

CONTRIBUTIONS TO THE KARYOMORPHOLOGICAL
DATA AND THEIR TAXONOMIC IMPLICATIONS
OF SECT. *KUDOJA* AND SECT. *MONOPODIAE* IN *GENTIANA* L.*

Liu Jianquan Ho Tingnong Chen Shilong

(Northwest Plateau Institute of Biology, the Chinese Academy of Sciences, Xining, 810001)

Abstract

This paper reports the karyomorphological observations on one species and two varieties in Sect. *Kudoja*, and one species in Sect. *Monopodiae* of the genus *Gentiana* L. for the first time. The chromosomes of all taxa under study are commonly of the complex chromocenter type and interstitial type respectively at the resting stage and mitotic-prophase. The karyotype formulas are: *G. altorum* $2n = 24 = 16m + 8sm = 2L + 6M_2 + 16M_1$; *G. arethusae* var. *delicatula* $2n = 24 = 16m + 8sm = 2L + 6M_2 + 16M_1$; *G. veitchiorum* var. *futtereri* $2n = 24 = 22m(2SAT) + 2sm = 12M_2 + 10M_1 + 2S$ and *G. cephalantha* $2n = 24 = 18m(4SAT) + 6sm = 2L + 8M_2 + 14M_1$. The karyomorphological characteristics of Sect. *Kudoja* are summarized and the systematic position of sections *Kudoja* and *Monopodiae* are also discussed.

Key words: *Gentiana*; Sect. *Kudoja*; Sect. *Monopodiae*; Karyomorphology; Cytotaxonomy

In the genus *Gentiana* L., Sect. *Kudoja*, as circumscribed by Satake & Toyokuni in 1960, comprises 3 series and 27 species and Sect. *Monopodiae*, a monoserial section, consists of 10 species. Both sections are distributed in C. & SE. Asia; Sect. *Monopodiae* from SW. China through C. & S China to Indo-China and Indonesia; Sect. *Kudoja* from Kashmir, along the Himalayas to W. China and one species (*G. yakushimensis*) extending into Taiwan of China and the Yakushima Island of Japan. The overlapping distribution area of both sections occurs in W. Sichuan and NW. Yunnan [1]

The chromosome numbers have been reported for six species in Sect. *Kudoja* and for five species in Sect. *Monopodiae* by Zhukova (1967), Hsu (1968), Yuan & Kupfer (1993), Chen et al. (1997) and Ho et al. (1997), etc. (Table 1). However, karyomorphological studies are only limited to four species of Sect. *Kudoja* (Table 2) by Yuan & Kupfer (1993). This paper is the third in a series of reports (Ho et al. 1997; Chen et al. 1997) dealing with karyomorphological observations on Chinese gentians. We attempt to add more chromosome data on the genus *Gentiana*, with a hope to have a better understanding on the cytotaxonomy of the genus.

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Table 1 The chromosome numbers of Sect. *Kudoa* and Sect. *Monopodiae*

Taxon	Locality and Altitude	Chrom. No.	Reference or Voucher
	Specimens		
Sect. <i>Kudoa</i>			
<i>G. stipitata</i>			
subsp. <i>tizuensis</i>	Litang, Sichuan, 3800 m	26	Chen et al. 1997 ^[5]
<i>G. szechenyii</i>			
(<i>G. callistantha</i>)	Xiahe, Gansu, 2950 m	26	Yuan & Philippe 1993 ^[4]
<i>G. yakushimensis</i>	Japan	26	Shigenbu 1984 ^[17]
<i>G. arethusae</i>			
var. <i>delicatula</i>	Deqin, Yunnan, 3800 m	24	Liu Jianquan 320 *
<i>G. altorum</i>	Kangding, Sichuan, 3600 m	24	Liu Jianquan 290 *
<i>G. cachemirica</i>	Unknown	16	Zhukova 1967 ^[3]
<i>G. veichiorum</i>	Litang, Sichuan, 3600 m	24	Chen et al. 1997 ^[5]
	Xiahe, Gasu, 2950 m	24	Yuan & Philippe 1993 ^[4]
var. <i>futtereri</i>	Zokog, Qinghai, 2770 m	24	Liu Shangwu 3550 *
<i>G. ampla</i>	Lijiang, Yunnan, 3700m	24	Chen et al. 1997 ^[5]
<i>G. sino-ornata</i>	Xiahe, Gansu, 3500 m	48	Yuan & Philippe 1993 ^[4]
<i>G. lawrencei</i>			
var. <i>farreri</i>	Menyuan, Qinghai, 3500m	48	Chen et al. 1997 ^[5]
(<i>G. farreri</i>)	Xiahe, Gansu, 2950 m	48	Yuan & Philippe 1993 ^[4]
	Maqu, Gansu, 3200 m	48	Yuan & Philippe 1993 ^[4]
	Menyuan, Qinghai, 3500 m	48	Chen et al. 1997 ^[5]
Sect. <i>Monopodiae</i>			
<i>G. cephalantha</i>	Lijiang, Yunnan, 3000m	24	Liu Jianquan 352 *
<i>G. duclouxii</i>	Kunming, Yunnan, 2800m	24	Yuan & Philippe 1993 ^[4]
<i>G. rigescens</i>	Kunming, Yunnan, 2000m	24	Yuan & Philippe 1993 ^[4]
	Dali, Yunnan, 2300m	24	Yuan & Philippe 1993 ^[4]
<i>G. melandrifolia</i>	Dali, Yunnan, 2100m	n=12	Yuan & Philippe 1993 ^[4]
<i>G. davidii</i>			
var. <i>formosana</i>			
(<i>G. formosana</i>)	Unknown	26	Hsu 1968 ^[3]

* " " indicates voucher specimens for the materials in the present paper.

Materials and Methods

The localities and origin of 4 taxa under study are tabulated in Table 2. The voucher specimens are preserved in the herbarium of Northwest Plateau Institute of Biology, the Chinese Academy of Sciences (HNWP).

The method taken in the present paper is the same as that described by Ho et al. (1997). The symbols

for the karyotype descriptions followed Levan et al. (1964). The terminology used for chromosome complement of relative length (C.R.L.) was according to Kuo et al. (1972). The classification of karyotype asymmetry followed Stebbins (1971). The intrachromosomal asymmetry index (A1) and the interchromosomal asymmetry index (A2) proposed by Romero Zarco (1986) as well as index of the karyotypic asymmetry (As.K%) proposed by Hisao Arano (1963) were adopted.

Table 2 The origins and localities of the studied taxa

Taxon	Locality and Altitude	Chrom. No.	Voucher specimen
<i>G. arethusae</i>			
var. <i>delicatula</i>	Deqin, Yunnan, 3800m	24	Liu Jianquan 320
<i>G. altorum</i>	Kangding, Sichuan, 3600m	24	Liu Jianquan 290
<i>G. weichiorum</i>			
var. <i>futtereri</i>	Zokog, Qinghai, 2770m	24	Liu Shangwu 3550
<i>G. cephalanth</i>	Lijiang, Yunnan, 3000m	24	Liu Jianquan 352

Results

The resting chromosomes of all taxa showed several darkly stained, aggregated chromocenters and several large heteropycnotic bodies varying in size and number (Plate I: 1) in the their nuclei. Thus, the resting chromosomes could be classified as the complex chromocenter type.

The heterochromatic segments were found in the distal, proximal and interstitial regions of the prophase chromosomes of all taxa (Plate I: 2). Thus, the mitotic-prophase chromosomes could be classified as the interstitial type.

1. *Gentiana altorum* H. Smith ex Marq. [Sect. *Kudoa*] Table 3, 5; Plate I: 6, 10.

The chromosomes at mitotic-metaphase were counted to be $2n = 24$ with 16 median and 8 submedian chromosomes. The complement of relative length exhibits 2 long (2L), 6 longer (6M₂) and 16 shorter (16M₁) chromosomes. The chromosome complement has the total length of 34.46 μm . The mean length is 2.87 μm with lengths ranging from 2.22 to 4.22 μm . The chromosome bimodality is indistinct. The karyotype was categorized as 2A type.

The chromosome number and karyomorphology of this species are reported for the first time.

2. *Gentiana arethusae* Burk. var. *delicatula* Marq. [Sect. *Kudoa*] Table 3, 5; Plate I: 1, 2, 5, 8.

This species has the chromosome number of $2n = 24$ at mitotic-metaphase with 16 median and 8 submedian chromosomes. The complement of relative length shows 2 long (2L), 6 longer (6M₂) and 16 shorter (16M₁) chromosomes. The total length of the chromosome complement is 31.04 μm and the mean length 2.59 μm . The lengths range from 2.06 to 3.56 μm . The chromosome bimodality is indistinct. The karyotype was classified as 2A type.

The chromosome number and karyomorphology of this species are reported here for the first time.

Table 3 The chromosome parameters in *G. altorum* and *G. arethusae* var. *delicatula*

<i>G. altorum</i>						<i>G. arethusae</i> var. <i>delicatula</i>					
No.	RL	RS	RT	AR	PC	No.	RL	RS	RT	AR	PC
1	7.25	4.99	12.24	1.45	m	1	6.31	5.16	11.47	1.22	m
2	5.89	4.35	10.24	1.35	m	2	5.74	4.59	10.33	1.25	m
3	5.54	4.18	9.72	1.33	m	3	5.85	2.98	8.83	1.96	sm
4	5.46	3.63	9.09	1.50	m	4	4.59	4.01	8.60	1.14	m
5	5.25	2.93	8.18	1.79	sm	5	5.73	2.52	8.25	2.27	sm
6	5.08	2.81	7.89	1.81	sm	6	4.59	3.44	8.03	1.33	m
7	4.09	3.71	7.80	1.10	m	7	5.16	2.87	8.03	1.80	sm
8	5.63	2.09	7.72	2.69	sm	8	4.47	3.44	7.91	1.30	m
9	3.63	3.54	7.16	1.03	m	9	4.24	3.33	7.57	1.27	m
10	4.00	2.96	6.96	1.35	m	10	4.24	2.98	7.22	1.42	m
11	3.45	3.08	6.53	1.12	m	11	3.67	3.44	7.11	1.07	m
12	4.18	2.26	6.44	1.85	sm	12	4.36	2.29	6.65	1.90	sm

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.

3. *Gentiana veichiorum* var. *futtereri* (Diels et Gilg) T N Ho. [Sect. *Kudoa*] Table 4, 5; Plate I: 4, 9.

The chromosome number at mitotic-metaphase was found to be $2n=24$ with 22 median and 2 submedian chromosomes. On the short arms of the third pair chromosomes, two satellites were detected. The complement of relative length shows 12 longer ($12L_1$), 10 shorter ($10M_2$) and 2 short ($2M_1$) chromosomes. The chromosome complement has a total length of $39.28 \mu\text{m}$ and a mean length of $3.05 \mu\text{m}$. The lengths range from 2.39 to $4.09 \mu\text{m}$. The chromosome bimodality is indistinct. The karyotype was formulated as 2A type.

The chromosome number and karyomorphology of this species are reported for the first time.

4. *Gentiana cephalantha* Franch. ex Hemsl. [Sect. *Monopodiae* (H. Smith) T. N. Ho, Table 4, 5; Plate I: 3, 7.

This species shows the chromosome number of $2n=24$. The mitotic-metaphase chromosome complement consists of 18 median and 6 submedian chromosomes. Satellites were detected on the 7th and 8th pairs of chromosomes. The complement of relative length exhibits 2 long, 8 longer and 14 shorter chromosomes. The total length of the chromosome complement is $31.37 \mu\text{m}$ with the length range from 2.07 to $3.92 \mu\text{m}$ and the mean length of $2.61 \mu\text{m}$. The chromosome bimodality is indistinct. The karyotype was classified as 1A type.

The chromosome number and karyomorphology of this species is reported for the first time.

Table 4 The chromosome parameters in *G. cephalantha* and *G. veichiorum* var. *futtereri*

<i>G. cephalantha</i>						<i>G. veichiorum</i> var. <i>futtereri</i>					
No.	RL	RS	RT	AR	PC	No.	RL	RS	RT	AR	PC
1	7.97	4.53	12.50	1.76	sm	1	5.89	4.53	10.42	1.32	m
2	5.80	3.98	9.78	1.46	m	2	5.62	4.71	10.33	1.19	m
3	6.15	3.54	9.69	1.74	sm	3	5.44	4.53	9.97	1.21	m

续表

<i>G. cephalantha</i>						<i>G. veitchiorum</i> var. <i>futtereri</i>					
No.	RL	RS	RT	AR	PC	No.	RL	RS	RT	AR	PC
4	5.58	3.63	9.21	1.54	m	4	4.98	4.53	9.51	1.10	m
5	4.78	3.76	8.54	1.27	m	5	4.80	4.08	8.88	1.18	m
6	4.11	3.86	7.97	1.06	m	6	4.80	3.99	8.79	1.20	m
7	4.33	3.54	7.87	1.23	m	7	4.26	3.99	8.25	1.07	m
8	3.89	3.41	7.30	1.14	m	8	4.08	3.62	7.70	1.13	m
9	3.67	3.28	6.95	1.12	m	9	4.26	2.72	6.98	1.57	m
10	3.63	3.19	6.82	1.14	m	10	4.08	2.72	6.80	1.50	m
11	3.41	3.32	6.73	1.03	m	11	3.44	2.90	6.34	1.19	m
12	4.21	2.39	6.60	1.76	sm	12	4.17	1.90	6.07	2.19	sm

See table 3 for explanation of abbreviations.

Table 5 The karyotype information in section *Kudoa* and *Monopodiaceae*

Taxon	Population	Karyotype structure	Length (μm)	L/S	P	T	A1	A2	As.K%
Sect. <i>Kudoa</i>									
<i>G. szechenyii</i>									
(<i>G. callistanta</i>)	Gansu	$2n=2m(\text{SAT})+24\text{sm}$	1.80-3.10	1.70	0.00	1A	0.176	0.143	?
<i>G. veitchiorum</i>	Gansu	$2n=18m+6\text{sm}$	2.70-4.40	1.63	0.00	1A	0.306	0.131	?
var. <i>futtereri</i>	Qinghai	$2n=22m(2\text{SAT})+2\text{sm}$ $=12M_2+10M_1+2S$	2.39-4.09	1.72	0.08	2A	0.21	0.19	55.79
<i>G. sino-ornata</i>	Gansu	$2n=40m+8\text{sm}$	2.00-3.11	1.52	0.13	2A	0.298	0.130	?
<i>G. altorum</i>	Sichuan	$2n=16m+8\text{sm}$ $=2L+6M_2+16M_1$	2.22-4.22	1.70	0.23	2A	0.300	0.210	59.46
<i>G. arethusae</i>	Yunnan	$2n=16m+8\text{sm}$ $=2L+6M_2+16M$	2.06-3.56	1.76	0.15	2A	0.290	0.160	58.95*
var. <i>delicatula</i>									
<i>G. yakushimensis</i>	Japan	$2n=24m(2\text{SAT})+2\text{sm}$ $=12M_2+10M_1+2S$	1.50-3.10	2.07	0.00	1B	0.247	0.174	57.34**
Sect. <i>Monopodiaceae</i>									
<i>G. cephalantha</i>	Yunnan	$2n=18m(4\text{SAT})+6\text{sm}$ $=2L+8M_2+14M_1$	2.07-3.92	1.89	0.00	1A	0.23	0.21	57.55

L: length of the longest chromosome in a karyot;

S: length of the shortest chromosome in a karyotype;

P: proportion of the chromosomes of which the arm ratios are more than 2 in a karyotype;

T: referring to the classification of karyotypes of Stebbins (1971)^[11];

A1 and A2: the intrachromosomal and interchromosomal asymmetry index defined by Romero (1986)^[12];

AS.K %: Karotypic asymmetry proposed by Hisao (1963)^[10];

*: referring to reports of Yuan & Philippe 1993^[4]. **: referred to Shigenobu 1984^[17].

Discussion

1. Four species and one variety of Sect. *Monopodiaceae* of *Geniana* L. (Table 1) were counted chromosomes. But the karyotype study is only limited to one species presented in the present paper (Table 2). Therefore, it is still difficult to summarize the karyomorphological characteristics of Sect. *Monopodiaceae*.

2. All the three taxa under study in Sect. *Kudoa* have the same chromosome number $2n = 24$, $X = 12$ and the similar symmetrical karyotypes, which are congruent with the previous karyomorphological reports on this section. According to the available data (Table 1 and Table 2), the karyomorphological characteristics of Sect. *Kudoa* may be summarized as follows. (1) The resting and mitotic-prophase chromosomes are of the complex chromocenter type and the interstitial type respectively. (2) Although the different numbers of $2n = 16$, 24 , 26 and 48 are now found in 8 species and 2 varieties of the whole section, the commonest chromosome number is $2n = 24$, $X = 12$. The chromosome number of $2n = 16$ reported by Zhukova (1967) for *G. cachemirica* deviated far from the norm of this section and needs to be confirmed. The basic number of Sect. *Kudoa* might be $X = 12$. (3) The chromosome complement consists of median (m) and submedian (sm) chromosomes with no distinct satellites. (4) The chromosome complement comprises mainly M_2 and M_1 , and a few L and S. The chromosomes show a gradual decrease from the longest to the shortest with no obvious bimodality. (5) The karyotypes, classified as 1A and 2A, are very symmetrical. In addition, the intrachromosomal asymmetry index A_1 ranges from 0.176 to 0.306 and 0.263 in mean while the interchromosomal asymmetry index A_2 from 0.143 to 0.190 and 0.161 in mean, and $As.K\%$ varies from 55.79 to 59.46. (6) The chromosome lengths range from 1.80 to 4.40 μm . The karyomorphological characteristics of all the taxa studied in Sect. *Kudoa* are very similar to those found in other sections of *Gentiana*.

3. The ploidy levels in Sect. *Kudoa* usually vary with the increase of the elevation. Two ploidy levels (diploids and tetraploids) were found in Sect. *Kudoa*. According to the irreversibility law of the ploidy level from low to high, tetraploids are undoubtedly more advanced than diploids. In Sect. *Kudoa*, the tetraploids were found on areas of high altitudes apparently more in number than those on areas of low altitudes. For example, *G. futtereri* and *G. szechenyii* at the altitude 2770~2950 m were found to be diploids whereas *G. sino-ornata* and *G. lawrencei* var. *farreri* on high mountains of altitudes 3500~4900 m were tetraploids.

4. Sect. *Kudoa* and Sect. *Monopodiae* were placed under Sect. *Frigida* as two of the four parallel series by Marquand (1937). However, a cladistic analysis of *Gentiana* indicated these four series were apparently aggregated into two independent and parallel lines. Sect. *Kudoa* and Sect. *Monopodiae* of the same line share three synapomorphies (plant with a terminal vegetative rosette, calyx lobes subequal and triangular to narrowly triangular, rhizome short slender and distinct). Sect. *Kudoa* is more advanced than Sect. *Monopodiae* by having more apomorphies (upper stem leaves similar to linear-spatulate or linear calyx lobes; flower solitary and terminal; corolla plicate symmetrical and narrowly triangular). The two sections are similar to Sect. *Frigida* in having the same dominant number $X = 12$, and seed coats covered with membranous lamellae to form honeycomb-like pits, but different from Sect. *Frigida* in the stem leaves increasing in size and crowded towards the stem apex, and calyx tube not split on one side. Sect. *Frigida* is a relatively isolated group and distantly related to Sect. *Kudoa* and sect. *Monopodiae* because it has more plesiomorphies (highly developed intracalycular membrane, calyx tube split down one side with irregular teeth, complex cyme with many lax, pedicellate flowers, etc.).

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龙胆属华丽组和多枝组植物的核型资料及其分类学意义

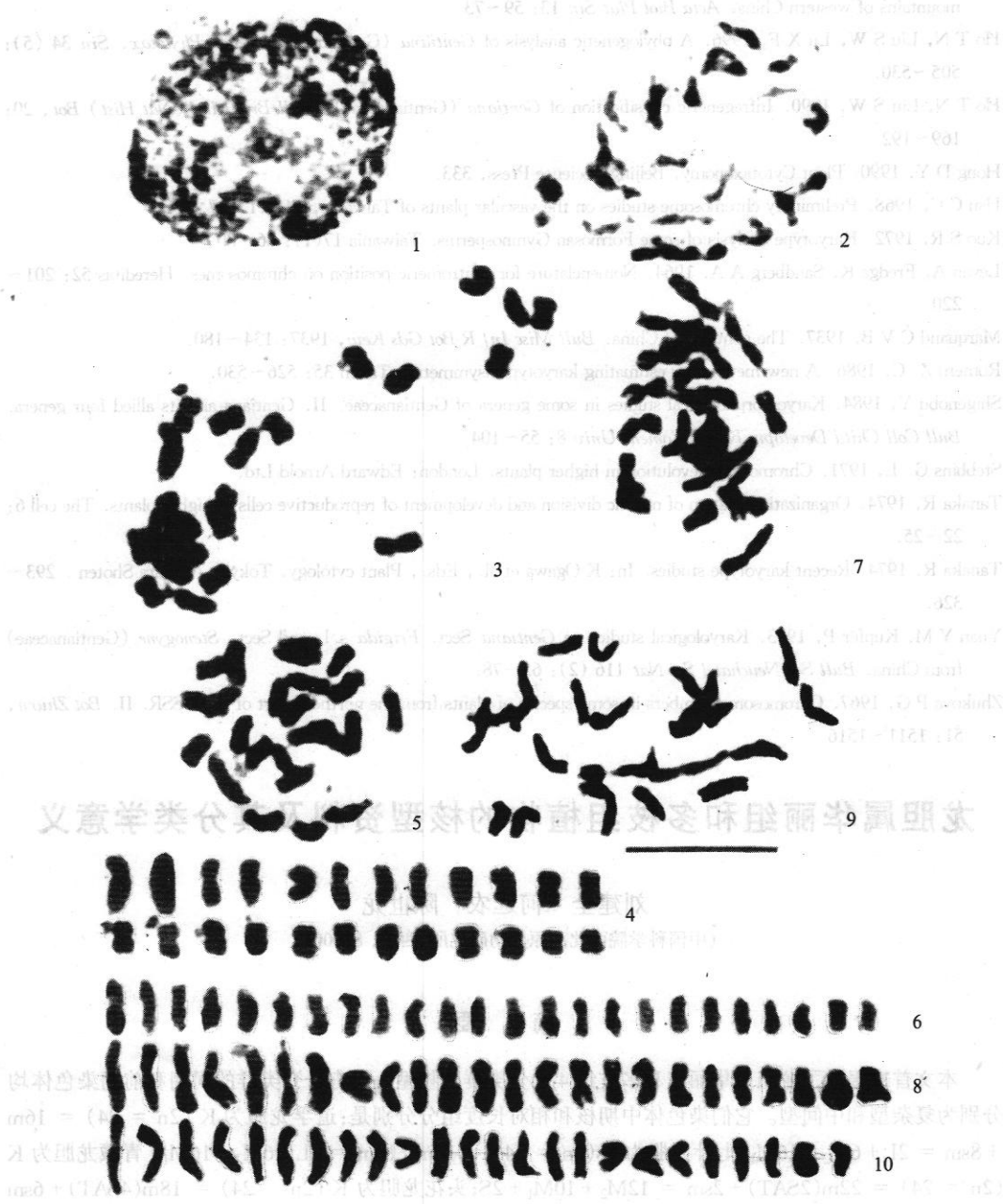
刘建全 何廷农 陈世龙

(中国科学院西北高原生物研究所, 西宁, 810001)

摘 要

本文首次报道了龙胆属华丽组和多枝组 4 个分类群的核型。所有研究类群的间期和前期染色体均分别为复杂型和中间型。它们染色体中期核和相对长度组分分别是: 道孚龙胆为 $K(2n = 24) = 16m + 8sm = 2L + 6M_2 + 16M_1$; 七叶龙胆为 $K(2n = 24) = 16m + 8sm = 2L + 6M_2 + 16M_1$; 青藏龙胆为 $K(2n = 24) = 22m(2SAT) + 2sm = 12M_2 + 10M_1 + 2S$; 头花龙胆为 $K(2n = 24) = 18m(4SAT) + 6sm = 2L + 8M_2 + 14M_1$ 。本文总结了华丽组的核型特征, 还讨论了华丽组和多枝组的系统位置。

关键词: 龙胆属; 华丽组; 多枝组; 核型; 细胞分类



1, 2, 5, 6. Somatic chromosomes of *Gentiana arethusae* var. *delicatula*: 1. Resting stage. 2. Mitotic prophase.
 3, 4. Somatic chromosomes of *G. cephalata*: 3. Mitotic metaphase. 4. Karyotypes.
 7, 8. Somatic chromosomes of *G. veichiorum* var. *futtereri*: 7. Mitotic metaphase. 8. Karyotypes.
 9, 10. Somatic chromosomes of *G. altorum*: 9. Mitotic metaphase. 10. Karyotypes. Scale bars = 10 μ m