# **CARYOLOGIA**

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### Karyological studies of ten *Ligusticum* species (Apiaceae) from the Hengduan Mountains Region of China

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**Abstract** — Karyological studies on ten species of the genus Ligusticum (Apiaceae) from the Hengduan Mountains Region of China were carried out. Five species of them are reported for the first time. All species have the same basic chromosome number, x = 11, but they could be differentiated by their karyotype formula and quantitative parameters of the karyotypes. L. capillaceum and L. pteridophyllum are tetraploid with the chromosome number of 2n = 4x = 44, other species are diploid with the chromosome number of 2n = 2x = 22. Our cytological results suggest that polyploidy did not play an important role in the chromosome evolution of plants from the Hengduan Mountains Region. Relationships between Ligusticum and its affinities are also discussed. Ligusticum has great diversification in northwestern Yunnan of China, so this region is probably the most diversified center for it.

Key words: chromosome, Hengduan Mountains region, karyotype, Ligusticum, polyploidy.

#### **INTRODUCTION**

The genus *Ligusticum* L., with about 60 species (Pu and Watson 2005), is probably one of the largest members of the family Apiaceae (Pimenov and Leonov 1993). It is widely distributed in the Eurasia continent and North-America, with Himalayas (including the Hengduan Mountains of western China) and North America as its two distribution centers (Pu 1991). Forty species are distinguished in China (35 species are endemic), most of which are distributed in the alpine belt of southwestern China, with only a few species extending to northern region (Pu and Watson 2005).

Ligusticum is a large and widespread genus of complex taxonomy and its relationships with putatively allied genera Cnidium Cuss., Hymenidium DC., Pachypleurum Ledeb., Paraligusticum Tichom., Rupiphila Pimenov & Lavrova, Selinum L., Tilingia Regel & Tiling, and Ligusticopsis Leute are still being clarified (Pu and WATSON 2005). Leute (1969; 1970) established an informal alliance "Verwandtschaftskreis der Gattung Ligusticum" to mark a group of genera presum-

ably related to Ligusticum and Selinum, which includes these genera - Cortia DC., Cyatoselinum, Cenolophium W.D.J. Koch, Endressia J. Gay, Heteroptylis, Ligusticopsis, Ligusticum (incl. Pachypleurum), Selinum (incl. Cnidium and Lithosciadium Turcz.), and Sphenosciadium Gray. Among these genera, its relationships with Tilingia and Ligusticopsis are the most controversial. Tilingia was established by REGEL and TILING (1858). The diagnostic characters of it are the distinct calyx teeth and the carpels bearing a solitary vitta in each furrow (*T. ajanensis* is the type species). However, these characters could not differentiate it from Ligusticum, and it was transferred into Ligusticum by Kozo-Poljansky (1916). The genus Ligusticopsis, with 14 species occurring in China, was separated from Ligusticum based on the prominent calyx teeth of the former (LEUTE 1969). This treatment was not supported by the following botanists since its establishment (Pu 1991). Based on their studies of pollen morphology, WANG et al. (1991) supported Tilingia and *Ligusticopsis* as the synonyms of *Ligusticum*. This treatment was also reflected in Flora of China (vol.14, Pu and Watson 2005). Pu (1991) subdivided the *Ligusticum* into two sections: *L.* section Ligusticum L. and L. section Pinnatibracteola Pu. However, such a split was not reflected in our molecular analysis (ZHOU et al. 2008). All previ-

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ous molecular studies have shown that *Ligusticum* is a polyphyletic heterogenous group in need of further revision (Downie and Katz-Downie 1996; Plunkett *et al.* 1996; Katz-Downie *et al.* 1999; Downie *et al.* 1998, 2000; Valiejo-Roman *et al.* 2006; Zhou *et al.* 2008).

The value of cytological data in the study of plant evolution and diversification has long been recognized, especially for taxa occurring in extreme habitats such as alpine mountains (STEBBINS 1950; 1971; HONG 1990; STACE 2000). Previous chromosome studies on Ligusticum were mainly limited to chromosome counts (GAGNIDZE and CHKHEIDZE 1974; Constance et al. 1976; Rostovtseva 1976; 1979; Krogulevich 1978; Silvestre 1978; Skalin-SKA et al. 1978; UHRIKOVA 1978; AHMAD and KOUL 1980: Arano and Saito 1980: Vachova and Pa-CLOVA 1980; VASILYEVA et al. 1981; 1991; HAMAL et al. 1986; CHINNAPPA and CHMIELEWSKI 1987; Pashuk 1987; Nishikawa 1988; Ge et al. 1989; TAMMARO 1989; NIKOLOV 1991; WETSCHNIG and Leute 1991; Mesíček and Javůrková-Jarolímová 1992; ZHANG and FANG 1993; PIMENOV et al. 1998, 1999). All of these previous data showed a consistent basic chromosome number, x=11 (while in L. sinense, the basic chromosome number is x=10, ZHANG 1994), with B chromosome and polyploidy as rare exceptions. As aforementioned, Hengduan Mountains Region is one of the two distribution centers of Ligusticum. Moreover, according to the distribution of endemic species, this region is also thought to be its diversified center (Pu 1991). However, the cytological data from this region is known insufficiently. Polyploidy has been considered to play an important role in plant speciation, especially in the harsh environments of alpine regions (HANELT 1966; LÖVE and LÖVE 1967; 1975; Grant 1981). Ligusticum are largely restricted to such habitats in the Hengduan Mountains Region, so we expected to find relatively high levels of polyploidy among them. Therefore, the purpose of this paper is: (1) to present karyological data for ten *Ligusticum* species and investigate their possible systematic and evolutionary implications; (2) to test whether polyploidy take an important role in the evolution of *Ligusticum*.

#### MATERIALS AND METHODS

Living plants of 10 *Ligusticum* species were collected from Hengduan Mountains Region of southwestern China (Table 1). Voucher specimens are deposited at KUN (Herbarium of Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China).

Somatic chromosomes were studied in root meristems of transplanted plants. The root tips were pretreated in a mixture of 0.002mol/l 8-hydmxyquinoline and 0.1mol/L Colchicine (4:1) for 4-5 hours at room temperature, then fixed in Camoy's Fluid (95%ethanol: acetic acid=3:1) at 4°C for at least half an hour, before staining, the root tips were hydrolyzed with 1mol/l HCL and 45% acetic acid (1:1) for 5-8min at 60°C. Finally, samples were stained with carbolfuchsin and squashed. Slides were made permanent using neutral balsam (Shanghai reagent company, China) as the mounting medium.

Observations were made of somatic mitotic metaphase. The nomenclature used for the description of the chromosome morphology is that proposed by Levan *et al.* (1964): the abbreviations m, sm, and st designate metacentric, submetacentric, and subtelocentric chromosomes, respectively. Karyotype asymmetry was determined by centromeric terminalization value (the abbreviation, T.C., T.C% = sum of the long arms/total haploid length ×100%) according to Arano (1963), and the categories of Stebbins (1971).

Table 1 — Localities, altitudes, and voucher specimens of the investigated species of Ligusticum.

Species	Localities, altitudes (m), and voucher (KUN)
L. brachylobum Franch.	China, Yunnan, Shangri-La, Napa Sea; 3500; ZJ0533
L. capillaceum H. Wolff	China, Sichuan, Daocheng; 3740; ZJ0549
L. daucoides (Franch.) Franch.	China, Sichuan, DaochengLitang; 4500; ZJ0557
L. delavayi Franch.	China, Yunnan, Xiaozhongdian; 3257; ZJ810841
L. involucratum Franch.	China, Sichuan, YajiangKangding; 4200; ZJ0572
L. pteridophyllum Franch.	China, Yunnan, Wufengshan; 3500; ZJ810836
L. rechingerianum (Leute) R.H. Shan &F.D. Pu	China, Yunnan, Weixi, Lidiping; 3400; ZJ810838
L. scapiforme H. Wolff	China, Yunnan, Shudu lake; 3400; ZJ0522
L. sikiangense Hiroe	China, Sichuan, DaochengLitang; 4500; ZJ0563
L. tenuisectum H.de Bossieu	China, Yunnan, Lijiang, Sandawan; 3100; ZJ0505

#### **RESULTS**

All species investigated have 2n = 2x = 22, except for *L. capillaceum* and *L. pteridophyllum*, which have 2n = 4x = 44. The karyotype asymmetry of all species is categorized as type 2A except for *L. rechingerianum* with the type 1A. The metaphase chromosomes of each species are shown in Fig. 1: A-J. Their detailed parameters and karyotype formulae are listed in Table 2. Brief descriptions of the cytological features of each species are as follows:

1. *L. brachylobum* - This species is endemic to China with the altitudes of 1600-4100 m, and has

entire bracteoles. It is diploid with the karyotype formula of 2n = 22 = 2M + 14 m + 6 sm (Fig. 1: A; Fig. 2: A). Its arm ratio (sum of the long arms/sum of the short arms) is 1.37. The karyotype asymmetry is of type 2A with the T.C. % of 57.84%.

2. *L. capillaceum* - This species is endemic to Hengduan Mountains Region of China with the altitutes of 2500-4000 m, and is characteristic of pinnate bracteoles. It is tetraploid with the karyotype formula of 2n = 44 = 4M + 28 m + 12 sm (Fig. 1: B; Fig. 2: B). Its arm ratio is 1.38. The karyotype asymmetry is categorized as 2A with the T.C. % = 57.92%.

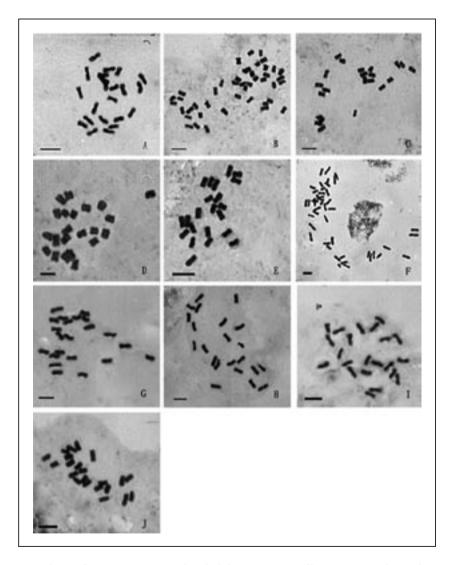


Fig. 1 — Mitotic metaphase of Ligusticum: A) L. brachylobum; B) L. capillaceum; C) L. daucoides; D) L. delavayi; E) L. involucratum; F) L. pteridophyllum; G) L. rechingerianum; H) L. scapiforme; I) L. sikiangense; J) L. tenuisectum. Bar = 10 µm.

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the long arms/total naploid length×100 %; Karyotype formula (KF); STEBBINS 8 asymmetry categories (S1).					
Taxon	AR	T.C%	KF	ST	
L. brachylobum	1.37	57.84	K (2n=2x)=2M+14m+6sm	2A	
L. capillaceum	1.38	57.92	K(2n=4x)=4M+28m+12sm	2A	
L. daucoides	1.31	56.78	K(2n=2x)=2M+16m+4sm	2A	
L. delavayi	1.41	58.53	K(2n=2x)=2M+12m+8sm	2A	
L. involucratum	1.32	56.81	K(2n=2x)=18m+4sm	2A	

54.82

56.54

57.72

55.65

57.34

Table 2 — The karyotype parameters of the 10 investigated species of *Ligusticum*: Arm ratio (AR); T.C%= sum of the long arms/total haploid length×100%; Karyotype formula (KF); STEBBINS's asymmetry categories (ST).

3. *L. daucoides* - This species has pinnate bracteoles, and is distributed in Hubei, Sichuan, Xizang, Yunnan of China with the altitudes of 2600-4800 m. Its karyotype formula is 2n = 22 = 2M + 16 m + 4 sm (Fig. 1: C; Fig. 2: C) with the arm ratio of 1.31. The karyotype asymmetry is of type 2A with the T.C. % = 56.78%.

1.21

1.30

1.37

1.25

1.34

L. pteridophyllum

L.rechingerianum

L. scapiforme

L. sikiangense

L. tenuisectum

- 4. *L. delavayi* This species is endemic to Hengduan Mountains Region of China with the altitudes of 2800-4500 m, and has entire bracteoles. Its karyotype formula is 2n = 22 = 2M + 12 m + 8 sm (Fig. 1: D; Fig. 2: D). Its arm ratio is 1.41. The karyotype symmetry is of type 2A with the T.C. % = 58.53%.
- 5. *L. involucratum* -This species is endemic to Hengduan Mountains Region of China with the altitudes of 2800-4900 m, and has pinnate bracteoles. It has the karyotype formula of 2n = 22 = 8 m + 4 sm (Fig. 1: E; Fig. 2: E). Its arm ratio is 1.32. The karyotype asymmetry is categorized as 2A with the T.C. % = 56.81%.
- 6. *L. pteridophyllum* This species is endemic to China with the altitudes of 1800-3600 m, and has entire bracteoles. It is a tetraploid with the karyotype formula of 2n = 44 = 8M + 32 m + 4 sm (Fig. 1: F; Fig. 2: F). Its arm ratio is 1.21. The karyotype asymmetry is categorized as 2A with the T.C. % = 54.82%.
- 7. L. rechingerianum This species is endemic to Hengduan Mountains region of China with the altitudes of 1500-4600 m, and has 2–3-pinnate bracteoles. It has the karyotype formula of 2n = 22 = 2M + 18 m + 2 sm (Fig. 1: G; Fig. 2: G). Its arm ratio is 1.30. The karyotype asymmetry is of type 1A with the T.C. % =56.54%.
- 8. L. scapiforme This species is endemic to Hengduan Mountains region of China with the altitudes of 2700-4800 m, and has 1-2-pinnate or apex 3-lobed bracteoles. Its karyotype formula is 2n = 22 = 2M + 18 m + 2 st (Fig. 1: H; Fig. 2: H).

Its arm ratio is 1.37. The karyotype asymmetry is of type 2A with the T.C. % = 57.72%.

2A

1A

2A

2A

2A

K(2n=4x)=8M+32m+4sm

K(2n=2x)=2M+18m +2sm

K(2n=2x)=2M+18m+2st

K (2n=2x)=2M+18m+2sm

K (2n=2x)=18m+4sm

- 9. L. sikiangense Its bracteoles is various, with entire or pinnate types. This species is endemic to Hengduan Mountains region of China with the altitudes of 3400-4500 m. It has the karyotype formula of 2n = 22 = 2M + 18 m + 2 sm (Fig. 1: I; Fig. 2: I). Its arm ratio is 1.25. The karyotype asymmetry is of type 2A with the T.C. % = 55.65%.
- 10. *L. tenuisectum* This species is endemic to China with the altitudes of 2000-4500 m, and has entire bracteoles. It has the karyotype formula of 2n = 22 = 18 m + 4 sm (Fig. 1: J; Fig. 2: J). Its arm ratio is 1.34. The karyotype asymmetry is of type 2A with the T.C. % = 57.34%.

#### **DISCUSSION**

*Karyological aspects and polyploidy* - The karyotypes of ten Ligusticum species investigated are shown in Fig. 2: A-J. Chromosome numbers and karyotypes of L. brachylobum, L. delavayi, L. pteridophyllum, L. sikiangense, L. tenuisectum are reported for the first time. The chromosome numbers of the remaining species agree with those published previously under synonymous Ligusticopsis (PIMENOV et al. 1999). All the species exhibited a karyotype asymmetry of type 2A except for L. rechingerianum which is of type 1A. As a whole, Ligusticum is characterized by symmetrical karyotypes, with a predominance of median centromeres (Table 2). The chromosome analysis of *Ligusticum* showed that the karyotypes of all species analyzed have very similar patterns (Fig. 2). Small differences in karyotype formulae and asymmetry indices found among species suggest that chromosome structure changes may have contributed to the diversification of the genus. Of the 30 species have been studied cytologically (including the 10 species in

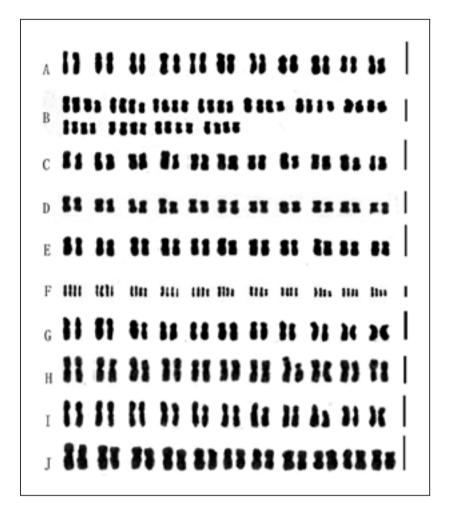


Fig. 2 — Karyotypes of Ligusticum: A) L. brachylobum; B) L. capillaceum; C) L. daucoides; D) L. delavayi; E) L. involucratum; F) L. pteridophyllum; G) L. rechingerianum; H) L. scapiforme; I) L. sikiangense; J) L. tenuisectum. Bar =  $10 \, \mu m$ .

present study), ten were analyzed under synonymous *Tilingia* and *Ligusticopsis* (three and seven, respectively).

All species investigated are diploid except for *L. capillaceum* and *L. pteridophyllum*, which are tetraploid with 2n = 4x = 44. In total, 9.4% polyploidy occurred in all studied populations of *Ligusticum*. Cytological statistical analysis on plants of the Hengduan Mountains Region showed that polyploidy, especially infrageneric polyploidy, has played a minor role in the evolution of the Hengduan Mountain flora (NIE *et al.* 2005). Our result was consistent with their inference that polyploidization is a minor factor in the species diversification of *Ligusticum*. Several other studies on karyological researches from Hengduan Mountains also indicated similar inference and inferred that chromosome evolution mainly oc-

curred at diploid level (Liu 2000; Gong et al. 2001; Nie et al. 2002; Cai et al. 2004; Pan et al. 2004; Yang et al. 2004; Zhang et al. 2007). Therefore, the lower levels of polyploidy maybe a main character for the evolution of Hengduan Mountain flora, unlike the global situation, where it is far more common.

Systematic position of L. delavayi - Karyotypes evolved from symmetry to asymmetry (STEBBINS 1971). According to Arano (1963), the karyotype asymmetry of Ligusticum delavayi is the largest (T.C. % = 58.53%). Due to its membranous margined bracts and slightly dorsally compressed fruits, L. delavayi has been transferred into Hymenidium (PIMENOV and KLJUYKOV 1999). Molecular results confirmed this treatment in which L. delavayi comprises a well-supported clade with Pleurospermum hookeri var. thomsonii and P. yunnanense (ZHOU

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et al. 2008), both of which were also referred to Hymenidium by the same authors (PIMENOV and KLJUYKOV 2000). L. delavayi is obviously more closely related to Hymenidium. However, as its basic chromosome number (x = 11) is different from that of Hymenidium (x =9, PIMENOV and KLJUYKOV 2000), and as *Hymenidium* is not monophyletic as presently circumscribed (PIMENOV and KLIUYKOV 2000; Zhou et al. 2008), so the position of L. delavayi within Hymenidium deserve further study. Systematic affinities for Ligusticum - Pu (1991) inferred an evolutionary trend of morphological characters for *Ligusticum*. That is, bracteoles evolved from entire to pinnate, and mericarps evolved from lateral-compressed to dorsal-compressed. He also arranged the species of Ligusticum into two sections: L. section Ligusticum L. with entire bracteoles, and L. section Pinnatibracteola Pu with pinnate bracteoles. In our study. L. brachylobum, L. delavayi, L. pteridophyllum, L. tenuisectum have entire bracteoles, while bracteoles of L. capillaceum, L. daucoides, L. involucratum, L. rechingerianum, L. scapiforme are pinnate (L. sikiangense has entire or pinnate bracteoles). As indicated in Table 2, no major differences were detected in karyotypes formulae between these two sections, both with M, m and sm centromeres. A molecular analysis on Ligusticum showed that species with entire bracteoles did not constitute a monophyletic group, while those with pinnate ones fell into the tribe Selineae (ZHOU et al. 2008). Considering *Ligusticum* is not monophyletic (PIMENOV and LEONOV 1993), this infrageneric subdivision is in need of further revision.

The genus *Ligusticopsis*, with 14 species occurring in China, was separated from Ligusticum based on the prominent calvx teeth of the former (LEUTE 1969). These prominent calyx teeth, however, actually occur in both genera. Other characters, e.g. basic chromosome number (x = 11), centromere types (M, m, sm) and pollen morphology (WANG et al. 1991), also could not differentiate Ligusticopsis from Ligusticum. All species investigated in this study have been referred to Ligusticopsis save the three (L. delavayi, L. involucratum and L. sikiangense). Molecular analysis indicated that species referred to Ligusticopsis (Ligusticum daucoides, L. oliverianum, L. scapiforme, and L. acuminatum) fell into two distant clades-- Selineae and Sinodielsia clade (ZHOU et al. 2008). Therefore, Ligusticopsis is not monophyletic and deserves further study. For *Tilingia*, it has consistent basic chromosome number (x = 11) with Ligusticum, but more studies need be done to clarify their relationships. Therefore, until a final revision and a general consensus reached, we adopt traditional classification regarding Ligusticopsis and Tilingia as synonyms of *Ligusticum*.

In the Flora Reipublicae Popularis Sinicae, *Ligusticum* was placed near *Selinum* and *Cnidium* (Chang 1979). Molecular studies also confirmed its close relationship to *Cortia*, *Cortiella* C. Norman, *Conioselinum scopulorum* Coult. & Rose and the monotypic genus *Trochiscanthes* W.D.J. Koch (Papini and Mosti 2006; Valiejo - Roman *et al.* 2006; Zhou *et al.* 2008). Leute (1969; 1970) estab-

Table 3 — A comparison of the basic chromosome numbers for the genera that are presumably related to *Ligusticum* – "*Ligusticum* affinity circle" as defined by Valiejo-Roman *et al.* (2006). Note: '?' indicated that no cytological materials were encoded for this genus).

Genus	Basic number	Genus	Basic number
Arafoe	?	Ligusticopsis	11
Cenolophium	10,11	Ligusticum	11
Cnidium	11	Lithosciadium	11
Cnidiocarpa	?	Lomatocarpa	11
Cortia	11	Macrosciadium	11
Cyatoselinum	?	Magadania	?
Dimorphosciadium	11	Mutellina	;
Endressia	?	Notopterygium	11
Hansenia	11	Oreocome	5
Halosciastrum	?	Pachypleurum	11
Heteroptylis	?	Paraligusticum	5
Hymenidium	?	Rupiphila	11
Kadenia	11	Selinum	11
Kailashia	?	Sphaenolobium	11
Karatavia	11	Sphenosciadium	11
		Tilingia	11

lished an informal alliance "Verwandtschaftskreis der Gattung Ligusticum" to mark a group of genera presumably related to Ligusticum and Selinum. Molecular and immunochemical analysis on this informal alliance confirm the separate status of some genera, e.g Magadania Pimenov & Lavrova, Sphaenolobium Pimenov, Dimorphosciadium Pimenov, Lomatocarpa Pimenov, Paraligusticum, and Arafoe Pimenov & Lavrova, also point that Ligusticum is a heterogeneous assemblage of not very closely related plants in need of further taxonomical revision (Valiejo-Roman et al. 2006). As indicated in Table 3, the basic chromosome number was x =11 for almost all genera of the *Ligusticum* affinity circle (Valiejo-Roman et al. 2006). That is, these genera could not be differentiated by the basic chromosome number. The revision for *Ligusticum* will only achieved by expanded sampling from its allies and by multidisciplinary methods.

Diversity center - Ligusticum is a genus typical of temperate distribution. It has two main distribution centers, one in North America, and the other in the Himalayas (including the Hengduan Mountains of western China, Pu 1991). Among the 40 species distinguished in China, more than 20 species are concentrated in northwestern Yunnan (Pu and Watson 2005). Species in this region have highly diversified morphological characters, e.g., of the 13 species with pinnate bracteoles, twelve occur in this region. Species of this region also hold all of the four types of petioles anatomy of the genus (PAN et al. 1992). In this study, they also presented some variations on karyotypes. So we can infer that the northwest of Yunnan is probably the most diversified centre of *Ligusticum*.

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