

Chromosome counts and karyotypes in *Chaetoseris* and *Stenoseris* (Asteraceae-Cichorieae) from the Hengduan Mountains of SW China

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Abstract *Chaetoseris* and *Stenoseris* are two morphologically close genera from the tribe Cichorieae of the sunflower family and they are endemic in alpine eastern Himalayas to the Hengduan Mountains of SW China. Mitotic chromosome numbers and karyotypes are reported for 12 populations representing eight species of *Chaetoseris* and two species of *Stenoseris* from the Hengduan Mountains region. Eight species are new and the other two provide confirmation of previous reference. All *Chaetoseris* and *Stenoseris* taxa are diploidy with $2n = 16$ and their basic number is tentatively suggested as $x = 8$. Karyotypes of *Chaetoseris* and *Stenoseris* are similar to each other with 2A and 2B for the former and 2A for the latter. Cytological data of chromosomal numbers and karyotypes support a close relationship of the two genera. Currently no polyploids are found for these two genera and it seems that polyploidization has played a minor role in their evolutionary speciation in the Hengduan Mountains region.

Key words Asteraceae, *Chaetoseris*, Cichorieae, Hengduan Mountains, karyotype, *Stenoseris*.

Chaetoseris Shih and *Stenoseris* Shih are two independent genera segregated from the notoriously heterogeneous traditional *Lactuca* L. within the subtribe Lactucinae of Cichorieae by Shih (1991). *Chaetoseris* is composed of 13–18 species with involucre bracts in 3–5 rows, 10–40 florets in each capitulum, florets purple to violet, rarely yellow, and achenes compressed and beaked, margins thickened and winged (Shih, 1997; Zhu, 2004; Lack, 2007). In contrast, *Stenoseris* is a small genus with 3–6 species, characterized by involucre bracts 3 in a single row, receptacle naked, 3–5 florets in each capitulum, florets purple to violet, and achenes compressed with wings (Shih, 1997; Zhu et al., 2006; Lack, 2007).

Although the tribe Cichorieae of Asteraceae is well defined by its milky latex and ligulate florets, the delimitations and phylogenetic relationships of its subtribes and many of its genera and species are still disputed (Stebbins et al., 1953; Bremer, 1994; Koopman et al., 1998; Karol & Mraz, 2008). This debate also occurs in *Chaetoseris* and *Stenoseris* concerning their taxonomical relationships and systematic positions within Lactucinae. Members of *Chaetoseris* had been placed in many other genera, such as *Lactuca* and *Sonchus* L. (Don, 1825; Franchet, 1895; Handel-Mazzetti, 1936),

as well as *Cicerbita* Wallr. (Beauverd, 1910). However, Shih (1991) thought that *Chaetoseris* differs not only from *Cicerbita* in having beaks at apex of achenes (vs. apex truncate and beakless in *Cicerbita*), but also from *Lactuca* without an outermost ring of short pappus at apex of achenes. Similarly, *Stenoseris* is separated from *Lactuca* based on *Lactuca graciliflora* Wall. ex DC., which has beaks and an outermost ring of short pappus at the apex of achenes. However, Kilian et al. (2009) has treated *Chaetoseris* and *Stenoseris* as synonyms of *Cicerbita* and *Notoseris*, respectively. The reticulate relationships for *Chaetoseris*, *Stenoseris*, and related genera (e.g., *Lactuca*, *Cicerbita*, and *Notoseris*) in the *Lactuca-Prenanthes* complex make it one of the most problematic groups in Asteraceae (Koopman et al., 1998). As pointed out by Stebbins et al. (1953), more evidence, such as morphological, palynological, and karyological data, must be used to fully resolve the classification and relationships among Cichorieae taxa.

All members of *Chaetoseris* and *Stenoseris* are distributed in subalpine or alpine thickets in the Hengduan Mountains of SW China (Shih, 1997; Zhu, 2004), with four species extending into India, Sikkim, Myanmar, India, Bhutan, and Nepal (i.e., *C. grandiflora* (Franch.) Shih, *C. macrantha* (C. B. Clarke) Shih, *C. cyanea* (D. Don) Shih, and *S. graciliflora* (Wall. ex DC.) Shih). It is apparent that the Hengduan Mountains is the most diversified center of the two genera. Floristically, this region is one of the biodiversity hotspots of the world with a large concentration of species diversity and endemism

Received: 29 August 2010 Accepted: 9 December 2010

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(Wu, 1988; Li & Li, 1993; Boufford & Van Dyck, 1999; Myers et al., 2000). A high rate of polyploidy could be expected in this region because of the unusually high species diversity and endemism, the widespread alpine environment, and the importance of polyploidy in plant evolution. However, Nie et al. (2005) has indicated that polyploidy might have played a relatively minor role in the evolutionary diversification of plants in the region. As suggested by Yuan & Yang (2008) and Meng et al. (2010), further cytological data are badly needed in order to have a better understanding of the role of polyploidy in this biodiversity hotspot.

Chromosomal information has contributed extensively to our understanding of relationships within the Asteraceae and has resulted in heightened awareness of groups in need of taxonomic re-evaluation (Watanabe et al., 2007). Chromosome data of the two genera, however, are scant in contrast with the large amount of cytological data on the Cichorieae as a whole (Babcock et al., 1937; Stebbins et al., 1953; Turner et al., 1961; Tomb, 1977; Tomb et al., 1978; Jansen & Stuessy, 1980). Only two species of *Chaetoseris* and two of *Stenoseris* have chromosomal data (Stebbins et al., 1953; Mehra et al., 1965; Mathew & Mathew, 1988; Yuan & Yang, 2002). In this paper, chromosome numbers and karyomorphology of eight species of *Chaetoseris* and two *Stenoseris* species from the Hengduan Mountains, were investigated, in order to expand our karyological knowledge of the two genera in the Cichorieae and investigate whether polyploidy plays important role on their species evolution in the Hengduan Mountains.

1 Material and methods

Seeds of 12 populations from the Hengduan Mountains of SW China, representing eight *Chaetoseris* and two *Stenoseris* species, were used (Table 1). Voucher specimens were deposited in the Herbarium of the Kunming Institute of Botany, Chinese Academy of Sciences (KUN). Chromosome counts were made on somatic metaphase using standard squash techniques. Root-tip meristems were obtained by germinating seeds on wet filter paper in Petri dishes at approximately 20 °C. Root tips less than 1.5 cm long were cut and pretreated with 0.002 mol/L 8-hydroxyquinoline at room temperature for 3–5 h. The material was fixed in Carnoy's solution (3:1 v/v absolute ethanol : glacial acetic acid) for 2–5 h at 4 °C. Meristems were dissociated in a mixture of 1 mol/L HCl and 45% acetic acid (1:1) for 15–30 s at 60 °C. They were then washed three times with distilled water and stained in 1% acetic orcein for a minimum

of 5–6 h at room temperature. Squashes were made in 45% acetic acid. Preparations were made permanent using the standard liquid nitrogen method.

Chromosome numbers were determined for each population from at least 50 cells of at least two seedlings for mitotic observations. Slides were analyzed with a Zeiss microscope equipped with a digital camera. Measurements of chromosome arm length and total chromosome length were taken from five selected chromosomal spreads with a medium degree of chromosome condensation. Karyomorphological classification of the mitotic interphase nuclei and prophase chromosomes follows Tanaka (1971, 1977, 1989), and the designation of the centromeric position as median (m), submedian (sm), and subterminal (st) follows Levan et al. (1964). The traditional karyotype asymmetry is classified according to Stebbins (1971).

Another asymmetry index (AI) to measure karyotype asymmetry proposed by Paszko (2006) is also analyzed in this study. The AI is defined as the product of a component expressing the relative variation in chromosome length (CV_{CL}) and a component expressing the relative variation in centromeric index (CV_{CI}). Relationships between these parameters are summarised by the following equation: $AI = CV_{CL} \times CV_{CI} / 100$.

2 Results

Chromosome numbers of 12 collections representing eight species of *Chaetoseris* and two of *Stenoseris* were determined (Table 1). These are displayed in Figs. 1–16. The characteristics of their karyotypes are represented in Table 2. *Chaetoseris* and *Stenoseris* have the same interphase nucleus and mitotic prophase chromosomes. The interphase chromatin of the two genera has an almost homogeneous distribution throughout the nucleus, forming a fibrous network of the chromonemata (Figs. 1, 3). According to the system of Tanaka (1971, 1977), it can be categorized as a diffuse type. Their chromosomes at mitotic prophase stain darkly and homogeneously, showing several small elastic constrictions (Figs. 2, 4). There were no conspicuously heterochromatic or euchromatic segments in those species. Using the system of Tanaka (1971, 1977, 1989), the prophase chromosomes are classified as an interstitial type.

All species of *Chaetoseris* and *Stenoseris* have the same chromosome number of $2n = 16$. Karyotypes of these studied species were quite uniform, consisting of 2 medium, 8–10 submedium, and 4–6 subterminal chromosomes (Table 2). According to Stebbins (1971), all the karyotypes of *Chaetoseris* belong to 2B, except for

Table 1 Locality (China), geographical position, altitude, and voucher number of the investigated species of *Chaetoseris* and *Stenosseris*

No.	Taxon	Locality, province	Position	Altitude (m)	Voucher
1	<i>Chaetoseris beesiana</i> (Diels) Shih	Lijiang, Yunnan	27°00'N, 100°12'E	2790	Nie, Meng, and Deng 1638 (KUN)
2	<i>C. cyanea</i> (D. Don) Shih	Dali, Yunnan	27°01'N, 100°10'E	2419	Nie, Meng, and Deng 1673 (KUN)
3		Dali, Yunnan	27°01'N, 100°10'E	2540	Nie, Meng, and Deng 1675 (KUN)
4	<i>C. dolichophylla</i> Shih	Lijiang, Yunnan	27°00'N, 100°12'E	2790	Nie, Meng, and Deng 1621 (KUN)
5	<i>C. grandiflora</i> (Franch.) Shih	Gongshan, Yunnan	27°47'N, 98°32'E	3130	Nie, Meng, and Deng 1722 (KUN)
6	<i>C. hastata</i> (Wall. ex DC.) Shih	Gongshan, Yunnan	27°47'N, 98°32'E	3130	Nie, Meng, and Deng 1739 (KUN)
7	<i>C. likiangensis</i> (Franch.) Shih	Lijiang, Yunnan	27°00'N, 100°12'E	2790	Nie, Meng, and Deng 1640 (KUN)
8	<i>C. lyriformis</i> Shih	Kangding, Sichuan	29°51'N, 102°02'E	3289	Nie, Meng, and Deng 1345 (KUN)
9		Zhongdian, Yunnan	28°26'N, 99°47'E	3164	Nie, Meng, and Deng 1439 (KUN)
10	<i>C. taliensis</i> Shih	Lijiang, Yunnan	27°00'N, 100°12'E	2790	Nie, Meng, and Deng 1637 (KUN)
11	<i>Stenosseris graciliflora</i> (Wall. ex DC.) Shih	Gongshan, Yunnan	27°47'N, 98°32'E	3130	Nie, Meng, and Deng 1732 (KUN)
12	<i>S. leptantha</i> Shih	Muli, Sichuan	27°41'N, 101°13'E	3228	Nie, Meng, and Deng 1159 (KUN)

C. dolichophylla Shih and *C. hastata* (Wall. ex DC.) Shih as 2A, and *Stenosseris* have a karyotype of 2A (Table 2).

The ranges of chromosome size in *Chaetoseris* and *Stenosseris* species are given in Table 2. All *Chaetoseris* species have one pair of short metacentric chromosomes except for *C. dolichophylla*. The chromosomes of *C. dolichophylla* are more uniform than any other species with the lowest ratio of the longest to the shortest chromosome as 1.63.

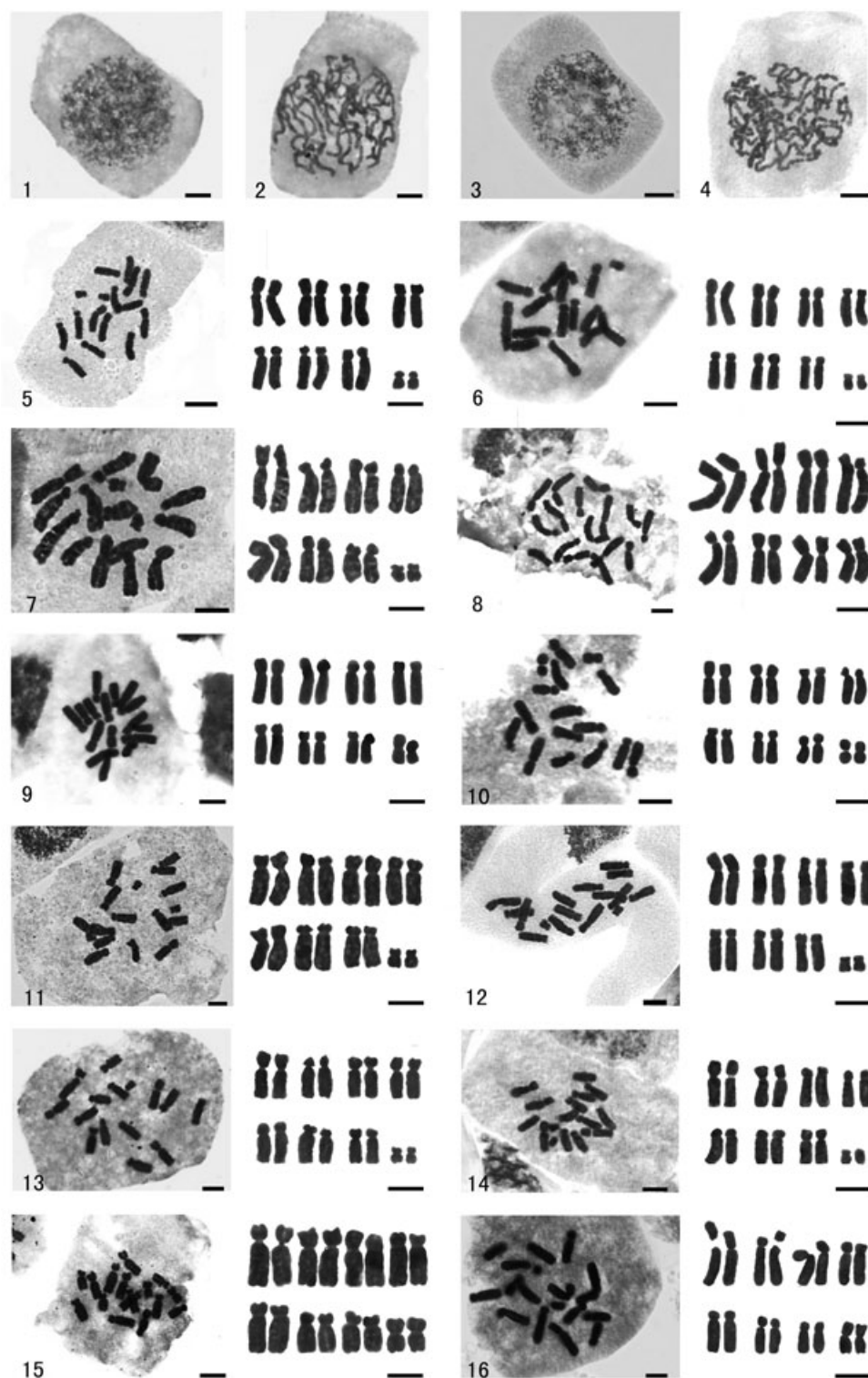
This is the first time the AI values for karyotypic asymmetry of the two genera have been reported. Species in *Chaetoseris* and *Stenosseris* have AI values varying from 3.24 to 6.44, and from 3.77 to 4.97, respectively.

3 Discussion

This paper reports a comprehensive survey of chromosome numbers in *Chaetoseris* and *Stenosseris* for the first time. Seven species of the former (*C. beesiana* (Diels) Shih, *C. cyanea* (D. Don) Shih, *C. dolichophylla*, *C. grandiflora* (Franch.) Shih, *C. likiangensis* (Franch.) Shih, *C. lyriformis* Shih, and *C. taliensis* Shih) and one of the latter (*S. leptantha* Shih) are reported for the first time. All species of *Chaetoseris* have the same chromosome number of $2n = 16$, consistent with previous counts, *C. hastata* (Stebbins et al., 1953; Mehra et al., 1965; Mathew & Mathew, 1988), and *C. macrantha* (C. B. Clarke) Shih (Stebbins et al., 1953). Therefore, the most likely basic chromosome number of the genus should be $x = 8$. *Stenosseris* contains only three species and two of them (*S. leptantha* and *S. graciliflora* (Wall. ex DC.) Shih) were counted as $2n = 16$ in this report, in agreement with two previous chromosome counts of *S. graciliflora* (Mehra et al., 1965) and *S. taliensis* (Franch.) Shih (Yuan & Yang, 2002). Thus, the basic number of those three species of *Stenosseris* should be supposed as $x = 8$.

To allow comparison of chromosome numbers in Lactucinae, all available chromosome numbers of *Chaetoseris* and *Stenosseris* and their possible closely related taxa (e.g., *Cicerbita*, *Lactuca*, *Notoseris*, and *Syncalathium souliei*) are listed in Table 3 (Shih, 1991; Kilian et al., 2009; Zhang et al., 2011). On the basis of morphological characters, Shih (1991) has separated *Chaetoseris* and *Stenosseris* from *Lactuca* and *Cicerbita*, respectively. However, Kilian et al. (2009) treated *Chaetoseris* and *Stenosseris* as synonyms of *Cicerbita* and *Notoseris*, respectively. As shown in Table 3, the basic number of *Stenosseris* ($x = 8$) differs from those of *Notoseris* ($x = 9$), therefore the cytological evidence does not support the transfer of *Stenosseris* into *Notoseris*. It is not clear for relationships between *Chaetoseris* and *Cicerbita* because the basic number of the former is $x = 8$, and that of the latter includes both eight and nine (Table 3). However, our cytological data strongly supported a close relationship between *Chaetoseris* and *Stenosseris*, as both of them having the same chromosome number of $2n = 16$ and similar karyotypes (Tables 2, 3). This is highly congruent with their morphological features, such as pappus in two rows, dimorphic, outer shortest, inner pappus longest, and with beaks at the apex of achenes. It is necessary to mention that the achene characters have been considered as important traits in classification in the Compositae (Singh et al., 1972; Mukherjee & Sarkar, 1995; Blanca & Guardia, 1997; Kilian, 1997; Dasgupta & Mukherjee, 2007; Das & Mukherjee, 2008). Recent studies based on morphological characters of herbarium and field observations suggested that *Chaetoseris* and *Stenosseris* are two closely specialized genera in the “*Lactuca-Prenanthes*” complex (Zhu, 2006). Moreover, molecular data also indicated a close relationship between them because *Stenosseris* is well supported to be nested within *Chaetoseris* (Zhang et al., 2011).

The AI index, a new asymmetry index, was developed by Paszko (2006) in order to give a single value that assesses karyotype asymmetry. The AI has the



Figs. 1–16. Mitotic nuclei, metaphase chromosomes, and karyotypes of *Chaetoseris* and *Stenoseres*. **1, 2.** Mitotic interphase and prophase nuclei of *Chaetoseris cyanea* (Dali). **3, 4.** Mitotic interphase and prophase nuclei of *Stenoseres graciliflora* (Gongshan). **5.** *C. beesiana* (Lijiang), $2n = 16$. **6.** *C. cyanea* (Dali), $2n = 16$. **7.** *C. cyanea* (Dali), $2n = 16$. **8.** *C. dolichophylla* (Lijiang), $2n = 16$. **9.** *C. grandiflora* (Gongshan), $2n = 16$. **10.** *C. hastata* (Gongshan), $2n = 16$. **11.** *C. likiangensis* (Lijiang), $2n = 16$. **12.** *C. lyriformis* (Kangding), $2n = 16$. **13.** *C. lyriformis* (Zhongdian), $2n = 16$. **14.** *C. taliensis* (Lijiang), $2n = 16$. **15.** *S. graciliflora* (Gongshan), $2n = 16$. **16.** *S. leptantha* (Muli), $2n = 16$. $2n$ indicates somatic chromosome number. Scale bar = 5 μm .

Table 2 Cytological characteristics of *Chaetoseris* and *Stenoseris* accessions in this study

No.	Taxon	Range SC–LC (μm)	Ratio LC/SC	S (μm) Mean (± SD)	L (μm) Mean (± SD)	CL (μm) Mean (± SD)	CI Mean (± SD)	AI	Type	Karyotype formula
1	<i>Chaetoseris beestiana</i>	2.63–7.12	2.71	1.56 (± 0.47)	4.28 (± 0.98)	5.81 (± 1.25)	27.16 (± 6.00)	4.75	2B	2n = 2x = 16 = 2m + 10sm + 4st
2	<i>C. cyanea</i> 1	2.18–6.80	3.12	1.47 (± 0.51)	3.78 (± 0.87)	5.24 (± 1.21)	27.88 (± 5.5)	4.60	2B	2n = 2x = 16 = 2m + 8sm + 6st
3	<i>C. cyanea</i> 2	2.55–9.57	3.75	1.54 (± 0.30)	3.94 (± 0.92)	5.49 (± 1.04)	27.16 (± 6.20)	6.44	2B	2n = 2x = 16 = 2m + 8sm + 6st
4	<i>C. dolichophylla</i>	6.26–10.22	1.63	2.48 (± 0.68)	5.74 (± 1.05)	8.18 (± 1.31)	30.68 (± 6.21)	3.24	2A	2n = 2x = 16 = 2m + 10sm + 4st
5	<i>C. grandiflora</i>	3.45–6.91	2.01	1.54 (± 0.30)	3.94 (± 0.92)	5.49 (± 1.04)	28.81 (± 6.87)	4.52	2B	2n = 2x = 16 = 2m + 10sm + 4st
6	<i>C. hastata</i>	3.23–6.11	1.89	1.37 (± 0.34)	3.39 (± 0.73)	4.75 (± 0.75)	29.38 (± 8.22)	4.43	2A	2n = 2x = 16 = 2m + 10sm + 4st
7	<i>C. likiangensis</i>	2.63–7.06	2.68	1.52 (± 0.40)	4.49 (± 1.13)	6.00 (± 1.37)	26.00 (± 6.01)	5.28	2B	2n = 2x = 16 = 2m + 8sm + 6st
8	<i>C. lyriformis</i> 1	2.17–7.51	3.46	1.54 (± 0.56)	4.44 (± 1.16)	5.94 (± 1.52)	26.11 (± 6.21)	6.13	2B	2n = 2x = 16 = 2m + 8sm + 6st
9	<i>C. lyriformis</i> 2	2.15–6.48	3.01	1.52 (± 0.41)	3.74 (± 0.96)	5.25 (± 1.22)	29.68 (± 6.37)	5.00	2B	2n = 2x = 16 = 2m + 10sm + 4st
10	<i>C. taliensis</i>	2.25–6.73	2.99	1.41 (± 0.44)	3.75 (± 0.92)	5.16 (± 1.22)	27.74 (± 5.69)	4.60	2B	2n = 2x = 16 = 2m + 10sm + 4st
11	<i>Stenoseris graciliflora</i>	4.24–8.20	1.93	1.68 (± 0.48)	4.27 (± 1.01)	5.95 (± 1.23)	28.58 (± 6.90)	4.97	2A	2n = 2x = 16 = 2m + 8sm + 6st
12	<i>S. leptantha</i>	4.77–8.41	1.76	1.94 (± 0.40)	4.80 (± 1.07)	6.73 (± 1.26)	29.30 (± 5.87)	3.77	2A	2n = 2x = 16 = 2m + 8sm + 6st

AI, asymmetry index according to Paszko (2006); CI, mean centromeric index; CL, mean length of chromosome; L, mean length of long arm; LC, longest chromosome length; m, metacentric; S, mean length of short arm; SC, shortest chromosome length; SD, standard deviation; sm, submetacentric; st, subtelocentric; Type, classification of karyotypes in relation to their degree of asymmetry according to Stebbins (1971).

advantage of allowing a high degree of precision and sensitivity to assess karyotype asymmetry, and higher values of the AI index are considered to indicate higher levels of karyotypic heterogeneity (Paszko, 2006). This is the first time the AI values for karyotypic asymmetry of the two genera have been reported. Generally, species in *Chaetoseris* (AI values = 3.24–6.44) have higher asymmetry karyotypes than that of *Stenoseris*. All *Chaetoseris* species have one pair of short metacentric chromosomes, except for *C. dolichophylla*. The chromosomes of *C. dolichophylla* are more uniform than any other species with the lowest ratio of the longest to the shortest chromosome as 1.63 and AI = 3.24. However, this unimodal karyotype of *C. dolichophylla* is also found in *Stenoseris*, which may indicate a close relationship between them. Further evidence, especially molecular data, is necessary to test this hypothesis.

Molecular data suggest that *Chaetoseris* and *Stenoseris* are close to *Synclathium souliei* (Franch.) Ling (Zhang et al., 2011). This finding is well supported by our cytological data. All of them have a base number of $x = 8$ with similar karyotype 2A (Zhang et al., 2007). Furthermore, they are all found in Himalayan areas and share similar achene morphology. Achenes of *Chaetoseris* and *Stenoseris* have three to six ridges and beaks at apex, whereas *Synclathium souliei* has four prominent ridges and short beaks on its achenes, different from other species of *Synclathium* that have one and two nerves on each face and lack beaks on their achenes (Zhang et al., 2009).

Stebbins et al. (1953) estimated a relatively low frequency (15%) of polyploids in the tribe Cichorieae. Tomb et al. (1978) found a relatively high incidence of 23% for the tribe excluding the polyploid agamosperous microspecies of *Taraxacum* and *Hieracium*. As shown in Tables 2 and 3, all species of *Chaetoseris* and *Stenoseris* were reported as diploid. Reports of the two genera are all from the Hengduan Mountains region of SW China. Similar results have been found from other genera of Asteraceae, such as *Cremanthodium* (Liu et al., 2001) and *Ligularia* (Liu, 2004). *Chaetoseris* and *Stenoseris* seem to be two more examples to corroborate the viewpoint proposed by Nie et al. (2005) that polyploidy might have played only a minor role in the evolutionary species diversification of Hengduan Mountains flora. This point of view is somewhat supported by chromosome studies of those genera in Asteraceae and many other families in the region's taxa, such as *Tibetia* (Fabaceae) (Nie et al., 2002), *Solmslaubachia* (Brassicaceae) (Yue et al., 2004), and *Delphinium* (Ranunculaceae) (Yuan & Yang, 2008). However, the results obtained from investigations on many other groups are very different. For example, polyploidy

Table 3 Somatic chromosome number (2n), locality, and data source of *Chaetoseris*, *Stenoseris*, and related taxa in Cichorieae

Taxon	Number	Locality	Data source
<i>Chaetoseris beesiana</i> (Diels) Shih	16/2n	Yunnan, China	Present paper
<i>C. cyanea</i> (D. Don) Shih	16/2n	Yunnan, China	Present paper
	16/2n	Yunnan, China	Present paper
<i>C. dolichophylla</i> Shih	16/2n	Yunnan, China	Present paper
<i>C. grandiflora</i> (Franch.) Shih	16/2n	Yunnan, China	Present paper
<i>C. hastata</i> (Wall. ex DC.) Shih (as <i>Lactuca hastata</i> DC.)	16/2n	India	Stebbins et al. (1953)
	8/n	India	Mehra et al. (1965)
	8/n	India	Mathew & Mathew (1988)
	16/2n	Yunnan, China	Present paper
<i>C. likiangensis</i> (Franch.) Shih	16/2n	Yunnan, China	Present paper
<i>C. lyriformis</i> Shih	16/2n	Sichuan, China	Present paper
	16/2n	Yunnan, China	Present paper
<i>C. macrantha</i> (C. B. Clarke) Shih (as <i>L. macrantha</i> Clarke)	16/2n	India	Stebbins et al. (1953)
<i>C. taliensis</i> Shih	16/2n	Yunnan, China	Present paper
<i>Stenoseris graciliflora</i> (Wall. ex DC.) Shih (as <i>L. graciliflora</i> DC.)	16/2n	India	Mehra et al. (1965)
	16/2n	Yunnan, China	Present paper
<i>S. leptantha</i> Shih	16/2n	Yunnan, China	Present paper
<i>S. taliensis</i> (Franch.) Shih	16/2n	Sichuan, China	Yuan & Yang (2002)
<i>Syncalathium souliei</i> (Franch.) Ling	16/2n	Yunnan, China	Zhang et al. (2007)
<i>Cicerbita haimanniana</i> (Asch. ex Dur. & Barr.) Beauverd	16/2n	Italy	Brullo et al. (1990)
<i>Ci. plumieri</i> (L.) Kirschl.	16/2n	Germany	Wegmuller (1994)
<i>Ci. prenanthoides</i> (Bieb.) Beauverd	16/2n	Georgia	Gagnidze & Chkheidze (1974)
<i>Ci. racemosa</i> (Willd.) Beauverd	16/2n	Georgia	Gagnidze et al. (1998)
<i>Ci. alpina</i> (L.) Wallr.	18/2n	Bulgaria	Van Loon & Van Setten (1982)
<i>Ci. petiolata</i> (K. Koch) Gagnidze	18/2n	Georgia	Gagnidze & Chkheidze (1974)
<i>Ci. pontica</i> (Boiss.) Grossh.	18/2n	Georgia	Gagnidze & Chkheidze (1974)
<i>Ci. tianschanica</i> (Regel & Schmalh.) Beauverd	18/2n	Germany cult.	Gemeinholzer & Faustmann (2005)
<i>Notoseris gracilipes</i> Shih	18/2n	Chongqing, China	Yuan & Yang (2002)
<i>N. guizhouensis</i> Shih	18/2n	Chongqing, China	Yuan & Yang (2002)
<i>N. porphyrolepis</i> Shih	18/2n	Chongqing, China	Yuan & Yang (2002)
<i>N. triflora</i> (Hemsl.) Shih	18/2n	Chongqing, China	Yuan & Yang (2002)
<i>Lactuca amorgina</i> Heldr. & Orph. ex Hal.	18/2n	Greece	Tzanoudakis (1986)
<i>L. capensis</i> Thunb.	18/2n	Cameroon	Morton (1993)
<i>L. graeca</i> Boiss.	9/n	Greece	Strid & Franzen (1981)
<i>L. indica</i> L.	18/2n	Taiwan, China	Peng & Hsu (1977)
<i>L. leptcephala</i> Stebbins	16/2n	Dem. Rep. Congo	Babcock et al. (1937)
<i>L. muralis</i> (L.) Fresen.	18/2n	Iceland	Löve & Löve (1982)
<i>L. parishii</i> Craib	18/2n	Japan	Pak (1991)
<i>L. perennis</i> L.	18/2n	Italy	Löve & Löve (1982)
<i>L. tenerrima</i> Pourret	9/n	USA	Tomb et al. (1978)
<i>L. undulata</i> Ledeb.	9/n	Iran	Ghaffari (1986)
<i>L. graminifolia</i> Michx.	17/n	Mexico	Keil (1981)
<i>L. canadensis</i> L.	34/2n	Canada	Löve & Löve (1982)
<i>L. floridana</i> (L.) Gaertn.	34/2n	Canada	Löve & Löve (1982)
<i>L. ludoviciana</i> (Nutt.) Riddell	34/2n	USA	Stebbins et al. (1953)

is found to be common in *Anaphalis* of Asteraceae (Meng et al., 2010), *Aconitum* subgenus *Lycotconum* of Ranunculaceae (Yuan & Yang, 2006), and *Buddleja* of Buddlejaceae (Chen et al., 2007). It is too early to evaluate the role of polyploids or diploids on plant speciation in this region because only a very small proportion of species have available chromosomal data (Nie et al., 2005; Yuan & Yang, 2008; Meng et al., 2010). The statistical analysis from Nie et al. (2005) was based on only 552 taxa with chromosome data reported from the Hengduan Mountains, whereas more than 8000 species have been recorded from this region. More plant groups with possibly different evolutionary backgrounds should be studied cytologically to gain a better understanding of the speciation patterns in this biodiversity hotspot.

Acknowledgements This study was supported by grants from the National Natural Science Foundation of China (Grant No. 30770167 to Ze-Long NIE, and Grant Nos. 30625004 and 40930209 to Hang SUN) and the Basic Research Program from the Ministry of Science and Technology of China (Grant No. 2007FY110100). We are grateful to Ms. Chun-Lin ZHANG for laboratory assistance.

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