

Research paper

Karyomorphology of three endemic plants (Brassicaceae: Euclidaeae and Arabideae) from the Qinghai-Tibet Plateau and its significance

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ABSTRACT

In the paper, chromosome number and karyotype of three endemic genera from China are reported for the first time. Our results show that *Anzhengxia yechengnica* has a karyotype formula $2n = 2x = 14 = 6m + 8sm$ and belongs to Stebbins-3A; *Shangrilaia nana* karyotype formula is $2n = 2x = 14 = 10m + 4sm (2sat)$ and belongs to Stebbins-1A; *Baimashania pulvinata* karyotype formula is $2n = 2x = 16 = 12m (2sat) + 4sm$ and belongs to Stebbins-1A. *Anzhengxia* and *Shangrilaia* are monospecific genera belonging to tribe Euclidaeae and both have a basic chromosome $x = 7$. *Baimashania*, which belongs to tribe Arabideae, has two species which have a basic chromosome $x = 8$. The implications of these cytological data are compared with morphological support and the implications for each tribe are discussed. We also summarize chromosomal number variation and its systematic implications of two tribes from the Qinghai-Tibet Plateau.

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1. Introduction

Plant karyotype research is important for understanding the origin and evolution plant species, molecular phylogeny, and floristic geography (Sun et al., 2019). Karyomorphological study provides insight into potential evolutionary characteristics of karyotypes, as well as the cytological mechanisms driving the evolution of plant diversity on a phylogenetic scale. In addition, karyomorphological study is a fast, inexpensive approach to classify plant species by identifying the basic cytological parameters of a species, including chromosome number, ploidy level, karyotype asymmetry, and karyotype coefficient of variation (Guerra, 2008). The number of chromosomes and karyotype of a species are stable characteristics that can reflect its basic genetic information.

Furthermore, differences in chromosome numbers between populations is important evidence for determining reproductive isolation. Investigating the cytological features of species (e.g., via chromosome atlas or polyploid frequency) at a regional or flora scale may uncover the influence of geo-ecological environmental shifts on chromosome ploidy.

Various hypotheses have been proposed to explain the origin and distribution of plant polyploids. The prevailing hypothesis is that the doubled genome of polyploids renders them more adaptable than diploids to extreme environments such as those encountered at high latitudes and high altitudes (Soltis and Soltis, 2000). For example, the region with the highest proportion of plant polyploids in the world is the Arctic Circle. Analysis of plant chromosome numbers in the Arctic indicates that the chromosome polyploid ratio in this region is more than 80% (Löve and Löve, 1975). In addition, previous research has shown that the ratio of polyploid species at high altitude environments is relatively high (Löve and Löve, 1967). Similarly, research has indicated that the polyploid frequency is much higher in the mountains than in the lowlands (Hanelt, 1966). The Qinghai-Tibet Plateau region is a well-known biodiversity hotspot that harbors numerous endemic plant species in extreme alpine environments. Although understanding

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species diversity in this area has been a long-term concern of scientists (Spicer, 2017; Sun et al., 2017), the underlying forces that have driven such species richness remains unclear. One potential explanation for the high level of endemic plant diversity in the Qinghai-Tibet Plateau is that increased polyploidization. Constructing regional chromosome data is a promising approach to shedding light on the formation and evolutionary history of this flora.

The Brassicaceae family comprises c. 4000 species including economically important crops and the model plant *Arabidopsis thaliana* (L.) Heynh. (Appel and Al-Shehbaz, 2003; Kiefer et al., 2014). Brassicaceae contains approximately 102 genera and 412 species in China (Zhou et al., 2001). *Anzhengxia* Al-Shehbaz & D. A. German, *Shangrilaia* Al-Shehbaz, J. P. Yue & H. Sun, *Baimashania* Al-Shehbaz are three recently established endemic genera of Brassicaceae from Qinghai-Tibet Plateau (Fig. 1). *Anzhengxia* (*A. ychengnica* (C. H. An) Al-Shehbaz & D. A. German) and *Shangrilaia* (*Shangrilaia nana* Al-Shehbaz, J. P. Yue & H. Sun) are monospecific genera (Al-Shehbaz and German, 2016; Al-Shehbaz et al., 2004). The genus *Baimashania* has two species (*Baimashania pulvinata* Al-Shehbaz and *B. wangii* Al-Shehbaz) (Al-Shehbaz, 2000). Although new species and genera of Brassicaceae are continually being described, few chromosomal data of related groups have been studied, which hampers comparative research. A statistical database has shown that chromosome numbers are generally known from 232 of the 338 (68.6%) genera and 1558 of the 3709 (42.0%) species of Brassicaceae (Koch and Al-Shehbaz, 2004). For Brassicaceae plants in China, there are 205 species in 74 genera with chromosome reports (statistical data by the authors). Cytological data can provide useful evidence for the systematics and taxonomy of Brassicaceae.

Despite their importance, the relationships among major lineages in Brassicaceae remain unresolved (Nikolov et al., 2019). To better understand the relationships in the Brassicaceae, we investigated the chromosome number and karyotype asymmetry patterns of *Anzhengxia*, *Shangrilaia*, and *Baimashania*, three endemic genera from the Qinghai-Tibet Plateau. To test the hypothesis that polyploidization is the primary driver of speciation in the Qinghai-Tibet Plateau region, we surveyed chromosome numbers and ploidy levels of species in two tribes (Euclidieae and Arabideae) of

Brassicaceae that have distributions limited the Qinghai-Tibet Plateau.

2. Materials and methods

2.1. Plant materials and treatments

Anzhengxia ychengnica, *Shangrilaia nana*, *Baimashania pulvinata* plants were collected from northwest and southwest China (Table 1). Voucher specimens have been deposited in the herbarium of the Kunming Institute of Botany (KUN).

Chromosome numbers were counted in more than 30 somatic cells from the root tips of seedlings of each taxon. Prior to germination, seeds were stored at 4 °C for at least one month. Subsequently, seeds were germinated in agarose at 24 °C. Fresh root tips (about 1–2 cm in length) were excised from the seedlings and pretreated in 0.002 or 0.003 mol/L 8-hydroxyquinoline solution at 24 °C in the dark for 2 h, then fixed in 3:1 Carnoy's solution (absolute ethanol: acetic acid, v/v) for at least 24 h at 4 °C. The fixed roots were hydrolysed in 1 mol/L HCl at 60 °C for 12 min, and then washed with distilled water, dyed with carbolfuchsin and squashed for observation. Karyotype analyses were based on measurements of mitotic–metaphase chromosomes taken from photographs.

2.2. Karyotype analysis

Karyotype analyses were based on at least six mitotic metaphase cells from each species. Chromosome classifications were made by the standardized nomenclature proposed by Levan et al. (1964). The degree of karyotype asymmetry was estimated with Stebbins's method (Stebbins, 1971). The index of Karyotypic Asymmetry (As.K %) was calculated as $As.K\% = \frac{\text{total of the longest in a chromosome set}}{\text{total of the a chromosome set}} \times 100$. Asymmetry index (AI) was calculated as $AI = \frac{CV_{CL} \times CV_{CI}}{100}$, where CV_{CL} is a component expressing the relative variation in chromosome length, and CV_{CI} is a component expressing the relative variation in the centromeric index. Karyotype parameters were measured using KaryoType software (Altunordu et al., 2016).



Fig. 1. Photographs of morphological traits and habits of *Anzhengxia*, *Shangrilaia* and *Baimashania*. 1–4: *A. ychengnica* (Photos by Hong-Liang Chen); 5–8: *S. nana* (Photos by Ji-Pei Yue); 9–12: *B. pulvinata* (Photos by Wen-Guang Sun).

Table 1
Voucher information for *Anzhengxia*, *Shangrilaia*, and *Baimashania*.

Taxon	Locality	Coordinates	Altitude/m	Voucher
<i>Anzhengxia yechengnica</i>	Yecheng, Xinjiang, China	E77°03'36", N37°11'34"	2450	YC-XZ115
<i>Shangrilaia nana</i>	Shangri-La, Yunnan, China	E99°35'13", N27°47'35"	4408	CHY-008
<i>Baimashania pulvinata</i>	Deqin, Yunnan, China	E99°01'20", N28°23'21"	4530	MS17-157

2.3. Polyploid frequency within the tribes Euclidiaceae and Arabideae

To quantify variation in chromosome number and polyploid frequency within the tribes Euclidiaceae and Arabideae, we surveyed published reports on species of the tribes (Table 2). For the same purpose, we consulted the network database from Index to Plant Chromosome Numbers (IPCN, <http://www.tropicos.org/NameSearch.aspx?projectid=9>) (Goldblatt and Lowry, 2011) and Chromosome Counts Database (CCDB, <http://ccdb.tau.ac.il/home/>) (Rice et al., 2015). For each taxon (including species and subspecies), we used the originally published names and proofread the name in The Plant List (TPL, <http://www.theplantlist.org/>).

We used these same sources to calculate n , $2n$ and polyploid frequency for species from the tribes Euclidiaceae (14 taxa, 8 genera) and Arabideae (18 taxa, 2 genera) that are distributed in the Qinghai-Tibet Plateau.

3. Results

3.1. *Anzhengxia yechengnica* (C. H. An) Al-Shehbaz & D. A. German

Anzhengxia, a monotypic genus of the tribe Euclidiaceae, is endemic in the Pamirs and Kunlun Mountains region (Al-Shehbaz and German, 2016). The karyotype formula for *A. yechengnica* is $2n = 2x = 14 = 6m + 8sm$ (Table 3). According to the nomenclature of Tanaka (1971), the interphase nuclei and prophase chromosomes can

be categorized as diffuse type (Fig. 2: A, B, C, D). The chromosomes varied in length from 5.05 to 7.11 μm . The proportion of the longest to the shortest chromosome length was 1.41, and the AI = 1.98. The karyotype asymmetry (KA) belongs to Stebbins's-3B (Table 4). This is the first report for the karyotype parameters of *A. yechengnica*.

3.2. *Shangrilaia nana* Al-Shehbaz, J. P. Yue & H. Sun

Shangrilaia is a monotypic genus of tribe Euclidiaceae with *S. nana* and exhibits a typical distribution in the Hengduan Mountains region, SW China (Al-Shehbaz et al., 2004). *S. nana* grows naturally in alpine gravel meadows or extremely weathered gravelly slopes at altitudes mostly above 4200 m. The karyotype of *S. nana* is $2n = 2x = 14 = 10m + 4sm$ (2sat) (Table 3). According to the nomenclature of Tanaka (1971), the interphase nuclei and prophase chromosomes can be categorized as diffuse type (Fig. 2: E, F, G, H). The second chromosome pair of diploid *S. nana* has a satellite chromosome on the short arm (Table 3). The chromosomes varied in length from 3.78 to 5.34 μm . The ratio of the longest to the shortest chromosome length was 1.41, and the AI = 1.17; KA is Stebbins's-1A (Table 4). This is the first report for the karyotype parameters of *S. nana*.

3.3. *Baimashania pulvinata* Al-Shehbaz

Baimashania is a genus of the Brassicaceae with two identified species (*B. pulvinata* and *B. wangii*) (Al-Shehbaz, 2000). *B. pulvinata*

Table 2
Base chromosome number, n and $2n$ for species of tribes Euclidiaceae and Arabideae.

Genus	No. Species Counted	Base Chromosome No. (x)	Chromosome No. (n)	Chromosome No. ($2n$)
Tribe Euclidiaceae				
<i>Anzhengxia</i>	1	7	7	14
<i>Braya</i>	21	6, 7, 8, 9, 10	9, 14, 16, 20, 21, 24, 25, 28, 32, 35, 42, 56	18, 28, 32, 40, 42, 48, 50, 56, 64, 70, 84, 112
<i>Christolea</i>	3	6, 7	6, 7	12, 14
<i>Cryptospora</i>	1	7	7	14
<i>Euclidium</i>	1	7	7	14
<i>Lachnoloma</i>	1	7	7	14
<i>Leiospora</i>	2	7	7	14
<i>Leptaleum</i>	1	7	7	14
<i>Octoceras</i>	1	7	7	14
<i>Parrya</i>	1	7	7	14
<i>Sisymbrium</i>	1	7	7	14
<i>Solms-laubachia</i>	8	7	7, 14	14, 28
<i>Streptoloma</i>	1	7, 10	7, 40	14, 80
<i>Tetracme</i>	2	7	7, 14	14, 28
Tribe Arabideae				
<i>Arabis</i>	104	4, 6, 7, 8, 9, 10, 11	4, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 20, 21, 24, 32	8, 12, 14, 16, 17, 18, 20, 22, 24, 28, 30, 32, 40, 42, 48, 64, 26
<i>Athysanus</i>	1	13	13	26
<i>Aubrieta</i>	12	8	8, 16	16, 32
<i>Baimashania</i>	1	8	8	16
<i>Draba</i>	204	6, 7, 8, 9, 10, 11, 12, 13, 15, 19	6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 18, 19, 20, 21, 22, 24, 25, 26, 27, 28, 30, 31, 32, 33, 36, 37, 38, 40, 41, 47, 48, 50, 56, 60, 64, 72	12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 36, 38, 40, 42, 44, 48, 50, 52, 54, 56, 60, 62, 64, 66, 72, 74, 76, 80, 82, 94, 96, 100, 112, 120, 128, 144

Table 3
Cytological characteristics of *Anzhengxia yechengnica*, *Shangrilaia nana*, and *Baimashania pulvinata*.

Species	Chromosome pair No.	L (%)	S (%)	L + S (%)	L/S	Chromosome type
<i>Anzhengxia yechengnica</i>	1	9.84	7.51	17.36	1.31	m
	2	10.92	4.33	15.26	2.52	sm
	3	9.36	5.87	15.23	1.60	m
	4	9.79	4.18	13.97	2.34	sm
	5	8.11	4.97	13.09	1.63	m
	6	9.55	3.28	12.83	2.91	sm
	7	8.33	3.95	12.28	2.11	sm
<i>Shangrilaia nana</i>	1	9.17	8.10	17.27	1.13	m
	2	10.44	5.82	16.26	1.79	sm (2sat)
	3	8.87	5.62	14.49	1.58	m
	4	7.66	6.30	13.96	1.22	m
	5	7.34	5.96	13.30	1.23	m
	6	7.90	4.43	12.33	1.78	sm
	7	7.35	5.05	12.39	1.46	m
<i>Baimashania pulvinata</i>	1	7.90	6.27	14.16	1.26	m
	2	7.29	6.66	13.94	1.09	m
	3	8.38	5.52	13.90	1.52	m
	4	6.66	5.73	12.38	1.16	m
	5	7.29	5.01	12.31	1.45	m (2sat)
	6	6.18	5.43	11.61	1.14	m
	7	5.87	5.62	11.48	1.04	m
	8	5.97	4.25	10.21	1.40	m

Abbreviations: L (%), relative length of long arm; S (%), relative length of short arm, L + S (%), relative length of total chromosome; L/S, arm ratio; m, metacentric; sm, sub-metacentric; sat: satellite chromosome.

is restricted mainly to alpine scree or weathered rocks in the Hengduan Mountains region at altitudes ranging from 4100 to 4600 m (Xu et al., 2014). This species is morphologically similar to plants in three genera (*Solms-laubachia* Muschler, *Leiospora* (C.A. Meyer) Dvorák, *Pycnoplathopsis* Jafri). The karyotype formula of *B. pulvinata* is $2n = 2x = 16 = 12m(2sat) + 4sm$ (Table 3). According to the nomenclature of Tanaka (1971), the interphase nuclei and prophase chromosomes can be categorized as simple type (Fig. 2: I, J, K, L). The fifth chromosome pair in the diploid has one satellite on the short arm (Table 3). The basic chromosome number of *Baimashania* was $x = 8$ and the somatic cells of the sampled

B. pulvinata were diploid. The chromosomes varied in length from 1.90 to 2.61 μm . The ratio of the longest to the shortest chromosome was 1.37, the AI = 0.76. KA is Stebbins's-1A (Table 4). This is the first report of the karyotype of *B. pulvinata*.

3.4. Summary of chromosome numbers for the tribes Euclidieae and Arabideae

Chromosome number for 1931 taxa of Brassicaceae in 258 genera have been reported (Goldblatt and Lowry, 2011; Rice et al., 2015; Warwick and Al-Shehbaz, 2006). In the Brassicaceae tribe

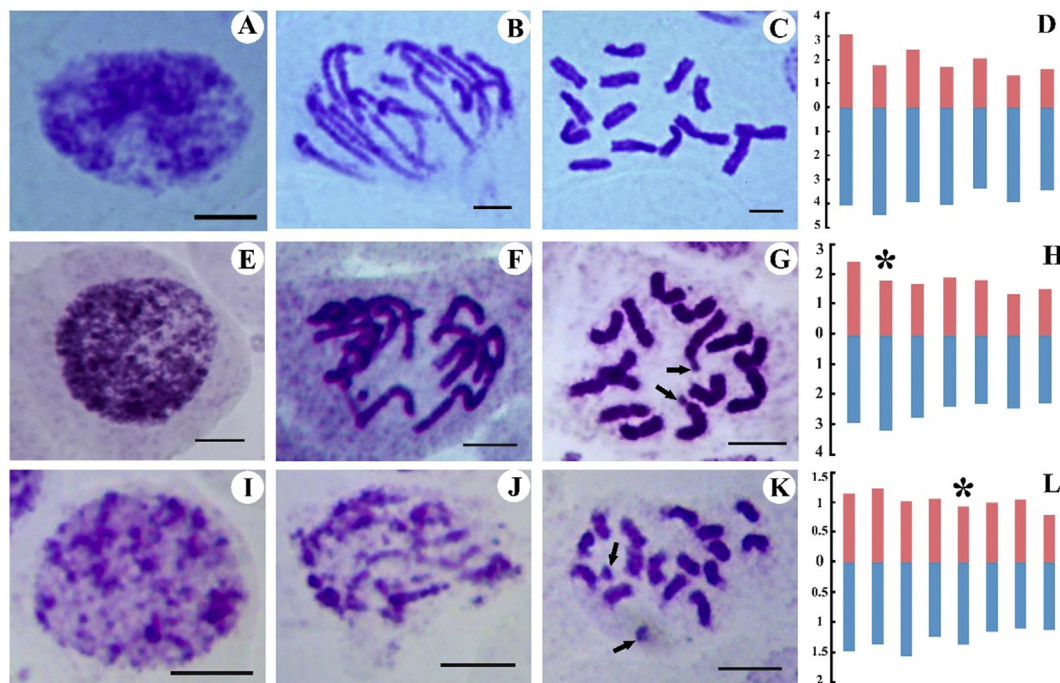


Fig. 2. Mitotic nuclei, metaphase chromosomes, and ideograms of *Anzhengxia*, *Shangrilaia* and *Baimashania*. A–D: *A. yechengnica*; E–H: *S. nana*; I–L: *B. pulvinata*. Scale bar = 5 μm ; Red: the relative length of short arm; Blue: the relative length of long arm; arrowheads and asterisks indicate satellite chromosomes.

Table 4
Karyotypic characteristics of three endemic species.

Taxon	Chromosome length range/ μm	Ratio LC/SC	L/ μm \pm SD	S/ μm \pm SD	TCL/ μm \pm SD	CI \pm SD	>2:1 As:K%	AI	THL \pm SD	CV _{CL}	CV _G	M _{CA}	KA	Chromosome No./Polyploidy	Karyotype Formula
<i>Anzhengxia yechengnica</i>	5.05–7.11	1.41	3.88 (± 0.36)	2.00 (± 0.54)	11.75 (± 0.67)	33.37 (± 5.90)	0.57	66.01	1.98	5.88 (± 0.67)	11.44	17.34	32.33	3 A	6 m + 8sm
<i>Shangrilaia nana</i>	3.78–5.34	1.41	2.57 (± 0.32)	1.80 (± 0.31)	8.75 (± 0.54)	41.17 (± 3.77)	0	58.81	1.17	4.37 (± 0.54)	12.43	9.40	17.85	1 A	10 m + 4sm (2sat)
<i>Baimashania pulvinata</i>	1.90–2.61	1.37	1.28 (± 0.32)	1.03 (± 0.12)	4.62 (± 0.24)	44.48 (± 0.32)	0	55.61	0.76	2.31 (± 0.24)	10.39	7.35	11.11	1 A	12 m (2sat) + 4sm

Abbreviations: LC/SC, the proportion of the longest chromosome length to the shortest chromosome length; L, long arm length (μm); S, short arm length (μm); TCL, mean length of chromosome (μm); CI, mean centromeric index; As:K%, index of karyotypic asymmetry (Arano, 1963); AI, asymmetry index (Paszko, 2006); THL, Total haploid (monoploid) length of chromosome set (μm); CV_{CL}, coefficient of variation of chromosome length (Paszko, 2006); CV_G, coefficient of variation of the centromeric index (Paszko, 2006); M_{CA}, mean centromeric asymmetry (Peruzzi and Eroglu, 2013); KA, karyotype asymmetry (Stebbins, 1971); m, metacentric; sm, submetacentric; sat, satellite chromosome; SD, standard deviation.

Euclidiaceae, chromosome numbers have been reported for 45 taxa in 14 genera. Chromosome number varies greatly in the tribe Euclidiaceae, with at least 16 different chromosome numbers, ranging from $2n = 12$ to $2n = 112$ (Table 2). Over 93.33% of taxa in tribe Euclidiaceae have the basic chromosome number $x = 7$.

Chromosome numbers have been reported for 322 taxa from 5 genera of tribe Arabideae. In the tribe Arabideae, at least 39 different chromosome numbers have been found, ranging from $2n = 8$ to $2n = 144$ (Table 2). Over 86.96% of taxa in the tribe Arabideae have the basic chromosome number $x = 8$.

Our survey of chromosome numbers and ploidy levels in tribes Euclidiaceae and Arabideae (367 species in 19 genera) showed that ploidy levels varied from $2x$ to $24x$ (Table 2).

We also surveyed chromosome number and ploidy levels for species that belong to the tribes Euclidiaceae and Arabideae but whose distribution is restricted to the Qinghai-Tibet Plateau region (Table 5). We found that the polyploid frequency of these species is about 36.11%.

4. Discussion

4.1. Karyomorphology of the three endemic plants

Our study presents an integral survey on the karyological variation of all currently recognized members of the tribes Euclidiaceae and Arabideae. In this study, we found that *A. yechengnica* and *S. nana* have the same chromosome number, $x = 7$, and that this number is the same as the basic chromosome number of plants in tribe Euclidiaceae. This finding supports the placement of the genera *Anzhengxia* and *Shangrilaia* in tribe Euclidiaceae (Chen et al., 2018). In addition, we report the first formulation of the karyotype of *B. pulvinata*, which has a basic chromosome number $x = 8$ and diploid number $2n = 16$.

We formulated the karyotype of *A. yechengnica* as $2n = 2x = 14 = 6m + 8sm$. This is the first report of karyotype parameters for *A. yechengnica*. Traditionally, *A. yechengnica* has been placed in *Microsymbrium* O. E. Schulz as *M. yechengicum* Z. X. An (An, 1981); however, *M. yechengicum* was transferred to *Sisymbriopsis* Botsch. & Tzvelev as *S. yechengicum* Z. X. An (1981) by Al-Shehbaz et al. (1999). Recent molecular phylogenetic study and morphological characters suggested that *S. yechengnica* is a monotypic genus of the tribe Euclidiaceae and should be treated as *A. yechengnica* (Al-Shehbaz and German, 2016). The occurrence of $2n = 2x = 14$ in *A. yechengnica* is similar to the karyotype of *Sisymbriopsis mollipila* (Maximowicz) Botschantzev (Ren et al., 2008), which has the same chromosome number as most species of the tribe Euclidiaceae.

The genus *Shangrilaia* of tribe Euclidiaceae is monotypic, consisting of *S. nana*, which is typically distributed in northwest Yunnan (Shangri-La County) (Al-Shehbaz et al., 2004). In this study, we found that the karyotype of *S. nana* is $2n = 2x = 14 = 10m + 4sm (2sat)$. In addition, we discovered that the second chromosome pair of diploid *S. nana* has a satellite chromosome on the short arm. Our results show that *S. nana* has the same chromosome count ($x = 7$) as *Solms-laubachia* (Yue et al., 2003, 2004), which is the most frequent chromosome count of the tribe Euclidiaceae. *S. nana* is also morphologically similar to *Solms-laubachia* in flowering pattern, petal color, and seed characteristics. However, the fruit of these two species differ; *Solms-laubachia* fruit are siliques, whereas *Shangrilaia* fruit are silicles (Fig. 1) (Al-Shehbaz et al., 2004).

Baimashania is a genus within Brassicaceae with two identified species (*B. pulvinata* and *B. wangii*) (Al-Shehbaz, 2000). Morphologically, these two species are closely related to the genera *Solms-laubachia*, *Leiospora*, and *Pycnophilthopsis*. In the

Table 5
Chromosome numbers (n, 2n) and polyploid levels for species of tribes Euclidieae and Arabideae from the Qinghai-Tibet Plateau.

Taxon	Chromosome No. (n)	Chromosome No. (2n)	Polyploidy
Tribe Euclidieae			
<i>Braya rosea</i>	14	28	4x
<i>Christolea crassifolia</i>	7	14	2x
<i>Euclidium syriacum</i>	7	14	2x
<i>Leiospora bellidifolia</i>	7	14	2x
<i>Leptaleum filifolium</i>	7	14	2x
<i>Neotorularia torulosa</i>	7	14	2x
<i>Solms-laubachia eurycarpa</i>	7	14	2x
<i>Solms-laubachia linearifolia</i>	7	14	2x
<i>Solms-laubachia minor</i>	7	14	2x
<i>Solms-laubachia pulcherrima</i>	7	14	2x
<i>Solms-laubachia retropilosa</i>	7, 14	14, 28	2x, 4x
<i>Solms-laubachia xerophyta</i>	7	14	2x
<i>Tetracme pamirica</i>	14	28	4x
<i>Tetracme quadricornis</i>	7	14	2x
Tribe Arabideae			
<i>Arabis amplexicaulis</i>	8, 16	16, 32	2x, 4x
<i>Arabis hirsuta</i>	16	32	2x
<i>Arabis pterosperma</i>	8	16	2x
<i>Arabis tibetica</i>	8	16	2x
<i>Draba alajica</i>	20	40	4x
<i>Draba alpina</i>	31, 32, 33, 37, 40, 56, 60	62, 64, 66, 74, 80, 112, 120, 64-66	2x
<i>Draba altaica</i>	8, 9	16, 18	2x, 4x
<i>Draba cana</i>	16	32	4x
<i>Draba draboides</i>	21	42	6x
<i>Draba eriopoda</i>	8	16	2x
<i>Draba glacialis</i>	8	16	2x
<i>Draba lanceolata</i>	16, 24	24, 32	3x, 4x
<i>Draba melanopus</i>	16	32	4x
<i>Draba nemorosa</i>	8	16	2x
<i>Draba nuda</i>	8	16	2x
<i>Draba olgae</i>	6	12	2x
<i>Draba oreades</i>	20	40	4x
<i>Draba subamplexicaulis</i>	24	48	6x

"Flora Reipublicae Popularis Sinicae", *B. pulvinata* was illustrated as *Solms-laubachia ciliaris* (Bur. et Franch.) Botsch. However, morphological studies established the new genus of *Baimashania* (Al-Shehbaz, 2000). Our study reveals that the basic chromosome number of *B. pulvinata* is $x = 8$, and chromosome pair five of the diploid has one satellite on the short arm. This finding is consistent with the base chromosome number in tribe Arabideae. Furthermore, the basic chromosome number and karyotype of *B. pulvinata* differs from *Solms-laubachia* (Yue et al., 2003, 2004) and is distinct from the base number $x = 7$ in tribe Euclidieae. Combined with previous studies (Yue et al., 2004; Yue et al., 2003), our findings support the placement of the genus *Baimashania* in tribe Arabideae.

4.2. Polyploid frequency in the tribes Euclidieae and Arabideae

Polyploidization is a key factor of plant diversity and speciation (Ehrendorfer, 1980; Lewis, 1980; Ramsey and Schemske, 2002; Stebbins, 1971). Our survey of chromosome numbers and ploidy levels in tribes Euclidieae and Arabideae (367 species in 19 genera) showed that ploidy levels varied from 2x to 24x (Table 2). In some species complexes, diploids are aneuploid, which may result in future hybridization and polyploidy and the creation of complex patterns of chromosome numbers. We have confirmed the existence of different cytotypes of the same ploidy level. More evidence is required of cytogenetics and genome size from related groups.

We found that the polyploid frequency in Euclidieae and Arabideae taxa distributed exclusively in the Qinghai-Tibet Plateau was about 36.11%. Although more taxa should be examined, this finding does not support the hypothesis that the polyploidy increases

adaptability to extreme environments encountered in the Qinghai-Tibet Plateau.

Authors' contribution

H.S. and Z-M.L. designed the study. W-G.S., H.-X.W. and R.W. performed the experiments. W-G.S. analyzed the data. W-G.S. wrote the first draft of the manuscript. All authors read and approved the final manuscript.

Declaration of Competing Interest

The authors declare that no potential conflict of interest.

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