



## Research paper

## Circumscription of the East Asia clade (Apiaceae subfamily Apioideae) and the taxonomic placements of several problematic genera

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## ABSTRACT

The East Asia (or *Physospermopsis*) clade was recognized in previous molecular phylogenetic investigations into the higher-level relationships of Apiaceae subfamily Apioideae. The composition of this clade, the phylogenetic relationships among its constituent taxa, and the placement of species previously determined to be problematic have yet to be resolved. Herein, nrDNA ITS sequences were obtained for 150 accessions of Apioideae, representing species whose distributions are in East Asia or genera having one or more species included within the East Asia clade. These data, along with published ITS sequences from other Apioideae (for 3678 accessions altogether), were subjected to maximum likelihood and Bayesian inference analyses. The results show that the East Asia clade contains representatives of 11 currently recognized genera: *Hansenia*, *Hymenolaena*, *Keraymonia*, *Sinolimprichtia*, *Acronema*, *Hymenidium*, *Physospermopsis*, *Pimpinella*, *Sinocarum*, *Tongoloo*, and *Trachydium*. However, the latter seven genera have members falling outside of the East Asia clade, including the generic types of all except *Tongoloo*. Within the clade, the species comprising these seven genera are widely intermingled, greatly increasing confusion among relationships than previously realized. The problematic species *Physospermopsis cuneata* is confirmed as falling within the East Asia clade, whereas *P. rubrinervis* allies with the generic type in tribe Pleurospermeae. *Physospermopsis kingdon-wardii* is confirmed as a member of the genus *Physospermopsis*, whereas the generic attributions of *P. cuneata* and *Tongoloo stewardii* remain unclear. Two species of *Sinocarum* (*S. filicinum* and *S. wolffianum*) are transferred into the genus *Meeboldia*. This is the most comprehensive molecular phylogenetic investigation of the East Asia clade to date, and while the results increase systematic understanding of the clade, they also highlight the need for further studies of one of the most taxonomically intractable groups in Apioideae.

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## 1. Introduction

Apiaceae (Umbelliferae) are a large family of flowering plants, with 442 genera and 3575 species recognized (Christenhusz and

Byng, 2016). While most members of its largest subfamily Apioideae are readily identifiable because of their characteristic inflorescences and fruits, their higher-level relationships have traditionally been obscure (Constance, 1971). A modern classification of Apioideae based on phylogenetic analyses of molecular data has elucidated the higher-level subdivisions within the subfamily and provided a framework for its classification (reviewed in Downie et al., 2001, 2010). However, several major clades have not yet been treated formally, pending confirmation from further studies (Downie et al., 2010).

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The East Asia (or *Physospermopsis*) clade is one of these problematic groups. Calviño et al. (2006) recognized species of *Physospermopsis* H. Wolff, *Trachydium* Lindl., *Tongoloo* H. Wolff, *Sinolimprichtia* H. Wolff, *Notopterygium* H. de Boissieu, *Haplosphaera* Hand.-Mazz., and *Hansenia* Turcz. as comprising the *Physospermopsis* clade. Included were species with an almost exclusively East Asian distribution. Zhou et al. (2008) thus suggested the alternative name “East Asia clade” and included species of *Pimpinella* L., *Sinocarum* H. Wolff ex R.H. Shan & F.T. Pu, and *Vicatia* DC. within. Subsequent molecular phylogenetic studies supported its monophyly and expanded its circumscription to include representatives of 16 genera (Zhou et al., 2009, 2020, 2021; Downie et al., 2010; Mousavi et al., 2021; Wen et al., 2021). The East Asia clade is a sister group to tribe Komarovieae (Zhou et al., 2009), or arises from within it based on limited sampling and using the universal Angiosperms353 probe set (Clarkson et al., 2021).

Taxonomic relationships within the East Asia clade are extraordinarily complex, having species-rich genera whose boundaries are poorly defined and several monotypic genera. Taxonomic challenges surround *Pimpinella*, *Sinocarum*, *Tongoloo*, and *Trachydium*. *Pimpinella* includes ~150 species that occur disjunctly in Africa, Europe, and Asia (Pimenov and Leonov, 1993; Pu and Watson, 2005). A few *Pimpinella* species are also distributed in South America, with one species found in western North America (Pimenov and Leonov, 1993). Members of *Pimpinella* can be recognized by their perennial (rarely biennial or annual) herbaceous habit, stem bases without fibrous remnant sheaths, slightly laterally compressed fruits constricted at the commissure, and filiform ribs. Authors have arranged the species of *Pimpinella* into various sections (de Candolle, 1827; Bentham and Hooker, 1867; Boissier, 1875; Wolff, 1910, 1927; Shan and Sheh, 1985a), and molecular phylogenetic studies have shown that the sectional classification of *Pimpinella* is highly artificial. Furthermore, *Pimpinella* is not resolved as a monophyletic group, with its members assigned to seven tribes and other major clades in Apioideae including the East Asia clade (Downie et al., 2010; Wang et al., 2014; Fereidounfar et al., 2016; Zhou et al., 2020). As the type species of *Pimpinella* (*P. saxifraga* L.) is placed within tribe Pimpinelleae, nomenclatural changes are required for those *Pimpinella* species falling outside of Pimpinelleae.

*Sinocarum* is a small genus of approximately 20 species and exhibits a typical Sino-Himalayan distribution ranging from Nepal to SW China (Pu et al., 2005). *Tongoloo* also occurs at high elevations in the Sino-Himalayan region, with 15 species recognized (Pan and Watson, 2005a; Pimenov, 2017). Both genera are poorly defined with diffuse generic boundaries, and relationship to putatively allied genera *Acronema* Edgew., *Pimpinella*, *Physospermopsis*, and *Trachydium* have been suggested. *Sinocarum* and *Tongoloo* were each determined to be non-monophyletic in their current circumscription (Downie et al., 2010; Zhou et al., 2020). Moreover, *Sinocarum* displayed conflicting placements in different phylogenetic studies (Zhou et al., 2008, 2009, 2020; Xiao et al., 2021). The proper circumscriptions of *Sinocarum* and *Tongoloo* need to be ascertained.

*Trachydium* is another taxonomically complex genus, and its generic delimitation has historically been the subject of considerable debate. Since its establishment, those high montane species from the Sino-Himalayan region having a prostrate habit or shortened stems were described in, or transferred to, *Trachydium* (Pimenov and Kljuykov, 2000). These include species previously attributable to *Aulacospermum* Ledeb., *Chamaesciadium* C.A. Mey., *Chamaesium* H. Wolff, *Ligusticum* L., *Physospermopsis*, *Pleurospermum* Hoffm., *Pseudotrachydium* (Kljuykov, Pimenov & V.N. Tikhom.) Pimenov & Kljuykov, *Schulzia* Spreng., and *Sinocarum*. However, Pimenov & Kljuykov (2000) considered *Trachydium* to be a monotypic genus (*T. roylei* Lindl.) and indicated that some of its species belong to *Sinocarum* or *Tongoloo*. Previous molecular results partly support

such a viewpoint, as the four species examined to date occur throughout the East Asia clade and are allied with *Sinocarum*, *Tongoloo*, and *Physospermopsis* (Zhou et al., 2008, 2009, 2020).

No traditional classification of Apioideae has grouped together those genera that are presently included in the East Asia clade. The morphological diversity among its members is high, making it particularly difficult to identify clade-specific diagnostic characters. In this study, we (1) identify additional members of the East Asia clade by increasing the sampling of species whose distributions are in East Asia or genera having one or more species already included in the clade; (2) assess the phylogenetic relationships of those members comprising the East Asia clade, placing emphasis on *Sinocarum*, *Tongoloo*, and *Trachydium*; and (3) confirm the phylogenetic placements of several species that have been treated variously (and perhaps erroneously) in previous molecular phylogenetic studies. The results obtained will be used to carry out nomenclatural transfers of some species and further clarify relationships within this taxonomically problematic group.

## 2. Materials and methods

### 2.1. Sampling

The nrDNA internal transcribed spacer (ITS) region was used for phylogenetic inference, as the numerous ITS sequences available in GenBank for Apiaceae subfamily Apioideae enabled an immediate consideration of these accessions for their possible inclusion in the East Asia clade. Comparative data for any specific chloroplast DNA locus does not yet exist across such a broad sampling of Apioideae.

To ascertain the limits of the East Asia clade, ITS sequence data were procured from 150 accessions of Apioideae (Table S1). These accessions included representation of species whose distributions in East Asia suggested possible close affinities with those taxa already included in the clade, or those genera whose species have already been unambiguously placed in the clade in earlier studies. Sampling of the genera *Tongoloo*, *Sinocarum*, and *Trachydium* was more comprehensive than the other genera. For those non-monophyletic genera whose species were previously determined to occur in several major clades, such as *Hymenidium* Lindl. and *Pimpinella*, those species that fell into the East Asia clade were resampled to confirm their phylogenetic positions. For those species having different ITS sequences in GenBank suggesting that at least one may be in error (i.e., *Physospermopsis rubrinervis* (Franch.) C. Norman and *P. cuneata* H. Wolff), we collected new leaf material from the type localities. Where possible, each included species was represented by more than one accession to represent morphological, geographical, or possible infraspecific molecular variation. Apioideae ITS sequences were downloaded from GenBank and screened using the strategies described by Zhou et al. (2020) for possible inclusion in the East Asia clade. We only used those sequences released after March 2018, as sequences prior to that date were extracted in a previous study to ascertain the broad phylogenetic placements of *Ligusticum* species (Zhou et al., 2020). Thirty-eight separate ITS1 and ITS2 sequences from the previous matrix of Zhou et al. (2020) were replaced with the resequencing of the entire ITS region (ITS1–5.8S–ITS2). In summary, 655 ITS sequences newly obtained from GenBank plus the 150 ITS sequences generated specifically for this study resulted in 805 sequences altogether. These were added to the matrix of Zhou et al. (2020) for a total of 3678 Apioideae ITS sequences.

### 2.2. DNA extraction

Total genomic DNAs were isolated from silica-gel dried materials or from herbarium specimens using a Plant Genomic DNA Kit

(Tiangen Biotech, China) according to the manufacturer's protocol. The entire ITS region was amplified using the primers ITS4 (5'-TCC TCC GCT TAT TGA TAT GC-3') and ITS5 (5'-GGA AGT AAA AGT CGT AAC AAG G-3'; White et al., 1990) or N-nc18S10 (5'-AGG AGA AGT CGT AAC AAG-3') and C26A (5'-GTT TCT TTT CCT CCG CT-3'; Wen and Zimmer, 1996). If the PCR amplification failed, the region was amplified in two parts, using ITS-u1 (5'-GGA AGK ARA AGT CGT AAC AAG G-3') and ITS-u2 (5'-GCG TTC AAA GAY TCG ATG RTT C-3') for ITS1, and ITS-u3 (5'-CAW CGA TGA AGA ACG YAG C-3') and ITS-u4 (5'-RGT TTC TTT TCC TCC GCT TA-3') for ITS2 (Cheng et al., 2016). Procedures for amplification are the same as described in Zhou et al. (2008, 2009). The PCR products were sequenced at the Sequencing Laboratory of the Institute of Botany using the same primers as for PCR on an ABI 3730 automated sequencer (Applied Biosystems, Foster City, California, U.S.A.). ITS sequence data acquired in this study were deposited in GenBank (Table S1).

### 2.3. Phylogenetic analysis

The sequences were assembled, aligned, and manually adjusted using the BioEdit sequence alignment editor (Hall, 1999). Initially, we performed maximum likelihood (ML) analyses using RAxML v.8.0.0 (Stamatakis, 2014) on XSEDE via the CIPRES Science Gateway (<http://www.phylo.org>). The settings were rapid bootstrap analysis with 1000 replicates and utilizing the GTR + I + G substitution model. Three species of tribe Bupleureae were used to root the trees as the tribe occupies a sister-group relationship to all other apioide genera excluding its most early-diverging branches (Downie et al., 2001; Calviño et al., 2006). When the circumscription of the East Asia clade was delimited through this ML analysis, we selected only its accessions to conduct Bayesian inference (BI) with MrBayes v.3.2.5 (Ronquist and Huelsenbeck, 2003; Ronquist et al., 2012). The BI trees were rooted with three members of tribe Komarovieae, as the tribe constitutes an immediate sister group to the East Asia clade (Zhou et al., 2009, 2020). For the BI analyses, we determined the appropriate nucleotide substitution models using the corrected Akaike information criterion (AIC) in jModeltest v.2.1.7 (Posada, 2008; Darriba et al., 2012). We performed the BI analysis using two independent runs of the Markov chain Monte Carlo (MCMC) for 10 million generations each and sampling one tree every 1000 generations. Analyses were run until the standard deviation of split frequencies was less than 0.001. Tracer was also used to graphically assess the convergence of runs, and to determine that the effective sampling size values exceeded 200. We discarded the first 25 % generations as burn-in, and the remaining trees were summarized into a 50% majority-rule consensus tree with posterior probabilities (PP).

### 3. Results

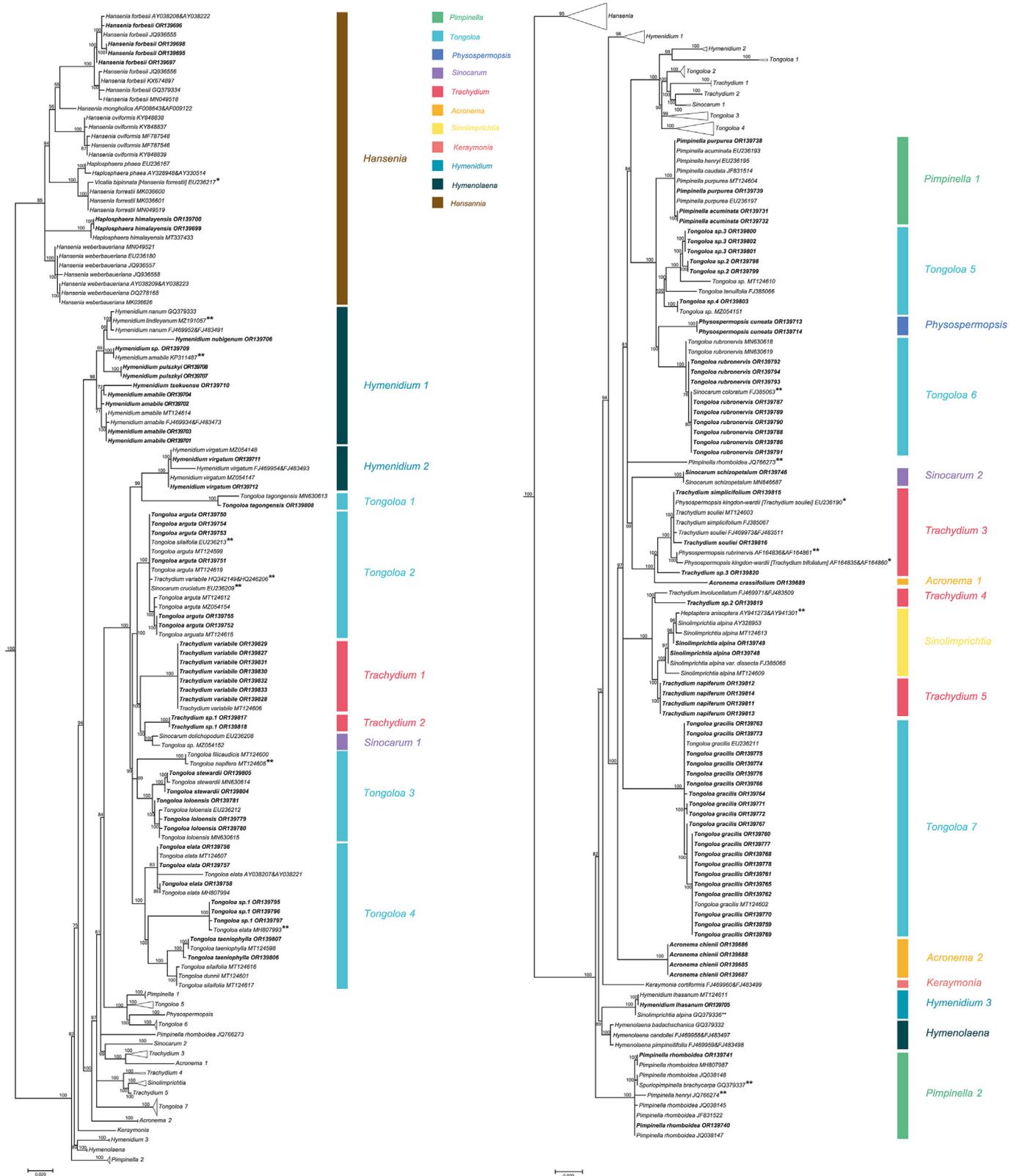
The aligned data matrix of 3678 ITS sequences contained 736 positions, with none excluded due to alignment ambiguities. Of these positions, 63 were autapomorphic, 63 were constant, and 610 were parsimony informative. Phylogenetic analysis of this data matrix resulted in a significant expansion of the East Asia clade from any previous circumscription. Two representatives from the genus *Acronema* are newly recognized members of the clade and the numbers of species from *Hymenidium*, *Tongoloa*, and *Trachydium* have increased substantially. Except for the genera *Hansenia*, *Hymenolaena* DC., *Keraymonia* Farille (including one accession), and *Sinolimprichtia* (a monotypic genus), all other genera comprising the East Asia clade are polyphyletic and greatly intermingled. The nomenclatural types of *Acronema*, *Hymenidium*, *Physospermopsis*, *Pimpinella*, *Sinocarum*, and *Trachydium* fall outside of the East Asia clade. The ML tree containing all 3678 representatives of Apioideae

is presented in Fig. S1, while a portion of this ML tree representing only the East Asia clade and its simplified phylogenetic tree showing relationships among groupings of taxa are presented in Figs. 1 and 2A, respectively. In addition, we extracted portions of the *Acronema* and *Sinodielsia* clades that contain taxa of interest, as shown in Figs. 3 and 4, respectively.

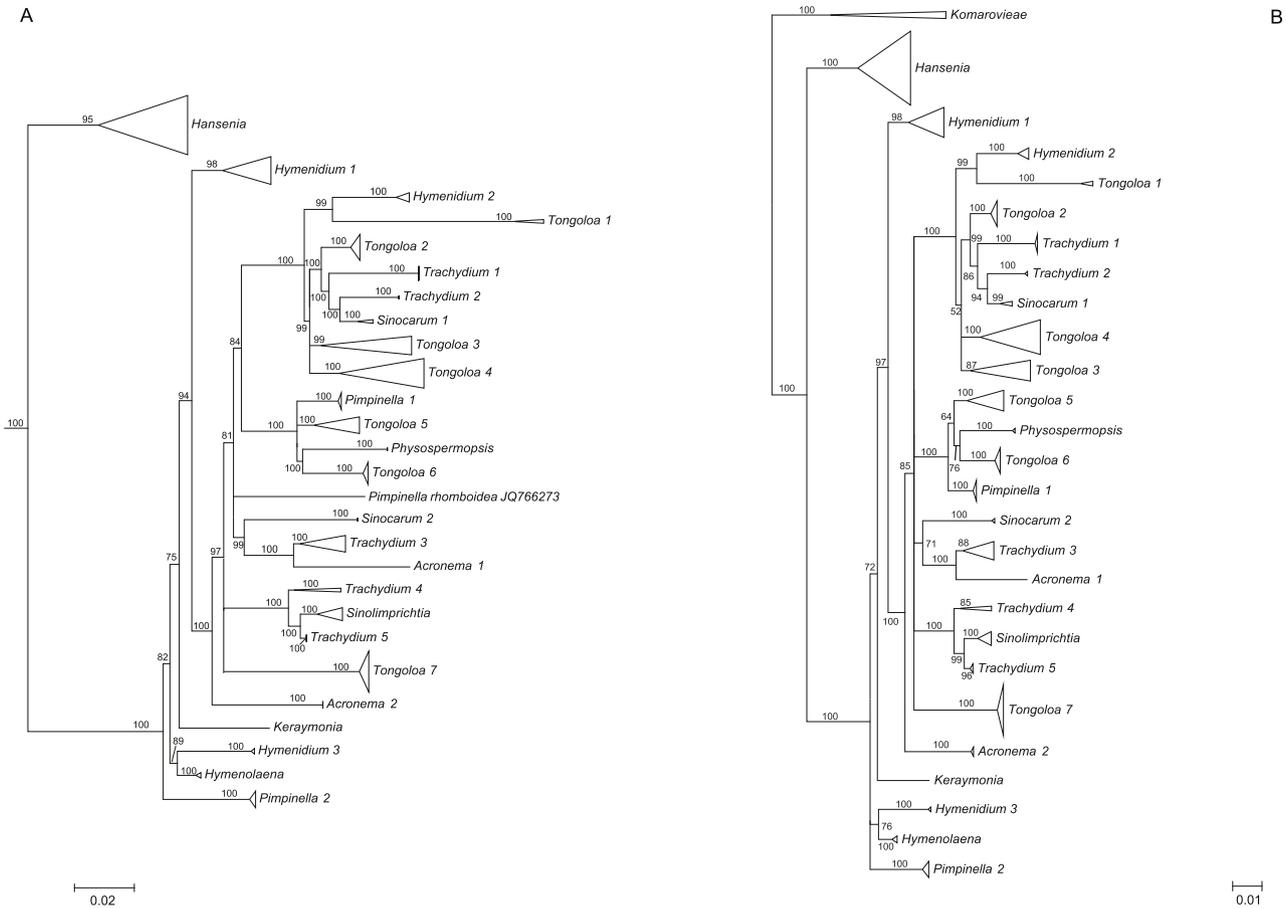
#### 3.1. Problematic sequences in GenBank

Simultaneous analysis of multiple ITS sequences from the same species indicated that some may be either misidentifications or resulting from contamination or improper laboratory practices because they did not fall as monophyletic in the phylogenetic trees. Sequences of some conspecific taxa differed considerably and occurred in different tribes and other major clades of Apioideae. *Physospermopsis cuneata* is confirmed as belonging to the East Asia clade. The placement of its two previously examined accessions (GenBank accession nos. EU236188 and EU236189) in tribe Pimpinelleae (Zhou et al., 2008, 2009) must be attributable to identification errors. The accession of *Physospermopsis rubrinervis* collected from its type locality (Luoping Mt., Yunnan Province, China) allies with other representatives of the same species within the tribe Pleurospermeae; the accession of *P. rubrinervis* (AF164836 and AF164861), previously attributable to the East Asia clade, is also a misidentification. Similar situations also occur for *Sinocarum coloratum* (Diels) H. Wolff ex R.H. Shan & F.T. Pu and *S. cruciatum* (Franch.) H. Wolff ex R.H. Shan & F.T. Pu, where sequences of the same species fell into both the *Acronema* clade (Fig. 3) and the East Asia clade (Fig. 1). After examination of their voucher materials, we considered that *Sinocarum cruciatum* accession MN846686 and *S. coloratum* accession MN846685 are correctly identified, whereas *S. coloratum* FJ385063 and *S. cruciatum* EU236209 in the East Asia clade and *S. coloratum* AY328927 and *S. cruciatum* AY038199, AY038213 and MH293141 in the *Acronema* clade are not. *Vicatia bipinnata* R.H. Shan & F.T. Pu (EU236217) and its synonymous species *Melanosciadium bipinnatum* (R.H. Shan & F.T. Pu) Pimenov et Kljuykov (JX514721) fell into the East Asia clade (Fig. 1) and tribe Selineae (Fig. S1), respectively. The voucher specimen of *V. bipinnata* is actually *Hansenia forrestii* (H. Wolff) Pimenov & Kljuykov, while the ITS sequence of *M. bipinnatum* (JX514721) is identical to that of *Pimpinella rhomboidea* var. *tenuiloba* R.H. Shan & F.T. Pu. The newly obtained *Melanosciadium genuflexum* Pimenov & Kljuykov is placed in the *Sinodielsia* clade and is sister group to the clade of *Tongoloa zhongdianensis* S.L. Liou, *Pterocyclus rivulorum* (Diels) H. Wolff, and *Sinodielsia delavayi* (Franch.) Pimenov & Kljuykov (Fig. 4). *Heptaptera anisoptera* Tutin (AY941273 and AY941301) and *Spuriopimpinella brachycarpa* (Kom.) Kitagawa (GQ379337) arise from within accessions of *Sinolimprichtia alpina* H. Wolff and *Pimpinella rhomboidea* Diels, respectively. However, other sequences of *H. anisoptera* and *S. brachycarpa* are placed into the *Opopanax* and *Acronema* clades, so we excluded these two problematic genera from the East Asia clade. With nearly identical ITS sequences, *Hymenidium lindleyanum* (Klotzsch) Pimenov & Kljuykov (MZ191057) comprises a group with *H. nanum* (Rupr.) Pimenov & Kljuykov in the East Asia clade, while another accession of *H. lindleyanum* (FJ469949 and FJ483488) falls into tribe Pleurospermeae (Fig. S1).

The accessions of *Physospermopsis kingdon-wardii* (H. Wolff) C. Norman (AF164835, AF164860 and EU236190) do not ally. We further checked their voucher specimens (W810822 for EU236190, and E00052566 for AF164835 and AF164860), which should be identified as *Trachydium souliei* H.de Boissieu and *T. trifoliatum* H. Wolff, respectively. The accession *Sinolimprichtia alpina* (GQ379336) is sister group to the clade comprising two accessions of *Hymenidium lhasanum* Pimenov & Kljuykov, and distantly away



**Fig. 1.** Portion of the large consensus tree (Fig. S1) obtained from maximum likelihood analysis of 3678 nrDNA internal transcribed spacer sequences from Apioaceae subfamily Apioideae showing only the East Asia clade (comprising 206 terminals). Support values  $\geq 50\%$  are provided. Clade designations are those defined in the text. The 106 newly sampled accessions in this portion of the tree are shown in bold. GenBank accession numbers of all sequences are provided; two numbers indicate sequences from separate ITS1 and ITS2 regions. \*Indicates that the identifications of original materials from these accessions were confirmed and that these sequences were used in the Bayesian inference analysis; names in [] are the correct ones. \*\*Indicates that the identifications of these sequences are problematic and thus these taxa were excluded from the Bayesian analysis.



**Fig. 2.** **A.** Simplified phylogenetic tree derived from maximum likelihood analysis of 3678 nrDNA internal transcribed spacer sequences from Apiaceae subfamily Apiioideae showing the groupings of taxa in East Asia clade, with support values ( $\geq 50\%$ ) provided next to the branches. **B.** Simplified phylogenetic tree derived from Bayesian inference analysis of 195 nrDNA internal transcribed spacer sequences showing the group of taxa from the East Asia clade and outgroups, with Bayesian posterior probabilities ( $\geq 50\%$ ) provided next to the branches.

from other accessions of the same species. With only one nucleotide difference between them, we consider that the species identified as *S. alpina* (GQ379336) is actually *H. lhasanum*. Three accessions of *Pimpinella henryi* Diels fall into both Pimpinelleae and the East Asia clade, with the two accessions in the East Asia clade not grouping together. Although we cannot confirm the identity of accessions with sequences EU236195 and MH710738, the one in the East Asia clade (JQ766274) arising from within *Pimpinella rhomboidea* is no doubt a misidentification. Furthermore, *Tongoloa napifera* (H. Wolff) C. Norman (MT124605) does not ally with its synonymous species *Trachydium napiferum* H. Wolff, and *Pimpinella rhomboidea* (JQ766273) forms an isolated lineage distantly away from its conspecific accessions. Other suspect sequences include *Hymenidium amabile* (Craib & W.W. Smith) Pimenov & Kljuykov (KP311487), *Tongoloa elata* H. Wolff (MH807993), *Tongoloa silaifolia* (H. de Boissieu) H. Wolff (EU236213), and *Trachydium variabile* H. Wolff (HQ342149 and HQ246206). In summary, 11 genera are recognized herein as constituting the East Asia clade (Table 1).

### 3.2. Phylogeny of the East Asia clade

The aligned 195 ITS sequences from taxa comprising the East Asia clade and three outgroup taxa (Komarovieae) resulted in a matrix of 620 positions, with none excluded because of alignment ambiguities. Of these positions, 249 were parsimony informative, 305 were constant, and 66 were autapomorphic. Gaps ranging in length from 1 to 3 bp were introduced to facilitate alignment. The

mean percentage G + C content across all sequences was 54.8%. The BI results are generally congruent in topology with the portion of the ML tree containing the East Asia taxa; branch support values are indicated (Figs. 2B and 5).

The seven species of *Hansenia* constituted a well-supported monophyletic group (BI = 100), with each of its species also arising as monophyletic. Two species of the former genus *Haplo-sphaera*, *Haplo-sphaera phaea* Hand.-Mazz. ( $\equiv$  *Hansenia phaea* (Hand.-Mazz.) J.B. Tan & X.G. Ma) and *H. himalayensis* Ludlow ( $\equiv$  *Hansenia himalayensis* (Ludlow) J.B. Tan & X.G. Ma), arise from within the *Hansenia* clade. The three species of *Hymenolaena* also allied as a strongly supported clade (BI = 100) and is sister group to *Hymenidium lhasanum*. The four newly sampled species of *Hymenidium* [*H. pulszkyi* (Kanitz) Pimenov & Kljuykov, *H. nubigenum* (H. Wolff) Pimenov & Kljuykov, *H. tsekuense* (R.H. Shan) Pimenov & Kljuykov, and *H. sp.*] ally with their congeners *H. amabile* and *H. nanum* in clade *Hymenidium* 1 (BI = 98). *Hymenidium virgatum* Pimenov & Kljuykov (clade *Hymenidium* 2) and *H. lhasanum* (clade *Hymenidium* 3) are separately placed in the East Asia clade and do not cluster with the aforementioned congeners.

With the exception of *Tongoloa zhongdianensis* and *T. paucir-adiata* H. Wolff that are placed into the *Sinodielsia* clade (Fig. 4), all other sampled accessions of *Tongoloa* fell into the East Asia clade, albeit in seven different groups (*Tongoloa* 1–7). *Tongoloa tagon-gensis* L.J. Gui & X.J. He (*Tongoloa* 1), *T. arguta* L.J. Gui & X.J. He (*Tongoloa* 2), *T. rubronervis* S.L. Liou (*Tongoloa* 6), and *T. gracilis* H. Wolff (*Tongoloa* 7) each comprises a separate, monophyletic group.





**Table 1**

Composition and distribution of the East Asia clade. Asterisks denote those genera that are not monophyletic based on the analyses presented herein. Distribution only involves species of the East Asia clade and does not include the undescribed species.

Genus	Number of species falling into the East Asia clade/Total number of species in genus and reference	Distribution of species falling into the East Asia clade
<i>Acronema</i> *	2/25 <sup>a</sup>	China
<i>Hansenia</i> (including <i>Notopterygium</i> and <i>Haplosphaera</i> )	7/8 <sup>b,c,d,e</sup>	Bhutan, China, India, Mongolia, Nepal, Russia
<i>Hymenidium</i> *	7/37 <sup>f</sup>	Bhutan, China, India, Kazakhstan, Kirghizia, Sikkim, Tajikistan
<i>Hymenolaena</i>	3/3 <sup>g</sup>	Afghanistan, India, Kazakhstan, Kirghizia, Pakistan, Tadzhikistan
<i>Keraymonia</i>	1/4 <sup>g</sup>	China, Nepal
<i>Physospermopsis</i> *	1/15 <sup>a,g</sup>	China
<i>Pimpinella</i> *	5/150 <sup>a</sup>	China, India, Myanmar, Nepal, Pakistan
<i>Sinocarum</i> *	2/20 <sup>a,f</sup>	China, Myanmar
<i>Sinolimprichtia</i>	1/1 <sup>a</sup>	China
<i>Tongoloo</i> *	12/17 <sup>a,f,h,i</sup>	Bhutan, China, India, Nepal
<i>Trachydium</i> *	6/10 <sup>a,f</sup>	Bhutan, China, India, Nepal

<sup>a</sup> Sheh et al. (2005).

<sup>b</sup> Pimenov et al. (2008).

<sup>c</sup> Jia et al. (2019).

<sup>d</sup> Tan et al. (2020).

<sup>e</sup> Jiang et al. (2022).

<sup>f</sup> Pimenov (2017).

<sup>g</sup> Pimenov and Kljuykov (2000).

<sup>h</sup> Gui et al. (2020a).

<sup>i</sup> Gui et al. (2020b).

the East Asia clade except for the genus *Hansenia*. Lastly, *Keraymonia cortiformis* Cauwet & S.B. Malla, the only included species of the genus, constitutes an isolated lineage without close relatives.

## 4. Discussion

### 4.1. Circumscription and distribution of the East Asia clade

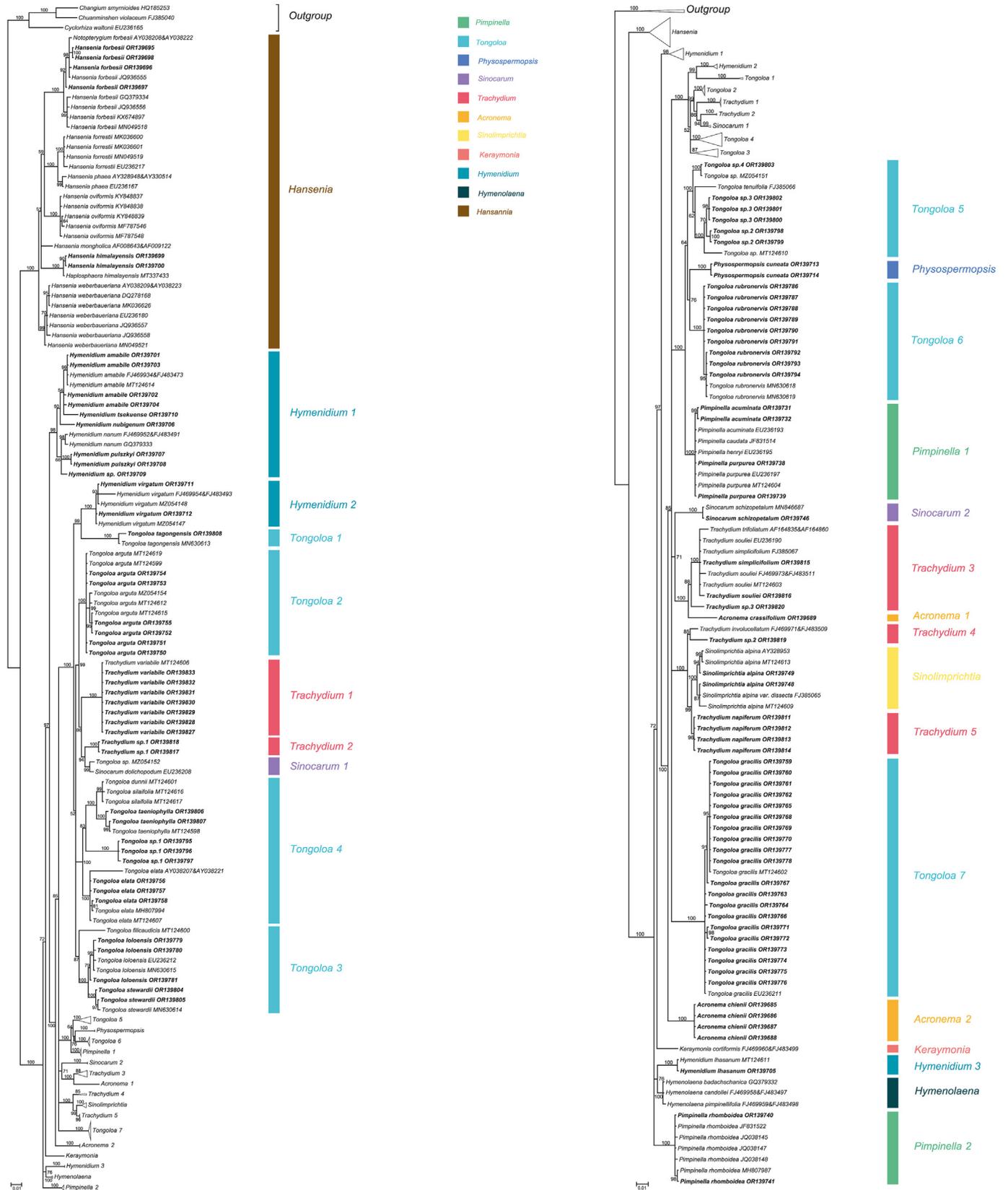
The East Asia clade has previously been considered as comprising representatives of 16 genera (Downie et al., 2010; Zhou et al., 2020, 2021). However, with the reduction of *Haplosphaera*, *Notopterygium*, and *Ligusticum litangense* F.T. Pu to *Hansenia* (Pimenov et al., 2008; Tan et al., 2020; Zhou et al., 2020), the exclusion of dubious sequences *S. brachycarpa*, *H. anisoptera*, and *V. bipinnata* from the clade, and the examination of additional sequences available in GenBank for possible inclusion, the East Asia clade is herein circumscribed to include 11 genera (Table 1). Seven of these genera (*Acronema*, *Hymenidium*, *Physospermopsis*, *Pimpinella*, *Sinocarum*, *Tongoloo*, and *Trachydium*) are each not monophyletic, and all have members falling outside of the East Asia clade. Within the East Asia clade each of these genera except *Physospermopsis* comprises two or more lineages with its species intermingled with other East Asia taxa, resulting in relationships more complex than previously realized. Excluding *Tongoloo*, the nomenclatural types of six genera fall into other tribes and major clades of Apiioideae indicating that substantial taxonomic rearrangements and new combinations will be inevitable. Upon expanded sampling of species distributed in East Asia and genera in which species have already been unambiguously placed in the clade, the number of species belonging to *Hymenidium*, *Tongoloo*, and *Trachydium* in the East Asia clade has increased greatly.

When the East Asia clade was first identified (as *Physospermopsis* clade, Calviño et al., 2006), it included species almost exclusively distributed in East Asia. With the expansion of its circumscription herein, its distribution now extends to Central and South Asia, and even Asian Russia. Two species, namely *S. schizopetalum* and *Pimpinella purpurea*, have also been reported to occur in Southeast Asia (Pimenov, 2017). All genera are native to Asia (the monotypic genus *Sinolimprichtia* is endemic to China). With the exception of *Hymenolaena*, whose distribution is limited to Central and South Asia (Afghanistan, India, Kazakhstan, Kirghizia, Pakistan, and Tajikistan; Pimenov and Kljuykov, 2000), all other genera have members distributed in China. The single species of *Keraymonia* (*K. cortiformis*) is distributed in China and Nepal (Pimenov, 2017). Six species of *Hansenia* [*H. forbesii* (H.de Boissieu) Pimenov & Kljuykov, *H. forrestii*, *H. oviformis* (R.H. Shan) Pimenov & Kljuykov, *H. phaea*, *H. weberbaueriana* (Fedde ex H. Wolff) Pimenov & Kljuykov, and *H. trifoliolata* Q.P. Jiang & X.J. He (not included in present analysis)] are confined to China, *H. himalayensis* is distributed in Bhutan, China, India and Nepal, and the type *H. mongolica* Turcz. occurs in Mongolia and Siberia, Russia (Sheh and Watson, 2005; Pimenov et al., 2008; Pimenov, 2017). Members of the remaining East Asia clade genera are distributed in Bhutan, China, India, Kazakhstan, Kirghizia, Myanmar, Nepal, Pakistan, Sikkim, and Tajikistan, with each genus having a species occurring in or endemic to China (Sheh et al., 2005; Pimenov, 2017; Pimenov and Kljuykov, 2000).

### 4.2. Morphological diversification and relationships within the East Asia clade

Unlike the tribes of Apiioideae inferred from molecular data that can also be delimited using morphological or anatomical synapomorphies (e.g., Bupleureae, Neves and Watson, 2004; Oenantheae, Hardway et al., 2004; Chamaesieae, Zhou et al., 2009), the East Asia clade is morphologically heterogeneous. The differences among its members are extreme, exhibiting a great diversity of habit, life form, flower morphology, umbel structures, and fruit morphology and anatomy. The fruit presents variation in shape, degree and direction of mericarp compression (laterally compressed or slightly dorsally compressed), surface of mericarp (tuberculate or glabrous), modifications of ribs (winged or filiform), and shape of the ventral endosperm (flat or concave). We are not aware of any morphological features that can be used to unambiguously define the East Asia clade.

Of the many distinct groupings of taxa within the East Asia clade, four are equivalent to generally recognized genera (*Hansenia*, *Sinolimprichtia*, *Hymenolaena*, and *Keraymonia*). With the incorporation of species from *Notopterygium* and *Haplosphaera*, as well as the recognition of a new species, *Hansenia* is now represented by eight species (Pimenov et al., 2008; Tan et al., 2020; Jiang et al., 2022). It is monophyletic and diagnostic morphologically, with its (sometimes somewhat unequally) broad wings on all ribs. *Sinolimprichtia* is a monotypic genus endemic to China and is characterized by scaphoid petals and dark purple anthers (Pan and Watson, 2005b). It falls as a sister group to *Trachydium napiferum* within the East Asia clade, which in turn is sister group to *T. involucellatum* and *Trachydium* sp. 2. These three species of *Trachydium* may be referred to *Sinolimprichtia*, but this remains to be confirmed. The genus *Hymenolaena* consists of three distinctive species distributed in western Himalaya, Afghanistan, and Middle Asia. Its pinnate leaves and large, conspicuous, and almost entirely membranous bracteoles well delimit the genus (Pimenov and Kljuykov, 2000); the group is also monophyletic in trees presented herein. *Keraymonia* currently comprises four species distributed in Nepal, Bhutan, and Xizang of China (Pimenov and



**Fig. 5.** Majority-rule consensus tree for the East Asia clade and outgroups inferred from Bayesian inference analysis (195 terminals). Numbers above the branches are Bayesian posterior probabilities. The 106 newly sampled accessions are shown in bold. GenBank accession numbers of all sequences are provided; two numbers indicate sequences from separate ITS1 and ITS2 regions. Clades designations are described in the text.

Kljuykov, 2000). The only species included in this study, *K. cortiformis*, forms an isolated lineage in the East Asia clade. The type species, *Keraymonia nipaulensis* Cauwet-Marc & Farill, allies closely with members of tribe Scandiceae in analyses of chloroplast gene *rbcl* sequences (Saslis-Lagoudakis et al., 2012). The generic status of *K. cortiformis* must be reconsidered.

*Tongoloa* is highly polyphyletic, however. Two of its species (*Tongoloa zhongdianensis* and *T. pauciradiata*) ally with the *Sinodielsia* clade, while the remainder form seven separate clades within the East Asia clade (Table 2). Some authors have suggested that *T. zhongdianensis* is conspecific with *T. loloensis* (Pan and Watson, 2005a). In our analysis, *T. zhongdianensis* is paraphyletic, with *Sinodielsia delavayi* arising from within. *S. delavayi* is the type of *Sinodielsia* H. Wolff, which is conspecific with *Meeboldia yunnanensis* (H. Wolff) Constance & F.T. Pu; thus, it has been renamed as *Meeboldia delavayi* (Franch.) W. Gou & X.J. He (Gou et al., 2021). All species of *Meeboldia* cluster together in the *Acronema* clade. *Tongoloa loloensis*, which has been variously designated as a species of *Carum*, *Pimpinella* or *Trachydium* (Franch, 1894; Boissieu, 1902; Hiroe, 1958), allies strongly with *Tongoloa stewardii*. *Tongoloa pauciradiata* is a poorly known species endemic to China and is not recorded in the Flora of China (Pan and Watson, 2005a); Hiroe (1979) considered it to be a species of *Pimpinella*. In the present study, *T. pauciradiata* allies with *Angelica paeoniifolia* R.H. Shan & C.Q. Yuan, both of which constitute a clade sister group to *Vicatia tibetica* H.de Boissieu (= *Sinodielsia tibetica* (H.de Boissieu) Kljuykov & P.K. Mukh.). The ITS sequences of four accessions of *T. pauciradiata* are identical to that of *A. paeoniifolia* (FJ237533), while the sequences of our own accessions of *A. paeoniifolia* (Zhou et al., unpublished data), all falling in the *Sinodielsia* clade, do not match those of other conspecific members. A comparison of our material of *A. paeoniifolia* (Z21-117 and Z21-124) with the types (PE00935513 and PE00617248) confirm that our collection is consistent with the types and protologue presented by Shan et al. (1980). Except for groups *Tongoloa* 3, *Tongoloa* 4, and *Tongoloa* 5, which each include two or more species of *Tongoloa*, the other *Tongoloa* species (including the type, *T. gracilis*) each constitute a separate clade. The morphological features characterizing the species comprising *Tongoloa* 4 are subtle and include ultimate segments (length vs. width ratio), plant height (< 30 cm vs. > 30 cm), and rays (thick vs. slender). These features make species identifications extremely difficult. In addition, the morphological characters of five undescribed species (i.e., *T. sp. 1*, *T. sp. 2*, *T. sp. 3*, *T. sp. 4*, and *T. sp. MT124610*) prevent them from being assigned to existing *Tongoloa* species and describing them now as new species would only add to the confusion, given the polyphyletic nature of the genus. Overall, *Tongoloa* is a rather critical genus, and its proper

**Table 2**

Clade designation of *Sinocarum*, *Tongoloa*, and *Trachydium* species based on results of this study. *Sinocarum filicinum* and *S. wolffianum* are excluded from *Sinocarum* based on these same results.

Species	Clade
<i>Sinocarum bellum</i> , <i>S. coloratum</i> , <i>S. cruciatum</i> , <i>S. muliense</i> , <i>S. vaginatum</i> , <i>S. sp. 1</i>	<i>Acronema</i> clade
<i>Sinocarum dolichopodum</i> , <i>S. schizopetalum</i> ; <i>Tongoloa arguta</i> , <i>T. dunnii</i> , <i>T. elata</i> , <i>T. filicaudicis</i> , <i>T. gracilis</i> , <i>T. loloensis</i> , <i>T. rubronervis</i> , <i>T. silaifolia</i> , <i>T. sp. 1</i> , <i>T. sp. 2</i> , <i>T. sp. 3</i> , <i>T. sp. 4</i> , <i>T. sp. MZ054152</i> , <i>T. sp. MT124610</i> , <i>T. taeniophylla</i> , <i>T. tenuifolia</i> , <i>T. tagongensis</i> , <i>T. stewardii</i> ; <i>Trachydium involucellatum</i> , <i>T. napiferum</i> , <i>T. simplicifolium</i> , <i>T. souliei</i> , <i>T. sp. 1</i> , <i>T. sp. 2</i> , <i>T. sp. 3</i> , <i>T. trifoliatum</i> , <i>T. variable</i>	East Asia clade
<i>Tongoloa pauciradiata</i> , <i>T. zhongdianensis</i> ; <i>Trachydium subnudum</i>	<i>Sinodielsia</i> clade
<i>Trachydium roylei</i>	Pleurospermeae

circumscription and taxonomy will be among the most difficult challenges remaining in Apioideae.

*Sinocarum* is closely related to, and difficult to distinguish from, *Acronema* because the characters used to delimit these genera are variable and overlapping (Pu et al., 2005). *Acronema* is characterized by long-linear or long-aristate petals; however, some species have acute or obtuse petals (e.g., *A. yadongense* S.L. Liou and A. chinense H. Wolff) that can also be seen in *Sinocarum*. Both genera have species with ultimate linear segments making them indistinguishable (e.g., *Acronema schneideri* H. Wolff, *A. graminifolium* (W.W.Smith) S.L. Liou & R.H. Shan, and *Sinocarum vaginatum*). In the present study, species of *Sinocarum* and *Acronema* fall into both the *Acronema* and East Asia clades (Table 2). In the *Acronema* clade, their species are intermingled, indicative of their close relationship. The generic type of *Sinocarum* (*S. coloratum*) was synonymized with *S. cruciatum* by Pimenov (2017). However, *S. coloratum* allies with *S. muliense*, both of which comprise a clade sister group to the clade of *S. cruciatum* and *S. vaginatum*. Upon examination of these specimens, we believe that *S. coloratum* and *S. cruciatum* should each be maintained as distinct species. *Sinocarum bellum* does not ally with its congeners. In a previous study (Xiao et al., 2021), *S. bellum* fell as sister group to all *Acronema* species. Two other species of *Sinocarum* in the *Acronema* clade, *S. filicinum* and *S. wolffianum*, form a sister group with three species of *Meeboldia*. Their fruits are similar, being ovoid with filiform ribs, tapering toward the apex, slightly laterally compressed, and having a concave seed face (Wolff, 1930; Xiao et al., 2021); all have recurved styles too (Wolff, 1930; Shan and Sheh, 1985b, Table 3). As a result, we transfer *S. filicinum* and *S. wolffianum* into the genus *Meeboldia* (see Taxonomic treatment section). The morphological characters of *S. dolichopodum*, such as its long rhizome, leaf morphology, and divided bracteoles, are rather uncharacteristic of *Sinocarum*, suggesting that the species may be better placed elsewhere (Pu et al., 2005). The present results support such a treatment, as the species allies with several species of *Tongoloa* and *Trachydium*. The most characteristic feature of *S. schizopetalum* (Franch.) H. Wolff is its petal apex being palmately 3–4-lobed. This species is sister group to the *Trachydium* 3 group plus *A. crassifolium*. Its broad-ovoid mature fruits and sub-rhomboidal pollen are also different from those *Sinocarum* species in the *Acronema* clade (Xiao et al., 2021). *A. crassifolium* is a newly described species characterized by thickly papery, ternate, abaxially dark purple leaves, terminal umbels with 8–13 rays, and no calyx teeth (Wang et al., 2013). Because the apex of its petals is linear (ca. 1.7 mm long), it was described under the genus *Acronema*. However, the species falls within the East Asia clade, distantly away

**Table 3**

Morphological comparisons of *Sinocarum filicinum* and *S. wolffianum* with *Meeboldia*.

Character	<i>S. filicinum</i>	<i>S. wolffianum</i>	<i>Meeboldia</i>
Roots	Taproot elongate, often branched	Taproot fusiform	Taproot fusiform
Basal leaves	2-pinnate	Bipinnatisect	3-pinnate/ pinnatifid
Bracteoles	Linear-lanceolate	Linear	Linear
Styles	Recurved	Recurved	Recurved
Calyx	Subulate	Subulate	Lanceolate-subulate
Fruits	Ovoid or oblong-ovate, slightly laterally compressed, tapering toward the apex, seed face concave	Ovate-oblong, slightly laterally compressed, tapering toward the apex, seed face concave	Narrowly ovoid, slightly laterally compressed, tapering toward the apex, seed face concave
Ribs	Filiform	Filiform	Filiform

from most of its congeners in the *Acronema* clade. With its roots conic or tuberous, ultimate segments linear or linear-lanceolate, and petal bases long clawed and with an acute apex, *Acronema chienii* is also separated from congeners and occupies an isolated position in the East Asia clade, further adding to the taxonomic complexities of the genus and the clade as a whole.

Of the 37 species of *Hymenidium* recognized by Pimenov (2017), seven species (and one unknown species) occur in the East Asia clade as three separate lineages. *H. amabile* is widely distributed in China (Sichuan, Yunnan, and Xizang Provinces), Bhutan, and India (Pimenov, 2017), and is easily identified by its showy leaf sheaths and bracteoles having its membranous and main veins dark purple. *Hymenidium tsekuense* is a narrowly endemic species of northwestern China (Qinghai Province) and is part of the *Pleurospermum hookeri* C.B. Clarke [= *H. hookeri* (C.B. Clarke) Pimenov & Kljuykov] complex (Pan and Watson, 2005c). The main morphological differences between *H. amabile* and *H. tsekuense* are that the latter is slender in habit and has fewer rays (Shan and Sheh, 1979). In the present study, *H. amabile* is paraphyletic with *H. tsekuense* contained within, whereas *H. hookeri* falls into the *Acronema* clade. Thus, *H. tsekuense* and *H. amabile* may be regarded as conspecific or possibly close relatives having geographical variants. *Hymenidium nubigenum* is another poorly known taxon recorded from only a few collections, with its bracteoles margins white-membranous and ribs crisped-winged (Pan and Watson, 2005c). The sample collected from its type locality (Que'er Mtn, Sichuan Province) yielded only a portion of its ITS sequence and this was enough to inform its phylogenetic position. *H. nubigenum* allies with *H. nanum*, as either a geographically distant species in the ML analysis (Fig. 1) or a poorly supported sister group to *H. tsekuense* and *H. amabile* in the BI analysis (Fig. 5). Both *H. virgatum* and *H. lhasanum* are newly described species endemic to China (Pimenov and Kljuykov, 2004). In the protologue, the authors considered *H. virgatum* to be closely related to the genera *Sinolimprichtia* and *Tongoloo*. In the present study, it is a sister group to *Tongoloo tagongensis*. However, the morphological features of *H. virgatum* and *T. tagongensis* are distinctly different. *Hymenidium lhasanum* forms a sister group to three species of *Hymenolaena*. Both taxa have clearly different morphologies, especially in the leaf blade (1-pinnate vs. bipinnatisect) and bracteoles (completely membranous vs. membranous-margined).

*Trachydium* has been described as a storage-box genus, holding all taxa with shortened stems from the alpine Sino-Himalaya. Besides the two clades to which *Trachydium* has been referred to previously (East Asia clade and Pleurospermeae; Downie et al., 2010), one species (*Trachydium subnudum*) is allied with the *Sinodielsia* clade (Table 2 and Fig. 4). *Trachydium subnudum* is characterized by its scabrous leaf surfaces and densely tuberculate fruit, especially on its ribs. It occurs as a sister group to the clade of *Tongoloo pauciradiata* and *V. thibetica*. These three species share several characteristics, such as long rhizomes, carrot-like roots, and scabrous leaves, and all are distant from their respective generic types and congeners. The type species of *Trachydium* (*T. roylei*) is clustered with several species of *Hymenidium* in the tribe Pleurospermeae. Whether these *Hymenidium* species are transferred into *Trachydium* or separated as a distinct genus remains to be seen. Species of *Trachydium* in the East Asia clade each comprise separate groups. The exception is *Trachydium* 3, which includes four species of *Trachydium*. *Trachydium souliei*, *T. simplicifolium*, and *T. trifoliatum* are morphologically distinct, but have almost identical ITS sequences. These species are distributed primarily in the Himalayas and their origins and low sequence divergence could be the result of rapid species radiation.

*Pimpinella rhomboidea* is endemic to China and is characterized by its terminal leaflets being broad-ovate or rhombic. It has two

varieties (*P. rhomboidea* and *P. rhomboidea* var. *tenuiloba*; Pu and Watson, 2005) that do not cluster together. In the protologue, the authors considered the main morphological differences between the varieties to refer to the basal leaves (ternate-2-pinnate vs. 2-ternate) and ultimate segments (1–1.5 × 0.5–1 cm vs. 5–8 × 2–5 cm); fruit characters were not used (Shan and Pu, 1989) for there are no ripe fruits on the type specimen (CDBI0172296). *Pimpinella rhomboidea* var. *tenuiloba* was synonymized with *M. bipinnatum* (≡ *V. bipinnata*, Pimenov and Kljuykov, 2006; Tan et al., 2015), which has close relationships to both *Angelica angelicifolia* (Franch.) Kljuykov and *A. yanyuanensis* (F.T. Pu) J. Zhou of tribe Selineae. The generic type of *Melanosciadium*, *M. pimpinelloideum* H.de Boissieu also belongs to Selineae, and it arises from within *Angelica* species. Thus, we consider that both *M. bipinnatum* (= *Pimpinella rhomboidea* var. *tenuiloba*) and *M. pimpinelloideum* will be transferred to *Angelica* pending confirmation from fruit characters. While *M. genuflexum* is away from congeners and falls into the *Sinodielsia* clade. *Pimpinella rhomboidea* occupies an isolated position in the East Asia clade. The other four species of *Pimpinella* in the East Asia clade comprise a polytomy. Considering that members of the genus *Pimpinella* are scattered in no less than seven major clades of Apioideae, there is still a long way to go to resolve its nomenclatural and taxonomic problems.

#### 4.3. Three species with ambiguous phylogenetic placements

*Physospermopsis cuneata* is a little-known species endemic to China. It is unusual within the genus because of its lack of conspicuous bracts and bracteoles (Pan and Watson, 2005d). Based on fruit structure, general habit, and leaf dissection, Pimenov and Kljuykov (1999) transferred it into the genus *Sinodielsia*, as *S. cuneata* (H. Wolff) Pimenov & Kljuykov. The results presented herein are consistent with our findings from prior studies in supporting its placement in the East Asia clade (Zhou et al., 2009, 2020). In this clade, it comprises a sister group to *Tongoloo rubronervis*, which in turn forms either a trichotomy with *Tongoloo* 5 and *Pimpinella* 1 (Fig. 1) or is a poorly supported sister group to *Tongoloo* 5 (Fig. 5). The type of *Sinodielsia* [*S. yunnanensis* H. Wolff (≡ *M. yunnanensis*)] falls into the *Acronema* clade. Upon the results presented herein, the species may be better placed in *Tongoloo*, or a new genus awaits description.

*Physospermopsis kingdon-wardii* was originally described as a species of *Trachydium* under the name of *T. kingdon-wardii* H. Wolff (1929). It was later transferred into the genus *Pleurospermum* as *P. kingdon-wardii* (H. Wolff) Hiroe (1979). Based on anatomical and micromorphological fruit characters, Pu and Liu (2005) considered it more appropriately placed in *Trachydium*. Pimenov (2017) classified it as synonymous with *Physospermopsis obtusiuscula* (DC.) C. Norman, while other authors have argued that *P. kingdon-wardii* differs from *P. obtusiuscula* in its reduced stem, dwarf plants, and small fruits with prominent and sinuate ribs (Xu et al., 2021). After careful comparison of the type specimens of *Physospermopsis kingdon-wardii* (E00000221) and *P. obtusiuscula* (K000697363), we believe that the treatment of Pimenov (2017) is justified. It is also supported by the present study, as accessions of *P. kingdon-wardii*, with its entire or divided bracteoles and shortened stems (OR139727, OR139725, OR139724 and OR139726), and *P. obtusiuscula* (OR139722, OR139723 and OR139728), with its stems not shortened, comprised a polytomy. Herein, the generic attribution of *P. kingdon-wardii* is confirmed in the genus *Physospermopsis*.

*Tongoloo stewardii* is disjunctly distributed in Central and Southwest China and is distinguished from other species of the genus by its ovate to lanceolate-ovate ultimate segments and margins irregularly pinnate or coarsely serrate. Hiroe (1958)

transferred the species to *Pimpinella* as *P. stewardii* (H. Wolff) Hiroe. Some authors considered it to be synonymous with *Tongoloa fortunatii* (H. de Boissieu) Pimenov & Kljuykov (Pimenov and Kljuykov, 1999; Pimenov, 2017). We have examined type materials of both species and conclude that *T. stewardii* and *T. fortunatii* cannot be separated from each other. Herein, *Tongoloa stewardii* is a sister group to *T. loloensis*, both of which fall into a large clade consisting of *Trachydium*, *Tongoloa*, and *Sinocarum*.

## 5. Conclusion

This is the most comprehensive study of the East Asia clade (Apiaceae subfamily Apioideae) carried out to date, specifically with regard to the number of new accessions examined, many of which are now included within the group. The clade is circumscribed to include representatives of 11 genera, seven (*Acronema*, *Hymenidium*, *Physospermopsis*, *Pimpinella*, *Sinocarum*, *Tongoloa*, and *Trachydium*) of which are not monophyletic and with some having their nomenclatural types falling outside of the group. Within the clade, the species comprising the polyphyletic genera are seriously intermingled, resulting in more confusing relationships than previously realized. The most perplexing taxonomic problems remaining in East Asia clade surround these polyphyletic genera, which are notoriously difficult to define. Thus, despite our attempt to clarify phylogenetic relationships of all genera comprising the East Asia clade, additional taxonomic study is warranted for the problematic species highlighted here.

## 6. Taxonomic treatment

***Meeboldia filicina*** (H. Wolff) J. Zhou, comb. nov.

≡ *Sinocarum filicinum* H. Wolff, 1929, Repert. Spec. Nov. Regni Veg. 27: 182, nom. inval. (Art. 35.1).

≡ *Carum chinense* M. Hiroe, 1979, Umbelliferae World: 872.

Type: CHINA. “Yunnan, eastern flank of the Tali Range, 2540 m a.s.l., Forrest 6863” (lectotype E! –barcode K00000440, designated by M. Farille in E; isolectotype K! –barcode K000685663).

***Meeboldia wolffiana*** (Fedde ex H. Wolff) J. Zhou, comb. nov.

≡ *Acronema wolffianum* Fedde ex H. Wolff, Repert. Spec. Nov. Regni Veg. 27: 328. 1930.

≡ *Sinocarum wolffianum* (Fedde ex H. Wolff) P.K. Mukh. & Constance, 1991, Edinburgh J. Bot. 48(1): 42.

≡ *Pimpinella feddeana* M. Hiroe, 1979, Umbelliferae World: 832.

Type: INDIA. “Himalaya, Sikkim, Jongri, 12,000 ft, 15. 10. 1875, Clarke 25796” (lectotype K! –barcode K000075372, designated by Mukherjee, Constance, 1991: 42).

## Author contributions

Jing Zhou: Writing – review & editing, Writing – original draft, Funding acquisition, Conceptualization. Zhenwen Liu: Writing – original draft, Conceptualization. Jia-Rui Yue: Investigation. Jun-Mei Niu: Formal analysis. Shi-Lin Zhou: Investigation. Xin-Yue Wang: Visualization, Data curation. Stephen R. Downie: Writing – review & editing

## Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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## Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.pld.2023.11.002>.

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