

Research paper

Crepis desertorum (Asteraceae, Cichorieae), a new species from northern Xinjiang (China) based on morphological and molecular dataJuan Qiu^a, Jianwen Zhang^b, Tiangang Gao^c, Dunyan Tan^{a, d, *}^a Xinjiang Key Laboratory of Grassland Resources and Ecology and Ministry of Education Key Laboratory for Western Arid Region Grassland Resources and Ecology, College of Grassland and Environment Sciences, Xinjiang Agricultural University, Urumqi 830052, China^b CAS Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China^c State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, Beijing 100093, China^d College of Biology and Environmental Sciences, Jishou University, Jishou 416000, China

ARTICLE INFO

Article history:

Received 15 June 2019

Received in revised form

12 November 2019

Accepted 15 November 2019

Available online 12 December 2019

Editor: Zelong Nie

Keywords:

Karyotype

Micro-morphology

Pericarp

Pollen

Taxonomy

ABSTRACT

Crepis desertorum from the Junggar Basin of northern Xinjiang, northwestern China, is described as a new species. Molecular studies indicate that the species is closely related to *Crepis frigida*. Morphological studies indicate that it is similar to *Crepis sancta* subsp. *bifida* but differs from the latter taxon in having glandular hairs on the stem, a flat receptacle and dimorphic achenes. Chromosome features and pollen and achene ultrastructure also are described for the new species.

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1. Introduction

Crepis L. is a large taxonomically controversial genus in tribe Cichorieae of Asteraceae containing over 200 species that are mainly distributed throughout the Northern Hemisphere and Africa (Enke and Gemeinholzer, 2008; Shi et al., 2011). The genus presumably originated in the Altai/Tien Shan region in Central Asia (Babcock, 1947). The present center of diversity of *Crepis* is the circum-Mediterranean area (Enke and Gemeinholzer, 2008). Babcock, 1947 divided *Crepis* into 27 sections worldwide and included *Lagoseris* as a section of the genus *Crepis* (e.g., Lack, 2007; Enke, 2010). However, recent molecular studies based on nuclear ITS and plastid *matK* sequences indicated that sect. *Lagoseris* may be a distinct genus (Enke and Gemeinholzer, 2008; Enke, 2010; Kilian et al., 2009). ITS and *matK* phylogenetic trees of the *Lagoseris* clade include *Crepis* species from sections *Lagoseris*, *Pterotheca*, *Microcephalum*, *Intybellia*, as well as the genera *Rhagadiolus* and *Lapsana* (Enke and Gemeinholzer, 2008; Enke, 2010).

During fieldwork (2012–2013) in a sand desert area of the Junggar Basin of northern Xinjiang in northwestern China, we discovered an ephemeral species of Asteraceae that could not be identified. Its annual habit and the receptacle with only a few setiform paleae indicated that the plant clearly was a member of *Crepis* sect. *Pterotheca* (Babcock, 1947a, 1947b) or *Lagoseris* subg. *Pterotheca* (Czerepanov, 1964). Detailed examination of these plants and a survey of the literature, including *Flora of the U.S.S.R.* (Czerepanov, 1964), *Flora of China* (Shi et al., 2011), *Flora Xinjiangensis* (An, 1999) and Babcock's monographs of *Crepis* (Babcock, 1947a, 1947b), showed that this unknown plant was similar to *Crepis sancta* subsp. *bifida* (Vis.) Thell. ex Babc. but distinguished from it by glandular hairs on the stem, bract shape, style color and shape of the dimorphic achenes. Morphological comparisons and nuclear ITS and plastid *matK* sequences indicated that this plant represented an undescribed species of *Crepis*, which we named *Crepis desertorum*.

2. Material and methods

2.1. Morphological description

The morphological description is based on live material. Details of bracts, flowers and achenes were examined under a Nikon

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Peer review under responsibility of Editorial Office of Plant Diversity.

SMZ1000 stereoscopic microscope (Nikon Corp., Tokyo, Japan) and measured with a digital caliper. Distribution, habitats and phenology of the new species are based on field observations. Live material was collected from Mosuowan, Shihezi city of Xinjiang, China (44°25.42'N, 86°01.21'E).

2.2. SEM observations on pollen and achene morphology

Mature pollen grains and achenes were mounted directly on aluminum stubs with double-coated conductive glue, coated with gold-palladium and examined under a Zeiss SUPRA 55VP (Carl Zeiss, Oberkochen, Germany) scanning electron microscope (SEM). Terminology for the description of pollen follows Skvarla and Turner (1966) and Ma et al. (2009). Vouchers for the pollen and achene material studied are provided in Table 1. All voucher specimens have been deposited in the Herbarium of Xinjiang Agricultural University (XJA) (see Table 1).

2.3. Karyotype analysis

Mature achenes were collected from a natural population (Mosuowan, Shihezi city of Xinjiang, China) in June 2013. They were incubated on wet filter paper in Petri dishes at 20/10 °C (12/12 h) and a 12 h daily light period for 4–5 days, during which time germination occurred. Root-tips were removed from roots 1–1.5 cm in length and pretreated with 0.002 M 8-hydroxyquinoline at room temperature (c. 20 °C) for 3 h and then fixed in ethanol: glacial acetic acid (3:1v/v) for 24 h. Subsequently, fixed root-tips were hydrolyzed in 1 M HCl for 20 min at 60 °C, stained with carbol fuchsin and then squashed in a drop of 45% acetic acid and mounted for cytological observations. Photomicrographs were taken under a Zeiss Axioskop 40 microscope (Carl Zeiss, Oberkochen, Germany) using a 100 × oil lens. Karyotypic analysis of chromosomes at mitotic-metaphase was determined from five well-spread metaphases. The symbols used to describe the karyotypes followed Levan et al. (1964) and Li and Chen (1985). The asymmetry classification of the karyotype follows Stebbins (1971) and Li and Chen (1985).

2.4. Molecular analysis

We sampled 17 populations representing 14 species of *Crepis* s.l., including the presumed new species, for molecular analyses. *Askellia flexuosa* was chosen for the outgroup based on Enke and Gemeinholzer (2008), Zhang et al. (2011), and our data. Sequences for other related taxa were obtained from GenBank (see Appendix S1). A list of samples, voucher information and GenBank accession numbers are provided in Appendix S1.

DNA was extracted from leaves dried over silica-gel using the CTAB method (Doyle and Doyle, 1987). DNA sequences of the chloroplast *matK* region and of nuclear ribosome internal

transcribed spacers (ITS) were amplified based on a PCR procedure of initial denaturation at 94 °C for 2 min, followed by 40 cycles of 40 s at 94 °C, 1 min 30 s at 50 °C and 2 min at 72 °C, with a final extension at 72 °C for 15 min. Amplification products were purified on 1.5% low-melting agarose gels, and the desired DNA was recovered with a UNIQ-10 kit (Shanghai SBS, Biotech Ltd., China), following directions provided by the manufacturer. Sequencing reactions were conducted with the forward or reverse primers of the amplification reactions, using the DYE-namic ET Terminator Kit (Amersham Pharmacia Biotech, Shanghai, China), with an ABI PRISM 3730 automatic DNA sequencer from Shanghai Sangon Biological Engineering Technology & Services Co., Ltd. (Shanghai, China). The PCR primers for the nuclear internal transcribed spacers (ITS) were ITS4 and ITS5 (White et al., 1990), and the chloroplast *matK* sequences were amplified in two overlapping parts using the primers trnK-710f (Johnson and Soltis, 1995) and *matK*-iR (Fehrer et al., 2007) for *matK* 1, *matK*-ifN and *matK*-rN (Enke and Gemeinholzer, 2008) for *matK* 2.

The program Sequencher 4.1 (Gene Codes Corp., Ann Arbor, Michigan, USA) was used to evaluate chromatograms for base confirmation and to edit contiguous sequences. After editing, all sequences were aligned in MAFFT v7.311 (Katoh et al., 2002; Katoh and Standley, 2013) and manually adjusted with MEGA 7.0.14 (Kumar et al., 2016). Phylogenetic analyses were conducted based on Bayesian inference (BI) in MrBayes v3.2.6 (Ronquist et al., 2012), Maximum Likelihood in RAxML 8.2.10 (Stamatakis, 2014) on CIPRES (Miller et al., 2010) and Maximum Parsimony (MP) in PAUP version 4.0b10 (Swofford, 2002).

For Bayesian inference (BI) analysis, jModeltest v2.1.7 (Darriba et al., 2012) was used to select the best-fit model of nucleotide substitution based on the Akaike information criterion (AIC). The SYM + I + G model was selected for the nrITS dataset and the GTR + I model for the cpDNA dataset. Four simultaneous Monte Carlo Markov chains (MCMCs) were run for five million generations for both nrITS, *matK* and combined sequences, and one tree was sampled every 1000 generations. The first 1250 trees (25% of total trees) were discarded as burn-in. The remaining trees were summarized in a 50% majority-rule consensus tree, and the Bayesian posterior probabilities (BP) were calculated.

For the maximum likelihood bootstrap (ML) analyses, we constructed the phylogeny using GTRCAT as the nucleotide substitution model and performed 1000 replicates for the bootstrap analyses.

For the maximum parsimony bootstrap (MP) analyses, 100 replicates of random stepwise addition with tree bisection-reconnection (TBR) branch swapping were performed using heuristic searches, with all most-parsimonious trees saved at each replicate (MulTree on). Support for each branch was assessed using bootstrap analyses with 100 bootstrap replicates, each with 10 stepwise additions.

Table 1

Voucher material for the *Crepis desertorum* J. Qiu & D.Y. Tan pollen, achene morphology and karyotype analysis.

	Location	Coordinate	Altitude	Date	Voucher
Pollen material	China, Xinjiang, Shihezi City Mosuowan District, 147 Regiment 22 Company	44°25.42'N, 86°01.21'E	300 m	6 May, 2013	J. Qiu 2013-0171 (XJA)
	China, Xinjiang, Jimsar County, Wucaiwan District, China national highway 216 514 km	44°23.71'N, 88° 47.21'E	530 m	27 Apr, 2013	J. Qiu 2013-0129 (XJA)
Achene material	China, Xinjiang, Shihezi City Mosuowan District, 147 Regiment 22 Company	44°25.42'N, 86°01.21'E	300 m	15 May, 2013	J. Qiu 2013-0195 (XJA)
	China, Xinjiang, Jimsar County, Wucaiwan District, China national highway 216 514 km	44°23.71'N, 88°47.21'E	530 m	12 May, 2013	D.Y. Tan 274 (XJA)

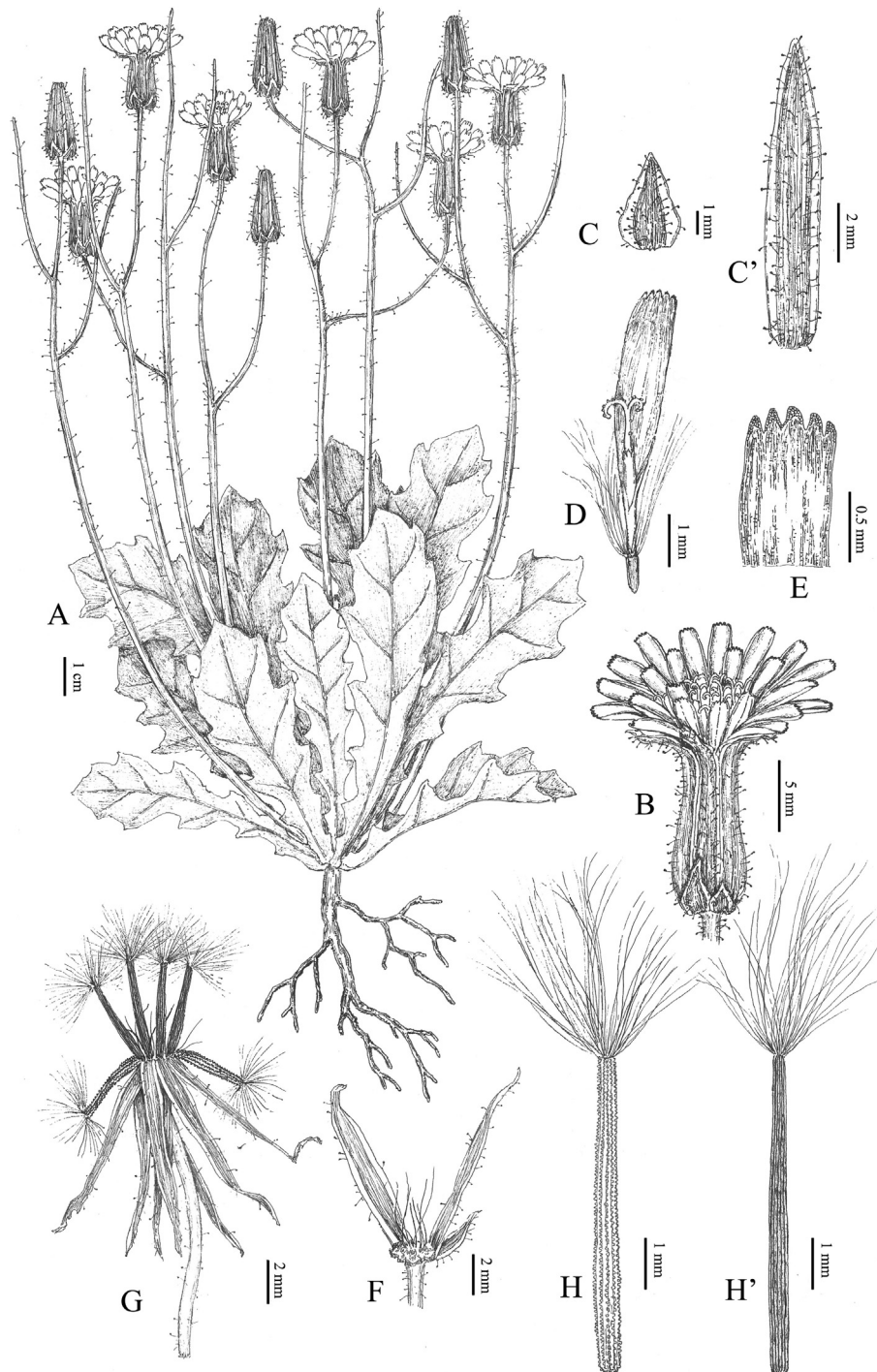


Fig. 1. Illustrations of *Crepis desertorum* J. Qiu & D.Y. Tan *sp.nov.* Drawn by C.D. Cui. (A) individual; (B) capitulum; (C) outer bract; (C') inner bract; (D) floret; (E) ligule teeth; (F) receptacle; (G) infructescence; (H) peripheral achene; (H') central achene.

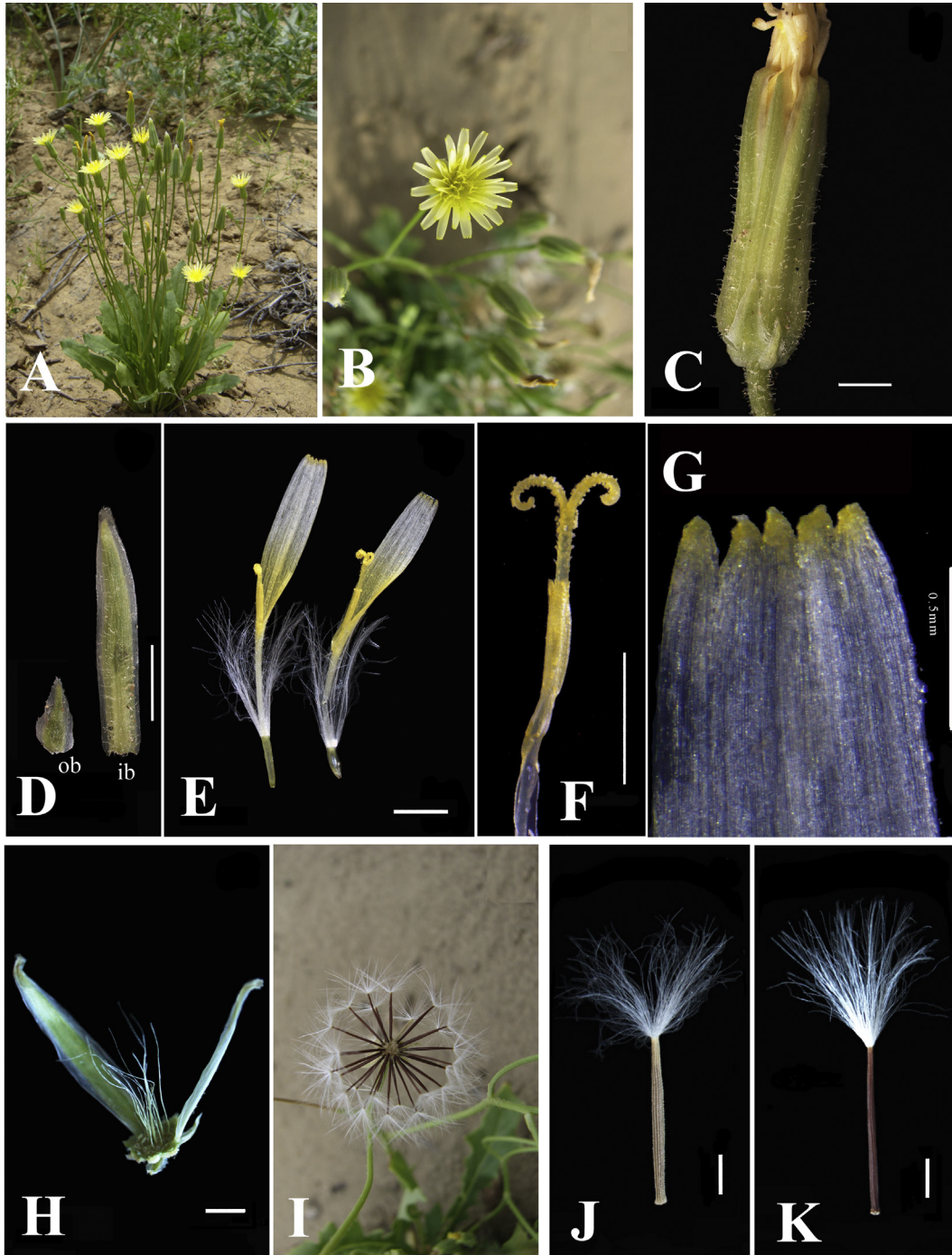


Fig. 2. Photographs of *Crepis desertorum* J. Qiu & D.Y. Tan. (A) individual; (B) capitulum; (C) involucre; (D) bracts (ob = outer bracts, ib = inner bracts); (E) ligulate florets; (F) style branches; (G) details of ligule teeth; (H) receptacle; (I) infructescence; (J) peripheral achene; (K) central achene. Scale bar: 1 mm.

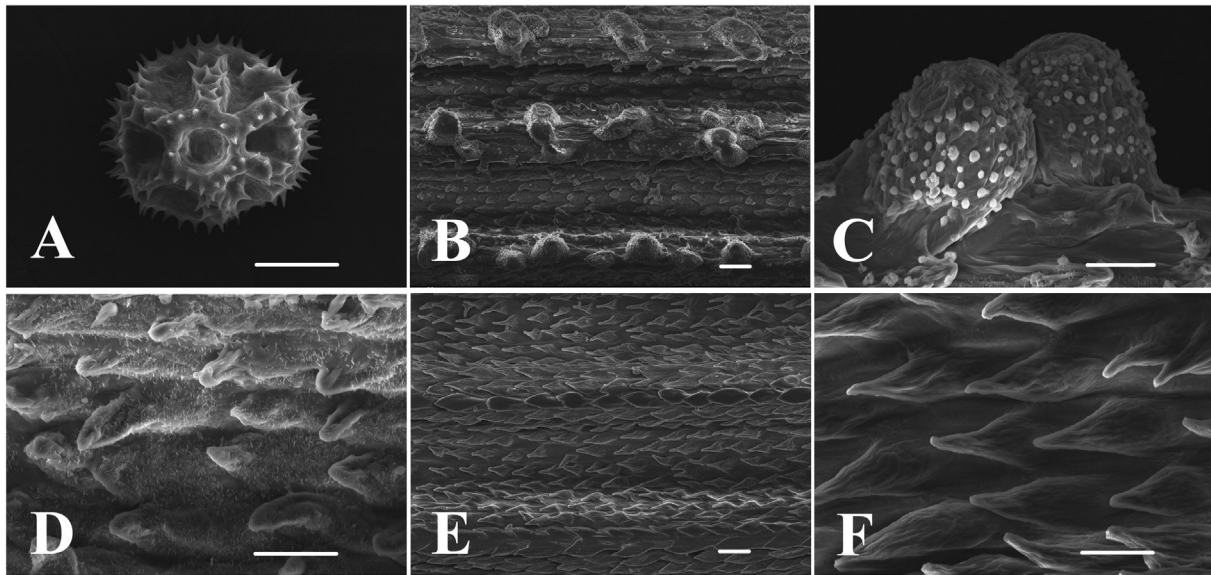


Fig. 3. SEM images of pollen and achenes of *Crepis desertorum* J. Qiu & D.Y. Tan. (A) pollen grain (polar view); (B–D) Peripheral achene (B) rough longitudinal ribs; (C) papilliform cells covered with white granules; (D) scaly cells covered with short tomentum; (E–F) Central achene (E) thin longitudinal ribs; (F) glabrous scaly cell. Scale bar: 10 μ m in A, C, D and F, 20 μ m in B and E.

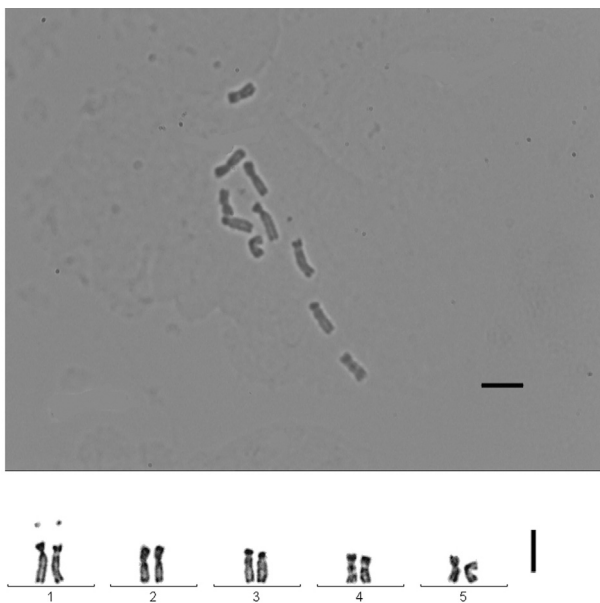


Fig. 4. Metaphase chromosomes and karyotype of *Crepis desertorum* J. Qiu & D.Y. Tan. Scale bar: 5 μ m.

3. Results

3.1. Taxonomic treatment

***Crepis desertorum* J. Qiu & D.Y. Tan, sp. nov** (Figs. 1 and 2).

Type: CHINA. Xinjiang, Mosuowan District, Shihezi city, sand dune, 44°25.42'N, 86°01.21'E, alt. 300 m, 30 Apr. 2013, J. Qiu & D. Y. Tan 2013-0146 (holotype: XJA, isotypes: KUN and PE).

3.2. Diagnosis

C. desertorum is similar to *C. sancta* subsp. *bifida*, but it is easily distinguished from the latter species by habitat, stem with glandular hairs, style color, receptacle and dimorphic achenes.

3.3. Description

Annual. Roots slender, hard. Stem erect or ascending, 7–25 cm high, cylindrical with glandular hairs, finely ribbed. Basal leaves numerous and forming a rosette, leaf blade linear-lanceolate, lanceolate or oblanceolate, 4–10 cm long (including petiole) and 0.7–1.4 cm wide, glabrous, base attenuate to petioles, apex obtuse to acute, margin irregularly sinuate-dentate or pinnatifid, spiny hairy marginally; cauline leaves arising from the branches, linear, ca. 0.3–0.4 mm long. Capitula many in corymbs. Involucre narrowly cylindrical to narrowly campanulate, 7–11 mm long and 2–4 mm wide. Involucral bracts with glandular hairs; outer bracts 4–5, triangular, longest 1/3–1/4 as long as inner ones, margin white scarios, apex acute; inner bracts 8–12, lanceolate, 10–12 mm long, ca. 2 mm wide, margin white scarios, apex acute. Receptacle covered with erect setaceous hairs, 3–7 mm long. Florets ligulate, 12–30, corolla 6–9 mm long, tube white, ca. 3 mm long, ligule yellow in lower part and yellowish-white in upper part, apex 5-dentate with teeth ca. 0.01 mm long; anther ca. 2 (–2.5) mm long; style branches yellowish, 0.5 mm long. Infructescences numerous. Achenes dimorphic; peripheral achenes 2–15, whitish-yellowish, terete, linear, 4.2–6.1 mm long and 0.2–0.5 mm wide, with 10 ribs covered with papilliform protuberances; central achenes 7–30, reddish-brown, terete, linear, 4.2–5.6 mm long and 0.2–0.4 mm wide, with 10 smooth ribs. Pappus many fine white bristles, 3–6 mm long. Fl. and fr. Apr.–Jun.

Distribution and habitat – *C. desertorum* is widely distributed in the Junggar Basin. It grows in stationary sand dunes at altitudes of 300–530 m (Fig. 5). Associated species include *Haloxylon ammodendron* (C.A.Mey.) Bunge, *Calligonum leucocladum* (Schrenk) Bge., *Eremurus anisopterus* (Kar. et Kir.) Regel, *E. inderiensis* (M. Bieb.) Regel, *Soranthus meyeri* Ledeb., *Astragalus flexus* Fisch. and some annual desert ephemerals.

Etymology – The specific epithet is derived from the desert habitat, from which the type of this species was collected.

Chinese name – Huang Mo Huan Yang Shen (荒漠还阳参).

Morphological evidence – By comparing the morphological characteristics of *C. desertorum* with those of its related species (Table 3), we found that *C. desertorum* is similar to the species *C. sancta* (with three subspecies) and more specifically to *C. sancta* subsp. *bifida*.

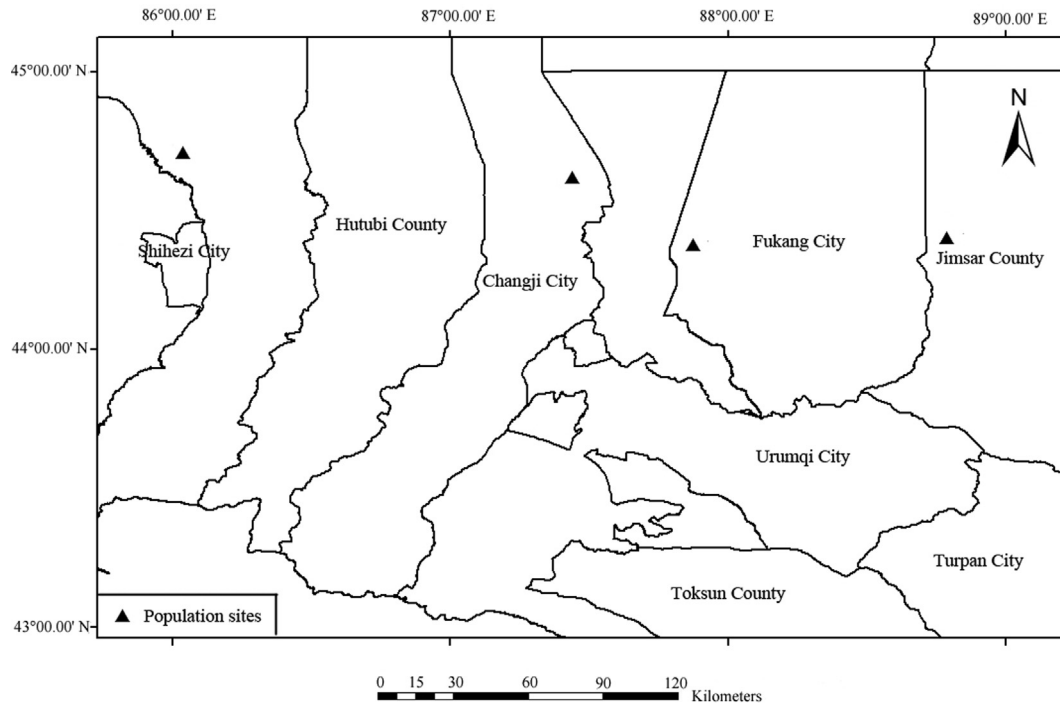


Fig. 5. Distribution of *Crepis desertorum* J. Qiu & D.Y. Tan in the Junggar Basin of Xinjiang, China. Mapped by H. F. Zhang.

However, it differs from *C. sancta* in having glandular hairs on the stem (Fig. 1A) (vs. yellow setiform hairs, subglabrous or glandular on the stem of *C. sancta*), a flat receptacle with some erect setaceous hairs in the center of the receptacle (Figs. 1F and 2H) (vs. flat receptacle with scales in *C. sancta*), style usually yellow (vs. green in *C. sancta* subsp. *bifida*) and dimorphic achenes (vs. trimorphic achenes in *C. sancta* and *C. sancta* subsp. *bifida*). The related species *C. frigida* is a perennial with monomorphic achenes (Table 3), whereas *C. desertorum* is an annual herb usually with dimorphic achene (Figs. 1H, H' and 2J, K).

Pollen evidence – *C. desertorum* pollen is echinoloplate and belongs to the *Cichorium intybus* type. It is isopolar, radially symmetrical, tricolporate and spheroidal. Grain size ranges from 28.21 to 35.48 μm (Fig. 3A). The endexine (a distinct exine layer between ectexine and intine) is thick, and the columellae are very thin and short.

Achene morphology – Peripheral and central achenes of *C. desertorum* differ in pericarp micro-morphology. Rough longitudinal ribs (Fig. 3B) on the surface of peripheral achenes are composed of papilliform cells covered with white granules (Fig. 3C). Epidermal cells between the longitudinal ribs are scaly and covered with short tomentum (Fig. 3D). However, thin

longitudinal ribs (Fig. 3E) on the surface of central achenes are composed of glabrous scaly cells (Fig. 3F), and the epidermal cells between the longitudinal ribs also are scaly and glabrous.

Karyotype evidence – The chromosome number of *C. desertorum* is $2n = 2x = 10$ (Fig. 4). The karyotype includes 5 pairs of chromosomes (Table 2): pair 1 subtelocentric (st), pairs 2–3 submetacentric (sm), and pairs 4–5 metacentric (m). The first pair has a satellite. The karyotype formula is $2n = 10 = 4m + 4sm + 2nd$ (2SAT). Karyotype asymmetry is of the 3A type.

Phylogenetic evidence – The Bayesian tree with MP, ML and BP support values for each clade is shown in Fig. 6. The sampled species of *Crepis* s.l. form a monophyletic group with strong support of BP = 1.00, when the genera *Lapsana* and *Rhagadiolus*, which are deeply nested within the clade of *Crepis* s.l., are included. The clade of *Lapsana* and *Rhagadiolus* is sister to the *Lagoseris* clade, which includes the new species *C. desertorum* and some species of the *C.* sect. *Lagoseris* (*C. frigida*, *C. sancta*, *C. purpurea*, *C. sahendi*, *C. multicaulis*, *C. elongata*). Within the clade, *C. desertorum* is sister to *C. frigida* but with moderate support of BP = 0.78.

Paratypes – CHINA. Xinjiang: Mosuowan District, Shihezi City, alt. 300 m, 12 June, 2012, D. Y. Tan 2012-0102 (XJA); same locality, 6 May, 2013, J. Qiu 2013-0171 (XJA); Wujiaqu City, alt. 490 m, 12 May, 2013, J. Qiu 2013-0190 (XJA); Wutonggou, Fukang City, alt. 446 m, 27 Apr., 2013, J. Qiu 2013-0142 (XJA); same locality, 14 May, 2013, J. Qiu 2013-0182 (XJA); Wucuiwan District, Jimsar County, alt. 530 m, 27 Apr., 2013, J. Qiu 2013-0093, 2013-0129 (XJA).

Table 2

Morphometrics of karyotype of *Crepis desertorum* J. Qiu & D.Y. Tan ($2n = 2x = 10$). Relative length (chromosome length/total length of chromosome set) $\times 100$, long arm length (L), short arm length (S), total length of chromosome set (TLC), centromeric index [CI = $100 \times (S/TCL)$] and arm ratio (AR = L/S).

Chromosome pair	Relative length			Centromeric index (CI)	Arm ratio (AR)	Chromosome types
	L	S	TLC			
1*	3.86	1.21	5.06	22.86	3.20	st
2	3.44	1.61	5.04	31.96	2.14	sm
3	3.39	1.21	4.60	25.92	2.81	sm
4	2.36	1.57	3.94	39.94	1.50	m
5	2.26	1.37	3.63	38.01	1.65	m

Note: *Chromosomes with satellites. st (subtelocentric), sm (submetacentric) and m (metacentric).

4. Discussion

The genus *Crepis* comprises about 18 species (five endemic in China, nine of which are distributed in Xinjiang (Shi et al., 2011)). The *Lagoseris* species previously reported as occurring in Xinjiang is *L. sancta* (L.) K. Maly (Hou, 1982). *L. sancta* also is recorded in *Flora Xinjiangensis* (An, 1999). However, neither Hou (1982) nor An (1999) described the distribution or habitat of

Table 3
Morphological comparison of *Crepis desertorum*, *C. frigida*, *C. sancta*, and *C. sancta* subsp. *bifida*.

Characters	<i>Crepis desertorum</i>	<i>Crepis frigida</i> ^{a,b}	<i>Crepis sancta</i> ^a	<i>Crepis sancta</i> subsp. <i>bifida</i> ^c
Life form	annual	perennial	annual	annual
Stem indumentum	glandular hairs	mostly scapellike, tomentose and pubescent	yellow setiform hairs, subglabrous or glandular	—
Outer bracts	triangular, longest 1/3–1/4 as long as inner ones, c. 0.3–0.4 mm long, margin white scarious, apex acute	narrowly ovate, acute	linear to ovate, 2.0–3.0 mm long, c. 1.5 mm wide, subglabrous or thinly glandular, margin white scarious	deltoid to subovate, acute, 1/8–1/3 as long as the inner bracts
Receptacle	flat, covered with erect setaceous hairs	flat, with scales	flat, with scales	—
Style color	yellow	yellow	greenish or yellow	green
Achene type	dimorphic	monomorphic	dimorphic or sometimes trimorphic	dimorphic or sometimes trimorphic
Peripheral achenes, shape	whitish-yellowish, terete, linear, 4.2–6.1 mm long and 0.2–0.5 mm wide, with 10 ribs covered with dense papilliform protuberances	light brown, cylindrical, c. 5.0 mm long, straight or curved, with 15 smooth ribs, slightly attenuate; epidermal cells obscure in outline with acute end wall, outer cell wall ornamentation smooth	white, cylindrical, 3.0–5.0 mm long, 0.6–1.5 mm wide, sulcate or smooth dorsally and mostly winged, stramineous (sometimes absent)	white, corticeous, strongly obcompressed, linear-lanceolate, dorsally smooth, the lateral alae narrow, thin and indurate (sometimes absent)
Intermediate achenes, shape	—	—	terete, slender, coarsely or finely spiculate	terete, slender, coarsely or finely spiculate
Central achenes, shape	reddish-brown, linear, 4.2–5.6 mm long and 0.2–0.4 mm wide, with 10 smooth ribs; the epidermal cells obscure in outline with acute end wall	—	brown or greenish, narrowly fusiform, 3.0–4.0 mm long, c. 0.4 mm wide, sometimes scabridulous	terete, slender, smooth

Note: —, Not described.

^a <http://cichorieae.e-taxonomy.net/portal/node/8>.

^b Kalmuk et al., 2018.

^c Babcock, 1947.

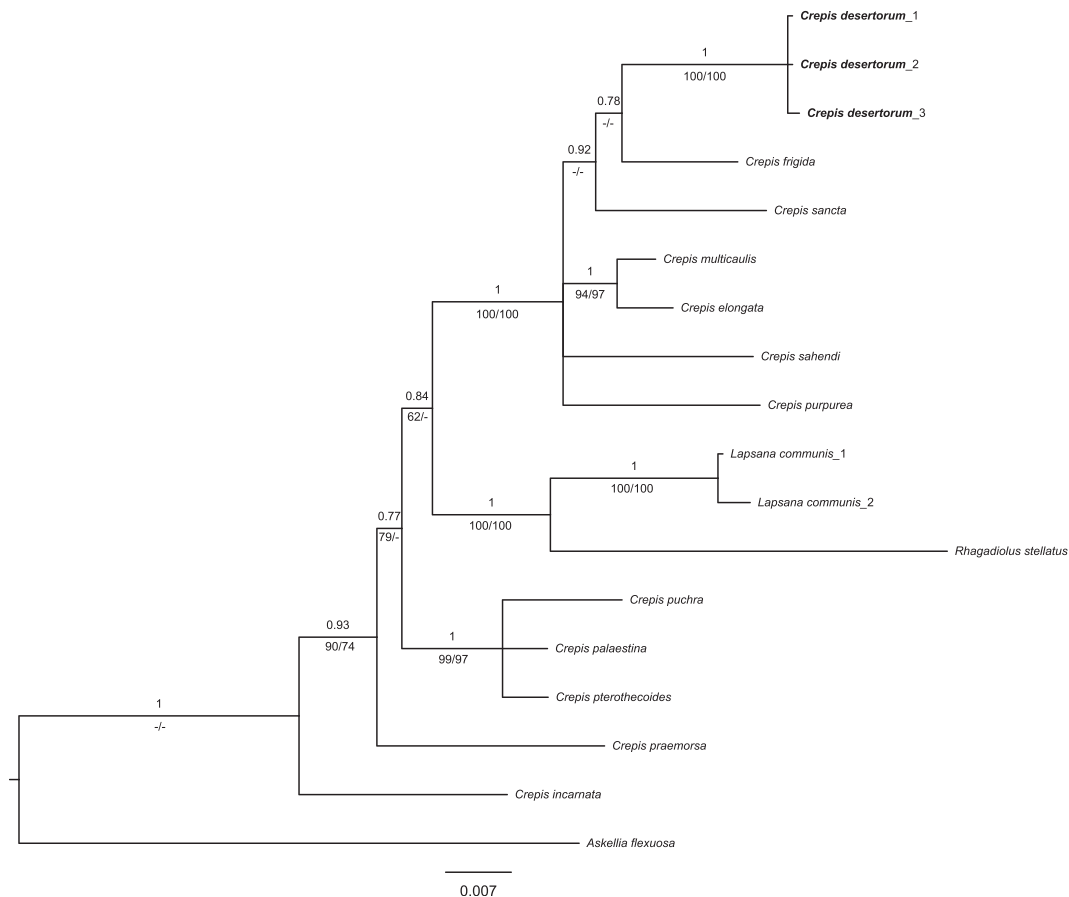


Fig. 6. Bayesian consensus tree of *Crepis desertorum* (bold) and related species of *Crepis*. Numbers above branches indicate Bayesian posterior probability (BP), numbers below branches are maximum likelihood bootstrap (ML) and maximum parsimony bootstrap (MP).

L. sancta in Xinjiang. Moreover, we did not find any voucher specimen in the herbaria of the Xinjiang Institution of Ecology and Geography, Chinese Academy of Sciences (XJBI), Shihezi University (SHI) or Xinjiang Agricultural University (XJA). In addition, no relevant records of specimens were found in the Chinese virtual herbarium (<http://www.cvh.ac.cn/>) or in the Specimen resources sharing platform for education of China (<http://mnh.scu.edu.cn/main.aspx>).

The pollen of *C. desertorum* and *C. sancta* belongs to the *Cichorium intybus* type, but the pollen of *C. desertorum* belongs to the *C. intybus* subgroup, while that of *C. sancta* belongs to the *Taraxacum officinalis* subgroup (Enke, 2010). However, *C. desertorum* has a chromosome number of $x = 5$, which differs from that of *C. frigida* ($x = 4$) (Enke and Gemeinholzer, 2008).

Molecular studies based on nuclear ITS and plastid *matK* sequences indicated that *C. desertorum* is more closely related to *C. frigida* than to *C. sancta* subsp. *bifida* (Fig. 6) but with low support (PP = 0.78). Although the micromorphology of the central achenes of *C. desertorum* is similar to that of *C. frigida* (Kalmuk et al., 2018), the two species differ greatly in life form, stem indumentum and outer bracts (Table 3). Babcock, 1947a, 1947b even treated *L. sancta* as a synonym of *C. sancta* subsp. *bifida*. *C. desertorum* is known only from the Junggar Basin in northern Xinjiang, China; *C. sancta* is distributed in Europe, the Caucasus region, Balkans-Asia Minor, Palestine, Afghanistan and the Indo-Himalayas, whereas *C. sancta* subsp. *bifida* is distributed in Afghanistan, Turkestan and N.W. Himalayas (Babcock, 1947; Czerepanov, 1964). Thus, the geographical distribution of *C. desertorum* is disjunct from that of *C. sancta* and *C. sancta* subsp. *bifida*. *C. desertorum* has some unique morphological characters, and it differs from *C. sancta* subsp. *bifida* in having glandular hairs on the stem, yellowish style branches, peripheral whitish-yellowish linear achenes with 10 ribs covered with papilliform protuberances and white pappus (Table 3).

Africa is a major distribution area of the genus *Crepis* with more than 40 species, and the achenes of some African species are dimorphic, such as *C. aspera*, *C. amplexifolia*, *C. pulchra*, and others (<http://cichorieae.e-taxonomy.net/portal/node/8>). There are significant differences in the achene shape and number of the ribs, surface structure and the pappus between *C. desertorum* and these African species with dimorphic achenes (Enke, 2010; Kalmuk et al., 2018; <http://cichorieae.e-taxonomy.net/portal/node/8>).

Declaration of Competing Interest

The author declares no conflict of interest.

Acknowledgements

We thank Drs. Carol C. Baskin and Jerry M. Baskin (University of Kentucky, Lexington, Kentucky, USA) for correcting the English, and we are grateful to Dr. H. L. Chen for molecular lab work and analysis. This study was supported by the National Natural Science Foundation of China (No. U1603231, No. 31650067 and No. 31570213) and Program for Tianshan Innovative Research Team of Xinjiang Uygur Autonomous Region, China (2018D14010).

Appendix S1

Taxon name, voucher information (for the first published sequences in part I and the downloaded sequences from GenBank that was placed in part II) and GenBank accession numbers for ITS and *matK* sequences used in this study.

Part I:

Taxa	Voucher	ITS	<i>matK</i>
<i>Crepis desertorum</i> J. Qiu & D.Y. Tan_1	LW-079 (XJA), Wucaiwan,	MN750316	MN764299
<i>Crepis desertorum</i> J. Qiu & D.Y. Tan_2	Xinjiang, China	MN750317	MN764300
<i>Crepis desertorum</i> J. Qiu & D.Y. Tan_3		MN750318	MN764301
<i>Crepis elongata</i> Babcock	SunH2522 (KUN), Demula, Tibet, China	MN750319–	MN764302

Part II:

Taxa	ITS	<i>matK</i>
<i>Askellia flexuosa</i> (Ledebour) W. A. Weber	EU363596	EU363544
<i>Crepis frigida</i> (Boiss. & Balansa) Babcock	EU363612	EU363555
<i>Crepis rubra</i> L. (= <i>C. incarnata</i> Vis.)	EU363608	EU363551
<i>Crepis multicaulis</i> Ledeb.	EU363642	EU363573
<i>Crepis palaestina</i> (Boiss.) Bornm.	EU363639	–
<i>Crepis praemorsa</i> (L.) Walther	EU363654	EU363578
<i>Crepis pteothecoides</i> Boiss.	–	EU363570
<i>Crepis pulchra</i> L.	AJ633369	AJ633144
<i>Crepis purpurea</i> (Willd.) M. Bieb.	EU363653	–
<i>Crepis sahendi</i> Boiss. & Buhse	EU363651	–
<i>Crepis sancta</i> (L.) Bornm.	AJ633372	AJ633150
<i>Lapsana communis</i> L._1	AJ633285	AJ633137
<i>Lapsana communis</i> L._2	AJ633286	AJ633138
<i>Rhagadiolus stellatus</i> (L.) Gaertn.	DQ451823	AJ633224

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