Acta Phytotaxonomica Sinica

毛冠菊属系统位置的核形态证据

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Systematic position of Nannoglottis Maxim. s.l. (Asteraceae) : karyomorphological data

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Abstract This paper describes for the first time the karyomorphology of 4 populations of 2 species of *Nannoglottis* Maxim. s.1. The two species both show the resting nuclei of the complex chromocenter type and the mitotic prophase chromosomes of the interstitial type. The karyotype formula of *N. gynura* is 2n = 18 = 14m + 2sm + 2st (SAT) in two populations while that of *N. carpesioides* is 2n = 18 = 14m + 2sm (2SAT) + 2st in two populations. The two species under study represent two sections of *Nannoglottis* s.1. *N. gynura*, the only species of sect. *Stenolepis*, is considered as the most primitive member of the genus. Accordingly, the basic chromosome number of the genus might be x = 9. Karyomorphological data indicate that *Nannoglottis* should be placed in the tribe Astereae rather than in the Inuleae and the Senecioneae.

Key words Nannoglottis Maxim.; Karyomorphology; Tribal classification

Nannoglottis Maxim. s.l., a small genus of the Asteraceae, is endemic to the Plateau Qinghai-Xizang (Tibet). This genus, as circumscribed by Ling & Chen (1965) to include the genera *Stereosanthus* Franch. and *Vierhapperia* Hand.-Mazz., comprises two sections and eight species. In terms of its tribal classification and systematic position, *Nannoglottis* has been one of the problematic genera in the Asteraceae (Ling & Chen 1965).

Nannoglottis s. s. is a monotypic genus, including only *N. carpesioides*. Its habit and leaves resemble those of *Carpesium* L. Therefore, the genus was originally classified in the tribe Inuleae by Maximovicz (1881), but was considered as an abnormal genus because of its trimorphous flowers. Hoffmann (1894) transferred it to the subtribe Senecioninae of the tribe Senecioneae as an isolated genus. Several years later, Franchet (1896) established another genus, *Stereosanthus* Franch., which includes four species. He proposed that *Stereosanthus* might represent an intermediate type between the Inuleae and the Senecioneae. Handel-Mazzetti (1937) acknowledged the above two genera and established an additional monotypic genus *Vierhapperia* Hand.-Mazz., which he placed in the tribe Astereae.

After examining the type specimens and other collections of *Nannoglottis*, *Stereosanthus* and *Vierhapperia*, Ling & Chen (1965) suggested that *Stereosanthus* and *Vierhapperia* be incorporated into *Nannoglottis*. They based this classification on the observation that the three genera share similar flower forms and the same achene and pappus structures. According to Ling & Chen (1965), though differences in disposition of involucral bracts and length of ligules are good criteria for dis-

1998-11-19 收稿,1999-07-13 收修改稿。

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Foundation Item: The National Natural Science Foundation of China(NSFC, 39670059); A grant from President Foundation of the Chinese Academy of Sciences.

criminating species, they are not sufficient for generic delimitation. Furthermore, they argued that Nannoglottis s.l. should be classified in the Senecioneae and treated as a primitive genus in the subtribe Senecioninae.

Nordenstam (1977) tentatively proposed that *Nannoglottis* s. 1. be excluded from the Senecioneae and transferred to the Astereae as Handel-Mazzetti (1937) treated the reduced *Vierhapperia*. This suggestion was followed by Jeffrey & Chen (1984), Jeffrey (1992), Zhang & Bremer (1992) and Bremer (1994), although they had not found more data to support this treatment and usually treated it as an isolated genus of the Astereae. However, in his systematic treatment of Chinese Asteraceae, Ling (1997) insisted that *Nannoglottis* should be placed in the Senecioneae, in a subtribe of its own, Nannoglottisinae. In addition, he thought that Nannoglottisinae might be closely related to his subtribe Tussilagininae s. s. (including only two genera, *Petasites* and *Tussilago*) based on the trimorphous flowers commonly found in these two subtribes (Ling 1997). At the same time, Ho *et al.* (1997) thought that *Nannoglottis* might have evolved from *Senecio* of the Senecioneae. All these suggestions for the tribal classification and systematic position of *Nannoglottis* is are related to three separate tribes: the Inuleae, the Senecioneae and the Astereae.

The karyomorphological information is one line of important evidence for clarifying the controversial systematic issues of the Asteraceae (Solbrig 1977). But the karyomorphological data of *Nannoglottis* have never been reported due to the difficulty of obtaining materials. In this paper, 4 populations of 2 species, which represent two sections of *Nannoglottis* s.1., were karyomorphologically investigated. Based on the karyomorphological data, the tribal classification of *Nannoglottis* was discussed.

1 Materials and Methods

The two species and their origins were listed in the Table 1. All woucher specimens are deposited in the Northwest Plateau Institute of Biology, the Chinese Academy of Sciences (HNWP). Table 1 Origins and vouchers of the studied species

Species	Locality	Voucher Specimens (in NWPB)			
Nannoglottis carpesioides	Xunhua, Qinghai, alt. 2000 m Huzhu, Qinghai, alt. 2100 m	Liu Jian-quan 538 Liu Jian-quan 551			
N. gynura	Yushu, Qinghai, alt. 3400 m Yushu, Qinghai, alt. 3600 m	H. B. G. 1942 H. B. G. 2335			

The roots were pretreated with a mixture of 0.05 % colchicine and 0.002 mol/L hydroxyquinoline for eight hours, and then fixed overnight in Carnoy 's fluid (absolute alcohol glacial acetic acid = 3 1). After being macerated in 1 mol/L hydrochloric acid at 60 for five minutes, they were stained and squashed with Carbol Fuchsin. The karyomorphological classifications of the resting and mitotic prophase followed Tanaka (1971). The symbols for the description of karyotypes followed Levan *et al.* (1964). The indices of relative length (IRL) suggested by Kuo (1972) were adopted. The asymmetry of karyotypes was classified according to Stebbins (1971).

2 Results

2.1 Nannoglottis carpesoides Maxim. (Table 2)

The resting nuclei were of the complex chromosome type (Fig. 1:1). The karyomorphological type of the mitotic prophase chromosomes belonged to the interstitial type (Fig. 1:2).

The metaphase chromosomes (Fig. 1:3) of both populations were counted to be 2n = 18, rang-

ing in length from 4.10 µm to 6.70 µm. Their karvotypes (Fig. 1:4.5) were similar, and were formulated as 2n = 18 = 14m + 2sm(2SAT) + 2st, belonging to Stebbins '2A type.

Nannoglottis gynura (C. Winkl.) Ling et Y. L. Chen (Table 2) 2 2

The resting nuclei and the mitotic prophase chromosomes were the complex chromosome type and the interstitial type respectively, similar to those of N. carpesoides. Both populations (Fig. 1: 7) had the chromosome number of 2n = 18, ranging in length from 4.15 µm to 7.22 µm. Their karvotypes (Fig. 1:6 ~ 8) were both formulated as 2n = 18 = 14m + 2sm + 2st (2SAT), belonging to Stebbins '2A type.

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	Nannoglottis	carpesioid	les			N. gyn	ura		
	Liu Jian-	quan 538				H. B. G.	1942		
NO	RL	AR	Т	IRL	No	RL	AR	Т	IRL
1	7.03 + 7.95 = 14.98	1.13	m	1.35	1	7.18+8.03=15.21	1.12	m	1.37
_2	5.67 + 8.07 = 13.74	1.42	m	1.24	2	5.22+6.91 = 12.13	1.32	m	1.09
3	4.92+6.88=11.80	1.40	m	1.06	3	4.41 + 7.10 = 11.51	1.61	m	1.04
4	5.03 + 5.95 = 10.98	1.18	m	0.99	4 5	4.89+6.43=11.32	1.31	m	1.02
5	4.57+6.23=10.97	1.36	m	0.99	5	4.20+6.43 = 10.63	1.53	m	0.96
6	2.55 + 7.14 = 9.69	2.80	sm *	0.87	6	2.30 + 8.08 = 10.38	3.51	st *	0.93
7	4.43+4.89=9.52	1.10	m	0.84	7	4.97 + 5.16 = 10.13	1.03	m	0.91
8	3.88+5.41=9.29	1.39	m	0.84	8	3.06 + 6.92 = 9.98	2.26	sm	0.90
9	1.78 + 7.50 = 9.28	4.21	st	0.84	9	3.60 + 5.40 = 9.00	1.50	m	0.81
	Liu Jian-	quan 551				H. B. G.	2335		
NO	RL	AR	Т	IRL	No	RL	AR	Т	IRL
1	5.94 + 7.31 = 13.25	1.23	m	1.19	1	5.88+7.90=13.09	1.34	m	1.24
_2	5.45 + 7.46 = 12.91	1.37	m	1.16	2	5.45+7.41 = 12.86	1.36	m	1.16
3	5.84+6.51 = 12.35	1.11	m	1.11	3	5.18+7.33=12.51	1.42	m	1.12
4	5.06+6.76=11.82	1.34	m	1.06	4	4.46+7.12=11.58	1.60	m	1.04
5	5.73 + 5.74 = 11.47	1.01	m	1.03	5	4.97+6.24=11.21	1.26	m	1.00
6	4.78 + 5.12 = 9.90	1.11	m	0.89	6	1.88 + 7.66 = 9.54	4.07	st *	0.86
7	2.57 + 7.33 = 9.90	2.85	sm *	0.89	7	4.72+4.96=9.48	1.10	m	0.85
8	3.80 + 5.84 = 9.64	1.54	m	0.87	8	2.84 + 6.50 = 9.34	2.29	sm	0.84
9	2.08 + 6.65 = 8.73	3.20	st	0.77	9	3.54 + 5.25 = 8.79	1.48	m	0.79

Table 2 Parameters of mitotic metaphase chromosomes of 4 populations of 2 species in Nannoglottis

RL: relative length. AR: arm ratio. T: type. IRL: index of relative length.

* indicating the satellite chromosomes

3 Discussion

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The two species of *Nannoglottis* s.1. under study have common karyomorphogical characteristics and similar karyotypes. N. carpesioides was the only species of Nannoglottis s.s. (Maximovicz 1881) while N. gynura was ascribed to Stereosanthus by Franchet (1896) and Handel.-Mazzetti (1937). Their similar chromosome data support Ling & Chen (1965) reducing Stereosanthus as a congeneric name of Nannoglottis.

Nannoglottis s.l. comprises two sections: sect. Stenolepis and sect. Nannoglottis. The former section includes only one species: N. gynura, and this species was considered as the most primitive member of the genus (Ling & Chen 1965). The latter section consists of seven species, including N. carpesioides. Although a further study of more species is needed, this research indicates x =9 might be the base chromosome number of Nannoglottis s.1.

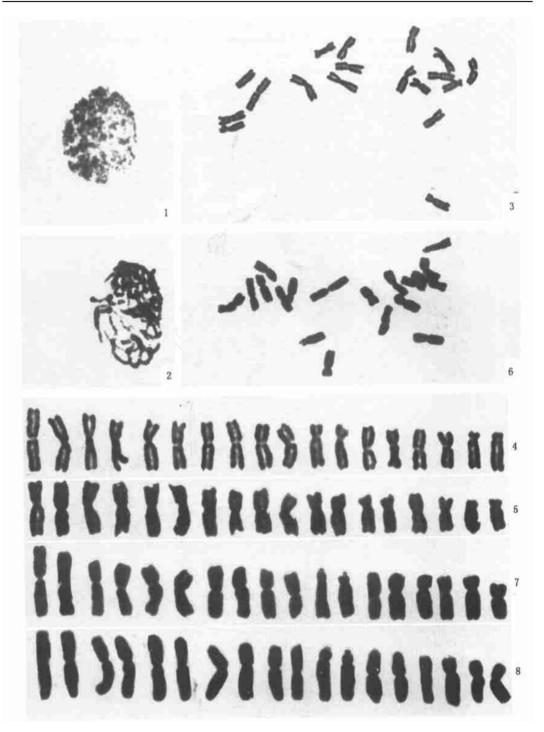


 Fig. 1 ~ 5. Nannoglottis carpesoides (1 ~ 4. Liu Jian quan 538; 5. Liu Jian quan 551).

 Fig. 6 ~ 8. N. gynura (6 ~ 7. H. B. G. 1942; 8. H. B. G. 2335). (1 ~ 3,6. ×2000; 4 ~ 5,7 ~ 8. ×3000)

As stated in the introduction, the tribal classification and systematic position of *Nannoglottis* have long been disputed. The base chromosome numbers of the Inuleae and the Senecioneae are x =

10. All genera postulated to be related to *Nannoglottis* in the Inuleae and the Senecioneae have the base chromosome numbers of x = 10 or x = 30 derived from x = 10 (Table 3). The chromosome data reject the suggestions for the tribal classification of *Nannoglottis* in the Inuleae and the Senecioneae, and the close relationships of *Nannoglottis* to some genera (e.g. *Carpesium*, *Senecio*, *Tussilago* and *Petasites*) of these two tribes (Ling 1997, Ho *et al*. 1997, Ling & Chen 1965, Franchet 1896,

Taxon	Base number	Reference	
Nannoglottis	x = 9	Present research	
Astereae	x = 9	Semple 1995	
Aster	x = 9	Aderson 1974	
Erigeron	x = 9	Semple 1995	
Inuleae	x = 10	Anderberg 1991	
Carpesium	x = 10	Anderberg 1991	
Senecioneae	x = 10	Robinson et al. 1997	
Senecio	x = 10	Robinson et al. 1997	
Petasites	x = 30	Robinson et al. 1997	
Tussilago	x = 30	Robinson et al. 1997	

Table 3 A comparison of the base chromosome numbers of *Nannoglottis* and related taxa

Hoffmann, 1894; Maximovicz 1881).

The common x = 9 of *Nannoglottis* and the Astereae indicates that Nannoglottis might have a close affinity with the Astereae. In addition, Astereae evolved in Eurasia, possibly in the region adjacent to the Indian Ocean (Xiang & Semple 1996). Nannoglottis is distributed in this region. Therefore, from the phytogeographical viewpoint, it is imaginable that Nannoglottis may have evolved with the Astereae from a common ancestor. Our results support the suggestion of Jeffrey & Chen (1984), Jeffrey (1992), Zhang & Bremer (1992) and Bremer (1994) that Nannoglottis should be treated in the Astereae. However, based on the current available data, it is still difficult to speculate about the systematic position of Nannoglottis in the Astereae. Gross - morphologically, Nannoglottis is

unique in the Astereae except that its style branches are similar to those of most genera in this tribe. In addition, st chromosomes were detected in *Nannoglottis* but not in all investigated genera of the Astereae (unpublished data). Both the tribal classification of *Nannoglottis* and its systematic position in the Astereae need to be confirmed and determined from other lines of evidence especially from the molecular data. The tribal classifications and systematic positions of many problematic genera of the Astereaee (e.g. *Adenocaulon, Corymbium and Eremothamus*) have been successfully determined by molecular methods (Jansen & Kim 1996).

Acknowledgments The first author wishes to express his sincere thanks to his supervisor Prof. Lu An-Ming for the guidance, encouragement and support. We are indebted to Profs. Yang Qin-Er and Li Mao-Xue for their valuable comments and constructive suggestions for the manuscript.

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摘要 首次记载了毛冠菊属 2 种 4 居群的核形态资料。两种植物的染色体间期和前期染色体为复杂型 和中间型。狭舌毛冠菊两居群的染色体数目与核型公式为 2n = 18 = 14m + 2sm + 2st (2SAT);毛冠菊两居 群的染色体数目与核型公式为 2n = 18 = 14m + 2sm (2SAT) + 2st。它们分别代表了整个毛冠菊属的两组 植物,并包含了形态学上最原始的种类,因此,该属的染色体基数可能为 x = 9。核形态证据表明毛冠菊 属放在紫菀族比放在旋覆花族和千里光族中更为合理。

关键词 毛冠菊属;核形态;族的归属

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