

## **Sinoseris (Crepidinae, Cichorieae, Asteraceae), a new genus of three species endemic to China, one of them new to science**

Authors: Wang, Ze-Huan, Kilian, Norbert, Chen, Ya-Ping, and Peng, Hua

Source: Willdenowia, 50(1) : 91-110

Published By: Botanic Garden and Botanical Museum Berlin (BGBM)

URL: <https://doi.org/10.3372/wi.50.50109>

---

BioOne Complete ([complete.BioOne.org](https://complete.BioOne.org)) is a full-text database of 200 subscribed and open-access titles in the biological, ecological, and environmental sciences published by nonprofit societies, associations, museums, institutions, and presses.

Your use of this PDF, the BioOne Complete website, and all posted and associated content indicates your acceptance of BioOne's Terms of Use, available at [www.bioone.org/terms-of-use](https://www.bioone.org/terms-of-use).

Usage of BioOne Complete content is strictly limited to personal, educational, and non - commercial use. Commercial inquiries or rights and permissions requests should be directed to the individual publisher as copyright holder.

---

BioOne sees sustainable scholarly publishing as an inherently collaborative enterprise connecting authors, nonprofit publishers, academic institutions, research libraries, and research funders in the common goal of maximizing access to critical research.

ZE-HUAN WANG<sup>1</sup>, NORBERT KILIAN<sup>2\*</sup>, YA-PING CHEN<sup>3</sup> & HUA PENG<sup>3\*</sup>

## *Sinoseris* (Crepidinae, Cichorieae, Asteraceae), a new genus of three species endemic to China, one of them new to science

Version of record first published online on 12 March 2020 ahead of inclusion in April 2020 issue.

**Abstract:** Studies to elucidate the systematic position of two Chinese species described originally as *Lactuca hirsuta* and *L. scandens*, of which only historical specimens from the late 19<sup>th</sup> and early 20<sup>th</sup> centuries were known, revealed the occurrence of three different species. Molecular phylogenetic analysis of these species based on sequences of the nuclear ribosomal internal transcribed spacer (nrITS) region and three plastid DNA markers (*trnL-F*, *psbA-trnH*, *matK*) uncovered a hitherto unknown lineage in a first comprehensive phylogenetic backbone of the subtribe *Crepidinae* (Asteraceae, tribe *Cichorieae*). Substantiated by comparative morphological studies, this lineage is described as a new genus, named *Sinoseris*, endemic to the Chinese provinces Sichuan and Yunnan. One of its three species is new to science, while another is conspecific with both *L. hirsuta* and *L. scandens*. The third was meanwhile described by other authors as *Nabalus muliensis* and is now transferred to *Sinoseris*.

**Key words:** Asteraceae, China, Cichorieae, Compositae, Crepidinae, molecular phylogenetics, *Nabalus*, new genus, new species, Sichuan, *Sinoseris*, taxonomy, Yunnan

**Article history:** Received 28 October 2019; peer-review completed 21 January 2020; received in revised form 30 January 2020; accepted for publication 4 February 2020.

**Citation:** Wang Z.-H., Kilian N., Chen Y.-P. & Peng H. 2020: *Sinoseris* (Crepidinae, Cichorieae, Asteraceae), a new genus of three species endemic to China, one of them new to science. – Willdenowia 50: 91–110. doi: <https://doi.org/10.3372/wi.50.50109>

## Introduction

Investigations into the flora of China have considerably increased our knowledge of its rich plant diversity during the last decades and have also pointed out knowledge gaps. Many taxa, also including members of tribe *Cichorieae* (Asteraceae, sunflower family) are still insufficiently known. One of the least known species in this tribe was described as *Lactuca hirsuta* Franch. (Franchet 1895) from Yunnan and was known from only a few collections from the late 19<sup>th</sup> and early 20<sup>th</sup> centuries. Shih (1997) assigned

*L. hirsuta* to *Chaetoseris* C. Shih, which was later determined to be a congener of *Melanoseris* Decne. (Shih & Kilian 2011; Wang & al. 2013; Kilian & al. 2017). Doubts on this systematic position of *L. hirsuta* were already expressed by Shih & Kilian (2011). In the context of the general poverty of morphological features in the *Cichorieae* coupled with extensive parallel evolution, which renders the recognition of lineages difficult (Kilian & al. 2009a), the scarcity of fruiting material available and the absence of any recent collection of this taxon have hindered redressing its systematic position.

1 Department of Medicinal plants and cultivation, College of Pharmacy, Guizhou University of Traditional Chinese Medicine, Guiyang 550025, China.

2 Botanischer Garten und Botanisches Museum Berlin, Freie Universität Berlin, Königin-Luise-Str. 6–8, 14195 Berlin, Germany.

3 Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China.

\* Authors for correspondence: Norbert Kilian, <https://orcid.org/0000-0003-0890-4373>, e-mail: [n.kilian@bgbm.org](mailto:n.kilian@bgbm.org); Hua Peng, e-mail: [hpeng@mail.kib.ac.cn](mailto:hpeng@mail.kib.ac.cn)

The situation changed when the first author discovered a specimen among the plant collections of the fourth national survey of traditional Chinese medicine resources, which matched the description and historical specimens of *Lactuca hirsuta* from Dayao County, Yunnan. Further studies, including field trips guided by the re-evaluated historical collections, unveiled the identity of another taxon, described as *L. scandens* C. C. Chang (1934) and not so far identified with any of the known species (Shih & Kilian 2011), and brought to light a separate lineage of three species, one of them hitherto unknown to science.

The aims of our study were to test the previous hypotheses on the systematic position of *Lactuca hirsuta* and its two allies by morphological and molecular phylogenetic analyses, and to draw taxonomic conclusions from the phylogenetic evidence.

## Material and methods

**Plant material** — The study was based on live plants observed and photo-documented in the field during two trips to Sichuan and Yunnan in 2017 and 2018 as well as on newly collected and historical specimens of *Lactuca hirsuta* and its allies. Specimens were studied from the herbaria GH, LBG, P, PE and W (herbarium codes follow *Index herbariorum*; <http://sweetgum.nybg.org/science/ih/>). Newly collected specimens were deposited in KUN, with duplicates in B and PE. For comparative morphological studies of *L. hirsuta*, its allies and related genera, we consulted specimens in the herbaria of B, KUN and PE.

**Morphological studies** — For scanning electron microscopic (SEM) study, achenes and pollens were mounted on SEM stubs with double-sided sticky tape, coated with 20 nm Pt-Pd using a Cressington 108Auto sputter-coater and examined using a ZEISS SIGMA 300.

**Sampling, DNA extraction, amplification, sequencing and phylogenetic analysis** — Multiple samples of *Lactuca hirsuta* and its two allies were sequenced and included in the molecular phylogenetic analysis based on the nuclear ribosomal internal transcribed spacer (nrITS) and three plastid DNA markers (*trnL-F*, *psbA-trnH*, *matK*). Otherwise, mostly published sequences of our own studies were included, as well as those from other authors when considered reliable. Table 1 lists the samples used in the analyses. The sampling for the nrITS matrix was designed to represent all genera of the *Crepidinae* (except for the extremely rare monotypic *Spiroseris* Rech. f. of Pakistan of which no sequence data are available) and its sister subtribe *Chondrillinae* (see Kilian & al. 2009b+; for current systematics). The plastid DNA matrix is more restricted in its sampling due to sequence availability. Its focus is on the position of the three species among the more closely

related lineages. *Launaea sarmentosa* (Willd.) Kuntze (*Hyoseridinae*) was used as the outgroup and root of the phylogenetic trees. INSDC (International Nucleotide Sequence Database Collaboration) accession numbers of published sequences follow the taxon name in the trees (Fig. 1; Fig. 2).

Extraction of DNA and amplification and sequencing of the *trnL-F* and *psbA-trnH* regions were done as described by Wang & al. (2013) and of the *matK* as described by Liu & al. (2013). The final DNA sequences were submitted to ENA (<http://www.ebi.ac.uk/ena/>) using the software tool *annonex2embl* (Gruenstaedl 2019). INSDC accession numbers of the newly generated sequences are listed with the specimen data in Table 1.

Sequences were aligned with MAFFT version 7 using default parameters (Katoh & al. 2017) and the alignments adjusted manually using PhyDE version 0.9971 (Müller & al. 2010). Indels were coded as binary characters using simple indel coding (Simmons & Ochoterena 2000) implemented in SeqState v.1.40 (Müller 2005). The nrITS matrix was subdivided into the four partitions ITS1, 5.8s, ITS2, indels. The plastid DNA matrix was subdivided into the four partitions *trnL-F*, *psbA-trnH*, *matK* and indels; two length-variable poly-T stretches of 3 and 7 nucleotides, respectively, in the *psbA-trnH* partition were excluded because of homology uncertainty. The alignments are made available as Supplemental Content in the online edition of this paper.

Phylogenetic relationships were inferred using maximum parsimony (MP), maximum likelihood (ML) and Bayesian inference (BI). MP was performed with the parsimony ratchet using PRAP v.2.0 (Müller 2004) with 10 additional random cycles and default parameters in combination with PAUP v.4.0b10 (Swofford 2003); Jackknife (JK) support values were calculated in PAUP with 10 000 jackknife replicates using the TBR branch swapping algorithm with 36.788% of characters deleted and one tree held during each replicate. ML analyses were done with the MPI version of RAXML-NG 0.9.0 (Kozlov & al. 2019) on the high-performance computing system of the Freie Universität Berlin. The best-fitting models of sequence evolution for the DNA partitions had been assessed with ModelTest-NG (Darriba & al. 2019) and selected according to the Bayesian Information Criterion (BIC): TIM3+I+G4 for ITS1 and 5.8S, TPM3uf+G4 for ITS2; TVM+G4 for the *trnL-F* region and *matK*, TPM1uf+G4 for *psbA-trnH*; the binary indel partitions were not included in the ML analyses due to software restrictions. The tree space was explored with 50 tree searches using 25 random and 25 parsimony-based starting trees, followed by standard bootstrapping, employing the bootstopping test with a maximum replicate number of 1500 and a bootstrap convergence requirement with 3% default cutoff. The BS support values were mapped onto the best-scoring ML tree obtained. The BI analyses were performed with the MPI version of MrBayes (Ronquist & al. 2012) on the high-performance computing sys-

tem of the Freie Universität Berlin. Instead of a priori testing, the optimal substitution model was sampled across the entire general time reversible (GTR) model space in the Bayesian MCMC analysis (Huelsenbeck & al. 2004). Two simultaneous runs of four parallel chains each were performed for  $3 \times 10^7$  generations with a sample frequency of 1 tree per 2000 generations. Convergence of the runs was checked by making sure that the average standard deviation of split frequencies of the post-burn-in runs was below 0.01 and the effective sampling size (ESS) well above 200 in either run for all parameters. TreeGraph v.2 (Stöver & Müller 2010) was used to visualize the trees with statistical node support.

## Results

The aligned nrITS region had a length of 691 characters; together with the coded indels the matrix included a total of 782 characters of which 356 were parsimony-informative. The MP analysis resulted in 140 most parsimonious trees ( $L = 1767$ ,  $CI = 0.440$ ,  $RI = 0.739$ ,  $RC = 0.325$ ,  $HI = 0.560$ ), largely congruent in topology with the trees of the BI and ML analyses. Fig. 1 shows the BI majority consensus phylogram with the BI posterior probabilities (PP) and ML bootstrap (BS) support values (bootstrapping converged after 1100 replicates) below the branches and the MP jackknife (JK) support values above the branches.

The aligned concatenated plastid DNA markers had a length of 2301 and, together with the coded indels, 2391 characters, of which 286 were parsimony-informative. The MP analysis resulted in 46 most parsimonious trees ( $L = 747$ ,  $CI = 0.775$ ,  $RI = 0.825$ ,  $RC = 0.639$ ,  $HI = 0.225$ ), largely congruent in topology with the trees of the BI and ML analyses. Fig. 2 shows the BI majority consensus phylogram with the BI posterior probabilities (PP) and ML bootstrap (BS) support values (bootstrapping converged after 1250 replicates) below the branches and the MP jackknife (JK) support values above the branches.

Both the nrITS tree (Fig. 1) and the plastid DNA tree (Fig. 2) place the species originally described as *Lactuca hirsuta* and its two allies into a separate, well-supported clade (nrITS: JS = 98.1, PP = 1, BS = 70; plastid DNA: full JS, PP and BS support). In the nrITS phylogeny the clade is part of the large, chiefly E Asian *Dubyaea-Nabalus-Soroseris-Syncalathium* polytomy. In contrast, this polytomous clade received no statistical support in the plastid DNA phylogeny and is shown in Fig. 2 only for easier comparison with the nrITS tree; the deeper nodes of the *Crepidinae* are entirely unresolved, but the terminal clades are largely the same as in the nrITS tree. The main difference in the composition of the *Crepidinae* clade concerns the well-known presence of *Faberia* Hemsl. in the plastid DNA tree in contrast to the nrITS tree (Liu & al. 2013). With only moderate statistical sup-

port, the plastid DNA tree indicates a sister group relationship of the clade under study with *Nabalus tatarinowii* (Maxim.) Nakai. Finding the three species nested in one clade agrees with the conspicuous overall morphological similarity of them. The sister group relationship (with full statistical support) of two of them in the nrITS tree (Fig. 1, as *Sinoseris scandens* and *S. muliensis*), also corresponds with the stronger morphological similarity between these two species compared to the third (Fig. 1, as *S. changii*), which is apparent in particular with respect to achene morphology and the capitulum size. The plastid DNA phylogeny (Fig. 2), however, contrasts with the sister group relationships being vice versa.

The three species of this clade are also morphologically clearly distinct from their closer relatives, which all appear as members of the *Dubyaea-Nabalus-Soroseris-Syncalathium* polytomy in the nrITS tree. Diagnostic for the clade under study is a synflorescence of second, subspiciform to paniculiform paracladia, the involucre with very few, inconspicuous outer phyllaries, beaked achenes with more than two secondary ribs per main rib and a dirty white to pale brownish pappus of moderately coarse, scabrid bristles (Table 2). Their pollen is echinolophate tricolpate of the widespread *Cichorium* type; the three species share moderately narrow interlacunar gaps, but differ in the extent and spine number of the polar areas, ranging from moderately to very extensive and with c. 12 to >20 spines (see Taxonomy, below).

Consequently, this lineage is best classified as its own genus, for which we have chosen the name *Sinoseris* (see Taxonomy, below). This genus is endemic to China, where its species are restricted to Yunnan and Sichuan (Fig. 3). Only the most widespread of the three species has been known to science for a longer time. Its original name *Lactuca hirsuta* is illegitimate as a younger homonym of *L. hirsuta* Muhl. ex Nutt. of North America. Considered to be different from *L. hirsuta*, the Chinese species was described a second time 40 years later by Chao Chien Chang (1900–1972) as *L. scandens*, which is now the basionym for the name of this species. The conspecificity of both taxa was blurred by infraspecific variation and incorrectly described features in the protologue of *L. hirsuta* (see Taxonomy, below). We discovered the second species (see Taxonomy below, under *S. muliensis*) first among the historical specimens from the early 20<sup>th</sup> century determined as *L. hirsuta* before we re-collected it in the wild. While this paper was in preparation, it was published as *Nabalus muliensis* Y. S. Chen, L. S. Xu & R. Ke (Chen & al. 2019). We discovered the third species (*S. changii*) in the field and do not know historical herbarium material of it. However, sequences of the nrITS region published under the name *L. scandens* (INSDC acc. no. KF732051 to KF732056, see Fig. 1) and included in our phylogenetic reconstruction were found nested in the same clade as our sequences of this hitherto undescribed species.

Table 1. INSDC (International Nucleotide Sequence Database Collaboration) accession numbers of newly generated nrITS and plastid DNA sequences with specimen data of samples used.

Taxon name	DNA Bank ID and specimen	Locality	Marker: accession no.
<i>Acanthocephalus benthamianus</i> Regel	B:DNA Bank:DB 464, <i>L. Martins &amp; T. Janssen 1005</i> (JE)	Kyrgyzstan, Jalal-Abad Oblast, Bazar-Korgon Rayon, Dscharadar	ITS: LR743481
<i>Chondrilla chondrilloides</i> (Ard.) H. Karst.	B:DNA Bank:DB 309, <i>Wraber 102782</i> (B 10 0138369)	Italy, Udine, prope Venzone	ITS: LR743477
<i>Chondrilla juncea</i> L.	B:DNA Bank:DB 310, <i>K. H. Rechinger 62177</i> (B 10 0027072)	India, Kashmir, Karawring S Srinagar versus Chari Sharif	ITS: LR743478
<i>Chondrilla letosperma</i> Kar. & Kir.	B:DNA Bank:DB 306, <i>T. Dürbye 1754</i> (B 10 0096856)	Kyrgyzstan, Tien-Shan, Issyk-Kul-See, Ak-Sakji,	ITS: LR743476
<i>Chondrilla ramosissima</i> Sm.	B:DNA Bank: DB303/2005, <i>R. Willing &amp; E. Willing 119544</i> (B 10 0142299)	Greece, Nomos Korinthias, N Galatas	ITS: LR743475
<i>Crepidiastrum tenuifolium</i> (Willd.) Sennikov	B:DNA Bank:DB 26539, <i>Burkhardt</i> (herb. M. Ristow)	Russia, W Siberia, Altay Mts	<i>matK</i> : LR743493
<i>Crepis multicaulis</i> Ledeb.	B:DNA Bank:DB 43961, <i>E. v. Raab-Straube 020302</i> (B 10 0149449)	Russia, S Siberia, Altay Mts	<i>matK</i> : LR743494
<i>Heteroderis pusilla</i> (Boiss.) Boiss.	[NK131] B:DNA Bank:DB 39434, <i>K. H. Rechinger 35031</i> (B 10 1013626)	Afghanistan, Tirin	ITS: LR743479
<i>Lagoseriopsis popovii</i> (Krasch.) Kirp.	B:DNA Bank:DB 26499, <i>Boischantzev &amp; al.</i> (LE)	Tajikistan, N Olimabad, 600 m	<i>matK</i> : LR743491
<i>Sinoseris changii</i> 1	<i>Wang Zehuan &amp; Chen Yaping WZH20171001</i> (KUN)	China, Yunnan, Dayao County, Tanhua village	ITS: LR743482; <i>trnL-F</i> : LR760722; <i>psbA-trnH</i> : LR760713; <i>matK</i> : LR743495
<i>Sinoseris changii</i> 2	<i>Wang Zehuan &amp; Chen Yaping WZH20171011</i> (KUN)	China, Yunnan, Dayao County, Guthua village	ITS: LR743483; <i>trnL-F</i> : LR760723; <i>psbA-trnH</i> : LR760714; <i>matK</i> : LR743496
<i>Sinoseris changii</i> 3	<i>Wang Zehuan &amp; Chen Yaping WZH20171018</i> (KUN)	China, Yunnan, Yongren County, Yongxing village	ITS: LR743484; <i>trnL-F</i> : LR760724; <i>psbA-trnH</i> : LR760715; <i>matK</i> : LR743497
<i>Sinoseris multiensis</i> 1	<i>Wang Zehuan &amp; Li Huimin WZH20181001a</i> (KUN)	China, Sichuan, Muli County, Xiamaidi village	ITS: LR743488; <i>trnL-F</i> : LR760728; <i>psbA-trnH</i> : LR760719; <i>matK</i> : LR743501
<i>Sinoseris multiensis</i> 2	<i>Wang Zehuan &amp; Li Huimin WZH20181001b</i> (KUN)	as above	ITS: LR743489; <i>trnL-F</i> : LR760729; <i>psbA-trnH</i> : LR760720; <i>matK</i> : LR743502
<i>Sinoseris multiensis</i> 3	<i>Wang Zehuan &amp; Li Huimin WZH20181001c</i> (KUN)	as above	ITS: LR743490; <i>trnL-F</i> : LR760730; <i>psbA-trnH</i> : LR760721; <i>matK</i> : LR743503

(continued on next page)

Table 1 (continued from previous page)

Taxon name	DNA Bank ID and specimen	Locality	Marker: accession no.
<i>Sinoseris scandens</i> 1	Wang Zehuan & Chen Yaping WZH20171019a (KUN)	China, Sichuan, Yanchuan County, Gesala village	ITS: LR743485; <i>trnL-F</i> : LR760725; <i>psbA-trnH</i> : LR760716; <i>matK</i> : LR743498
<i>Sinoseris scandens</i> 2	Wang Zehuan & Chen Yaping WZH20171019b (KUN)	as above	ITS: LR743486; <i>trnL-F</i> : LR760726; <i>psbA-trnH</i> : LR760717; <i>matK</i> : LR743499
<i>Sinoseris scandens</i> 3	Wang Zehuan & Chen Yaping WZH20171019c (KUN)	as above	ITS: LR743487; <i>trnL-F</i> : LR760727; <i>psbA-trnH</i> : LR760718; <i>matK</i> : LR743500
<i>Sonchella dentata</i> (Ledeb.) Sennikov	B:DNA Bank:DB 26502, V. Chanminkhum & al. (B 10 0517804)	Russia, Siberia, Tuvniskaja ASSR	<i>matK</i> : LR743492
<i>Syncalathium disciforme</i> (Mattf.) Y. Ling	[NK168] T. N. Ho & al. 1196 (CAS 919951)	China, Qinghai, 4300 m	ITS: LR743480

## Discussion

The clade including the species under study is nested in the Asian-North American *Dubyaea-Nabalu-Sorosseris-Syncalathium* polytomy, which is one of six major terminal clades resolved in our phylogenetic backbone of the subtribe *Crepidinae* based on nrITS (Fig. 1). This phylogenetic position seems surprising in view of their previous classification as members of *Lactuca* L. or the *Lactucinae*. It must be considered, however, that in the late 19<sup>th</sup> and early 20<sup>th</sup> centuries the generic concept of *Lactuca* was extremely wide and spanned members of several of the modern subtribes (Kilian & al. 2017). Disentangling the subtribes *Crepidinae* and *Lactucinae* has, moreover, proven particularly difficult due to the scarcity of non-homoplastic morphological synapomorphies (Bremer 1994).

The *Dubyaea-Nabalu-Sorosseris-Syncalathium* polytomy was found in several studies with varying partial representation of its members (Kilian & al. 2009a; Zhang & al. 2011; Liu & al. 2013; Kilian & al. 2017). Divergence time estimations for the *Crepidinae* by Zhang & al. (2011) revealed that it is likely of Pliocene origin, with a crown age of around 5 myr only; for genera such as *Sorosseris* Stebbins or *Syncalathium* Lipsch., a crown age of less than 2 and 3 myr, respectively, has been estimated. The comparatively young age of this polytomy may be responsible for the shallow genetic differentiation among many of its members (Zhang & al. 2011), in particular within lineages such as *Sorosseris* or *Nabalu* Cass. (in the sense of the type, *N. trifoliolatus* Cass., of that generic name), as indicated by branch lengths in Fig. 1 and Fig. 2. Distinctly longer branches of and within the *Sinoseris* clade in both the nrITS and the plastid DNA phylogram are indicative for a comparatively deeper genetic differentiation of its species and of the genus from related genera.

The authors of the recently described *Nabalu muliensis*, Chen & al. (2019), inferred its generic placement through a plastid DNA tree in which this species is nested in a clade together with *N. tatarinowii* from China and *N. trifoliolatus* (which provides the type of the name *Nabalu*) from North America (in press, Chen & al. pers. comm.). This topology is, however, the result of a restricted sampling among the members of the *Dubyaea-Nabalu-Sorosseris-Syncalathium* polytomy. Both the nrITS trees (see already Kilian & al. 2017 and Fig. 1) and the plastid DNA tree (Fig. 2) show that *Nabalu* in its current sense is actually polyphyletic. The nrITS tree indicates three separate lineages, two of them present in North America (*N. trifoliolatus* [*Nabalu sensu typi*] clade, *N. sagittatus* (A. Gray) Rydb. clade) and one in E Asia (*N. tatarinowii* clade; see also Kilian & al. 2017). *Nabalu muliensis* and its two allies are resolved separate from all of them. Members of the *N. sagittatus* clade were not included in the plastid DNA tree because the partial *matK* sequences available are insufficient for resolving

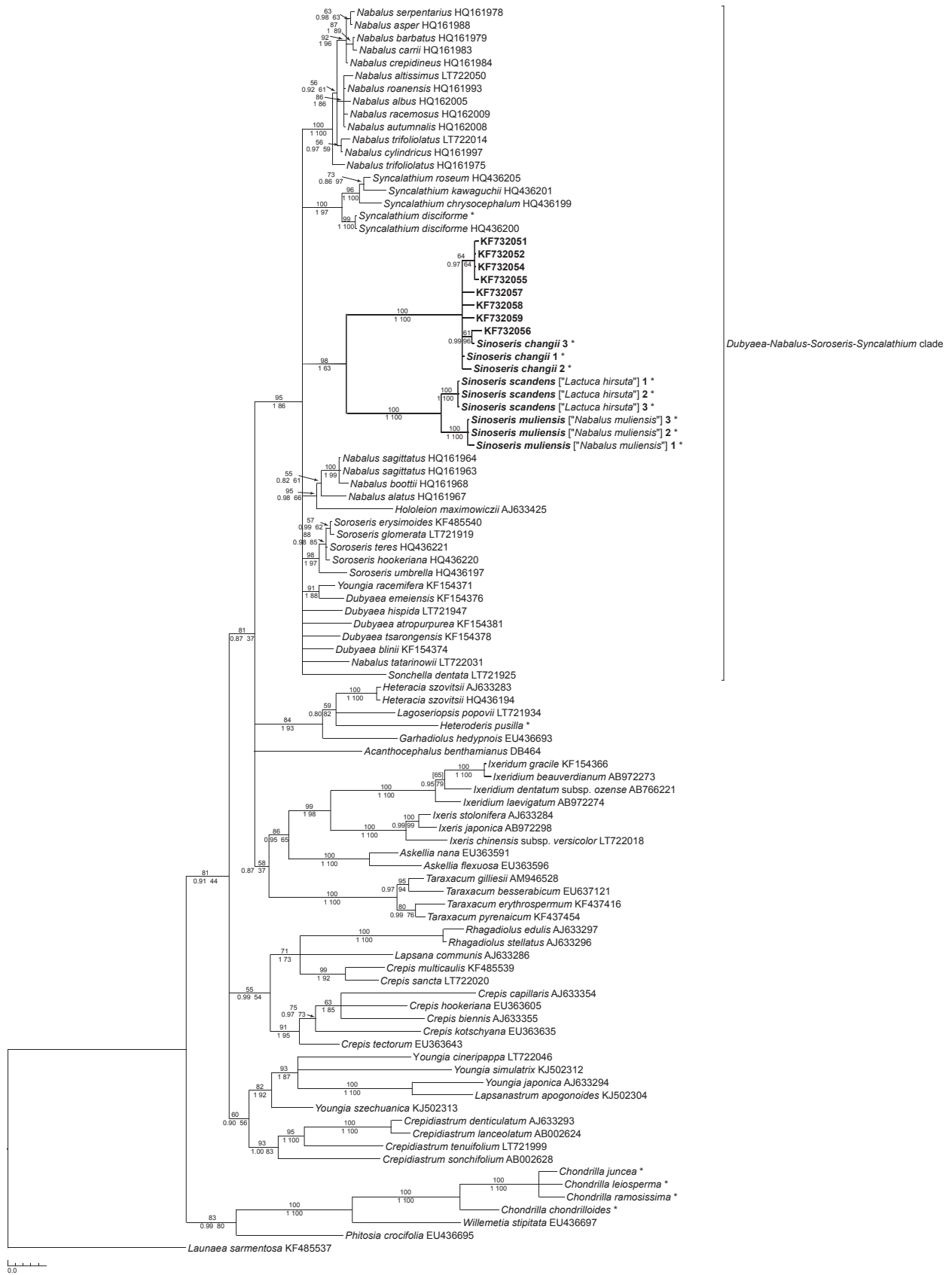


Fig. 1. Majority consensus phylogram of the *Crepidinae* from the Bayesian analysis (support values: first line: maximum parsimony jackknife; second line: Bayesian posterior probability / maximum likelihood bootstrap) based on the nrITS region. An asterisk following the sample designation indicates newly generated sequence(s); see Table 1.

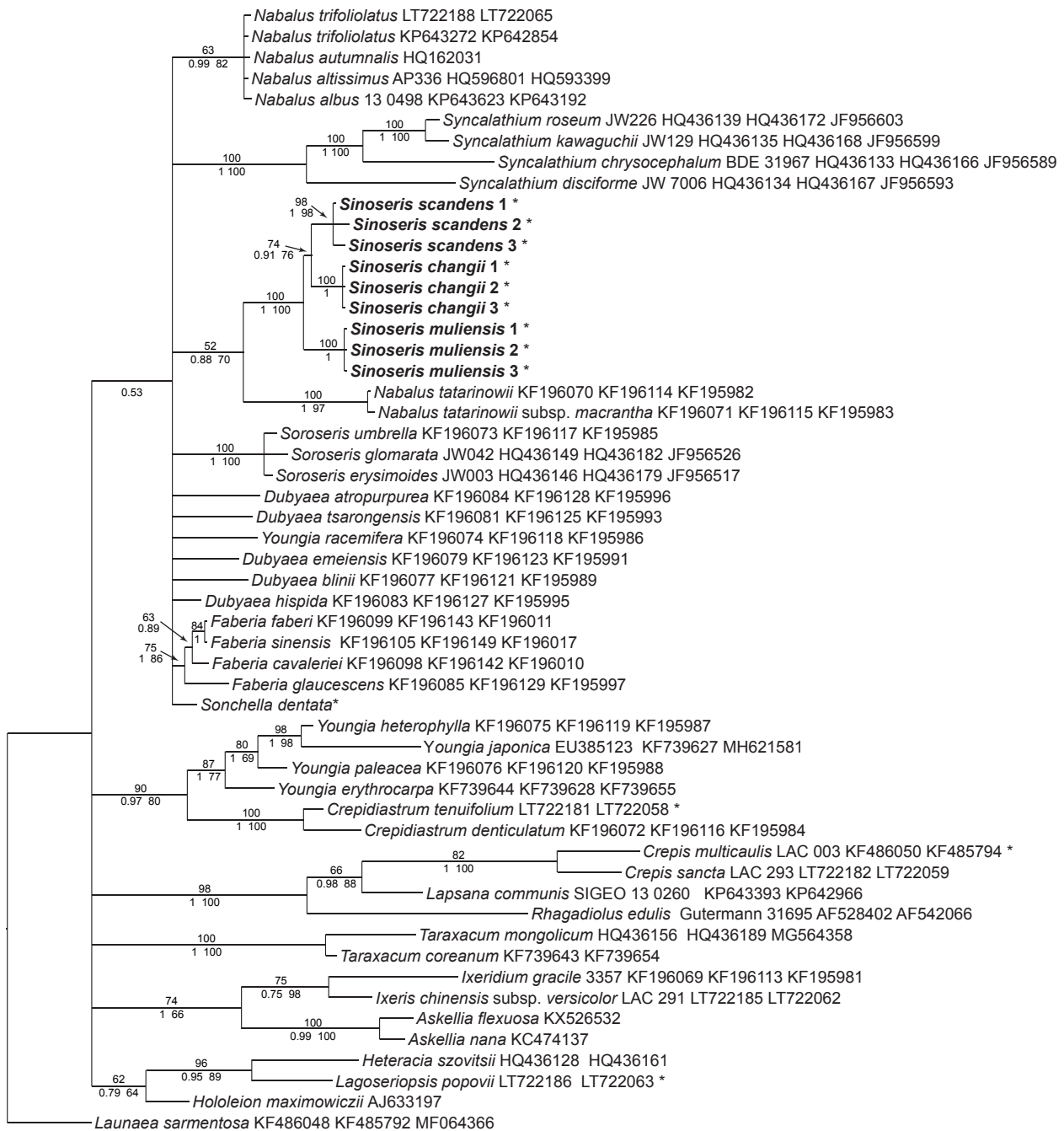


Fig. 2. Majority consensus phylogram of the *Crepidinae* p.p. from the Bayesian analysis (support values: first line: maximum parsimony jackknife; second line: Bayesian posterior probability / maximum likelihood bootstrap) based on the plastid DNA *trnL-F*, *psbA-trnH* and *matK* markers. An asterisk following the sample designation indicates newly generated sequence(s); see Table 1.

their position; *Nabalus sensu typi* and the *N. tatarinowii* clade are resolved as lineages clearly separate from each other and from *Sinoseris*.

The sister-group relationship between *Sinoseris* and *Nabalus tatarinowii* is only moderately supported and morphologically not apparent. A possible taxonomic conclusion of their congenerity appears therefore premature. Morphologically the *Crepidinae* appear comparatively diverse, but characterization of their genera mostly relies on rather complex combinations of features responsible for a certain characteristic overall ap-

pearance, whereas identification of synapomorphies is rather difficult (Bremer 1994) and still in its infancy. Micromorphological characters are no exception; pollen morphology, for example, across the *Crepidinae* shows certain differences within the common *Cichorium* L. pollen type, but the number of representatives investigated of the various genera is still fairly limited (Wang & al. 2009). The significance of such differences is uncertain yet, and the range of states we observed even in a small genus such as *Sinoseris* rather enhances this uncertainty.



Table 2. Comparison of diagnostic morphological features between genera of the *Dubyaea-Nabalus-Sorosoris-Syncalathium* clade and *Sinoseris* (compare the *Crepidinae* backbone, Fig. 1).

Genus	Life form	Division of leaves †	Indumentum of leaves and stems	Synflorescence	Differentiation of involucre ‡	Outer phyllaries of involucre	Corolla colour §	Achene apex ¶	Achene ribbing pattern: main ribs / secondary ribs per main rib	Achene indumentum	Pappus colour
<i>Dubyaea</i> DC.	perennial	UD to PD	mostly hispid, glandular or eglandular, more rarely none	corymbiform, rarely umbelliform, or capitula solitary	I to D	several, imbricate	Y or C	T	5/≥2	none (or with short appressed papillae)	yellowish, brownish, rarely white
<i>Hoteleion</i> Kitam.	rhizomatous perennial	UD	none	paniculiform to corymbiform	D	several, imbricate	Y	T	5 weak/indistinct	none	straw-coloured
<i>Nabalus</i> Cass., s.l.	perennial	UD to PD	± tomentose, or more rarely hispidulose, scabrid or villose, very rarely none	paniculiform, racemiform or spiciform	D	several, imbricate	Y or W or C	T	5/≥2	none	straw-coloured to brown
<i>Sonchella</i> Sennikov	perennial	UD	± none	racemiform or paniculiform	D	several, imbricate	Y	T	5/1-2	with short appressed papillae	white
<i>Sorosoris</i> Stebbins	perennial	UD to PD	none to pilose	syncalathia	D	2	Y or W	T, rarely B	5/1 or ≥2	none or with short appressed to spreading-erect papillae	whitish to straw-coloured, distally often greyish
<i>Syncalathium</i> Lipsch.	perennial	UD to PD	none or villous	syncalathia	U	0	Y or C	T	5/≥2	none	greyish white
“ <i>Youngia</i> ” <i>racemifera</i>	perennial	UD	none	racemiform, secund	D	several, imbricate	Y	T	5/2-3	none	straw coloured to pale brown
<i>Sinoseris</i>	annual (to monocarpic biennial)	UD to LP	conspicuously stiff, eglandular	paniculiform of secund, subspiciform to paniculiform paracladia	D	few, very small, inconspicuous	Y	B	5/≥2	with appressed to (apically) spreading-erect linear flattened acute papillae	dirty white to pale brownish

†: UD = undivided; PD = pinnately divided; LP = lyrate pinnatisect. – ‡: I = imbricate; D = differentiated in inner and outer series; U = uniseriate. – §: Y = yellow; C = cyanic; W = white. – ¶: B = beaked; T = truncate.

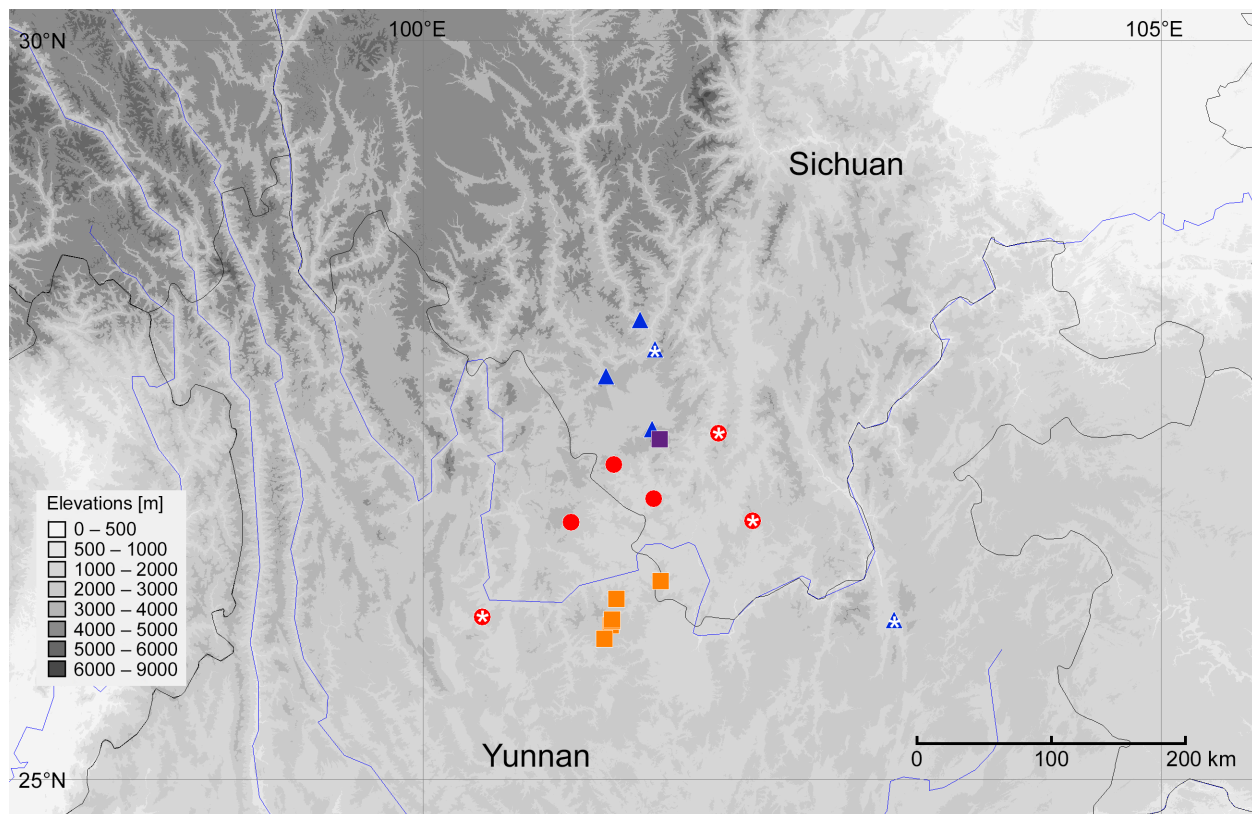


Fig. 3. Distribution of *Sinoseris*; red circles: *S. scandens*; blue triangles: *S. muliensis*; orange squares: *S. changii*; violet square: population with putative introgression between *S. muliensis* and *S. scandens*; occurrences marked with a white asterisk are known only from historical herbarium specimens. – Georeferenced map generated with DIVA-GIS (Hijmans 2012) using an adaptation of the SRTM 90 m digital elevation data (CGIAR-CSI 2019).

All three *Sinoseris* species are annuals (or perhaps monocarpic biennials) and grow in the subtropical (warm-temperate) highlands of Sichuan and Yunnan and preferably in open, rocky habitats. All other members of the *Dubyaea-Nabalus-Sorosseris-Syncalathium* clade are, in contrast, perennials and confined to the higher montane or alpine zones (*Dubyaea*, *Sorosseris*, *Syncalathium*, and “*Youngia*” *racemifera*, the last described in *Youngia* Cass. but of unclear generic affinity) or more continental and either colder (*Nabalus*, *Hololeion* Kitam.) or more arid (*Sonchella* Sennikov) climates. The *Sinoseris* lineage is therefore somewhat outstanding, which deserves further attention.

It is not fully clear from the data available whether *Sinoseris* diversified in principal by allopatric speciation, as the distribution areas (Fig. 3) seem to indicate, but there is evidence for a lack of a reproductive isolation on secondary contact: whereas the name *Nabalus muliensis* is typified by a specimen with 3-flowered capitula, one further gathering cited and illustrated (*Y. S. Chen & al. 152119*) by its authors clearly represents *Sinoseris scandens* (with 5 florets). A third gathering of a population with 3- to 5-flowered capitula likely represents an introgressive population, for which intermediate and variable, otherwise constant, numbers of florets (and inner phyllaries) are characteristic, resulting from hybridization with *S. scandens*.

All three species have been rarely collected so far, which appears surprising as they are not inconspicuous. Reasons may be their late flowering from late September onward and their scattered occurrence, perhaps due to their preference of rocky habitats.

## Taxonomy

*Sinoseris* N. Kilian, Ze H. Wang & H. Peng, **gen. nov.**  
Type: *Sinoseris scandens* (C. C. Chang) Ze H. Wang, N. Kilian & H. Peng

*Diagnostic features* — Annual (or monocarpic biennial) herbs; stems, leaves and involucre with conspicuous indumentum of stiff hairs; basal leaves distinctly petiolate; synflorescence of secund, subspiciform to paniculiform paracladia; capitula with 3–12 florets; involucre with inconspicuous outer phyllaries; achenes beaked; achene corpus with 5 main ribs alternating with (2 or)3 or 4 secondary ribs; pappus dirty white to pale brown, of moderately coarse, scabrid bristles.

*Description* — Annual (or monocarpic biennial) herbs with leafy stem and conspicuous, stiff indumentum on stem, leaves and involucre, late flowering (Sep–Nov).



Fig. 4. Photograph of the lectotype of *Lactuca scandens* C. C. Chang in the herbarium LBG.



Fig. 5. *Sinoseris scandens* – A: habit; B: flowering capitula; C: fruiting capitula with mature achenes; D: basal leaf; E: sequence of stem leaves (upward, right to left). – Photographs by Wang Zehuan from Sichuan, near Gesala Village on 14 Oct 2017 (A, B, D, E) and 12 Nov 2018 (C); population voucher: Wang Zehuan & Chen Yaping WZH20171019 (KUN).

*Basal and lowermost cauline leaves* with petiole-like portion as long as or longer than lamina. *Capitula* 3–12 flowered, in  $\pm$  secund, subspiciform to narrowly paniculiform paracladia from axils of cauline leaves, pendent in bud, subsistent at anthesis and pendent again at fruiting. *Involucre* narrowly cylindrical at anthesis, strongly differentiated into an equal inner and very inconspicuous

outer phyllary series. *Receptacle* epaleate, glabrous, smooth. *Florets* with yellow corolla, styles greyish to blackish. *Pollen* echinolophate, tricolpate, of *Cichorium* type (sensu Blackmore 1986) with polar areas either triangular, moderately extensive and each with c. 12 spines, or very extensive, approximately hexagonal and each with >20 spines, and with moderately narrow interlacu-

nar gaps (Fig. 6E, F; Fig. 8E, F; Fig. 10E, F). *Achenes* beaked; corpus somewhat flattened,  $\pm$  subconic, with 5 main ribs (best discernible near base) alternating with (2 or)3 or 4 secondary ribs (fully developed in middle third and then similar in shape to main ribs), dark brown, with appressed to spreading-erect (in distal portion of corpus) linear, flattened, acute papillae; beak slender, shorter than or as long as corpus. *Pappus* dirty white to pale brown, caducous, of scabrid bristles similar in length and diameter, with 7–12(–14) rows of cells in cross-section near base.

*Etymology* — The generic name *Sinoseris* is a compound of the Latin “Sina” for China and “seris” (σέρης), the classical Greek name for salad (more precisely of *Cichorium* species).

### Key to the species of *Sinoseris*

1. Involucre with usually 8 inner phyllaries; capitula with 8–12 florets; anther tube golden yellow to brownish; achenes abruptly contracted into a slender beak as long as the obconic and broad-shouldered corpus . . . . . **3. *S. changii***
- Involucre with 5 or fewer inner phyllaries; capitula with 6 or fewer florets; anther tube blackish; achenes attenuate into a slender beak much shorter than the narrowly ellipsoid corpus . . . . . **2**
2. Involucre with (4 or)5 inner phyllaries; capitula with 4–6 florets . . . . . **1. *S. scandens***
- Involucre with 3 inner phyllaries; capitula with 3 florets . . . . . **2. *S. muliensis***

**1. *Sinoseris scandens*** (C. C. Chang) Ze H. Wang, N. Kilian & H. Peng, **comb. nov.**  $\equiv$  *Lactuca scandens* C. C. Chang in Contr. Biol. Lab. Sci. Soc. China, Bot. Ser. 9: 133. 1934. – **Lectotype (designated here):** [China] Szechuan, Yien-Pien Hsian [Sichuan, Yanbian County, c. 26.90°N, 101.56°E], 2600 m, 16 Oct 1932, *T. T. Yü 1702* (LBG00092879! [see Fig. 4]; isolectotypes: LBG00092880!, PE01106722!).

= *Lactuca hirsuta* Franch. in J. Bot. (Morot) 9: 258. 1895, nom. illeg. [non *Lactuca hirsuta* Muhl. ex Nutt., Gen. N. Amer. Pl. 2: 124. 1818]  $\equiv$  *Chaetoseris hirsuta* C. Shih, Fl. Reipubl. Popularis Sin. 80(1): 282. 1997  $\equiv$  *Melanoseris hirsuta* (C. Shih) N. Kilian in Wu & al., Fl. China 20–21: 220. 2011. – **Lectotype (designated here):** China, Yunnan, lieux ombragés au mont Che-tscho-tze, au-dessus de Tapintze [a village at c. 26.10°N, 100.40°E], 10 Oct 1882, *J. M. Delavay 627* (P00288022! [marked as “holotype”]; isolectotype: P00750292! [marked as “isotype”]).

*Description* — Annual (to monocarpic biennial) herbs, 15–80 cm tall, strongly covered with stiff, eglandular, reddish-purplish hairs, with a taproot. *Stem* solitary or, if branched right from base, plants seemingly with several

stems, erect or arched erect, branching, leafy. *Basal and lower cauline leaves* abruptly contracted into a petiole-like portion to 15 cm long, base semi-amplexicaul to more often winged and distinctly clasping stem; lamina broadly triangular, ovate to broadly lanceolate, or oblanceolate, 3–14 cm long, 2.5–13.5 cm wide, entire to lyrate-pinnatisect, with a broadly ovate to broadly triangular terminal lobe, cordate or obtuse to cuneate at base and acute at apex, with 1 or 2 pairs of much smaller triangular to rhombic, acute to obtuse lateral lobes, or up to 5 pairs of very small ovate to elliptic lateral lobes; lamina margin variably shallowly or deeply sinuate-dentate, often irregularly so, and denticulate. *Middle and upper cauline leaves* oblanceolate or ovate to lanceolate, smaller, with winged or  $\pm$  without petiole-like basal portion, otherwise similar to lower cauline leaves, base distinctly clasping. *Synflorescence* of a flowering stem in well-developed plants with several paracladia from axils of cauline leaves, all subspiciform to narrowly paniculiform and  $\pm$  secund, each with a few to more than a dozen capitula pendent in bud, subpendent at anthesis and pendent again at fruiting. *Capitula* with (4 or)5(or 6) florets; peduncle in most cases less than 1 cm long. *Involucre* narrowly cylindrical, 10–13 mm long; strongly differentiated into inner and outer phyllary series, the latter very inconspicuous; phyllaries abaxially reddish hirsute as remainder of plant; outer phyllaries up to 3, very inconspicuous, narrowly linear, c. 0.9  $\times$  0.2 mm; inner phyllaries usually 5, linear-lanceolate and similar in length, green, sometimes (partly) with a purplish tinge. *Receptacle* epaleate, glabrous, smooth. *Florets* with bright yellow corolla; ligule broadly elliptic to obovate,  $\pm$  horizontally spread, 14–16 mm long, to 3 mm wide, tube c. 6 mm long; anther tube blackish, fertile part 4.6–4.8 mm long, apical appendages rounded, c. 0.2 mm long, basal appendages c. 0.6 mm long; *style* and style arms blackish. Pollen of *Cichorium* type (sensu Blackmore 1986) with triangular, moderately extensive polar areas, each with c. 12 spines, and moderately narrow interlacunar gaps (Fig. 6E, F). *Achenes* 8–9 mm long, corpus narrowly ellipsoid to subconic, subcompressed, dark brown mottled white, covered with linear, flattened, acute, antrorse papillae, shorter and appressed in proximal two thirds of corpus, longer and spreading-erect in distal third, with 5 main ribs (best discernible near base) alternating with (2 or)3(or 4) secondary ribs (fully developed in middle third and then similar in shape to main ribs), apex attenuate into a slender, whitish beak of 3–4 mm (Fig. 6A–D). *Pappus* 6–7 mm long, dirty white to pale brownish, caducous, bristles of similar length and diameter, near base of 8–14 rows of cells in cross-section. – Fig. 5; Fig. 6.

*Distribution* — China: NW Yunnan and SW Sichuan.

*Habitat and ecology* — *Sinoseris scandens* occurs at altitudes between 1750 and c. 3000 m on rocky slopes with open grassland vegetation. Fl. and fr. Sep–Nov.

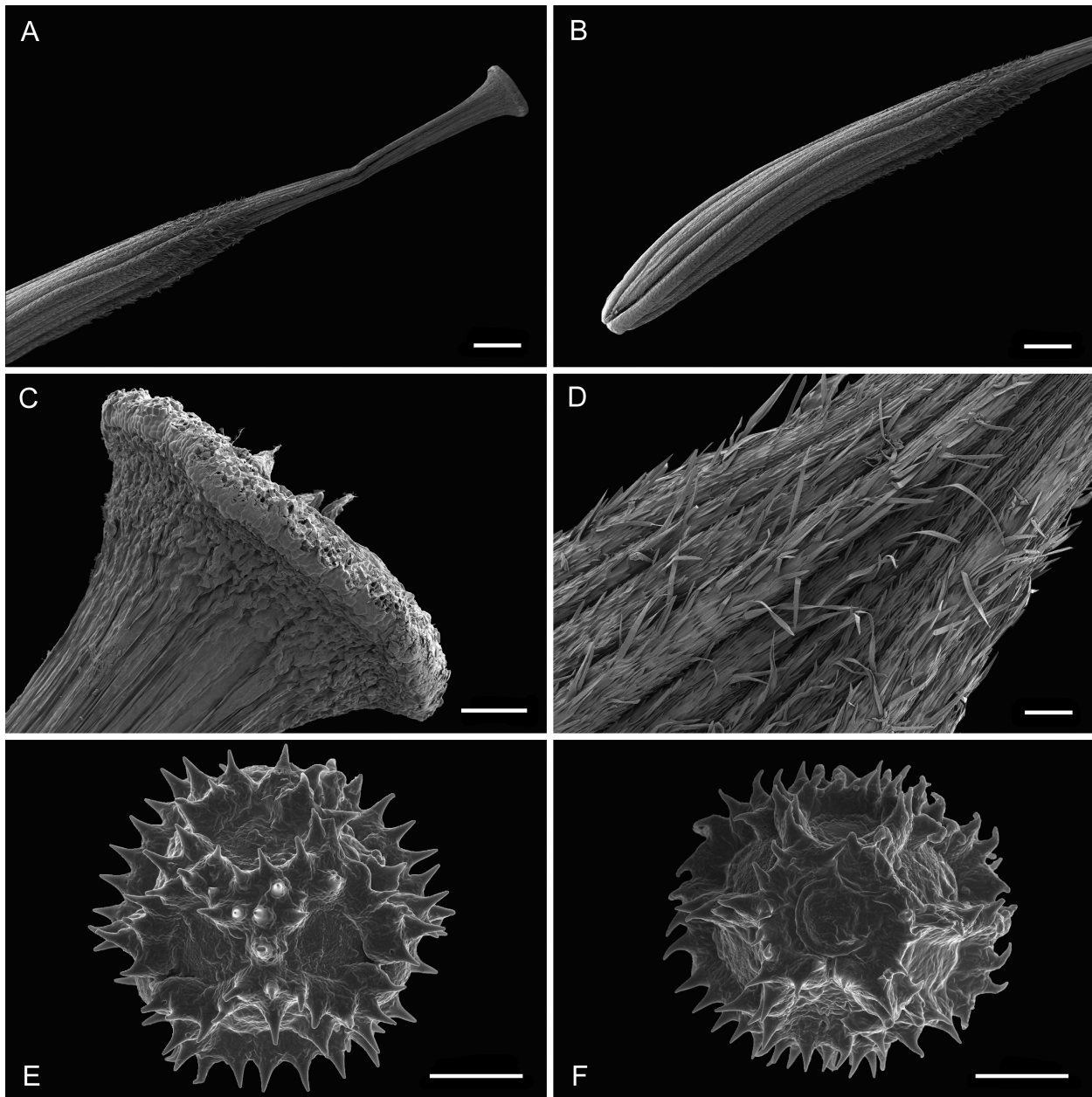


Fig. 6. *Sinoseris scandens* – A–D: achene; A: apical portion; B: basal portion; C: pappus disk with detached pappus bristles showing cross-section of bristles; D: apex of corpus with parts of papillae longer and spreading. – E, F: pollen; E: polar view; F: equatorial view. – Scale bars: A, B = 500  $\mu\text{m}$ ; C = 100  $\mu\text{m}$ ; D = 200  $\mu\text{m}$ ; E, F = 10  $\mu\text{m}$ . – From Wang Zehuan & Chen Yaping WZH20171019 (KUN).

**Threat status** — *Sinoseris scandens* has been collected so far at five separate localities in Sichuan and Yunnan. Three were made between 1882 and 1932. At the two current localities, Gesala and Ninglang, <500 individuals in 2017 and <100 individuals in 2018 were counted, respectively. Population sizes seem to vary considerably from year to year as observed in Gesala comparing 2017 and 2018. A formal threat status assessment for this species according to the IUCN Red List categories and criteria (IUCN 2012) requires more data on the actual and historical distribution and population sizes in relation to land-use changes. Although the scarcity of collections may be partly due to its late flowering in the year,

*S. scandens* seems to be a rare species with a scattered distribution endemic to a small part of the two provinces. Its status should therefore be of concern and addressed by further investigations.

**Remarks on typification and synonymy** — The description in the protologue of *Lactuca scandens* is detailed and corresponds well with the type material traced in LBG and PE. The eglandular, stiff, reddish indumentum in combination with capitula of (mostly) 4 or 5 yellow florets, blackish anther tubes and styles, and an involucre of (4 or) 5 inner and very inconspicuous outer phyllaries diagnose the taxon perfectly. The author compared the

species with *L. hirsuta* as its “nearest ally”, stating that *L. scandens* differs by a red (versus “white”, actually dirty white: “setis sordidis”) hispid eglandular (versus mixed eglandular-glandular) indumentum, a “white” (versus dirty white) pappus, and undivided (versus lyrate-pinnate) leaves. The descriptions of the pappus in the protologue of *L. scandens* are contradictory: the English description states “white”, whereas the Latin description states “setae ... sordide albae”, i.e. dirty white, which agrees with our observation and also with the description of *L. hirsuta*. The leaves in *L. hirsuta* are lyrate-pinnatisect but they are variable within populations, ranging from entire to pinnatisect. The indumentum in the type specimens of *L. hirsuta* looks in fact dirty white, but this is likely only an effect of drying; the statement about presence of glandular hairs in the protologue of *L. hirsuta* is erroneous, as well as the number of 8 florets per capitulum. With the help of the curators in P their number has been confirmed as 5 or 6. The number of inner phyllaries is correctly given as 5, in agreement with *L. scandens*. It can safely be concluded that both taxa are conspecific.

The type gathering of *Lactuca scandens* collected by T. T. Yü is stated in the protologue to come from the “vicinity of Pa-hsien (Chungking)”, which is apparently erroneous. The label of the specimens LBG00092879 (Fig. 4) and PE01106722 clearly state its provenance as Yien-Pien Hsian (= Yanbian county). The first, more complete specimen, is selected by us as lectotype. The locality as given in the protologue is also unlikely because it is more than 500 km away from the other collections of the species and the genus.

The gathering of Père Jean Marie Delavay, the original material of *Lactuca hirsuta*, was made in the mountains above the village “Tapintze” [= Dapingzi], where Père Delavay lived from August 1882 onward for some years as missionary. This Dapingzi (there are other homonymous places) is situated at c. 26.10°N, 100.40°E, some 55 km NNE of Dali in the valley of the Loulou river, a tributary of the Jinsha Jiang (the upper Yangtze), which passes c. 12 km to the NE (Kilpatrick 2014: 69, 102; reproducing a map of the area drawn by Père Delavay). Technically the two sheets of the same gathering by Père Delavay of *L. hirsuta* at P are syntypes so that a lectotype has to be designated. We have selected the one marked as “holotype”, with the original label of the collector and the determination in Franchet’s hand.

*Additional specimens seen* — CHINA: SICHUAN: in regio subtropica convallis fluminis Yalung ad affluentem versus Yenyüen in altograminetis ad viam Gwanyingai, 27°20'N [c. 102°E], subtr. calceo, 1750 m, 29 Sep 1914, *H. Handel-Mazzetti* 5342 [Diar. Nr. 887nota] (W 1940-348); in montis Lungdschu-schan prope urbem Huili regione temperata, rupibus supra vicum Djindjiatsun in limite reg. calide temperatae, 2800 m, [c. 26.75°N, 102.23°E], 16 Sep 1914, *H. Handel-Mazzetti* 5186 [Diar. Nr. 839] (W 1940-347); Panzhihua, Yanbian

County, Gesala Village, 27.130136°N, 101.287422°E, elev. 2523 m, 14 Oct 2017, *Wang Zehuan & Chen Yaping* WZH20171019 (B, KUN, PE). — YUNNAN: Lijiang, Ninglang Yi Autonomous County, from Zhanhe Village to Yongningping Village, 26.742985°N, 101.000726°E, elev. 2934 m, 20 Oct 2018, *Wang Zehuan & Li Huimin* WZH20181005 (KUN).

**2. *Sinoseris muliensis*** (Y. S. Chen, L. S. Xu & R. Ke) Ze H. Wang, N. Kilian & H. Peng, **comb. nov.** ≡ *Nabulus muliensis* Y. S. Chen, L. S. Xu & R. Ke in *Phytotaxa* 416: 258. 2019. — Holotype: China, Sichuan, Muli County, Xia-maidi, Mianbu, 27°22'N, 101°33'E, 3000 m, stony grassy slopes and stony thicket slopes, 8 Oct 2016, *Y. S. Chen & L. S. Xu* 160248 (IBSC; isotypes: IBSC, PE).

*Description* — Annual (or monocarpic biennial) herbs with taproot, 15–90 cm tall, strongly covered with stiff, eglandular, pale to dark reddish-purplish hairs. *Stem* solitary, erect, branching from base or higher up, leafy. *Basal and lower cauline leaves* abruptly contracted into a petiole-like portion up to 6 cm long, base semi-amplexicaul or winged and distinctly clasping stem; lamina orbicular (in particular in basal leaves) to broadly triangular or ovate, or oblanceolate, 4–8 cm long, 2.8–5.5 cm wide, entire or lyrate-pinnatifid to pinnatisect, with a large orbicular to broadly triangular terminal lobe with cordate or obtuse to cuneate base and acute apex, and 1 to several pairs of (much) smaller ovate or elliptic to rhombic or ± triangular, acute to obtuse lateral lobes; lamina margin variably shallowly or deeply sinuate-dentate, often irregularly so, and denticulate. *Middle and upper cauline leaves* ovate to lanceolate, smaller, with winged or ± without petiole-like basal portion, otherwise similar to lower cauline leaves, base distinctly clasping stem. *Synflorescence* of a flowering stem in well-developed plants with several paracladia from axils of cauline leaves, all subspiciform to narrowly paniculiform and ± secund, each with a few to more than 12 capitula pendent in bud, subpendent at anthesis and pendent again at fruiting. *Capitula* with 3 florets; peduncles mostly shorter than involucre. *Involucre* narrowly cylindrical, 10–12 mm long; strongly differentiated into inner and ± inconspicuous outer phyllary series; phyllaries abaxially pale to reddish hirsute as remainder of plant; outer phyllaries 2, narrowly linear, 2–4 × 0.2–0.3 mm; inner phyllaries 3, linear-lanceolate and similar in length, green, sometimes (partly) with a purplish tinge. *Receptacle* epaleate, glabrous, smooth. *Florets* with yellow corolla; ligule elliptic, reflexed, 9–12 mm long, to c. 2 mm wide, dorsally pale yellow, tube 5–6 mm long; anther tube blackish, fertile part 2.8–3.6 mm long, apical appendages rounded, c. 0.2 mm long, basal appendages c. 0.3 mm long; *style* and *style arms* blackish. Pollen of *Cichorium* type (sensu Blackmore 1986) with very extensive, approximately hexagonal polar areas, each with >20 spines, and with moderately narrow interlacunar gaps (Fig. 8E, F). *Achenes* 7–9 mm long, corpus



Fig. 7. *Sinoseris muliensis* – A: habit; B: flowering capitula; C: stem leaf; D: mature achene. – Photographs from Sichuan, near Xiamaidi Village by Chen Yaping on 11 Oct 2018 (A–C) and by Wang Zehuan on 13 Nov 2018 (D); population voucher: *Chen Yaping, Jiang Lei & Zheng Hailei EM652* (KUN).

subconic, with 5 main ribs (best discernible near base) alternating with 3(or 4) secondary ribs (fully developed in middle third and then similar in shape to main ribs), dark brown, with linear, flattened, acute, antrorse papillae, shorter and appressed in proximal two thirds of corpus, longer and spreading-erect in distal third; apex of corpus attenuate into a slender, whitish beak of 1–2 mm (Fig. 8A–D). *Pappus* 6–7 mm long, dirty white, caducous, bristles of similar length and diameter, near base of 8–12 rows of cells in cross-section. – Fig. 7; Fig. 8.

*Distribution* — China: E Yunnan and SW Sichuan.

*Habitat and ecology* — *Sinoseris muliensis* grows on rocky stream banks and slopes with open, bushy vegetation at altitudes between c. 2200 and 3250 m. Fl. and fr. Sep–Nov.

*Threat status* — *Sinoseris muliensis* is known from two historical and four current localities. At the three popula-

tions in Muli County, only 10, 80 and 250 individuals were counted, respectively, so that the population sizes seem in general smaller than those of the other two species. *Sinoseris muliensis* occurs scattered in its distribution, similar to *S. scandens*, which may be due to its requirement of open, rocky habitats. Nearly a third of the few-flowered capitula of many individuals was found infected in 2018 by an insect and therefore without fruits. *Sinoseris muliensis* is certainly rare and of localized distribution. Its status should therefore be of concern and addressed by further investigations. The threat evaluation by Chen & al. (2019, under *Nabalus muliensis*) as Endangered, although based on an even more limited knowledge of the species, is likely justified, not the least in view of putative introgression with *S. scandens*, which is likely the result of secondary contact between the formerly isolated species resulting from human activities.

*Remarks* — Attention should be paid to introgression with *Sinoseris scandens*, the occurrence of which can be



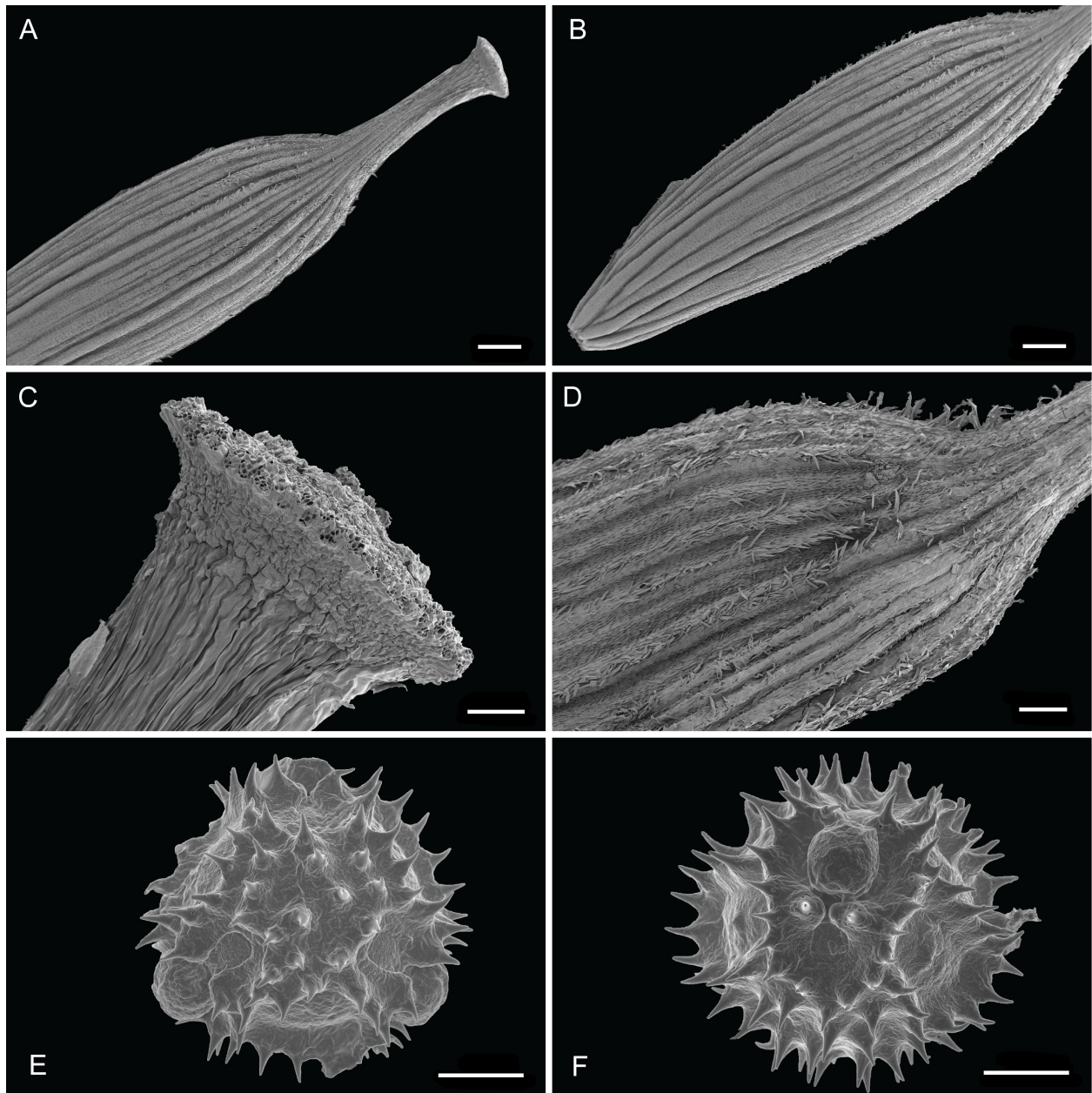


Fig. 8. *Sinoseris muliensis* – A–D: achene; A: apical portion; B: basal portion; C: pappus disk with detached pappus bristles showing cross-section of bristles; D: apex of corpus with parts of papillae longer and spreading. – E, F: pollen; E: polar view; F: subequatorial view. – Scale bars: A, B = 500  $\mu\text{m}$ ; C = 100  $\mu\text{m}$ ; D = 200  $\mu\text{m}$ ; E, F = 10  $\mu\text{m}$ . – From Wang Zehuan & Li Huimin WZH20181001 (KUN).

concluded from gatherings reported by Chen & al. (2019) from Yanyuan County (Yanjin, Gongmushan Village, Bailingshan mountain, [27.36°N, 101.56°E], stony grassy or thicket slopes, 3188 m, *Y. S. Chen & L. S. Xu 160231*, IBSC, PE). Hybrids can be recognized by variable and intermediate numbers of inner phyllaries and florets.

*Specimens seen* — CHINA: SICHUAN: inter oppidum Yenyüen et castellum Kwapi [between the town Yanyuan and the fortress Kwapi, = Yanyuan Xian, Guabie; Wodi-xiang on some Chinese maps, pers. comm. David Boufford], c. 27.45°N [actually 27.91°N, 101.57°], ad viam vico Tangetu oppositam [at the road opposite

the village Tangetu, place not traced], substr. arenaeo, 3250 m, 4 Oct 1914, *H. Handel-Mazzetti 5476* [Diar. Nr. 923] (GH, W 1940-349); Yi Autonomous Prefecture of Liangshan, Muli Tibetan Autonomous County, Xiamaidi Village, from Mianbu pass to Muli County, 27.730082°N, 101.236879°E, elev. 3021 m, 11 Oct 2018, *Chen Yaping, Jiang Lei & Zheng Hailei EM652* (KUN); Yi Autonomous Prefecture of Liangshan, Muli Tibetan Autonomous County, Xiamaidi Village, from Mianbu pass to Muli County, 27.730014°N, 101.236871°E, elev. 3022 m, 19 Oct 2018, *Wang Zehuan & Li Huimin WZH20181001* (B, KUN, PE); Yi Autonomous Prefecture of Liangshan, Muli Tibetan

Autonomous County, Sanjiaoya Town, on way from Biji to Guoquanyan, 28.107632°N, 101.467566°E, elev. 2275 m, 13 Oct 2018, *Chen Yaping, Jiang Lei & Zheng Hailei EM672* (KUN). — YUNNAN: Lou-Pou, prefecture de Tong Tchouan [= Dongchuan, city, 26.082872°N, 103.18783°E], 19 Oct 1906, *F. Ducloux 4477* (P3732867, P03732866 [label text: “Yunnan, Lou Pou à deux journées de Tong Tchouan, plante cueillie par Joseph Tschang, 19 Oct 1906, *F. Ducloux 4477*”]).

**3. *Sinoseris changii* Ze H. Wang, N. Kilian & H. Peng, sp. nov.**

Holotype: China, Yunnan, Chuxiong Autonomous Prefecture, Dayao County, Tanhua Village, mountain behind Tanhua Temple, 25.950745°N, 101.232407°E, elev. 2719 m, 12 Oct 2017, *Wang Zehuan & Chen Yaping WZH20171001* (KUN!; isotypes: B!, KUN!, PE!).

*Description* — Annual (or monocarpic biennial) herbs with taproot, 20–100 cm tall, strongly covered with stiff, eglandular, pale to dark reddish-purplish hairs. Stem solitary or, if branched right from base, plants seemingly with several stems, erect, branching, leafy. Basal, lower and middle cauline leaves abruptly contracted into a petiole-like portion up to 17 cm long with 0–3 pair(s) of lobes, otherwise unwinged, and with base semi-amplexicaul to at most weakly clasping; lamina rhombic, ovate, triangular or lanceolate in outline, 3–11 cm long, 3–8 cm wide, entire to lyrate-pinnate with 1 or 2(or 3) pair(s) of smaller, acute or obtuse lateral lobes and a large terminal lobe, fresh green on upper surface, paler, greyish green on lower surface; margin irregularly sinuate-dentate and denticulate; apex ± acute, base distinctly cordate. Upper cauline leaves similar to middle ones but smaller, or ± oblanceolate and entire or lyrate-pinnatifid lamina attenuate



Fig. 9. *Sinoseris changii* – A: habit; B, C: flowering capitula; D, E: leaf indumentum; F: achene. – Photographs by Chen Yaping (A) and Wang Zehuan (B–F) from Yunnan, near Tanhua Temple on 12 Oct 2017; population voucher: *Wang Zehuan & Chen Yaping WZH20171001* (KUN).

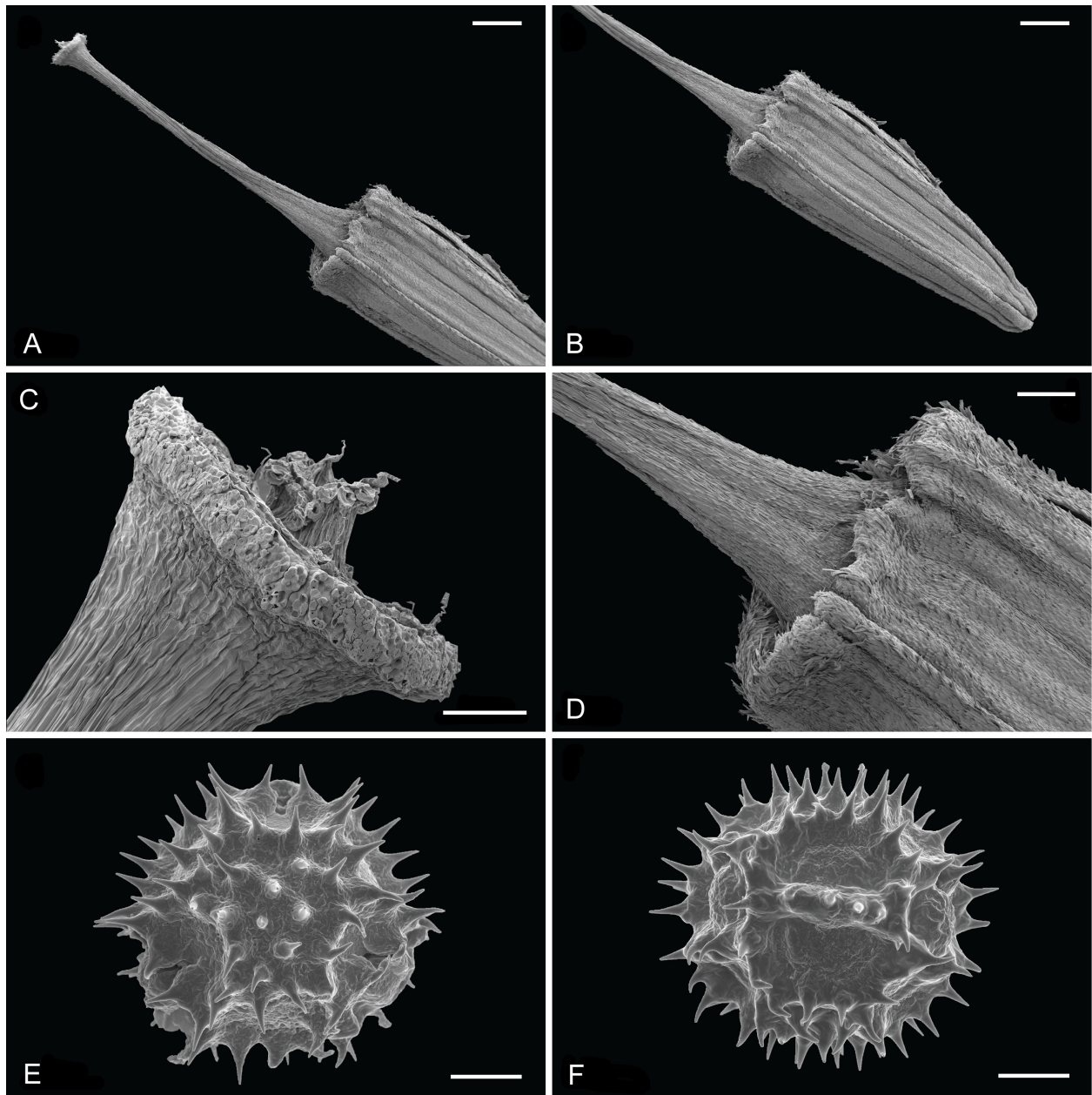


Fig. 10. *Sinoseris changii* – A–D: achene; A: apical portion; B: basal portion; C: pappus disk with detached pappus bristles showing cross-section of bristles; D: apex of corpus with parts of papillae longer and spreading. – E, F: pollen; E: polar view; F: parapolar view. – Scale bars: A, B = 500  $\mu\text{m}$ ; C = 100  $\mu\text{m}$ ; D = 200  $\mu\text{m}$ ; E, F = 10  $\mu\text{m}$ . – From Wang Zehuan & Chen Yaping WZH20171001 (KUN).

into a petiole-like portion much shorter than lamina, or  $\pm$  lanceolate and sessile with base semi-amplexicaul to weakly clasping. *Synflorescence* of a flowering stem paniculiform to corymbiform of some to many capitula erect in bud, spreading-erect to subpendent at anthesis and pendent at fruiting; in well-developed plants with several paracladia from axils of cauline leaves. *Capitula* with 8–12 florets; peduncles mostly longer than involucre. *Involucre* narrowly cylindrical, 9–14 mm long; strongly differentiated into inner and  $\pm$  inconspicuous outer phyllary series; phyllaries abaxially pale to reddish hirsute as remainder of plant; outer phyllaries 2–5, narrowly linear, 0.7–1.9  $\times$  c. 0.3 mm; inner phyllaries usually 8,

linear-lanceolate and similar in length, green, sometimes (partly) with a purplish tinge. *Receptacle* epaleate, glabrous, smooth. *Florets* with yellow corolla; ligule broadly elliptic to obovate,  $\pm$  horizontally spread, 10–12 mm long, to 3 mm wide, dorsally pale yellow, tube 5–6 mm long; anther tube golden yellow to brownish, fertile part 2.6–2.8 mm long, apical appendages rounded, c. 0.3 mm long, basal appendages c. 0.5 mm long; *style* and style arms pale greyish to blackish. *Pollen* of *Cichorium* type (sensu Blackmore 1986) with very extensive, approximately hexagonal polar areas, each with >20 spines, and with moderately narrow interlacunar gaps (Fig. 10E, F). *Achenes* 6–7 mm long, corpus subconic, with 5 main

ribs (best discernible near base) alternating with 3 (or 4) secondary ribs (fully developed in middle third and then similar in shape to main ribs), dark brown, with linear, flattened, antrorse papillae, spreading-erect at apex and appressed and shorter in rest, at widest diameter abruptly contracted into a slender, pale brown, basally appressed papillate beak of about same length as corpus, corpus below beak broad-shouldered (Fig. 10A–D). *Pappus* 5–6 mm long, dirty white to pale brownish, caducous, bristles of similar length and diameter, near base of 7–12 rows of cells in cross-section. – Fig. 9; Fig. 10.

*Distribution* — China: C Yunnan.

*Habitat and ecology* — The species is confined to open, rocky habitats at altitudes between c. 1900 and 2750 m. Fl. and fr. Sep–Oct.

*Threat status* — The occurrence of *Sinoseris changii* is less scattered and rare compared to the other two species. Between Tanhua and Wanbi, for example, the species is present with high frequency on sunny, rocky slopes, although the individual populations usually do not exceed a few hundred mature individuals. Considering its localized distribution in C Yunnan, its status should nevertheless be of concern and addressed by further investigations.

*Etymology* — We dedicate this species to the memory of Chao Chien Chang (1900–1972), one of the early modern Chinese botanists. He worked at the Kunming Institute of Botany of the Chinese Academy of Sciences, and studied Chinese *Asteraceae*, in particular of Yunnan.

*Additional specimens seen* — CHINA: YUNNAN: Chuxiong Autonomous Prefecture, Dayao County, Wanbi Village, Gao-ping-zi, 26.224444°N, 101.308611°E, elev. 2229 m, 15 Oct 2015, *Exped. Dayao team ly334* (KUN); Chuxiong Autonomous Prefecture, Dayao County, Tanhua Temple to Guihua Village, 26.042925°N, 101.273300°E, elev. 2103 m, 12 Oct 2017, *Wang Zehuan & Chen Yaping WZH20171003* (KUN); Chuxiong Autonomous Prefecture, Dayao County, Tanhua Temple to Guihua Village, 26.074892°N, 101.284225°E, elev. 1945 m, 12 Oct 2017, *Wang Zehuan & Chen Yaping WZH20171004* (KUN); Chuxiong Autonomous Prefecture, Dayao County, Guihua Village, 26.082596°N, 101.284981°E, elev. 2719 m, 13 Oct 2017, *Wang Zehuan & Chen Yaping WZH20171011* (KUN); Chuxiong Autonomous Prefecture, Yongren County, Yongxing Village, 26.344374°N, 101.614891°E, elev. 2123 m, 13 Oct 2017, *Wang Zehuan & Chen Yaping WZH20171018* (KUN).

## Acknowledgements

The authors are grateful to the staff of the herbaria GH, P, PE and W for the loan of material and to the staff of

the herbaria LBG and P for their courtesy in providing photographs of, and data on, type specimens. The use of high-performance computing resources at the Scientific Computing Service of the Freie Universität Berlin is gratefully acknowledged. The first author also thanks the staff of KUN and the Institute of Cultivation and Processing of Chinese Medicinal Materials for research facilities. This study was supported by the National Natural Science Foundation of China (grant no. 31500168). We thank Gabi Dröge, BGBM, for performing the sequence submission to ENA. Special thanks are due to David Boufford (Harvard University Herbaria) and three anonymous reviewers for valuable comments on earlier versions of this paper, and to Nick Turland for his excellent thorough editing.

## References

- Blackmore S. 1986: The identification and taxonomic significance of lophate pollen in the *Compositae*. – *Canad. J. Bot.* **64**: 3101–3112.
- Bremer K. 1994: *Asteraceae*: cladistics and classification. – Portland: Timber Press.
- Chang C. C. 1934: Contributio ad cognitionem generis *Lactucae* sinicae. – *Contrib. Biol. Lab. Sci. Soc. China* **9**: 127–133.
- Chen Y.-S., Xu L.-S. & Ke R. 2019: *Nabalus muliensis* (*Asteraceae*, *Cichorieae*), a new species from China. – *Phytotaxa* **416**: 257–262.
- CGIAR-CSI [Consortium of Spatial Information] 2019: NASA Shuttle Radar Topographic Mission (SRTM) 90 m digital elevation data (DEMs). – Available from <http://srtm.csi.cgiar.org/>
- Darriba D., Posada D., Kozlov A. M., Stamatakis A., Morel B. & Flouri T. 2019: ModelTest-NG: a new and scalable tool for the selection of DNA and protein evolutionary models. – *Molec. Biol. Evol.* **37**: 291–294.
- Franchet M. A. 1895: Plantes nouvelles de la Chine occidentale. – *J. Bot. (Morot)* **9**: 258–259.
- Gruenstaeudl M. 2019: annonex2embl: automatic preparation of annotated DNA sequences for bulk submissions to ENA. – bioRxiv 820480 [preprint; doi <https://doi.org/10.1101/820480>].
- Hijmans R. 2012: DIVA-GIS, ver. 7.5. – Available from <http://diva-gis.org/>
- Huelsenbeck J. P., Larget B. & Alfaro M. E. 2004: Bayesian phylogenetic model selection using reversible jump Markov chain Monte Carlo. – *Molec. Biol. Evol.* **21**: 1123–1133.
- IUCN 2012: IUCN Red List categories and criteria. Version 3.1, ed. 2. – Gland & Cambridge: IUCN.
- Katoh K., Rozewicki J. & Yamada K. D. 2017: MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. – *Briefings Bioinformatics* **20**: 1160–1166.

- Kilian N., Gemeinholzer B. & Lack H. W. 2009a: Tribe *Cichorieae*. – Pp. 343–383 in: Funk V. A., Susanna A., Stuessy T. F., Bayer R. J. (ed.), *Systematics, evolution, and biogeography of the Compositae*. – Vienna: IAPT.
- Kilian N., Hand R. & Raab-Straube E. von (general ed.) 2009b+: *Cichorieae* Systematics Portal. – Published at <http://cichorieae.e-taxonomy.net/portal/>
- Kilian N., Sennikov A., Wang Z.-H., Gemeinholzer B. & Zhang J.-W. 2017: Sub-Paratethyan origin and Middle to Late Miocene principal diversification of the *Lactucinae* (*Cichorieae*, *Compositae*) inferred from molecular phylogenetics, divergence-dating and biogeographic analysis. – *Taxon* **66**: 675–703.
- Kilpatrick K. 2014: *Fathers of botany: the discovery of Chinese plants by European missionaries*. – Chicago: University of Chicago Press.
- Kozlov A. M., Darriba D., Flouri T., Morel B. & Stamatakis A. 2019: RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. – *Bioinformatics* **35**: 4453–4455.
- Liu Y., Chen Y.-S. & Yang Q.-E. 2013: Generic status, circumscription, and allopolyploid origin of *Faberia* (*Asteraceae*: *Cichorieae*) as revealed by ITS and chloroplast DNA sequence data. – *Taxon* **62**: 1235–1247.
- Müller K. 2004: PRAP—computation of Bremer support for large data sets. – *Molec. Phylogen. Evol.* **31**: 780–782.
- Müller K. 2005: SeqState: primer design and sequence statistics for phylogenetic DNA datasets. – *Appl. Bioinformatics* **4**: 65–69.
- Müller K., Müller J. & Quandt D. 2010: PhyDE: Phylogenetic Data Editor, version 0.9971. – Available from <http://www.phyde.de/index.html>
- Ronquist F., Teslenko M., Van der Mark P., Ayres D. L., Darling A., Höhne S., Larget B., Liu L., Suchard M. A. & Huelsenbeck J. P. 2012: MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. – *Syst. Biol.* **61**: 539–542.
- Shih C. 1997: *Compositae* (10), *Cichorioideae*, *Lactuceae*. – In: Ling Y. & Shih C. (ed.), *Flora Reipublicae Popularis Sinicae* **80(1)**. – Beijing: Science Press.
- Shih C. & Kilian N. 2011: *Cichorieae* [excl. *Tragopogon*, *Taraxacum*, *Hieracium* and *Pilosella*]. – Pp. 195–207, 211–270, 325–350 in: Wu Z.-Y., Raven P. H. & Hong D.-Y. (ed.), *Flora of China* **20–21**. – Beijing: Science Press & St Louis: Missouri Botanical Garden Press.
- Simmons M. P. & Ochoterena H. 2000: Gaps as characters in sequence-based phylogenetic analyses. – *Syst. Biol.* **49**: 369–381.
- Stöver B. C. & Müller K. 2010: TreeGraph 2: combining and visualizing evidence from different phylogenetic analyses. – *BMC Bioinformatics* **11**: 7.
- Swofford D. L. 2003: PAUP\*: Phylogenetic Analysis Using Parsimony (\*and other methods), version 4.0b 10. – Sunderland: Sinauer Associates Inc. Publishers.
- Wang H., Wortley A. H. & Blackmore S. 2009: Pollen morphology of *Crepidinae* and *Lactucinae* (*Asteraceae*: *Cichorieae*) and its systematic significance. – *Grana* **48**: 160–178.
- Wang Z.-H., Peng H. & Kilian N. 2013: Molecular phylogeny of the *Lactuca* alliance (*Cichorieae* subtribe *Lactucinae*, *Asteraceae*) with focus on their Chinese centre of diversity detects potential events of reticulation and chloroplast capture. – *PLoS ONE* **8**: e82692.
- Zhang J.-W., Nie Z.-N., Wen J. & Sun H. 2011: Molecular phylogeny and biogeography of three closely related genera, *Sinoseris*, *Stebbinsia*, and *Syncalathium* (*Asteraceae*, *Cichorieae*), endemic to the Tibetan Plateau, SW China. – *Taxon* **60**: 15–26.

## Willdenowia

Open-access online edition [bioone.org/journals/willdenowia](http://bioone.org/journals/willdenowia)



Online ISSN 1868-6397 · Print ISSN 0511-9618 · 2018 Journal Impact Factor 1.156

Published by the Botanic Garden and Botanical Museum Berlin, Freie Universität Berlin

© 2020 The Authors · This open-access article is distributed under the CC BY 4.0 licence