Karyological studies on Gentiana sect. Frigida s.l. and sect. Stenogyne (Gentianaceae) from China

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Objekttyp: **Article**

Zeitschrift: **Bulletin de la Société Neuchâteloise des Sciences Naturelles**

Band (Jahr): **116 (1993)**

PDF erstellt am: **20.09.2024**

Persistenter Link: https://doi.org/10.5169/seals-89407

KARYOLOGICAL STUDIES ON *GENTIANA* SECT. *FRIGIDA* S. L. AND SECT. *STENOGYNE* (*GENTIANACEAE*) FROM CHINA

by

YONG-MING YUAN AND PHILIPPE KÜPFER

WITH 19 FIGURES AND 3 TABLES

INTRODUCTION

Section *Frigida* Kusn. s. l. refers to the circumscription of the section by SMITH (1961) and PRINGLE (1978). They lumped section *Isomeria* Kusn. with the section *Frigida* Kusn. both of which were recognized by KUSNEZOW (1895) in his first comprehensive monograph of the genus. But some other authors split the group into several sections or even genera; for examples, LÖVE & LÖVE (1972) established two genera for this group, mainly according to the basic chromosome numbers (see below): the monotypic *Favargera* Löve et Löve based on *Favargera froelichii* (Jan ex Reichenb.) Löve et Löve (= *Gentiana froelichii* Jan ex Reichenb.) and *Gentianodes* Löve et Löve which included all the other members of this group. But, in their very recent revision of the classification of *Gentiana* L., HO (1985) and HO & LIU (1990) adopted a rather narrower concept for the section and rejected the splitting of the group into different genera. They recognized the sections *Isomeria* and *Frigida* of KUSNEZOW (1895) and established three additional sections: *Monopodiae* T. N. Ho and *Phyllocalyx* T. N. Ho, split from the section *Frigida* sensu Kusnezow, and *Microsperma* T. N. Ho split from *Isomeria* sensu Kusnezow. The diagnostic characters of these newly established sections were mainly the branching patterns, habits and seed characters. For the sake of convenience, we follow their narrower sections in the following discussion.

According to HO & LIU (1990), the section *Frigida* sensu Ho & Liu consists of eighteen species distributed in the northern temperate area, from Europe to Asia and North America, with a high concentration in the mountainous regions of Southwestern China and Northeastern Burma (15 species). Two species, *G. frigida* Haenke and *G. froelichii*, are endemic to the Alps, Carpathians and Southwestern Bulgaria. North America shares 2 species, *G. algida* Pallas and *G. glauca* Pallas with Northeastern and Eastern Asia. The sections *Monopodiae* and *Microsperma*, consisting of 37 and 10 species respectively, are restricted to Eastern and Southeastern Asia and the

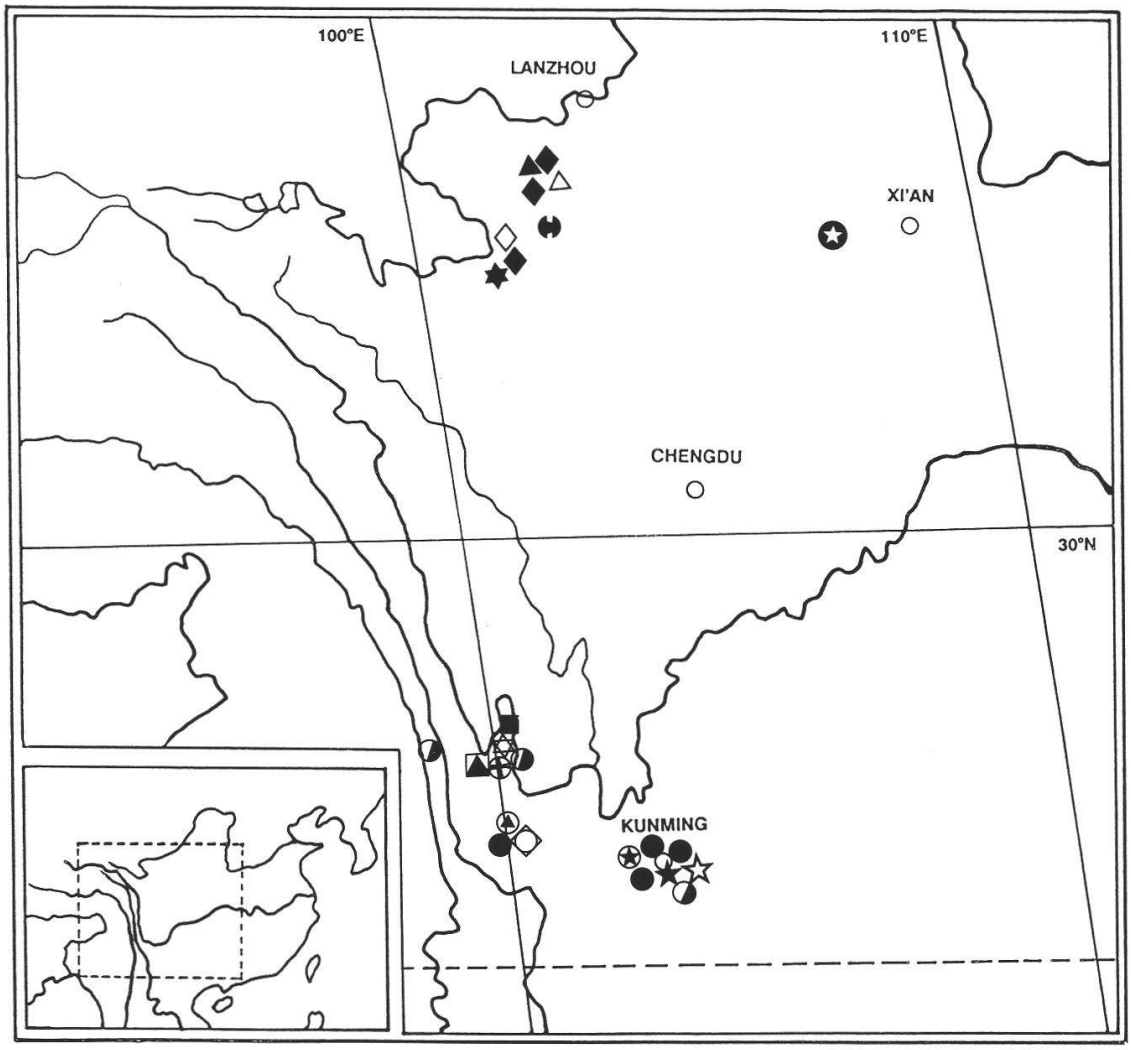


Fig. 1. The sampling sites of the populations of *Gentiana* species examined and their corresponding chromosome numbers.

▲ *G. callistantha* 2*n* = 26; ◆ *G. farreri* 2*n* = 48; ◇ *G. sino-ornata* 2*n* = 48; ⊕ *G. yunnanensis* 2*n* = 24; ■ *G. expansa* 2*n* = 34; ☆ *G. primuliflora* 2*n* = 42; ◭ *G. cephalantha* 2*n* = 24; ◈ *G. melandrifolia* 2*n* = 24; △ *G. veitchiorum* 2*n* = 24; ✪ *G. apiata* 2*n* = 24; ★ *G. gentilis* 2*n* = 42; ◑ *G. rhodantha* 2*n* = 46; ✯ *G. duclouxii* 2*n* = 24; ● *G. regescens* 2*n* = 24; ✡ *G. delavayi* 2*n* = 26; ✸ *G. nubigena* 2*n* = 24; ◬ *G. pterocalyx* 2*n* = 34; ◖ *G. striata* 2*n* = 46.

adjacent Himalayan area. The highest diversity occurs in the southwestern provinces of China and the eastern Himalayan region. The monotypic section *Phyllocalyx* includes only *G. phyllocalyx* C. B. Clarke found in the Himalaya and Southwestern China.

Chromosome numbers have been reported for seven species and one variety of this group, from Europe, Northeastern and Eastern Asia, and North America (cf. Table 1). Among them, *G. algida*, the most widespread species of this group, and *G. glauca* have been well studied. The numbers reported for the whole group are of $2n = 24$ for most species. Nevertheless, a few species differ. Thus *G. froelichii* was always counted as having $2n = 42$ chromosomes (FAVARGER 1965; LOVKA *et al.* 1971, 1972). It is precisely based on this distinct number that LÖVE & LÖVE (1972) esta-

TABLE 1.

The previous reports of chromosome numbers on *Gentiana* sect. *Frigida* s.l.

Taxon	*Origin*	*Chrom. no. (2n)*	*Reference*
sect. *Frigida* s.s.			
G. algida	Siberia	24	KRASNOBOROV & ROSTOVTSEVA (1975)
	Siberia	24	KRASNOBOROV *et al.* (1980)
	Tunkinsky Mt.	24	KROGULEVICH (1976)
	Sayanskiy Mt.	24	KROGULEVICH (1978)
	Colorado	24	LÖVE & LÖVE (1975)
	Japan	24	SHIGENOBU (1984)
	Altai	26	SOKOLOVSKAYA & STRELKOVA (1938)
	NE Yakutsk	24	YURTSEV & ZHUKOVA (1982)
	W Chukotka	24	ZHUKOVA (1967a)
	unkown	26	ZHUKOVA (1967b)
	Anyuy Mt.	24	ZHUKOVA (1980)
	W Chukotskiy	24	ZHUKOVA & PETROVSKY (1976)
G. algida var. *igaraskii*	Japan	24	SHIGENOBU (1984)
G. frigida	Czechoslovakia	24	MURIN (1974)
	Tatry Mt.	24	SKALINSKA (1951)
G. froelichii	Slovenia	42	FAVARGER (1965)
	Slovenia	42	LOVKA *et al.* (1971, 1972)
G. glauca	Alaska	24	DAWE & MURRAY (1979)
	Alaska	24	JOHNSON & PACKER (1968)
	Yukon	24	MULLIGAN & PORSILD (1969)
	Kamchatka	24	SOKOLOVSKAYA (1963, 1968)
	W Chukotskiy	24	ZHUKOVA (1966)
	Chukotskiy Yuzhnyy	24	ZHUKOVA (1969)
	Anyuyskiy Mt.	24	ZHUKOVA (1980)
	Chukotka	24	ZHUKOVA (1982)
	Chukotskiy	24	ZHUKOVA & TIKHONOVA (1971)
G. romanzowii	Kamchatka	24-26	SOKOLOVSKAYA (1963)
sect. *Monopodiae*			
G. formosana	Taiwan	26	HSU (1968)
G. yakushimensis	Japan	26	SHIGENOBU (1984)

blished the genus *Favargera* typified on *G. froelichii*. In addition, *G. formosana* Hayata (= *G. davidii* Franchet var. *formosana* (Hayata) T. N. Ho) from Taiwan and *G. yakushimensis* Makino from Japan were found to have $2n = 26$ chromosomes (HSU 1968; SHINGENOBU 1984). Although there is a high diversity of species, no observation has been made on the

Chinese and the Himalayan species, not even on some of the beautiful ornamental species such as *G. sino-ornata* Balf. f. and *G. farreri* Balf. f. which were introduced in Europe more than 50 years ago.

Stenogyne Franchet is a poorly known section both taxonomically and cytologically; nevertheless it has often been accepted (PRINGLE 1978; HO & LIU 1990). According to the current circumscription of HO & LIU (1990), the section contains fourteen species: ten are completely restricted to Southwestern China, two are relatively widespread in Northwestern and Central China, one is extending to Eastern Burma from Southwestern China and one is endemic to Thailand. None of them has been studied cytologically. Chromosome numbers are completely unkown for this section.

Following our reports on sections *Cruciata* Gaudin (YUAN, in press) and *Chondrophyllae* Bunge (KÜPFER & YUAN, submitted), this paper contributes additional chromosome data from China on the genus *Gentiana*.

MATERIALS AND METHODS

25 populations of 18 species were observed in this investigation. The species names and populations, along with their origins and chromosome numbers are listed in Table 2. The sampling sites are shown in Fig. 1. All the voucher specimens were deposited in the herbaria of the University of Neuchâtel, Switzerland (NEU) and of Lanzhou University, China (LZU). Seeds and flower buds were collected in the field and the flower buds were fixed with Carnoy. Chromosomes were observed either from mitosis in young ovaries and root tips germinated from seeds, or from meiosis of pollen mother cells, as indicated in Table 2. For observations on mitosis of root tips, the aceto-orcein squashing method was used and the procedure is the same as in our previous reports (YUAN, in press). SNOW's (1963) method was employed for the observations of meiosis and ovary mitosis.

The terminologies for centromeric positions introduced by LEVAN *et al.* (1964), the karyotype classification of STEBBINS (1971) and the karyotype asymmetry indices defined by ROMERO ZARCO (1986) were followed.

RESULTS

1. Sect. *Frigida* s.l.

Most species of the section *Frigida* s. l. have $2n = 24$ or $n = 12$ chromosomes. This confirms their diploid level and the basic number of $x = 12$ (Table 2). This, for example, is the case for *G. cephalantha* Franchet ex Hemsley, *G. duclouxii* Franchet, *G. melandrifolia* Franchet ex Hemsley, *G. regescens* Franchet ex Hemsley, *G. veitchiorum* Hemsley, *G. yunnanensis* Franchet, *G. apiata* N. E. Br. and *G. nubigena* Edgew. (Fig. 3-4, 6-7, 9 and 11-13). Tetraploid numbers were found for the first time for *G. farreri* and *G. sino-ornata* with $n = 24$ (Fig. 5) and $2n = 48$ (Fig. 8). Furthermore, the basic number of $x = 13$ was also found in this group, in *G. callistantha* Diels et Gilg and in *G. delavayi* Franchet, which were diploid with $2n = 26$ (Fig. 2 and 10). According to Ho (1988), these two species belong respectively to the sections *Monopodiae* and *Microsperma* (cf. Table 2).

TABLE 2.
Origins of the materials examined and their chromosome numbers

Taxon	*Collection number*	*Locality and altitude*	*Examined organs*	*Chromosome number*
sect. *Monopodiae*				
G. callistantha	G173	Xiahe, Gansu, 2950m	root	$2n = 26$
G. cephalantha	G135	Dali, Yunnan, 2800m	ovary	$2n = 24$
G. duclouxii	G142	Kunming, Yunnan, 2050m	ovary	$2n = 24$
G. farreri	G045	Xiahe, Gansu, 2950m	anther	$n = 24$
	G156	Xiahe, Gansu, 2950m	root	$2n = 48$
	G194	Maqü, Gansu, 3200m	root	$2n = 48$
G. melandrifolia	G137	Dali, Yunnan, 2100m	anther	$n = 12$
G. regescens	G090	Kunming, Yunnan, 2000m	anther	$n = 12$
	G136	Dali, Yunnan, 2300m	anther	$n = 12$
	G144	Kunming, Yunnan, 2150m	anther	$n = 12$
	G150	Kunming, Yunnan, 2200m	ovary	$2n = 24$
G. sino-ornata	G177	Maqü, Gansu, 3500m	root	$2n = 48$
G. veitchiorum	G200	Xiahe, Gansu, 2950m	root	$2n = 24$
sect. *Microsperma*				
G. delavayi	G112	Lijiang, Yunnan, 2850m	anther	$n = 13$
			ovary	$2n = 26$
G. yunnanensis	G107	Lijiang, Yunnan, 2500m	anther	$n = 12$
sect. *Frigida* s.s.				
G. apiata	G077	Taibaishan, Shaanxi, 3700m	root	$2n = 24$
G. nubigena	G030	Maqü. Gansu, 3800m	ovary	$2n = 24$
sect. *Stenogyne*				
G. expansa	G117	Lijiang, Yunnan, 2850m	root	$2n = 34$
G. gentilis	G152	Kunming, Yunnan, 2200m	anther	$n = 21$
G. pterocalyx	G106	Lijiang, Yunnan, 2500m	anther	$n = 17$
G. primuliflora	G151	Kunming, Yunnan, 2200m	root	$2n = 42$
G. rhodantha	G091	Bijiang, Yunnan, 1500m	ovary	$2n = 46$
	G098	Lijiang, Yunnan, 2500m	ovary	$2n = 46$
	G143	Kunming, Yunnan, 2200m	ovary	$2n = 46$
G. striata	G188	Lüqu, Gansu, 3050m	root	$2n = 46$

Observations on meiosis in some species (cf. Table 2) indicated that both the diploid species, e.g. *G. yunnanensis, G. regescens,* and the tetraploid species such as *G. farreri* have regular pairing and segregation of homologous chromosomes. Only bivalents were observed in the diakinesis of these species. However, the meiosis of some species such as *G. melandrifolia* and *G. cephalantha* are not synchronous, contrary to *G. regescens* and *G. yunnanensis* where the meiosis are fairly synchronous.

Karyotype analysis of selected species indicated that their chromosomes were dominantly metacentric and therefore the karyotypes were rather symmetrical, which can be seen from both the karyotype classification (1A or 2A) and the asymmetry indices (A_1 and A_2). The sizes of chromosomes were small to medium (Table 3).

2. Sect. *Stenogyne*

In section *Stenogyne*, three different numbers were discovered (Table 2). *G. expansa* H. Sm. and *G. pterocalyx* Franchet ex Hemsley had $2n = 34$ and $n = 17$ chromosomes (Fig. 14 and 16); their basic number therefore should be $x = 17$. *G. gentilis* Franchet and *G. primuliflora* Franchet had $n = 21$ and $2n = 42$ chromosomes respectively (Fig. 15 and 17); their basic number is therefore probably $x = 21$. Whereas *G. rhodantha* Franchet ex Hemsley and *G. striata* Maxim. had $2n = 46$ and $x = 23$ (Fig. 18 and 19). All these numbers are new for the section. Among them, $x = 17$ and 23 are also recorded for the first time for the genus *Gentiana*. In addition, *G. rhodantha* shows very specific heteropycnosis. Its chromosomes form very obvious chromocentres which scatter in late prophase nuclei (Fig. 18).

The karyotypes of the section were more asymmetrical with a higher proportion of submetacentric and acrocentric chromosomes. The classification of karyotype was of 2A and 3A types. The karyotype asymmetry indices further indicated that the asymmetry was mainly intrachromosomal, that is, due to the difference between the arms of each individual chromosome. The intrachromosomal asymmetry indices (A_1) of *G. expansa* and *G. primuliflora* were as high as 0.459 and 0.503 respectively, while their interchromosomal asymmetry indices (A_2) were equal to or even slightly lower than those of the members of other sections. Chromosome sizes of the species of this section were smaller (Table 3).

DISCUSSION

Our results have documented chromosome numbers for the first time for all the 18 species of *Gentiana* investigated and revealed two new basic numbers, $x = 17$ and 23, for the genus. These two newly found numbers fill the only gaps of the spectrum of chromosome numbers of *Gentiana* (YUAN, in press; KÜPFER & YUAN, submitted); thus a continuous series of gametic chromosome numbers from 6 to 26 can be found in the genus, which suggests rather complicated and reticulate relationships among the different cytotypes. Both dysploidization and polyploidization were probably important processes in the chromosome evolution of this genus. There is no simple relationship between the chromosome numbers and classification, because each basic chromosome number is not simply confined to a single infrageneric group.

Referring to the section *Frigida* s.s., the basic number is dominantly $x = 12$, with the exception of *G. froelichii* with $x = 21$ or $x = 7$ ($2n = 42$). Moreover, *G. algida* was generally found to have $2n = 24$ chromosomes in North America, Northeastern and Eastern Asia (cf. Table 1), except for the two reports of $2n = 26$ by SOKOLOVSKAYA & STRELKOVA (1938) and

TABLE 3.
Karyotype structures of some species of *Gentiana* sect. *Frigida* s.l. and sect. *Stenogyne*

Taxon	*Coll. No.*	*Karyotype*	*Length range (μm)*	*L/S*	*P*	*Type*	*A1*	*A2*
G. callistantha	G173	$2n = 2m$(SAT) $+24m$	1.8-3.1	1.70	0.00	1A	0.176	0.143
G. sino-ornata	G177	$2n = 40m + 8sm$	2.0-3.1	1.52	0.13	2A	0.298	0.130
G. veitchiorum	G200	$2n = 18m + 6sm$	2.7-4.4	1.63	0.00	1A	0.306	0.131
G. apiata	G077	$2n = 20m + 4sm$	2.1-3.0	1.40	0.00	1A	0.282	0.103
G. expansa	G117	$2n = 2m$(SAT) $+ 8m + 24sm$	1.7-2.8	1.69	0.29	2A	0.459	0.134
G. primuliflora	G151	$2n = 12m + 24sm + 6st$	1.4-1.9	1.40	0.71	3A	0.503	0.095

L: length of the longest chromosome in a karyotype.
S: length of the shortest chromosome in a karyotype.
P: proportion of the chromosomes of which the arm ratio is higher than two in a karyotype.
Type: referring to the classification of karyotype of STEBBINS (1971).
A1: the intrachromosomal asymmetry index defined by ROMERO ZARCO (1986).
A2: the interchromosomal asymmetry index defined by ROMERO ZARCO l.c.

ZHUKOVA (1967b). In section *Monopodiae*, in addition to the common number for many species of $2n = 24$ that was revealed by our investigation, $2n = 26$ was also reported for *G. formosana* from Taiwan (HSU 1968), *G. yakushimensis* from Japan (SHIGENOBU 1984) and *G. callistantha* from Western China by our present investigation. So, both the basic number $x = 12$ and 13 are present and their relationships and taxonomic implications need to be confirmed by more studies. The situation in section *Microsperma* seems similar to that in section *Monopodiae*: the only two chromosome reports on this section contributed by our present study show that both $x = 12$ and 13 exist. Therefore, at least three different basic numbers, $x = 12$ (6?), 13, 21 (7?), exist in section *Frigida* s.l.

LÖVE & LÖVE (1972) simply divided this group into two genera according to their basic chromosome numbers: the monotypic *Favargera* with a basic number of $x = 7$ (21?) based on *G. froelichii*, and *Gentianodes* with a basic number of $x = 6$ (12?) including all the other members of sect. *Frigida* s.l. However, some species such as *G. delavayi* which they included in their $x = 6$ genus have in fact another basic number ($x = 13$). Additional careful and critical reconsiderations of these groups are therefore necessary.

Furthermore, HO (1985) recognized smaller sections in this group. The present investigation shows that these sections are also chromosomally polybasic. In particular, she recognized the section *Microsperma* mainly by its

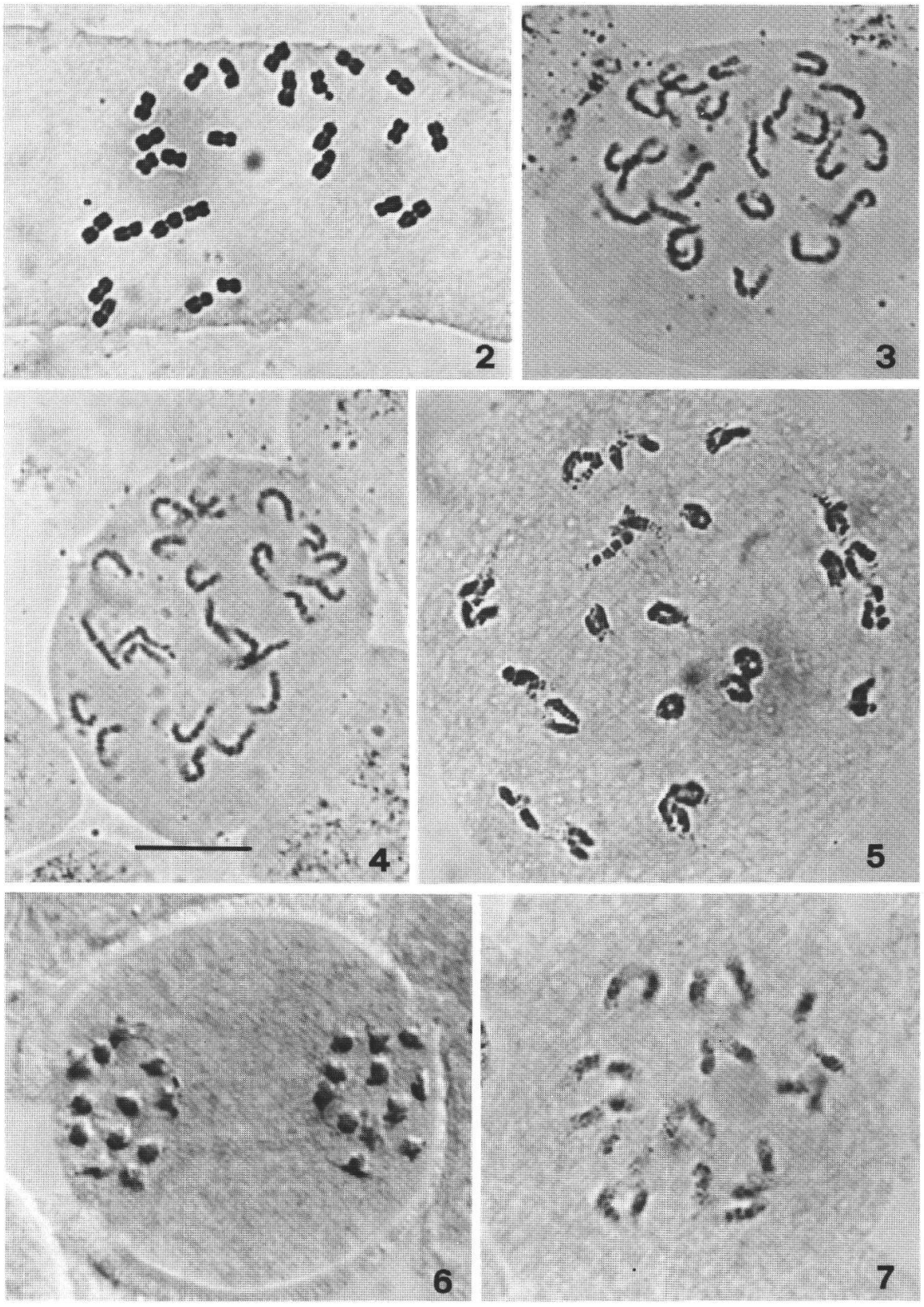
annual (or rather biennial) habit, but as demonstrated in section *Chondrophyllae* (KÜPFER & YUAN, submitted), plant habits are not congruent with chromosome numbers in the genus. The two annual species belonging to the section *Microsperma*, *G. delavayi* and *G. yunnanensis*, also have different basic numbers ($x = 13$ and 12 respectively).

Stenogyne is a poorly known section. Our present investigation took its chromosome number into account for the first time and revealed numbers very distinct from those of other members of the genus. In addition to the numbers $2n = 42$ and $n = 21$ of *G. gentilis* and *G. primuliflora* which have been reported for the European *G. froelichii* of the section *Frigida*, the other numbers of $2n = 34$ or $n = 17$ of *G. expansa*, *G. pterocalyx* and $2n = 46$ of *G. rhodantha* and *G. striata* have not been recorded in the genus *Gentiana* before. The higher and obviously secondary basic numbers $x = 17$, 21 and 23 suggest a specialized and isolated position of this section in the genus. The karyotype data also supports that: all the species of the section analyzed have rather small chromosomes and more asymmetrical karyotypes; their intrachromosomal karyotype asymmetry indices are much higher than that of others (Table 3). According to STEBBINS (1971, p. 90), there is a predominant trend in flowering plants toward increasing asymmetry of the karyotype. Therefore, from the point of view of chromosome number and karyotype asymmetry, the section *Stenogyne* is a more advanced group than the other sections of the genus.

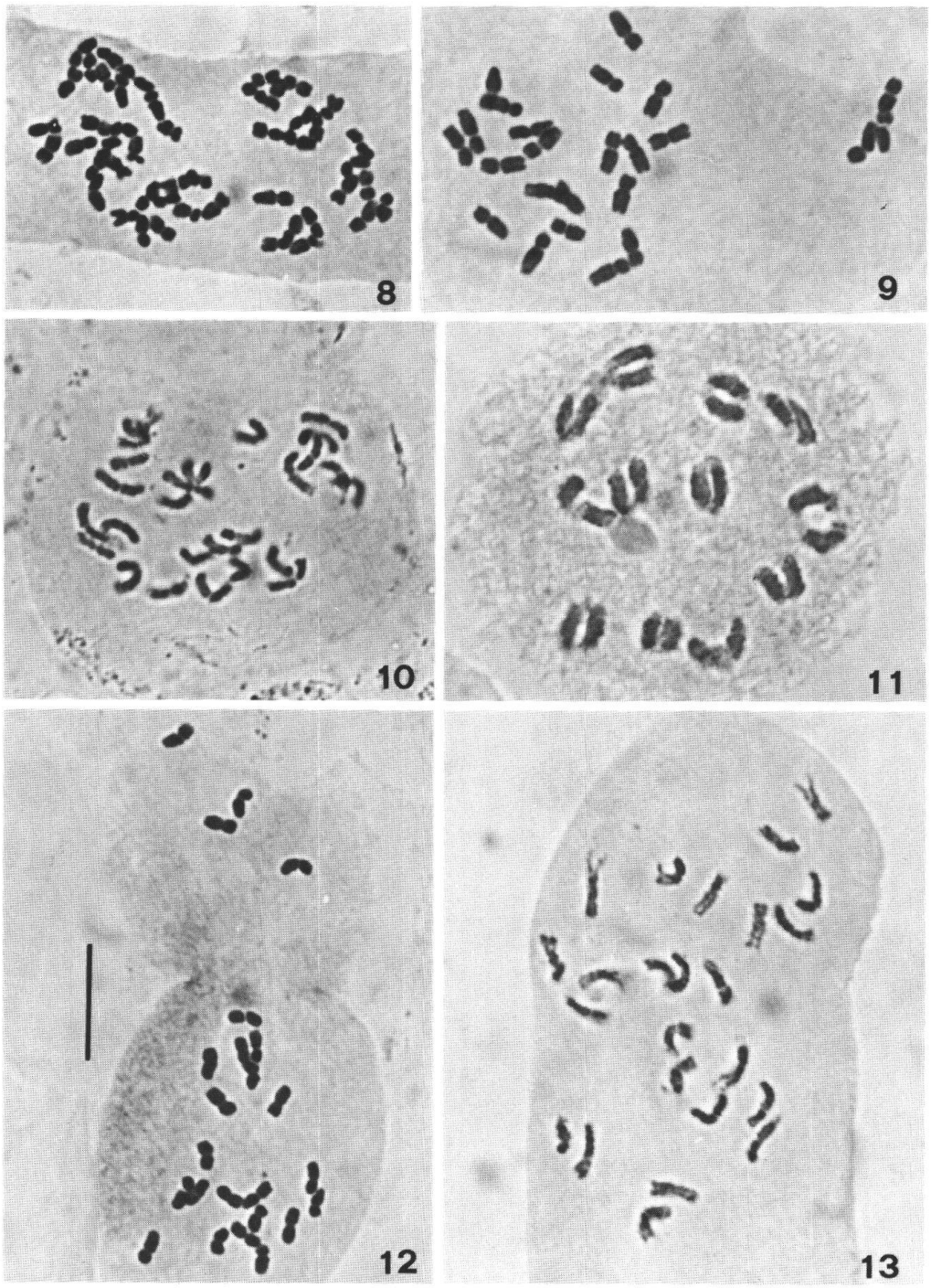
In addition, we demonstrated previously that the common chromosome numbers of *G. aristata* Maxim. and *G. nivalis* L. ($2n = 14$), *G. squarrosa* Ledeb. and *G. terglouensis* Hacq. ($2n = 38$) of sections *Chondrophyllae* and *Calathianae* Froelich may have derived independently (KÜPFER & YUAN, submitted). This could also be the case for the $2n = 42$ of *G. primuliflora* and *G. gentilis* of the section *Stenogyne* revealed here and *G. froelichii* of section *Frigida* reported previously (FAVARGER 1968; LOVKA et al. 1971, 1972), because the former two species are very isolated both morphologically and geographically from the latter. These phenomena suggest that the same basic number may not necessarily indicate a monophyletic origin and therefore, chromosome number cannot become a good criterion for classification until the cytogenetic mechanism influencing the variation of chromosome numbers in the genus *Gentiana* is well understood.

Acknowledgement

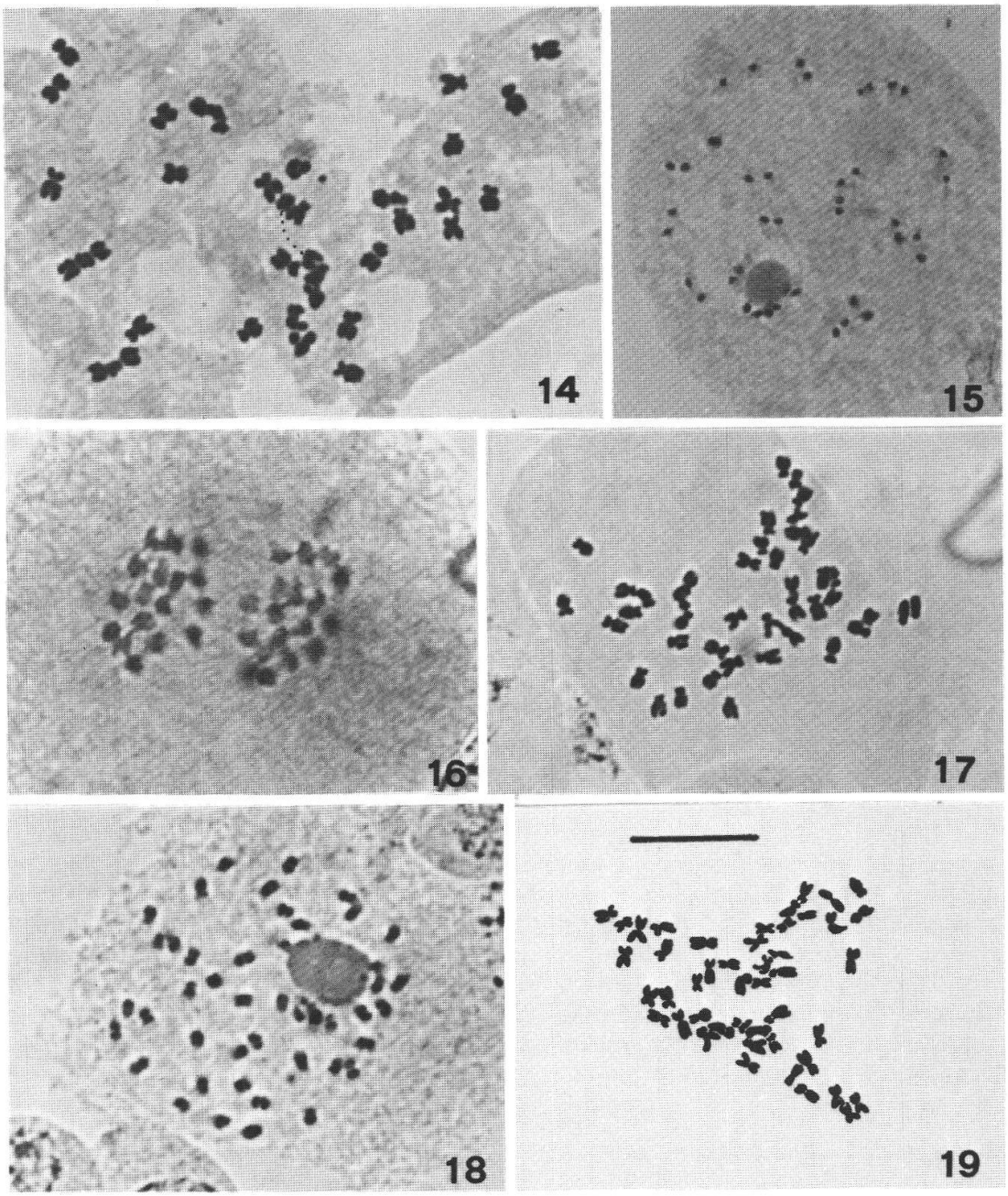
We thank Prof. Xun-Ling Wang, Mr. Xun Pu, Mr. Ji-Zhou Sun and Ms. Hui Ma for their kind help in collecting materials and Mr. E. Fortis for preparing the photographs. Our appreciation is also due to Dr. F. Felber for his critical reading of the manuscript and Ms. E. Boss and C. Fischer for correcting its English.



Figs. 2-7. Chromosomes of *Gentiana* sect. *Frigida* s.l. 2. *G. callistantha*, mitotic metaphase of root-tip, $2n = 26$; 3. *G. cephalantha*, mitotic prophase of ovary, $2n = 24$; 4. *G. duclouxii*, mitotic prophase of ovary, $2n = 24$; 5. *G. farreri*, diakinesis, $n = 24$; 6. *G. melandrifolia*, meiotic anaphase I, $n = 12$; 7. *G. regescens*, diakinesis, $n = 12$. — bar = 10 μm.



Figs. 8-13. Chromosomes of *Gentiana* sect. *Frigida* s.l. 8. *G. sino-ornata*, mitotic metaphase of root-tip, $2n = 48$; 9. *G. veitchiorum*, mitotic metaphase of root-tip, $2n = 24$; 10. *G. delavayi*, mitotic prophase of ovary, $2n = 26$; 11. *G. yunnanensis*, diakinesis, $n = 12$; 12. *G. apiata*, mitotic metaphase of root-tip, $2n = 24$; 13. *G. nubigena*, mitotic prophase of ovary, $2n = 24$. — bar = 10 μm.



Figs. 14-19. Chromosomes of *Gentiana* sect. *Stenogyne*. 14. *G. expansa*, mitotic metaphase of root-tip, $2n = 34$ (the dotted line indicates the chromosome which was broken by squashing); 15. *G. gentilis*, diakinesis, $n = 21$; 16. *G. pterocalyx*, meiotic anaphase I, $n = 17$; 17. *G. primuliflora*, mitotic metaphase of root-tip, $2n = 42$; 18. *G. rhodantha*, mitotic prophase of ovary, $2n = 46$; 19. *G. striata*, mitotic metaphase of root-tip, $2n = 46$; — bar = 10 μm except that in Fig. 15 the bar represents 20 μm.

Résumé

Les nombres chromosomiques de 18 espèces appartenant aux sections *Frigida* Kusn. s.l. (sect. *Monopodiae* T.N. Ho et sect. *Microsperma* T.N. Ho inclus) et *Stenogyne* Kusn. du genre *Gentiana* sont mentionnés pour la première fois. Les 25 populations étudiées proviennent des montagnes de l'ouest et du sud-ouest de la Chine. Dans la section *Frigida* s.l., *G. apiata* N. E. Br., *G. cephalantha* Hemsley, *G. duclouxii* Franchet, *G. melandrifolia* Hemsley, *G. nubigena* Edgew., *G. regescens* Hemsley, *G. veitchiorum* Hemsley et *G. yunnanensis* Franchet offrent toutes la même valence chromosomique à $2n = 24$ chromosomes; en revanche, *G. callistantha* Diels et Gilg and *G. delavayi* Franchet possèdent $2n = 26$ chromosomes; enfin, *G. farreri* Balf. f. et *G. sino-ornata* Balf. f. se sont révélés tetraploïdes à $2n = 48$ chromosomes. La polyploïdie est signalée pour la première fois dans la section. Le découpage de la section *Frigida* s.l. par HO & LIU (1990) n'a pas conduit à une meilleure adéquation des données caryologiques et morphologiques; chacune des petites sections reste polybasique. Le sect. *Frigida* s.s. paraît le plus homogène, toutes les espèces offrant $2n = 24$, à l'exception de l'espèce européenne *G. froehlichii* à $2n = 42$.

Les données relatives au sect. *Stenogyne* sont fragmentaires et hétérogènes. *G. expansa* H. Sm. et *G. pterocalyx* Hemsley ont $2n = 34$ chromosomes; *G. gentilis* Franchet et *G. primuliflora* Franchet offrent $2n = 42$ chromosomes alors que *G. rhodantha* Hemsley et *G. striata* Maxim. partagent un troisième nombre somatique, $2n = 46$. Tous ces nombres sont nouveaux pour la section, les nombres $2n = 34$ et $2n = 46$ sont même inédits pour le genre. Sur la base des données caryologiques, la section *Stenogyne* paraît relativement isolée au sein du genre. Elle contraste non seulement par ses nombres chromosomiques somatiques relativement élevés, aux relations phylétiques incertaines, mais aussi par ses chromosomes relativement petits et ses caryotypes particulièrement asymétriques.

L'ensemble de nos données récentes (YUAN, in press; KÜPFER & YUAN, submitted) ont montré que le genre *Gentiana* possédait une série continue de nombres gamétiques de $n = 6$ à $n = 26$. La polyploïdie et la dysploïdie ont donc participé d'une manière particulièrement intense à l'évolution du genre. D'une manière générale, l'identité de nombres chromosomiques entre deux espèces du genre *Gentiana* n'indique pas nécessairement une parenté étroite mais relève sans doute, dans plusieurs cas, d'homoplasies. L'interprétation des données caryologiques nécessite donc une extrême prudence et implique l'étude parallèle des caractères morphologiques, biochimiques et phytochimiques.

Summary

Chromosome numbers are documented here for the first time for 18 species including 25 populations of *Gentiana* sect. *Frigida* Kusn. s.l. and sect. *Stenogyne* Kusn. from the high altitude regions of Western and Southwestern China. In the sect. *Frigida* s.l., *G. apiata* N. E. Br., *G. cephalantha* Hemsley, *G. duclouxii* Franchet, *G. melandrifolia* Hemsley, *G. nubigena* Edgew., *G. regescens* Hemsley, *G. veitchiorum* Hemsley and *G. yunnanensis* Franchet all had $2n = 24$ chromosomes; whereas *G. callistantha* Diels et Gilg and *G. delavayi* Franchet had $2n = 26$ chromosomes; *G. farreri* Balf. f. and *G. sino-ornata* Balf. f. were tetraploids with $2n = 48$ chromosomes. The tetraploid number $2n = 48$ was found for the first time for the section. In sect. *Stenogyne*, *G. expansa* H. Sm. and *G. pterocalyx* Hemsley had $2n = 34$ chromosomes; *G. gentilis* Franchet and *G. primuliflora* Franchet had $2n = 42$ chromosomes; *G. rhodantha* Hemsley and *G. striata* Maxim. had $2n = 46$ chromosomes. All these chromosome numbers were found for the first time for the section, among them $2n = 34$ and $2n = 46$ were new numbers for the genus. Systematic relationships of these species are discussed on the basis of their chromosome numbers.

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