diverse breeding materials. For example, with leathery leaflets, sample 12 could provide potential resistance against the powdery mildew and downy mildew (*Botrytis cinerea*). Tetraploid samples 9 and 13, which have the same ploidy level with most of the modern rose cultivars, will expectedly improve the success rate of distant hybridization. In sum, a better understanding of the cytological data that contribute to breeding systems and desired traits will definitely lead to improved modern rose cultivars.
