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Cytological studies of 14 Chinese species of *Parnassia* L. (Parnassiaceae) and its phylogenetic implications

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Abstract — The chromosome numbers and karyomorphology of 14 Chinese species of the genus *Parnassia* were investigated. The chromosome numbers of 11 species were reported for the first time. The report of 2n=48 for *P. monochrofolia* Franch was new to the Chinese species of the genus. There are about 30 species cytologically studied up to now. From the available data, the species of *Parnassia* with the basic chromosome numbers of x=7, 8 and 9 were found in China and the Himalayas, in which the more species with x=9, as well as mainly in western N America, while x=8 was only found in eastern N. America. Polyploidization was common in the genus, more extensively in Northern America. Based on our results and the previously reported data, the basic chromosome numbers and polyploidization are discussed. Combined with gross morphology and geographical distribution of *Parnassia*, the phylogenetic implications of the cytological data are also discussed. It is suggested that eastern Asia and western N America are probably the modern divergent centers of the genus.

Key words: China, Chromosome numbers, Karyomorphology, *Parnassia,* Phylogenetic Implications

INTRODUCTION

Parnassia L. was treated in a family of its own, Parnassiaceae (Gray 1821), which was not commonly recognized until Hutchinson (1969), Dahlgren (1983) and Takhtajan (1969, 1997). As a subfamily, it had been belonging to a member of Saxifragaceae for a long time (Dandy 1927; Engler 1930; Thorne 1976; Dahlgren 1980; Cronquist 1981; Ku 1987; Gu and Hultgård 2001). In Parnassioideae, *Parnassia* was also included in Droseraceae (Pace 1912; Schoenagel 1931), and closely related to Hypericaceae (Arber 1913, 1915; Jay 1971), or even Crassulaceae (Bensel and Palser 1975). Recent molecular systematic studies revealed that Parnassiaceae, including *Parnassia* and *Lepturopetalon* Ell. was a sister group of Celastraceae (Chase *et al*. 1995; Apg 1998; Soltis *et al*. 2000; Apg-II 2003).

The genus *Parnassia*, comprising about 70 species, occurred in the North Hemisphere, in which most species are growing in China and the Himalayas, with approximately 10 species in the North America (Ku 1987; Gu and Hultgård 2001; Simmons 2004). The center of distribution of *Parnassia* is in China and the Himalayan regions, to which most species are endemic (Ku 1987; Wu *et al*. 2003).

Previous cytological studies of *Parnassia* have investigated over 20 species in North America, Europe and the Himalayas (Erlandsson 1942; Hamel 1953; Packer 1964; Zhukova 1966; Hedberg 1967; Löve and Ritchie 1966; Gastony and Soltis 1977; Bye and Soltis 1979; Löve and Löve 1980, 1982; Funamoto 1986). Although as many as 63 species are distributed in China (Gu and Hultgård 2001), the chromosome counts have been only reported from about nine species (Löve 1954; Krogulevich 1978; Murin *et al*. 1980; Malla *et al*. 1979; 1981; Funamoto *et al*. 1994; 1996; 1997; 1998; 2001). Cytological studies may contribute to discussions on evolutionary tends through chromosome changes (Guerra 1990). As part of an integrated study on Chinese *Parnassia*, the present paper reported the chromosome numbers and karyomorphology of 14 species from China, in which 8 species are endemic to China. The chro-

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mosome numbers of 11 species are reported for the fist time.

MATERIALS AND METHODS

The materials studied with voucher specimens were showed in Table 1. All species studied were collected from fields of natural populations in Yunnan, Sichuan and Xinjiang, some species collected from the fields then cultivated for six to twelve months in the Botanical Garden at Kunming Institute of Botany, the Chinese Academy of Sciences.

Table 1 — Species of *Parnassia* investigated.

Species	Localities	Vouchers
P. bifolia	Tianshan, Xinjang	Ding Wu 03019
P. brevistyla	Wenzhang, Sichuan	Ding Wu 02014
P. chinensis	Dali, Yunnan	Ding Wu 02003
P. delavayi	Lijiang, Yunnan	Ding Wu 02004
P. epunctulata	Qiaojia, Yunnan	Ding Wu 03890
P. esquirolii	Yiliang, Yunnan	Ding Wu 03016
P. faberi	Emeishan, Sichuan	Ding Wu 02017
P. monochorifolia	Qiaojia, Yunnan	Ding Wu 03022
P. mysorensis	Lijiang, Yunnan	Ding Wu 02010
P. pusilla	Zhongdian, Yunnan	Ding Wu 03028
P. subscaposa	Zhongdian, Yunnan	Ding Wu 03012
P. tenella	Lijiang, Yunnan	Ding Wu 02002
P. trinervis	Deqin, Yunnan	Ding Wu 03064
P. venusta	Gongshan, Yunnan	Ding Wu 03022

Root tips were pretreated in 2 mM hydroxyquinolone for 4-6 hr at room temperate, and then fixed in carnoy's liquid (3 ethanol: 1 glacial acetic acid) at 4 °C for 6-8 hr, finally kept in 70% ethanol. After maceration in 1N hydrochloric acid and 45% acetic acid (v/ v) for 40-50 seconds, materials were stained with Carbol Fuchsin and squashed for microscopic observation. Permanent slides were made by using the standard liquid nitrogen method.

Five individuals were investigated for each species. Chromosome measurements were obtained from the photographs of the best mitotic metaphase plates of each species. The karyomorphological classification of the interphase and prophase chromosomes followed Tanaka (1971; 1977). The symbols for the description of karyotypes followed Leven *et al.* (1964). The symmetry of karyotypes classified according to the Stebbins (1971). Taxonomical treatment followed Gu and Hultgård (2001).

RESULTS

All fourteen species investigated shared the same simple chromocenter type of the resting chromosomes and the proximal type of mitotic prophase chromosome (Figs 1A, 1B). They had a common gradual chromosome decrease in length from the longest to the shortest chromosomes at mitotic metaphase chromosomes. The parameters of chromosomes in the 14 species of *Parnassia* are listed in Table 2.

Sect. *Saxifragstrum* Drude - *Parnassia esquirolii* Level. The karyotype formula is 2n=18=16m +2sm. The chromosome number was reported for the first time. Metaphase chromosome ranging from 2.8 μm to 1.6 μm, the ratio of the longest to the shortest chromosome is ca. 1.8, and belonging to Stebinns'2A type (Figs 1G, 2E). This species is endemic to China and distributed in northeastern Yunnan and western Guizhou.

***Parnassia tenella* Hook f. et Thomas.** The karyotype formula is 2n=18=16m+2sm. The chromosome number was reported for the first time. Metaphase chromosome ranging from 1.6 μm to 1.3 μm, the ratio of the longest to the shortest chromosome is ca. 1.2, and belonging to Stebinns'2A type (Figs 1E, 2C). It is distributed in southwestern China, extending to Nepal and Sikkim.

Sect. *Cladoparnassia* Engl. - *Parnassia faberi* Oliv. The karyotype formula is 2n=18=16m+2sm. The chromosome number was reported for the first time. Metaphase chromosome ranging from 2.4 μm to 1.9 μm, the ratio of the longest to the shortest chromosome is ca.1.3, and belonging to Stebinns'2A type (Figs 1F, 2D). This species is endemic to China and distributed in central Sichuan, northeastern Yunnan.

Sect. *Nectarobilobos* Ku - *Parnassia bifolia* Nekress. The karyotype formula is 2n=36=24m +12sm. The chromosome number was reported for the first time. Metaphase chromosome ranging from 2.6 μm to 1.0 μm, the ratio of the longest to the shortest chromosome is ca. 2.6, and belonging to Stebinns'2B type (Figs 1O, 2M). Distributed in Xinjiang, Hazakhistan.

Sect. *Nectarotrilobos* Drude - Subsect. *Xiphosandra* Franch. - *Parnassia brevistyla* Hand.-Mazz. The karyotype formula is 2n=14=12m +2sm. The chromosome number corresponded with the counts made by Funamoto, et al. (2001).

Table 2 — Chromosome comparison in the fourteen investigated species of *Parnassia* (RLR: relative length ratio; P: percentage of chromosomes with arm ratio over 2:1; M: median region; SM: submedian; X: chromosome basic number).

Species	Chromosome numbers (2n)	Chromosome sizes (μm)	RLR	P (%)	Symmetry class	M	SM	X
Sect. *Saxifragastrum*								
P. esquirolii	18	1.6-2.8	1.8	33.3	2A	16	2	9
P. tennella	18	1.3-1.6	1.2	16.7	2A	16	2	9
Sect. *Cladoparnassia*								
P. faberi	18	1.9-2.4	1.3	11.1	2A	16	2	9
Sect. *Nectarotrilobos*								9
P. brevistyla	14	2.7-4.2	1.5	28.7	2A	12	2	7
P. delavayi	14	4.1-5.8	1.4	28.7	2A	12	2	7
P. chinensis	18	1.6-2.4	1.5	33.3	2A	14	4	9
P. epunctulata	18	2.0-3.1	1.5	44.4	2A	16	2	9
P. mysorensis	18	1.7-3.1	1.8	22.2	2A	14	2	9
P. pusilla	18	3.9-4.5	1.2	11.1	2A	12	2	9
P. subscaposa	18	2.1-3.5	1.7	22.2	2A	14	4	9
P. trinervis	18	1.9-3.0	1.6	11.1	2A	14	4	9
P. venusta	18	2.1-2.6	1.2	11.1	2A	16	2	9
Sect. *Nectarobilobos*								
P. bifolia	36	1.0-2.6	2.6	29.1	2B	24	12	9
Sect. *Allolobos*								
P. monochorifolia	48	0.8-1.8	2.3	45.8	2B	30	18	8

Metaphase chromosome ranging from 4.1 μm to 2.7 μm, the ratio of the longest to the shortest chromosome is ca.1.5, and belonging to Stebbins'2A type (Figs 1C, 2A). This species is endemic to China and distributed in southwestern and northwestern China.

***Parnassia delavayi* Franch.** The karyotype formula is 2n=14=12m+2sm. The chromosome number agrees with the counts made by FUNAMOTO *et al.* (1998, 2001). Metaphase chromosome ranging from 5.8 μm to 4.1 μm, the ratio of the longest to the shortest chromosome is ca.1.4, and falling into Stebinns'2A type (Figs 1D, 2B). The species is distributed in southwestern, northwestern and central China and Bhutan.

Sect. *Nectarotrilobos* Drude - Subsect. *Nectarotrilobos* Ku - *Parnassia chinensis* French. The karyotype formula is 2n=18=14m+4sm. The chromosome number was reported for the first time. Metaphase chromosome ranging from 2.4 μm to 1.6 μm, the ratio of the longest to the shortest chromosome is c. 1.5, and belonging to Stebbins'2A type (Figs 1H, 2F). It is distributed in southwestern China, extending to Bhutan, northern Myanmar, Nepal and Sikkim.

***Parnassia epunctala* J. T. Pan** The karyotype formula is 2n=18=16m+2sm. The chromosome number was reported for the first time. Metaphase chromosome ranging from 3.1 μm to 2.0 μm, the ratio of the longest to the shortest chromosome is c. 1.5, and belonging to Stebbins'2A type (Figs 1K, 2I). This species is endemic to China and distributed in northwestern Yunnan.

***Parnassia mysorensis* Heyhe.** The karyotype formula is 2n=18=14m+4sm. The chromosome number was reported for the first time. Metaphase chromosome ranging from 3.1 μm to 1.7 μm, the ratio of the longest to the shortest chromosome is c. 1.8, and belonging to Stebinns'2A type (Figs 1J, 2H). Distributed in southwestern China, northern India, Sikkim.

***Parnassia pusilla* Wall. ex Arn.** The karyotype formula is 2n=18=14m+4sm. Metaphase chromosome ranging from 4.5 μm to 3.9 μm, the ratio of the longest to the shortest chromosome is c. 1.2, and belonging to Stebinns'2A type (Figs 1N, 2L). The species is distributed in southern Xizang, Bhutan, northern India, Nepal, and Sikkim.

***Parnassia subscaposa* C. Y. Wu ex Ku** The karyotype formula is 2n=18=14m+4sm. The chromosome number was reported for the first time. Metaphase chromosome ranging from 3.5 μm to 2.1 μm, the ratio of the longest to the shortest chromosome is c.1.7, and belonging to Stebinns'2A type (Figs 1I, 2G). This species is endemic to China and distributed in northwestern Yunnan.

***Parnassia trinervis* Drude**: The karyotype formula is 2n=18=14m+4sm. The chromosome number agrees with counts made by FUNAMOTO, *et al.* (1996). Metaphase chromosome ranging

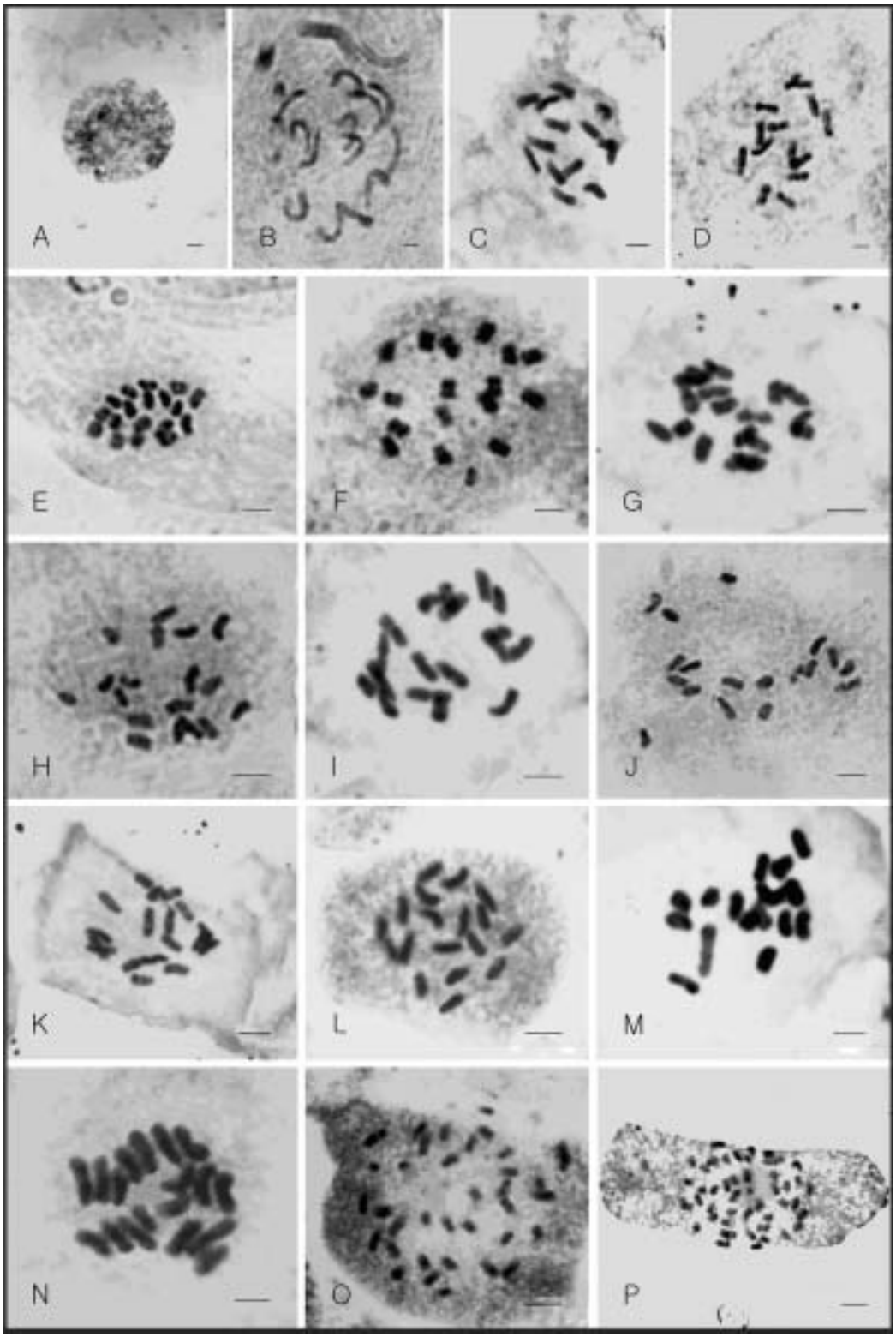

Fig. 1 — Karyomorphology of 14 *Parnassia* species. A: Resting state, B: Mitotic prophase, C: *P brevistyla*, D: *P. delavayi*, E: *P. tenella*, F: *P. faberi*, G: *P. esquirolii*, H: *P. chinensis*, I: *P. subscaposa*, J: *P. mysorensis*, K: *P. epunctulata*, L: *P. venusta*, M: *P. trinervis*, N: *P. pusilla,* O: *P. bifolia*, P: *P. monchorifolia*. All bar=3μm.

from 3.0 μm to 1.9 μm, the ratio of the longest to the shortest chromosome is c. 1.6, and belonging to Stebbins'2A type (Figs 1M, 2K). This species is endemic to China and distributed in southwestern and northwestern China.

***Parnassia venusta* Jien.** The karyotype formula is 2n=18=16m+2sm. The chromosome number was reported for the first time. Metaphase chromosome ranging from 2.6 μm to 2.1 μm, the ratio of the longest to the shortest chromosome is c. 1.2, and belonging to Stebbins'2A type (Figs 1L, 2J). This species is endemic to China and distributed in northwestern Yunnan.

Sect. *Allolobos* Ku - *Parnassia monochorifolia* French. The karyotype formula is 2n=48=30m +18sm. The hexaploid chromosome number was reported for the first time in China. Metaphase chromosome ranging from 1.8 μm to 0.7 μm, the ratio of the longest to the shortest chromosome is ca.2.3, and belonging to Stebinns'2B type (Figs 1P, 2N). This species is endemic to China and distributed in northeastern Yunnan.

DISCUSSIONS

1. Basic Chromosome Number Variation - The basic chromosome number is of importance to determine the systematic position of a taxon at higher taxonomic level (Raven 1975). As showed in Table 3, together with previously studied species, the chromosome numbers of about 30 species in the genus *Parnassia* were presently known, representing about 41% of the total number of species in the genus. Based on previous reports and our own studies, there are three basic chromosome numbers (*i.e.* x=7,8, and 9) in *Parnassia* (Funamoto *et al.* 1998; Simmons 2004).

The genus *Parnassia* might be divided into three groups, based on the chromosome base number. The first group with the basic chromosome number of x=9 was reported from about 20 species, accounted for more than 70% of species studied, and including type species of *Parnassia*, *i.e. P. palustris*. There were obvious differences in morphology among species, especially in the floral characteristics. These species distributed in N America had most highly elaborated and branched staminodia, while those in E Asia were with staminodia unlobbed or, when deeply lobbed, rarely more than half their length (Ku 1987; Wu *et al.* 2003). The second group included five species with the basic chromosome number x=8, led from 2n=32 and mainly distributed in N America. Two species with the same basic chromosome numbers were distributed in China, *Parnassia yunnunensis* var. *longistipitata*, which was of low and small, 3 minutely lobed staminodia. (Funamoto *et al.* 1998), and *P. monochorifolia* being with flat five-lobed staminodia. The third group with the basic chromosome number x=7 included *P. brevistyla* and *P. delavayi*, both from the Himalayas and SW China. Their fertile stamens were with the anther connection elongated beyond the anther sacs. Based on this character state, Frenchet (1897) proposed an alternative intrageneric classification, by dividing the genus into two sections, one of which consisted of *P. delavay*i and *P. brevistyla*. However, the odd difference of the chromosome base number in an Asian species *P. wightiana* (2n=36, Malla *et al.* 1981; 2n=14, Funamoto *et al.* 1998) suggested that *P. wightiana* needed to be reinvestigated by using material from different localities.

The center of diversity for *Parnassia* is in E Asia, especially in China and the Himalayas where the majorities of the species occur (Phillips 1982; Ku 1987; 1995; Wu *et al.* 2003). Most species with the basic chromosome number of x=9 were distributed in East Asia. Two species in North America had the same chromosome number, one being *P. palustris* which is the most widespread species of the genus, with populations in North America, Europe, and Asia, and south to Morocco (Korta 1972), the other being *P. kotzebuei*, which is distributed across Siberia and western North America. The chromosome numbers of *P. glauca* is very interesting, with two basic chromosome numbers x=8 (Gastony and Soltis 1977), and 9 (Löve and Löve 1977).

A second center of diversity is in N America where 10 species occur (Phillips 1982; Ku 1987 1995; Wu *et al.* 2003). *Parnassia townsedii* is the southernmost species and is endemic to the Sierra Madre Occidental of Mexico (Bye and Soltis 1979). The basic chromosome number of the western North America species is x=9 (Packer 1964; Bye and Soltis 1979; Jorgenson *et al.* 1977; Löve and Ritchie 1966; Funamoto *et al.* 1998), while the eastern N America species have a basic chromosome number of x=8 (Gastony and Soltis 1977; Löve and Ritchie 1966). It was suggested that the eastern species were more highly divergent from the western N America and Asian species (Philips 1982).

Based on the distribution of the three basic chromosome numbers, together with the morphological evidence, it is suggested here that X=9 might be original basic chromosome number in

Table 3 — Chromosome numbers and geographical distributions of *Parnassia* species

Species	Chromosome Numbers (2n)	Distributions	References
Sect. *Saxifragstrum*.			
P. esquirolii	2n=18	NE Yunnan, W Guizhou	The present study
P. tenella	2n=18	SW China; Nepel, Sikkim	The present study
P. yunnanensis var. *longistipitata*	2n=32	SW Yunnan, W Sichuan	Funamoto *et al*. 1997
Sect. *Cladoparnassia*			
P. faberi	2n=18	C Sichuan, NE Yunnan	The present study
Sect. *Nectarobilobos*			
P. bifolia	2n=36	Xijiang; Kazakhstan	The present study
Sect. *Nectarotrilobos*			
P. brevistyla	2n=14	SW, NW China	The present study
P. acuminum	2n=18	W Sichuan, S Qinghai	Funamoto *et al.* 1998
P. chinensis	2n=18	SW China; Bhutan, N Myanmar, Nepal, Sikkim	The present study
P. delavayi	2n=14	SW, NW, C China; Bhutan	The present study
P. epuenctulata	2n=18	NW Yunnan	The present study
P. laxianii	2n=18, 36	C Xinjiang; Kazakhstan, Mongolia, Si-beria	Krogulevich 1978
P. mysornsis	2n=18	SW China; N India, Sikkim	The present study
P. nubicola	2n=18	SW China; Afghanistan, Bhutan, India, Kashmir, Nepal, Pakistan	Hamel 1953
P. oreophila	2n=18, 36	NW, N China	Funamoto *et al.* 1994; 1996
P. pusilla	2n=18	S Xizang; Bhutan, N India, Nepal, Sikkim	The present study
P. scaposa var. *yushuensis*	2n=18	W Sichuan, S Xizang, S Qinghai	Funamoto *et al.* 1996
P. subscaposa	2n=18	NW Yunnan	The present study
P. trinervis	2n=18	NW Yunnan, Sichuan, Xizang, Qinghai, Gansu	The present study
P. venusta	2n=18	NW Yunnan	The present study
P. viridifolia	2n=18, 36	SW, NW China	Funamoto *et al*. 1998; 2001
Sect. *Allolobs*			
P. monochorifolia	2n=48	NE Yunnan	The present study
P. wightiana	2n=36	SW, NW, C China; SE Asia	Malla *et al.* 1981
	2n=14		Funamoto *et al*. 1998
Sect. *Parnassia*			
P. asarifolia	2n=32	Eastern N America	Löve and Ritchie 1966 Gastony and Soltis 1977
P. caroliniana	2n=32	Eastern N America	Gastony and Soltis 1977
P. fimbriata	2n=36	Western N America	Packer 1964; Taylor and Brochman 1966
P. glauca	2n=32	Eastern N America	Gastony and Slotis 1977
	2n=36		Löve and Löve 1977
P. grandifolia	2n=32	Eastern N America	Löve and Ritchie 1966
P. kotzebuei	2n=18, 36	Western N America; Si-beria	Jorgenson *et al*. 1958; Johnson and Packer 1968
P. palustris	2n=18,27, 36,45,54	N America; Europe; C Asia	Funamoto *et al*., 1998
P. townsedii	2n=36	Western N America	Bye and Soltis 1979

Parnassia, and x=8 and x=7 were derived from it by means of chromosome reorganization (such as chromosome fission, fusion and dysploidy). It is noted that the basic chromosome number x=7 is only reported in China. There is a tendency the chromosome number decrease (in evolution line) in the genus. However, further evidence is needed to test this hypothesis.

2. Polyploidization - Polyploidization has occurred extensively during the evolution of angiosperms (Stebbins 1971; Grant 1981; Masterson 1994; Ku *et al.* 2000). The importance of polyploidy as an active process was manifested by the estimated number of speciation events, as many as 2-4% (Otto and Whiffon 2000) and historical success of polyploidy in different floras

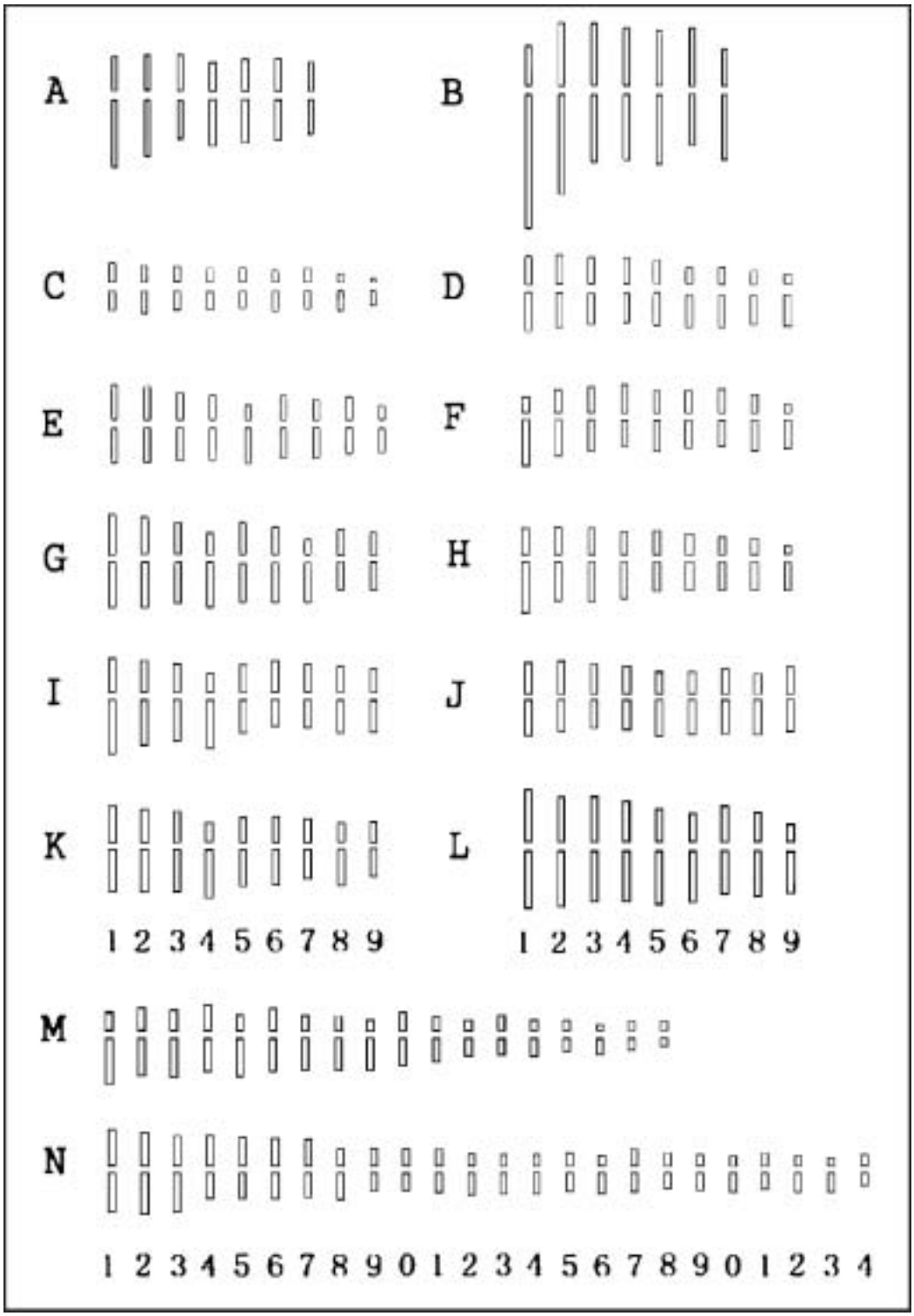

Fig. 2 — The haploid ideograms of 14 *Parnassia* species. A: *P. brevistyla*, B: *P. delavayi* C: *P. tenella,* D: *P. faberi,* E: *P. esquirolii*, F: *P. chinensis,* G: *P. subscaposa*, H: *P. mysorensis*, I: *P. epunctulata*, J: *P. venusta*, K: *P. trinervis*, L: *P. pusilla*, M: *P. bifolia*, N: *P. monchorifolia*.

(STEBBINS 1971). In *Parnassia*, as showed in Table 3, polyploidization appeared frequently, as many as 50 % of the observed species were polyploids.

Parnassia palustris is with wide geographical distribution throughout most of the Holarctic region. It includes diploid, triploid, tetraploid, pen-

taploid, and hexaploid individuals (2n=18, 27, 36, 45, and 54) (Funamoto *et al*. 1998 and references cited therein). Other species with both diploids and tetraploids are *P. kotzebuei* from Siberia and N America (2n=18 and 36) (Jorgenson *et al*. 1958; Löve and Ritchie 1966), *Parnassia laxmanii* from northern Asia extending to Xinjiang (2n= 18 and 36) (Krogulevich 1978; Murin *et al*. 1980), *Parnassia oreophyla* from China (2n=18 and 36) (Funamoto *et al*. 1994; 1996), *Parnassia viridifolia* from China (Funamoto *et al.* 1998; 2001). The tetraploids have been considered to be autoploids (e.g., *P. oreophyla*, Funamoto *et al*. 1996; *P. palustris,* Wentworth and Gornull 1996) or intraspecific hybrid polyploidy (e.g. *P. palustris*, Hultgärd 1987). Furthermore, the only difference in gross-morphology between diploid and tetraploid populations of *P. palustris* are the generally larger pollen grains and seeds in tetraploids (Hultgärd 1987). Rodriguez (1996) pointed out that demographic stochastic and iteroparity of a polyploidy can enhance its chance of successful establishment in a diploid population. This difference in colonizing ability between cytotypes might have helped autotetraploids to escape minority cytotype exclusion in diploid parental populations after the last glaciation. For instance, in Britain and Scandinavia, diploid populations of *P. palustris* have a southern distribution, whereas tetraploid populations have a more northern distribution (Hultgärd 1987; Wentworth and Gornall 1996). The tetraploids of *P. palustris* appear to be autopolyploids with no significant reduction in fertility (Wentworth and Gornall 1996), which were better than the diploids to spread north as the glaciers receded.

However, the present study revealed that most of the 14 studied species were diploids, mostly 2n=18, except for *P. brevistyla* and *P. delavayi* with 2n=14. In this report, two polyploids were *P. bifolia* from Xinjiang and Kazakhstan (2n=4x=36), and *P. monochorifolia* from northeastern Yunnan (2n=6x=48). The only other tetraploids was *P. yunnanensis* var. *longistiptata* with 2n=32 from southwestern Yunnan and western Sichuan (Funamoto *et al.* 1997). Obviously, fewer polyploids were reported in China, especially in southwestern China. Out of the 10 species distributed in N America, eight species including the Holarctic *P. palustris* were all polyploids (Table 3). Although most species distributed in Asia, only 6 species out of the 20 studied species were polyploidy (*P. laxmanii* 2n=18, 36, *P. oreophyla* 2n=18, 36, *P. viridifolia* 2n=18, 36; *P. yunnanensis* var. *longistiptata* 2n=32; *P. bifolia* 2n=36 and *P. monochorifolia* 2n=48). At present, only 20 out of the 63 of the Chinese species were studied, but it seems that the Asian species of *Parnassia* have been adopted a different evolutionary strategy from those of the North American species. As mentioned earlier, all three basic chromosome numbers were reported in Asia, while only x=9 and 8 were reported in N America.The polyploidization of the genus needs further study.

The fact that the tetraploid species were mostly distributed in N America, whereas diploids were mostly distributed in Asia, especially in the mountains of SW China implied that the mountains of SW China is the center of diversification. This area was considered to be one of the world's "hot spots" of biodiversity (Myers 1988; Boufford and Van Dijk 1999; Myers *et al*. 2000). More than 60% species of the genus were distributed in these mountains, accounted for about 80% species in China (Ku 1987; 1995).

3. Karyotype Evolution - *Parnassia* grows in temperate to arctic region, preferentially in open, moist habitats, from shore meadows to mountainsides. It is easy distinguished by the basal rosette of levels, generally with long peduncles, single-flowered inflorescences, penta-merous flowers, commissural stigmas, and the presence of staminodia opposite to petals. The classification of the genus heavily based on the shape of staminodia and the petals (Drude 1875; Engler 1930; Handel-Mazzetti 1941; Ku 1987; 1995; Wu *et al.* 2003).

Firstly, karyomorphology in *Parnassia* is more or less symmetric. Most studied species were with karyotype of Stebbins' 2A type. This is similar to that of *P. accuminum* (Funamoto *et al.* 2001), which had median-centromeric chromosomes of the chromosome complements in centromeric position at mitotic metaphase, while the other species had median- and submedian- centromeric chromosome. Obviously, the karyomorphology of *P. accuminum* was symmetric. According to Stebbins (1971), it is postulated that the karyotypes of *Parnassia* may have evolved towards the decrease of symmetry by the increase of median-centromeric chromosome in the chromosome complements. Second, it seems that the basic chromosome number x=7 in *P. brevistyla* and *P. delavayi* (both of the Sect. *Nectarotrilobos)* were caused by chromosome fusion. Both species had relatively larger chromosomes (see Table 2). For instance, the chromosomes of *P. brevistyla* are about twice larger than those of *P. chinensis* of the same section. *Parnassia delavayi* showed the chromosome

size twice larger than those of *P. viridiflora* (Funamoto *et al*. 1998), also the same section. The other seven species in Sect. *Nectarotrilobos*, all with smaller chromosomes, were with the basic chromosome number x=9.

4. Karyotype and Classification - Several different classifications were proposed for *Parnassia* (Drude 1875; Franchet 1897; Engler 1930; Handel-Mazzetti 1941; Ku 1987; 1995; Wu *et al*. 2003). Drude (1875) recognized four sections based on characteristic of the staminodes, ovary position, and carpel numbers. Ku (1987; 1995) recognized nine sections for the Chinese species. Philips (1982) recognized two sections for the N American species. In spite of the accumulating molecular data, chromosome information continues to be important in assessing phylogenetic relationships (Carr *et al.* 1999). Although the cytological data on *Parnassia* is not complete, it was concluded that the basic chromosome numbers for the genus are x=7, 8 and 9. Members of section *Parnassia* are primarily distributed in N America. Although *P. kotzebei* also extends into Siberia and *P. palustris* occurs throughout much of N America, Europe, and Asia. It was considered that Sect. *Parnassia* could be divided into two sections according to the basic chromosome numbers and geographical distributions (Philips 1982).

In addition, *Parnassia delavay*i and *P. brevistyla* possessed the feature of 3-lobed staminodia, were placed in Sect. *Nectarotriolbos* (Drude 1875; Engler 1930; Handel-Mazzetti 1941; Ku 1987; 1995). However, the basic chromosome number for *P. brevistyla* (2n=14) and *P. delavayi* (2n=14) is x=7. These species are restricted to China and Himalayas. The other characteristics were that their anther connectives elongated beyond the anther sacs. It was suggested that the both should be erected to a section of their own, as proposed by Franchet (1897) and Wu *et al.* (2003).

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