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## 獐牙菜属 5 种植物的核型研究

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**摘要:** 首次报道了中国 5 种獐牙菜属植物的染色体数目和核型。它们染色体中期核型和相对长度组分分别是: 四数獐牙菜为  $2n = 14 = 4m + 8sm + 2st = 2L + 6M_2 + 4M_1 + 2S$ ; 华北獐牙菜  $2n = 28 = 12m + 14sm + 2st = 6L + 8M_2 + 8M_1 + 6S$ ; 二叶獐牙菜为  $2n = 28 = 14m + 4sm + 10st = 2L + 14M_2 + 10M_1 + 2S$ ; 抱茎獐牙菜为  $2n = 20 = 6m + 12sm + 2st = 8M_2 + 12M_1$ ; 浙江獐牙菜为  $2n = 20 = 8m + 4sm + 8st = 8M_2 + 12M_1$ 。

**关键词:** 獐牙菜属; 染色体数目; 核型

**中图分类号:** Q 949      **文献标识码:** A

## A karyomorphological study on 5 species of *Swertia* (Gentianaceae)

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**Abstract:** The present paper reports the karyomorphological data of 5 species of *Swertia*. The karyotype formulae are as follows: *S. teraptera*  $2n = 14 = 4m + 8sm + 2st = 2L + 6M_2 + 4M_1 + 2S$ ; *S. wolfgangiana*  $2n = 28 = 12m + 14sm + 2st = 6L + 8M_2 + 8M_1 + 6S$ ; *S. bifolia*  $2n = 28 = 14m + 4sm + 10st = 2L + 14M_2 + 10M_1 + 2S$ ; *S. franchetiana*  $2n = 20 = 6m + 12sm + 2st = 8M_2 + 12M_1$ ; *S. hickinii*  $2n = 20 = 8m + 4sm + 8st = 8M_2 + 12M_1$ . The chromosome numbers and karyotypes of all species are reported for the first time.

**Key words:** *Swertia*; chromosome number; karyotype

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*Swertia* (Gentianeaceae) comprises 11 sections with about 160 species, mainly distributed in Northern temperate zone. Most sections and species are concentrated on western China, a few species in North American and African and only one species extending to Europe. Southwest China and its adjacent area are its major center of distribution and diversity<sup>[1]</sup>. However, karyomorphological investigations on *Swertia* from this region are very poor. Following our reports of karyomorphological studies on Chinese plants of Gentianeaceae<sup>[2,3]</sup>, the present paper contributes karyomorphology of 5 species in *Swertia*.

## 1 Materials and Methods

The materials and their localities are tabulated in Table 1. The voucher specimens are preserved in the herbarium of Northwest Plateau Institute of Biology, the Chinese Academy of Sciences, The People's Republic of China (HNWP).

**Table 1 Locality and chromosome numbers of the examined taxon in *Swertia***

Taxon	Material	Chrom. No.	Locality and Voucher specimen altitude
<i>S. tetraptera</i>	Ovary	2n= 14	Maqenm Qinghai, Xue Chun-ying 02, 3800 m
<i>S. bifolia</i>	Ovary	2n= 28	Guinai, Qinghai, Liu Jian-quan 12, 3900 m
<i>S. wolfgangiana</i>	Ovary	2n= 28	M aduo, Qinghai, Zhou L i-hua 2242, 3700 m
<i>S. hicknii</i>	Roots	2n= 20	M t Nangya, Anhui, Shao Jian-zhang 91083, 1500 m
<i>S. franchetiana</i>	Ovary	2n= 20	Changdu, Xizang, Liu Jian-quan 154, 3800 m

For the observations of ovaries, the method introduced by Liu<sup>[4]</sup> was taken. For the growing root tips, the procedure was as same as our former reports<sup>[2-3]</sup>. The karyotype formulae are estimated according to Leavan et al<sup>[5]</sup>. The terminology used for chromosome complement of relative length (C. R. L. ) is that defined by Kuo et al<sup>[6]</sup>. The classification of karyotype asymmetry follows Stebbins<sup>[7]</sup>. The intrachromosomal asymmetry index (A 1) and the interchromosomal asymmetry index (A 2) proposed by Romero Zarco<sup>[8]</sup> as well as index of the karyotypic asymmetry (A s k%) proposed by Hisao Arano<sup>[9]</sup> were adopted.

## 2 Results

### 2.1 *Swertia tetraptera* Maxim. (sect **Herteranthos**). Table 2, Plate I: 1, 5

This species exhibits the chromosome number of 2n= 14; the mitotic metaphase complement consists of 4 median, 8 submedian and 2 subterminal chromosomes. The complement of relative length shows 2 long (L), 6 longer (M 2), 4 shorter (M 1) and 2 short (S) chromosomes. The total length of the chromosome complement is 26  $\mu\text{m}$  and the mean length 3.14  $\mu\text{m}$ . The lengths range from 4.6 to 1.73  $\mu\text{m}$ . The chromosome bimodality is distinct. The karyotype asymmetry was categorized to be the 2B type. The karyotype asymmetry indices are A 1= 0.45, A 2= 0.29 and A s k%= 66.46. The chro-

mosome number and karyomorphology of this species are reported here for the first time

**Table 2 The chromosome parameters in *S. tetraptera***

Parameters <i>S. tetraptera</i>						
No.	RL	RS	RT	AR	PC	C. R. L
1	16.02	4.90	20.92	3.27	st	1.46(L)
2	11.73	5.34	17.07	2.20	sm	1.20(M2)
3	10.25	5.43	15.68	1.89	sm	1.10(M2)
4	8.32	6.13	14.75	1.36	m	1.01(M2)
5	8.32	4.82	13.14	1.73	sm	0.92(M1)
6	7.44	3.42	10.86	2.18	sm	0.76(M1)
7	4.38	3.50	7.88	1.25	m	0.55(L)

RL = relative length of long arm, RS = relative length of short arm, RT = relative total length of chromosome, AR = arm ratio, PC = position of centromere; m = median, sm = submedian, st = subterminal; C. R. L = chromosome complement of relative length

**Table 3 The chromosome parameters in *S. bifolia* and *S. wolfangiana***

Parameters <i>S. bifolia</i>							<i>S. wolfangiana</i>						
No.	RL	RS	RT	AR	PC	C. R. L	No.	RL	RS	RT	AR	PC	C. R. L
1	7.59	2.15	9.74	3.54	st	1.36(L)	1	6.01	5.21	11.22	1.15	m	1.57(L)
2	6.60	1.99	8.59	3.32	st	1.20(M2)	2	6.81	3.00	9.81	2.27	sm	1.37(L)
3	4.73	3.62	8.35	1.31	m	1.17(M2)	3	5.29	4.05	9.34	1.31	m	1.31(L)
4	4.65	3.10	7.75	1.86	sm	1.09(M2)	4	5.21	2.80	8.01	1.86	sm	1.13(M2)
5	5.48	2.07	7.55	2.65	sm	1.06(M2)	5	4.41	3.41	7.82	1.29	m	1.10(M2)
6	3.93	3.38	7.31	1.16	m	1.02(M2)	6	4.29	3.45	7.74	1.24	m	1.05(M2)
7	5.52	1.73	7.25	3.02	st	1.02(M2)	7	5.65	1.60	7.25	3.53	st	1.02(M2)
8	3.66	3.58	7.24	1.02	m	1.01(M2)	8	4.37	2.68	7.05	1.63	m	0.99(M1)
9	3.89	2.62	6.51	1.48	m	0.91(M1)	9	4.81	1.60	6.41	3.00	sm	0.90(M1)
10	3.77	2.74	6.51	1.38	m	0.91(M1)	10	4.21	2.20	6.41	2.09	sm	0.90(M1)
11	3.50	2.98	6.48	1.17	m	0.90(M1)	11	4.05	1.96	6.01	2.06	sm	0.84(M1)
12	4.97	1.23	6.20	4.03	st	0.87(M1)	12	3.01	1.48	4.49	2.03	sm	0.63(S)
13	4.77	0.87	5.64	5.45	st	0.79(M1)	13	2.60	1.48	4.08	1.76	sm	0.57(S)
14	2.70	2.03	4.73	1.33	m	0.66(S)	14	2.40	1.60	4.00	1.50	m	0.56(S)

See Table 2 for the explanation of abbreviations

## 2.2 *Swertia bifolia* Batal (sect **Rugosa**) Table 3; Plate 1: 2, 6

This species exhibits the chromosome number of  $2n = 28$ ; the mitotic metaphase

complement consists of 14 median, 4 submedian and 10 subterminal chromosomes. The complement of relative length shows 2 long (L), 14 longer (M2), 10 shorter (M1) and 2 short (S) chromosomes. The total length of the chromosome complement is  $58.06 \mu\text{m}$  and the mean length is  $4.15 \mu\text{m}$ . The lengths range from  $5.60$  to  $2.53 \mu\text{m}$ . The chromosome bimodality is indistinct. The karyotype asymmetry was categorized to be the 2B type. The karyotype asymmetry indices are  $A_1 = 0.53$ ,  $A_2 = 0.27$  and  $A_{sk} = 68.34$ . The chromosome number and karyomorphology of this species are reported here for the first time.

### 2.3 *Swertia wolfgangiana* Gruning (sect *Rugosa*), Table 3; Plate I: 3, 7

This species exhibits the chromosome number of  $2n = 28$ . The mitotic metaphase complement consists of 12 median, 14 submedian and 2 subterminal chromosomes. The complement of relative length shows 6 long (L), 8 longer (M2), 8 shorter (M1) and 6 short (S) chromosomes. The total length of the chromosome complement is  $48.13 \mu\text{m}$  and the mean length is  $3.44 \mu\text{m}$ . The lengths range from  $5.40$  to  $1.93 \mu\text{m}$ . The chromosome bimodality is distinct. The karyotype asymmetry was categorized to be the 2B type. The karyotype asymmetry indices are  $A_1 = 0.42$ ,  $A_2 = 0.30$  and  $A_{sk} = 63.35$ . The chromosome number and karyomorphology of this species are reported here for the first time.

### 2.4 *Swertia hickinii* Burk (sect *Ophelia*, ser. *Ramosae*), Table 4; Plate I: 3, 8

Table 4 The chromosome parameters in *S. hickinii* and *S. franchetiana*

Parameters <i>S. hickinii</i>							<i>S. franchetiana</i>						
No.	RL	RS	RT	AR	PC	C.R.L	No.	RL	RS	RT	AR	PC	C.R.L
1	3.59	8.23	11.82	2.29	sm	1.18 (M2)	1	5.71	6.62	12.33	1.16	m	1.22 (M2)
2	5.33	6.28	11.60	1.18	M	1.16 (M2)	2	3.58	7.76	11.34	2.17	sm	1.12 (M2)
3	5.15	5.89	11.04	1.14	m	1.10 (M2)	3	5.10	6.24	11.34	1.22	m	1.12 (M2)
4	4.59	5.63	10.22	1.23	m	1.02 (M2)	4	3.80	7.15	10.95	1.88	sm	1.08 (M2)
5	3.72	6.11	9.83	1.64	m	0.98 (M1)	5	2.93	6.85	9.78	2.34	sm	0.96 (M1)
6	2.25	7.40	9.65	3.29	st	0.97 (M1)	6	4.30	5.02	9.32	1.17	m	0.92 (M1)
7	1.95	7.49	9.44	3.84	st	0.94 (M1)	7	2.44	6.58	9.02	2.70	sm	0.89 (M1)
8	1.99	7.27	9.26	3.65	st	0.93 (M1)	8	2.13	6.71	8.84	3.15	st	0.86 (M1)
9	1.60	7.27	8.87	4.54	st	0.89 (M1)	9	2.47	6.24	8.71	2.52	sm	0.85 (M1)
10	2.38	5.89	8.27	2.47	sm	0.83 (M1)	10	2.24	6.24	8.47	2.79	sm	0.84 (M1)

See Table 2 for the explanation of abbreviations

This species exhibits the chromosome number of  $2n = 20$ . The mitotic metaphase complement consists of 8 median, 4 submedian and 8 subterminal chromosomes. The com-

plement of relative length shows 8 longer and 12 shorter chromosomes. The total length of the chromosome complement is  $23.10 \mu\text{m}$  and the mean length is  $2.31 \mu\text{m}$ . The lengths range from  $1.91$  to  $2.73 \mu\text{m}$ . The chromosome bimodality is indistinct. The karyotype asymmetry was categorized to be the 3A type. The karyotype asymmetry indices are  $A_1 = 0.50$ ,  $A_2 = 0.12$  and  $A_s k\% = 67.45$ . The chromosome number and karyomorphology of this species are reported here for the first time.

## 2.5 *Swertia franchetiana* H. Smith (sect **Ophelia**, ser. **Ramosae**), Table 4; Plate I: 1, 9

This species exhibits the chromosome number of  $2n = 20$ . The mitotic metaphase complement consists of 6 median, 12 submedian and 2 subterminal chromosomes. The complement of relative length shows 8 longer and 12 shorter chromosomes. The total length of the chromosome complement is  $26.69 \mu\text{m}$  and the mean length is  $2.63 \mu\text{m}$ . The lengths range from  $2.23$  to  $3.59 \mu\text{m}$ . The chromosome bimodality is indistinct. The karyotype asymmetry was categorized to be the 3A type. The karyotype asymmetry indices are  $A_1 = 0.46$ ,  $A_2 = 0.14$  and  $A_s k\% = 65.34$ . The chromosome number and karyomorphology of this species are reported here for the first time.

## 3 Discussion

The chromosome counts of *Swertia*<sup>[10]</sup> are mainly limited to the Japanese species<sup>[10]</sup> and the Western Himalayan species<sup>[11]</sup>. So far, chromosome numbers of  $2n = 60, 52, 28, 26, 24, 22, 20, 18, 16, 14$  have been recorded for the genus<sup>[10-15]</sup>. From the chromosome data available, one finds that some sections (e.g. sect. *Ophelia*) are polybasic while some sections (e.g. sect. *Rugosa*) have a constant basic chromosome number. However, it is still difficult to connect the chromosome data with the gross morphology. The mechanisms of chromosome variation in the genus are still puzzling. One may expect to find high chromosome diversity in the mountain regions of Western China, which is the area of the highest specific diversity for this genus. In turn, the result may contribute more clues to understand the evolutionary mechanisms of chromosome variation in this genus. The chromosome studies on more species from this region is currently undertaken in our lab, which will assist in solving the above problems.

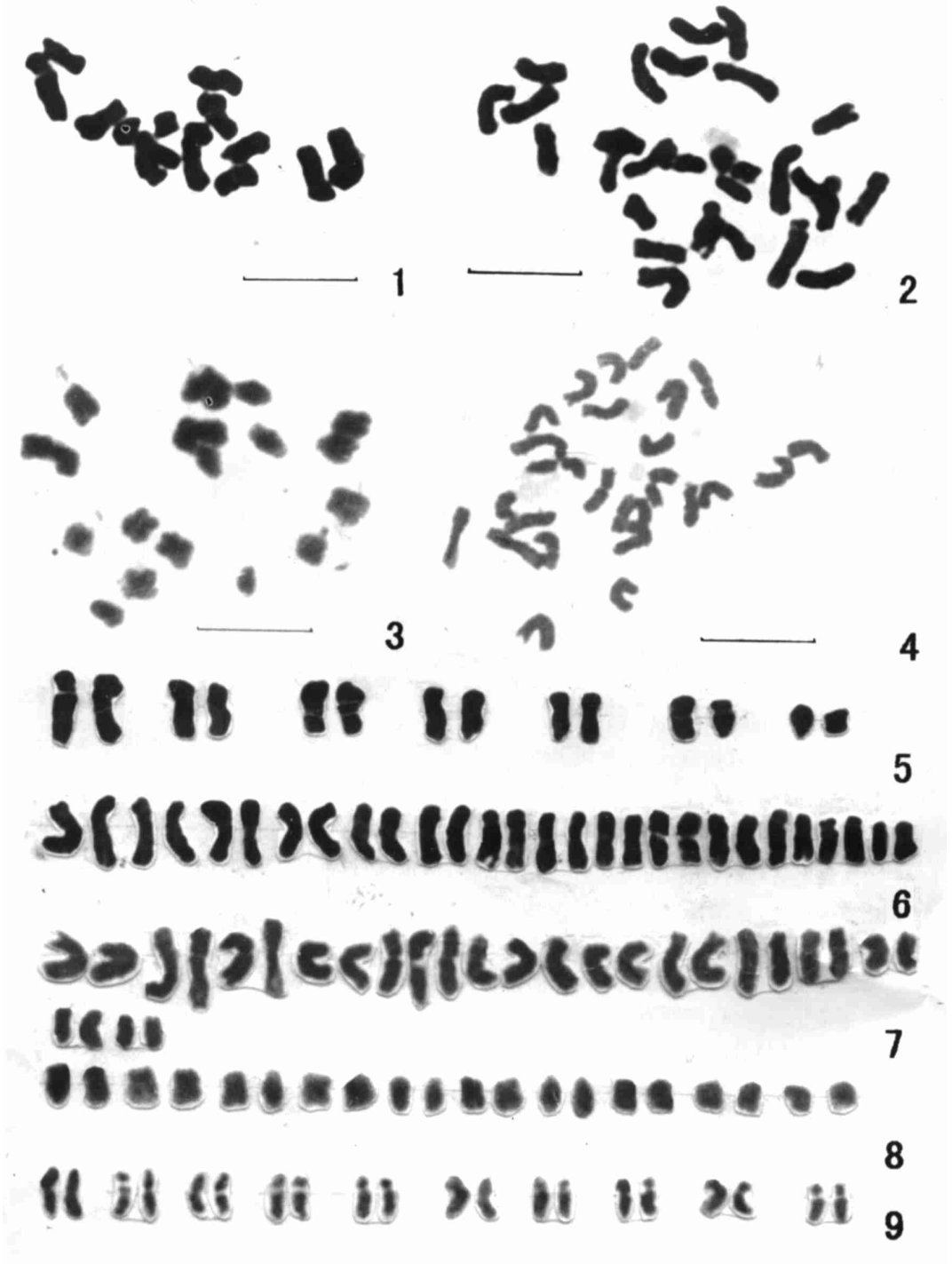
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### Explanation of Plate:

**Plate I** Fig. 1, 5. Somatic chromosomes of *S. tetraptera*, 1. Mitotic metaphase 5. Karyotypes Fig. 2, 6. Somatic chromosomes of *S. bifolia*, 2. Mitotic metaphase 6. Karyotypes Fig. 3, 7. Somatic chromosomes of *S. wolfgangiana*, 3. Mitotic metaphase 7. Karyotypes Fig. 4, 8. Somatic chromosomes of *S. hicknii*, 4. Mitotic metaphase 8. Karyotypes Fig. 9. Karyotypes of *S. franchetiana*. Scale bars= 10  $\mu$ m.



See explanation at the end of text