

# Taxonomy in the Kunming Institute of Botany (KIB): Progress during the past decade (2008–2018) and perspectives on future development

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## ABSTRACT

The development of new taxonomical theories and approaches, particularly molecular phylogenetics, has led to the expansion of traditional morphology-based taxonomy into the concept of “integrative taxonomy.” Taxonomic knowledge has assumed greater significance in recent years, particularly because of growing concerns over the looming biodiversity crisis. Since its establishment in 1938, the Kunming Institute of Botany (KIB), which is located in Yunnan province in Southwest China, has focused attention on the taxonomy and conservation of the flora of China. For the forthcoming 80th anniversary of KIB, we review the achievements of researchers at KIB and their associates with respect to the taxonomy of land plants, fungi, and lichen. Major taxonomic advances are summarized for families of Calymperaceae, Cryphaeaceae, Lembophyllaceae, Neckeraceae, Polytrichaceae and Pottiaceae of mosses, Pteridaceae and Polypodiaceae of ferns, Taxaceae and Cycadaceae of gymnosperms, Asteraceae, Begoniaceae, Ericaceae, Euphorbiaceae, Gesneriaceae, Lamiaceae, Orchidaceae, Orobanchaceae, Poaceae, Theaceae and Urticaceae of angiosperms, Agaricaceae, Amanitaceae, Boletaceae, Cantharellaceae, Physalacriaceae Russulaceae, Suillaceae and Tuberaceae of fungi, and Ophioparmaceae and Parmeliaceae of lichens. Regarding the future development of taxonomy at KIB, we recommend that taxonomists continue to explore the biodiversity of China, integrate new theories and technologies with traditional taxonomic approaches, and engage in creative monographic work, with support from institutions, funding agencies, and the public.

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## 1. Introduction

Taxonomy is the scientific discipline that encompasses the description, identification, nomenclature, and classification of organisms. It is both fundamental and crucial for biological study because the correct circumscription and naming of organisms is necessary prior to any further research (Peng et al., 2013). This is because the named taxa that taxonomists produce provide the mechanism for assembling and disseminating information about the biota. These names in fact provide the stable foundation upon which all biological sciences rely. Over the past decades, following the development of molecular technologies and the introduction of phylogenetic theory, taxonomy has undergone a revolutionary

change. In the e-flora era, classical taxonomy, which discriminates taxa primarily on morphology, has gradually developed into “integrative taxonomy” (Dayrat, 2005). This integrative approach incorporates evidence from multiple disciplines (e.g., molecular phylogenetics, biogeography, comparative anatomy, and ecology) to solve taxonomic problems (Padial et al., 2010; Schlick-Steiner et al., 2010; Valdecasas et al., 2008; Will et al., 2005). The utilization of new data and evidence, especially those from DNA, has enabled taxonomy to be more central to biology as a whole than ever before (Stuessy, 2009).

China is home to 30,000 of the approximately 350,000–400,000 species of vascular plants of the world (Wu et al., 1994–2013) and serves as the floristic museum and/or evolutionary cradle for various species (Lu et al., 2018). To explore, understand, and protect plant diversity in China, especially southwest China, taxonomy has long been one of the important research fields at the Kunming Institute of Botany (KIB). Professor Zhengyi Wu (Cheng-Yih Wu), an eminent botanist from KIB, devoted almost his entire life to the development of taxonomy and floristics in China (Peng et al., 2013).

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He was appointed as the fourth Editor-in-Chief of the Editorial Committee of *Flora Reipublicae Popularis Sincae* (FRPS) in 1987. Together with Prof. Peter H. Raven from the Missouri Botanic Gardens, Wu co-chaired the Committee that guided the compilation of all 25 volumes of *Flora of China*, the last of which was completed in 2014 (Zhou and Sun, 2016). Meanwhile, in 2012 researchers from KIB proposed and launched a next generation Flora project called iFlora. This initiative incorporates information from eFlora databases with technologically advanced data, especially those derived from next generation sequencing (NGS) techniques, DNA sequence methodologies, geographical information systems, and computer information technology. iFlora aims to deliver accurate and rapid species identifications and easy access to relevant, contemporary species-related digital information (Li et al., 2012). Additionally, sixty years after the publication of the first edition of *A Dictionary of the Families and Genera of Chinese Seed Plants* (Hou, 1958), a new edition of this work, *A Dictionary of the Families and Genera of Chinese Vascular Plants*, which integrates evidence from molecular phylogenetic studies, was recently published (Li, 2018).

In the review that follows, we summarize the progress achieved by KIB researchers with respect to the integrative taxonomy of land plants (i.e., ferns and seed plants), fungi, bryophytes, and lichens during the past ten years (Fig. 1). Some of the work was done in collaboration with researchers from other institutions. This review is done in connection with the celebration of the 80th anniversary of the establishment of KIB, which occurs this year.

## 2. Progress of taxonomy at KIB

### 2.1. Ferns

Ferns, with ca. 215 genera and 10,560 species, are vascular plants that produce spores and undergo an alternation of generations (i.e., with separate gametophyte and sporophyte generations existing as free-living plants) (Christenhusz and Byng, 2016; Christenhusz and Chase, 2014). Lu et al. (2015) explored the phylogenetic utility of the chloroplast genome in resolving difficult deep nodes in ferns. The results of this study supported the sister relationships between *Equisetum* L. and the Psilotales-Ophioglossales clade, between the Equisetales-Psilotaless-Ophioglossales clade and the clade of the leptosporangiate and marattioid ferns, as well as between the tree fern clade and polypods. In a study of the fern genus *Adiantum* L. (Pteridaceae) from China and neighboring areas, Wang et al. (2016) screened and evaluated five plastid regions (*rbcl*, *matK*, *trnH-psbA*, *trnL-F* and *rps4-trnS*) and eight nuclear regions (ITS, ITS2, *pgiC*, *gapC*, *LEAFY*, *IBR3\_2*, *DET1* and *SQD1\_1*). Their results showed that the two-barcode combination of *rbcl* + *trnH-psbA* appear to be the best choice for barcoding *Adiantum*, and perhaps for basal polypod ferns in general. A phylogenetic study of the fern subfamily Pteridoideae (Pteridaceae) by Zhang et al. (2017a) showed that three species traditionally placed in *Anogramma* Link. were more closely related to *Cerosora* Domin and *Pityrogramma* Lin than to other *Anogramma*. Consequently, a new genus, *Gastoniella* Li Bing Zhang & Liang Zhang, was established to accommodate the new systematic position of these species. Based on plastid phylogeny and other non-molecular evidence of the Old World fern genus *Pyrrosia* Mirb. (Polypodiaceae), the new genus *Hovenkampia* Li Bing Zhang & X. M. Zhou (Polypodiaceae) was established to accommodate the *Pyrrosia africana* Ballard group of three African species. This new genus was named in honor of Prof. Peter Hovenkamp, a specialist of *Pyrrosia*, based at the Naturalis Biodiversity Center, Leiden, Netherlands (Zhou et al., 2017c).

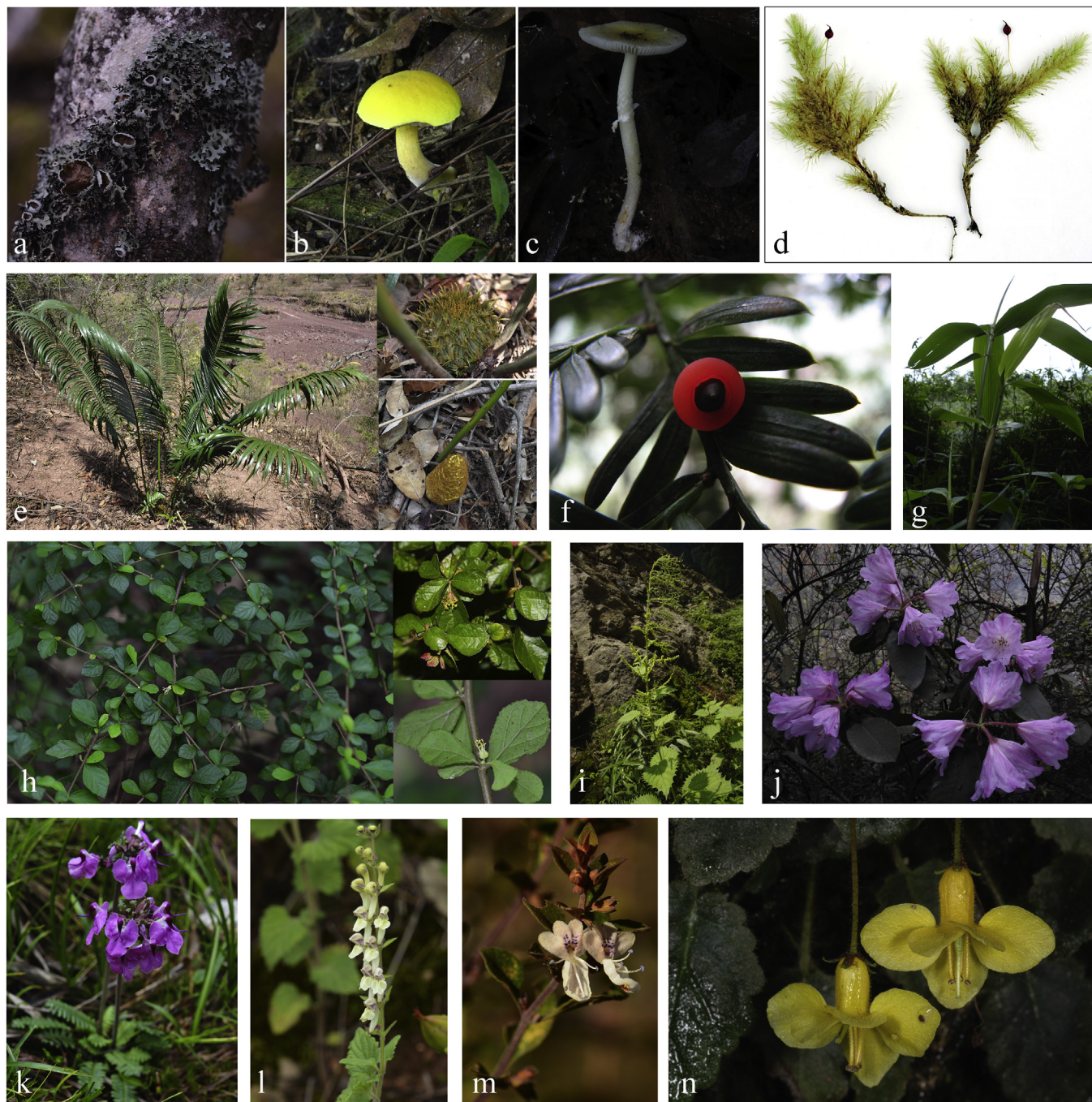
### 2.2. Seed plants

Gymnosperms, with ca. 1079 species in 83 genera, are seed plants with an ovule that is not enclosed in a carpel (Christenhusz and Byng, 2016; Christenhusz et al., 2011). The focal groups of gymnosperms studied at KIB are *Amentotaxus* Pilg., *Taxus* L. (Taxaceae) and *Cycas* L. (Cycadaceae). Based on both morphological and molecular sequence data, Shah et al. (2008) showed that the *Taxus* species from the Western Himalaya, including Pakistan, is *Taxus fuana* N. Li & R.R. Mill., not *Taxus wallichiana* Zucc. or *Taxus baccata* L. as previously thought. The distinct species status of the above three taxa was well supported and found to be correlated with their geographic distributions. Liu et al. (2011) used a DNA barcoding approach to successfully discriminate the four Eurasian species of *Taxus*: *Taxus baccata*, *Taxus cuspidata* Siebold & Zucc., *Taxus fuana* and *Taxus sumatrana* (Miq.) de Laub. They also identified seven lineages within the *T. wallichiana* group, some of them showing discrete geographical distributions and distinct morphologies, and potentially represent new species. Poudel et al. (2012) conducted a study of *Taxus* in the Hindu Kush-Himalaya and adjacent regions based on 743 samples from 46 populations. This work used morphological, molecular, and climatic data to confirm the existence of three distinct species within the area, namely, *Taxus contorta* Griff., *T. wallichiana* and *Taxus mairei* (Lemée & H. Lév.) S.Y. Hu. In a separate study of the *T. wallichiana* complex involving 1240 samples from 79 populations, Möller et al. (2013) combined 27 morphological characters with sequences of the chloroplast *trnL-F* intron/spacer region to define a number of taxonomically discrete units and delineate the geographic distribution of five species, including one new to science, namely, *Taxus calcicola* L.M. Gao & Mich. Möller. Finally, Gao et al. (2016) examined five DNA barcodes (*rbcl*, *matK*, *trnH-psbA*, *trnL-F* and nrITS) to evaluate their discrimination ability and to investigate the taxonomy of *Amentotaxus*. This study indicated that recent collections from Yunnan province (China), Lao Cai province (Vietnam), and Laos may represent a new species.

Cycads are the oldest and most primitive assemblages of living seed plants in the world. They have survived through periods of dramatic tectonic activity, climate fluctuation and environmental variations, making this plant group of great significance for research (Zheng et al., 2017). *Cycas chenii* X. Gong & W. Zhou was described and illustrated to honor Professor Jiarui Chen (Chia-Jui Chen), a botanist from the Institute of Botany, Chinese Academy of Sciences, for his significant work on the genus *Cycas* in China (Zhou et al., 2015). Research by Feng et al. (2016) involving species of the *Cycas segmentifida* D.Y. Wang & C.Y. Deng complex significantly altered our understanding of this group. Using cpDNA, nuclear gene *GTP*, and microsatellites, these authors rejected previous hypotheses that this complex comprised eight taxa. Instead, just two previously described species were recognized, namely, *Cycas guizhouensis* K. M. Lan & R. F. Zou and *C. segmentifida* D. Y. Wang & C. Y. Deng. *Cycas longlinensis* H. T. Chang & Y. C. Zhong was included within *C. guizhouensis* and the other five taxa were included within *C. segmentifida*.

Angiosperms (flowering plants), regarded as one of the most diverse and species-rich groups on Earth, include ca. 13,164 genera and 295,383 species (Christenhusz and Byng, 2016). Orchidaceae and Poaceae (Monocots), Begoniaceae, Euphorbiaceae and Urticaceae (Rosids), Asteraceae, Ericaceae, Gesneriaceae, Lamiaceae, Orobanchaceae and Theaceae (Asterids) are the main focal plant groups for taxonomists at KIB.

Orchidaceae is the largest vascular plant family, with ca. 736 genera and at least 28,000 species (Christenhusz and Byng, 2016). At KIB, several research groups have been working on this group.



**Fig. 1.** Selected new species published by researchers at KIB in the last decade. (a) *Anzia rhabdorhiza* Li S. Wang & M. M. Liang (b) *Zangia citrina* Yan C. Li & Zhu L. Yang (c) *Amanita melleialba* Zhu L. Yang, Q. Cai & Y. Y. Cui (d) *Taiwanobryum undulatifolium* (Tixier) W. Z. Ma, Enroth & Shevock (e) *Cycas chenii* X. Gong & W. Zhou (f) *Taxus calcicola* L. M. Gao & Mich. Möller (g) *Pseudosasa xishuangbannaensis* D. Z. Li, Y. X. Zhang & Triplett (h) *Tsaiodendron dioicum* Y. H. Tan, Z. Zhou & B. J. Gu (i) *Zhengyia shennongensis* T. Deng, D. G. Zhang & H. Sun (j) *Rhododendron bailiense* Y. P. Ma, C. Q. Zhang and D. F. Chamb (k) *Pedicularis wanhongiae* M. L. Liu & W. B. Yu (l) *Scutellaria wuana* C. L. Xiang & F. Zhao (m) *Isodon aurantiacus* Y. P. Chen & C. L. Xiang (n) *Oreocharis ninglangensis* W. H. Chen & Y. M. Shui.

Chen and Shui (2010) described a new species, *Anoectochilus malipoensis* W. H. Chen & Y. M. Shui, from Yunnan, China, they also provided an updated key to the fourteen species of *Anoectochilus* Blume from China and Vietnam. *Calanthe yaoshanensis* Z. X. Ren & H. Wang from northeastern Yunnan, China was described and illustrated as a new species; its habitat was investigated and its conservation status was assessed as ‘Critically Endangered’ (CR) (Ren et al., 2011). Tang et al. (2015b) provided a new framework for the complex phylogenetic relationships between East Asiatic

*Amitostigma* Schltr. and other genera traditionally included in its alliance. They also proposed a new classification of the genera and species in the East Asia Clade.

Poaceae is the fifth largest vascular family, with ca. 780 genera and at least 12,000 species (Christenhusz and Byng, 2016), and it includes the nearly ubiquitous group of monocots known as grasses. This family consists of 12 subfamilies (Stevens, 2001 onwards), and researchers at KIB have focused mainly on subfamilies Panicoideae and Bambusoideae. Within Panicoideae, Liu

and Peng (2010) established a new subgenus, *Miscanthus* subgen. *Rubimons* (B. S. Sun) Y. C. Liu & H. Peng and described a new species within it, *Miscanthus villosus* Y. C. Liu & H. Peng, from southwest Yunnan, China. These authors also described another new species, *Microstegium butuoense* Y. C. Liu & H. Peng from Sichuan, China (Liu and Peng, 2011).

For Bambusoideae, KIB researchers have focused on the tribes Arundinarieae and Bambuseae. The temperate woody bamboos (tribe Arundinarieae) comprise ca. 31 genera and 546 species (Bamboo Phylogeny Group, 2012; Clark et al., 2015) that are primarily distributed in the North Temperate Zone or at high elevations in the Old World tropics. Previous studies based mainly on plastid DNA fragments recognized 12 lineages for this tribe (Attigala et al., 2014; Yang et al., 2013a; Zeng et al., 2010; Zhang et al., 2016). However, conflicts between plastid and nuclear phylogenies have demonstrated that hybridization (introgression) and/or incomplete lineage sorting might occur in these temperate woody bamboos (Wang et al., 2017b; Zhang et al., 2012b), leading to a complicated evolutionary pattern for this lineage. In Zhang et al. (2013), *Pseudosasa xishuangbannaensis* D. Z. Li, Y. X. Zhang & Triplett was described and illustrated as a new species, the specific epithet referring to its distribution in the Xishuangbanna area of southern Yunnan, China. This species is characterized by glabrous culm leaf sheaths with dense setae at the base, several to many spikelets, and 5–7 glumes, and it can be distinguished from closely related species by these morphological features and molecular evidence. Zhang et al. (2017c) conducted herbarium and field studies, and molecular phylogenetic analyses to determine phylogenetic relationships for the six temperate woody bamboos from Madagascar. This work confirmed that the Malagasy temperate woody bamboos should be treated as members of the genus *Oldenania* Stapleton, and a new species, *Oldenania itremoensis* D. Z. Li, Y. X. Zhang & T. Haevermans, was described and illustrated.

Based on a phylogenetic reconstruction of *Bambusa* Schreb. and its allies, Yang et al. (2010) suggested that several species were misplaced and needed reassignment. Specifically, their research showed that i) the transfer of *Dendrocalamus rongchengensis* T.P. Yi & C.Y. Sia to *Bambusa* was supported; ii) the transfer of *Dendrocalamus membranaceus* Munro into *Bambusa* was not supported, noting that this species was better placed within *Dendrocalamus* Nees; iii) the placement of *Dendrocalamopsis stenoaurita* (W.T. Lin) Keng f. ex W.T. Lin in the *Dendrocalamus* complex rather than within *Bambusa* subg. *Dendrocalamopsis* L. C. Chia & H. L. Fung was supported. In addition, the authors also confirmed the position of *Bambusa*, *Dendrocalamus*, *Gigantochloa* Kurz ex Munro, *Melocalamus* Benth., *Neosinocalamus* Keng f., *Oxytenanthera* Munro and *Thyrostachys* Gamble as a closely related group of Bambusinae. Zhou et al. (2017a) used morphology and molecular phylogeny to describe and illustrate a new species of *Holttumochloa* K. M. Wong from the lowland montane forests of Diaolu Mountain on the Island of Hainan, South China, namely, *Holttumochloa hainanensis* M. Y. Zhou & D. Z. Li. The discovery of this new species greatly expanded the distribution area of *Holttumochloa* which had previously been known only from Malaysia. This study therefore demonstrated an affinity between the flora of Hainan and Malaysia. Zhou et al. (2017b) also conducted a near-complete, generic-level phylogeny of the paleotropical woody bamboos (PWB, 85% genera) based on 18 plastid DNA fragments. This study recovered phylogenetic relationships that were mostly supported by morphological and geographical evidence. Additionally, *Neohouzeaua cordata* T. H. Wen & Dai was transferred to *Melocalamus*, as *Melocalamus cordatus* (T.H. Wen & Dai) D. Z. Li & M. Y. Zhou.

Begoniaceae includes two genera and 1825 species (Christenhusz and Byng, 2016). Species from this family are distributed widely in the tropical and subtropical regions of the

world (Stevens, 2001 onwards), however, only the biggest genus, *Begonia* L., occurs in China. Jiao and Shui (2013) tested four candidate plant barcoding regions (*rbcl*, *matK*, *trnH-psbA*, ITS) in 136 samples representing 26 species of *Begonia*. Their results indicated that in contrast to the low interspecific variation of the three chloroplast DNA fragments, ITS/ITS2 sequences showed significant interspecific divergences, enabling a high level of species discrimination (96%–100%). *Begonia pellioides* Y. M. Shui & W. H. Chen, a species endemic to limestone areas in southeastern Yunnan, was illustrated (Wang et al., 2015). Through the collaborative surveys conducted by KIB and the Centre for Plant Conservation of Vietnam (CPC) in the transboundary karst regions in Northern Vietnam and Southern China, seven new species were described. These are *Begonia albopunctata* Y. M. Shui, W. H. Chen & H. Q. Nguyen, *Begonia erectocarpa* H. Q. Nguyen, Y. M. Shui & W. H. Chen, *Begonia gulongshanensis* Y. M. Shui & W. H. Chen, *Begonia minissima* H. Q. Nguyen, Y. M. Shui & W. H. Chen, *Begonia mollissima* Y. M. Shui, H. Q. Nguyen & W. H. Chen, *Begonia rhytidophylla* Y. M. Shui & W. H. Chen, *Begonia bambusetorum* H. Q. Nguyen, Y. M. Shui & W. H. Chen (Chen et al., 2018c). Additionally, *Begonia kingdon-wardii* Tebbit was rediscovered from northern Myanmar (Chen et al., 2018a).

Euphorbiaceae (the spurge family), with 209 genera and 6252 species, is distributed widely in pantropical and cool temperate regions (Christenhusz and Byng, 2016; Stevens, 2001 onwards). A new monotypic genus based on *Tsaiodendron dioicum* Y. H. Tan, Z. Zhou & B. J. Gu. was described and illustrated in Zhou et al. (2017d). This new taxon is from Yunnan province, southwestern China, and its phylogenetic position within tribe Euphorbieae (Acalyphoideae, Euphorbiaceae) was supported by phylogenetic as well as morphological and palynological evidence. The genus was named in honor of Prof. Xitao Cai (Hse-Tao Tsai), who devoted his life to the study of Chinese plants, the Xishuangbanna Tropical Botanical Garden (XTBG), and the Kunming Institute of Botany (KIB).

Urticaceae (the nettle family) comprises 53 genera and more than 2625 species (Christenhusz and Byng, 2016). Wu et al. (2013b) conducted the first densely sampled (122 species from 47 genera) molecular phylogeny of this family, which resolved major relationships of the deep nodes with substantial support. Within the family Urticaceae, Deng et al. (2013a) described a new monotypic genus, from Hubei province, central China, that was based on *Zhengyia shennongensis* T. Deng, D. G. Zhang & H. Sun. The genus *Zhengyia* T. Deng, D.G. Zhang & H. Sun was named in honor of Prof. Zhengyi Wu, a renowned Chinese botanist who studied Chinese plants for over 70 years. *Zhengyia* is distinguished from the related genera *Urtica* L., *Hesperocnide* Torr. and *Laportea* Gaudich. in the tribe Urticeae by its seed and stipule morphology; phylogenetic evidence also shows that it is distinct and is related to *Urtica* (including *Hesperocnide*) species and *Laportea cuspidata* (Wedd.) Friis. Other new species of Urticaceae have also been described from southwestern China (Lin et al., 2011; Wu et al., 2011a,b, 2013a).

Asteraceae is the second largest vascular plant family, with ca. 1623 genera comprising c. 24,700 species in 13 subfamilies (Christenhusz and Byng, 2016; Stevens, 2001 onwards). Zhang et al. (2011) used cytology, molecular phylogeny, morphology, and scanning electron microscopy of cypselae morphology to establish a new monotypic genus *Parasynalathium* J. W. Zhang, Boufford & H. Sun to accommodate the new combination *Parasynalathium souliei* (Franch.) J.W. Zhang, Boufford & H. Sun ( $\equiv$  *Lactuca souliei* Franch.). *Parasynalathium* is endemic to the Himalaya-Hengduan Mountains, although distinct from other members of the subtribe, *P. souliei* remained in Lactucinae and grouped within *Lactuca* L. s.l. However, Kilian et al. (2017) argued that *P. souliei* was nested within *Melanoseris*, based on both nrITS and the plastid DNA phylogeny. Deng et al. (2014) described and illustrated *Youngia zhengyiana* T.

Deng, D. G. Zhang, J. W. Zhang & H. Sun, a new species from Guizhou province of southern China belonging to *Youngia* sect. *Mesomeris* (Asteraceae: Crepidinae). In light of the molecular phylogenetic reconstruction and additional morphological data, Wang et al. (2013) discussed the conflicting taxonomies of the Chinese *Lactuca* alliance. These authors also outlined an improved new classification of the genera *Notoseris* C. Shih, *Paraprenanthes* C. C. Chang ex C. Shih, and *Melanoseris* Decne.

Ericaceae, with ca. 126 genera and more than 4000 species, is one of the largest families of angiosperm (APG IV, 2016; Stevens, 2001 onwards). Liu et al. (2010) conducted molecular phylogenetic analyses and provided a new classification of *Pyrola* L. (Pyroleae, Monotropoideae, Ericaceae). As a result, *Pyrola* was confirmed as a monophyletic group with two redefined sections and six series: *P.* sect. *Pyrola* (*P.* ser. *Pyrola*, ser. *Ellipticae* (Andres) Krísa and ser. *Rugosae* (Andres) Zhen W. Liu & H. Peng) and *P.* sect. *Scotophylla* Nutt. (*P.* ser. *Japonicae* Krísa, ser. *Scotophyllae* (Nutt.) Zhen W. Liu & H. Peng and ser. *Chloranthae* Krísa). Species within each section and series share similar morphological traits and/or geographical distributions. In another study of the family, Ma et al. (2013) described new species within the large and rapid-radiating genus *Rhododendron* L. Morphological and DNA barcoding data (*rbcl*, *matK*, *trnH-psbA* and *nrITS*) supported *Rhododendron baihuense* Y. P. Ma as a new species and to be genetically distinct from the related *Rhododendron hanceanum* Hemsl. and *Rhododendron genestierianum* Forrest. Another three new species, namely *Rhododendron bailiense* Y. P. Ma, C. Q. Zhang and D. F. Chamb, *Rhododendron longipedicellatum* Lei Cai & Y.P. Ma, and *Rhododendron xiaoxueshanense* R.L. Liao and Y. P. Ma, were also described (Cai et al., 2016b; Liao et al., 2015; Ma et al., 2015). Additionally, numerous new species and other taxonomic rearrangements have been made for *Gaultheria* L. (Fritsch et al., 2015a,b, 2016).

Gesneriaceae consists of ca. 152 genera and 3540 species (Christenhusz and Byng, 2016), and is a characteristic plant group inhabiting the limestone areas of Southwest China. During the past ten years, at least 19 new species within Gesneriaceae from Southwest China and adjacent regions (e.g., Vietnam) have been described and illustrated. These include *Ancylostemon dimorphosepalus* W. H. Chen & Y. M. Shui, *Ancylostemon hekouensis* Y. M. Shui & W. H. Chen, *Didymocarpus anningensis* Y. M. Shui, Lei Cai & J. Cai, *Hemiboea crystallina* Y. M. Shui & W. H. Chen, *Oreocharis crispata* W. H. Chen & Y. M. Shui, *Oreocharis grandiflora* W. H. Chen, Q. H. Nguyen & Y. M. Shui, *Oreocharis jinpingensis* W. H. Chen & Y. M. Shui, *Oreocharis longituba* W. H. Chen, Q. H. Nguyen & Y. M. Shui, *Oreocharis ninglangensis* W. H. Chen & Y. M. Shui, *Oreocharis synergia* Y. M. Shui & Mich Möller, *Paraboea hekouensis* Y. M. Shui & W. H. Chen, *Pa. manhaoensis* Y. M. Shui & W. H. Chen, *Petrocodon ainsliifolius* W. H. Chen & Y. M. Shui, *Pe. lithophilus* Y. M. Shui, W. H. Chen & Mich. Möller, *Pe. viridescens* W. H. Chen, Mich. Möller & Y. M. Shui, *Petrocosmea shilinensis* Y. M. Shui & H. T. Zhao, *Raphiocarpus jinpingensis* W. H. Chen & Y.M. Shui, *Raphiocarpus maguanensis* Y. M. Shui & W. H. Chen, *Tremacron hongheense* W. H. Chen & Y. M. Shui (Cai et al., 2015, 2016a; Chen et al., 2012a,b, 2013, 2014a, 2015a,b, 2016b, 2017, 2018b,d; Chen and Shui, 2006; Zhang et al., 2010; Zhao and Shui, 2010). Chen (2014b) investigated the taxonomic status and phylogenetic affinities of a presumed extinct monotypic genus *Paraisometrum* W. T. Wang from the karst mountain region of Southwest China. This study indicated that *Paraisometrum mileense* W. T. Wang (= *Oreocharis mileensis* (W. T. Wang) Mich. Möller & A. Weber) represents a relatively isolated and derived taxonomic unit within *Oreocharis*.

Lamiaceae (the mint or deadnettle family), consists of ca. 241 genera and 7530 species (Christenhusz and Byng, 2016). This family is the traditional research subject of KIB and Profs. Chengyih Wu and Hsiwen Li are renowned experts on this family. Dr. Chunlei

Xiang and his colleagues have been working on the taxonomy and systematics of Lamiaceae for 13 years, focusing on the genera *Caryopteris* Bunge, *Chelonopsis* Miq., *Elsholtzia* Willd., *Isodon* (Schrad. ex Benth.) Spach, *Phlomoides* Moench, *Salvia* L., *Schnabelia* Hand.-Mazz. and *Scutellaria* L. (Chen et al., 2014c,d, 2016c, 2017a,b; Hu et al., 2017; Xiang et al., 2009, 2014, 2016a,b, 2018; Xiang and Liu, 2012a; Zhao et al., 2017). Using phylogenetic analyses together with morphological and cytological data these studies have revealed that *Bostrychanthera* Benth. should be transferred to *Chelonopsis*, and as a consequence two species were transferred. Two major clades within the genus are concordant with the Sino-Japanese and Sino-Himalayan distribution patterns (Xiang et al., 2013). Species of the genus *Isodon* are often rich in diterpenoids and medically important (Li et al., 2013), serving as an excellent system for studying chemotaxonomy. A number of new species have been added to the genus in recent years (Chen et al., 2014c,d, 2016c; Xiang and Liu, 2012b), broadening our understanding of the diversity of this genus. Recently, based on molecular and morphological data, a new infrageneric classification of the genus *Schnabelia* was proposed by Xiang et al. (2018) and the genus was divided into two sections, sect. *Cylindricaulis* and sect. *Schnabelia*. In addition, *Caryopteris forrestii* Diels var. *minor* C. Pei & S. L. Chen ex C. Y. Wu was elevated to species rank based on molecular and morphological evidence.

*Pedicularis* L. is a large temperate hemiparasitic genus in the Orobanchaceae family, with ca. 600–800 species that are distributed mainly in arctic-alpine regions of the northern hemisphere. New species have been added to this species-rich genus (Yu et al., 2008, 2010). For example, *Pedicularis wanghongiae* M. L. Liu & W. B. Yu was described from the Gaoligong Mountains in Yunnan province, based mainly on molecular data (*nrITS*, *matK*, *rbcl* and *trnL-F*) and pollen morphology. The authors named the species in honor of their advisor, Prof. Hong Wang, who has been working on the taxonomy and systematics of *Pedicularis* for the past 24 years (Liu and Yu, 2015). Yu et al. (2015) reconstructed a phylogeny for *Pedicularis* based especially on species from the Himalaya-Hengduan Mountains; thirteen major clades were resolved with strong support values. A more comprehensive global phylogeny of *Pedicularis* is needed, one that combines morphological and geographic characters within a phylogenetic framework.

Theaceae (the tea family), which comprises ca. 261 species in 9 genera, is a plant group with great economic and ecological importance (APG IV, 2016; Yu et al., 2017b). The recent rediscovery by Yang et al. (2014) and Zhao and Yang (2012) of *Camellia grandibracteata* H. T. Chang & F. L. Yu and *Camellia tonkinensis* (Pit.) Cohen-Stuart extends the distribution range of these two species. Phylogenetic reconstructions of *Camellia* sects. *Longipedicellatae* H. T. Chang, *Chrysantha* H. T. Chang, and *Longissima* H. T. Chang (Fang et al., 2010), and of the *Pyrenaria* Blume complex (Li et al., 2011a) have been conducted based on chloroplast DNA fragments or *nrITS*. Additionally, chloroplast genomes have been used to investigate species relationships within *Camellia* L. and *Schima* Reinw. ex Blume, as well as the phylogenetic framework of the entire family (Yang et al., 2013b; Yu et al., 2017a,b).

### 2.3. Bryophyta

Mosses (Bryophyta) are a diverse plant group with over 12,700 species in more than 800 genera (Cox et al., 2010). The taxonomic study of Bryophyta at KIB has been greatly enhanced by several bryo-flora inventories conducted in collaboration with other institutions around the world. The most productive of these collaborations was the Sino-American Gao-Li-Gong-Shan (GLGS) project, which was managed jointly by California Academy of Sciences and Kunming Institute of Botany. The many specimens collected in

connection with this project were carefully studied. Two new genera, namely *Hamatostrepta* Vána & D. G. Long (Vána and Long, 2008) and *Yunnanobryon* Shevock, Ochyra, S. He & D. G. Long (Shevock et al., 2011), and six new species, namely *Bucklandiella shevockii* Bednarek-Ochyra & Ochyra (Ochyra and Bednarek-Ochyra, 2010), *Hyophila flavolimбата* S. He & Y. J. Yi (He et al., 2015), *Philonotis lizangii* T. J. Kop. (Koponen, 2010), *Pinnatella homaliadelphoides* Enroth, S. Olsson, S. He, Shevock & D. Quandt (Enroth et al., 2010), *Schistidium riparium* H. H. Blom, Shevock, D. G. Long & Ochyra and *Schistidium mucronatum* H. H. Blom, Shevock, D. G. Long & Ochyra (Blom et al., 2011) were published through international collaborations. Even after the project had officially ended, the monotypic genus *Cyptodontopsis* (Cryphaeaceae), which was formerly known only from the type species collected over 80 years ago, was rediscovered along Nujiang valley (Ma et al., 2014).

Over recent years a series of bryophyte flora inventories within several National Nature Reserves (NNR) in Yunnan province have produced significant results. For example, in Daweishan NNR, the genus *Arthrocormus* Dozy & Molk. (Calymperaceae) was reported new for the country (Ma and Shevock, 2015a) and the discovery of the capsules of *Taiwanobryum undulatifolium* (Tixier) W. Z. Ma, Enroth & Shevock (Neckeraceae) enabled clarification of its systematic position (Ma et al., 2018b). In Jin-Ping Fenshuiling NNR, *Pogonatum shevockii* NE Bell & Hyvonen (Polytrichaceae) was described as a new species endemic to Southeast Asia (Bell et al., 2017), and the sporophytic structures of *Bryocrumia vivicolor* (Ma et al., 2016b) and *Chiastocaulon fimbriatum* (Ma and Shevock, 2018) were both described for the first time since their protologues. Furthermore, *Erpodium perrottetii* (Mont.) Jaeg. & Sauerb. has been reported as a new distributional record for China (Ma and Shevock, 2015b).

The National Geographic Society funded the study of rheophytic mosses in western Yunnan province from 2015 to 2018. This collaborative project yielded a number of significant taxonomic outcomes. A new genus, *Mawenzhangia* Enroth, Shevock & Ignatov (Lembophyllaceae), endemic to northwestern Yunnan was described (Enroth et al., 2018) and *Reimersia diversiretis* (Broth. ex Hand.-Mazz.) Shevock, W. Z. Ma, S. He & D. G. Long was resurrected, based on newly collected materials (Shevock et al., 2018). Two rare species, *Anomodon perlingulatus* Broth. ex P. C. Wu & Y. Jia (Ma et al., 2016a) and *Buxbaumia minakatae* S. Okamura (Ma and Shevock, 2016) were identified as new for the province.

## 2.4. Fungi

Fungal taxonomy is an important component of taxonomic research at KIB. During the past decade, several groups, including Agaricaceae, Amanitaceae, Boletaceae, Cantharellaceae, Physalacriaceae, Russulaceae, Suillaceae and Tubercaceae, have received much attention.

One of the most important studies involved the Boletaceae, a family that contains several ecologically and economically important mushrooms. Using sequences of four gene fragments (nrLSU, *tef1- $\alpha$* , *rpb1*, and *rpb2*), Wu et al. (2014) constructed a molecular phylogenetic framework for the family in which seven subfamily-level lineages were clearly revealed. Furthermore, six subfamilies were proposed, namely Austroboletoidae, Boletoidae, Chalci-poroideae, Leccinoideae, Xerocomoideae, Zangioideae, with the latter four being new to science.

During the past decade, at least 12 new genera from the family Boletaceae have been erected, based on both morphological and molecular evidence. They are *Zangia* Yan C. Li & Zhu L. Yang, *Pseudoaustroboletus* Yan C. Li & Zhu L. Yang, *Borofutus* Hosen & Zhu L. Yang, *Crocino-boletus* N. K. Zeng, Zhu L. Yang & G. Wu, *Chiua* Yan C. Li & Zhu L. Yang, *Hymenoboletus* Yan C. Li & Zhu L. Yang,

*Tengioboletus* G. Wu & Zhu L. Yang, *Tylocinum* Yan C. Li & Zhu L. Yang, *Baorangia* G. Wu & Zhu L. Yang, *Lanmaoa* G. Wu & Zhu L. Yang, *Parvixerocomus* G. Wu & Zhu L. Yang, and *Rugiboletus* G. Wu & Zhu L. Yang (Hosen et al., 2013; Li et al., 2011b, 2014; Wu et al., 2016a,b; Zeng et al., 2012, 2014). In addition, ca. 85 new species of this family have been resolved and formally described (Cui et al., 2016; Li et al., 2011b; Wu et al., 2016a,b; Zeng et al., 2017; Zhu et al., 2014).

Agaricaceae is a rich source for edible mushrooms, and taxonomists from KIB have contributed significantly to the understanding of this species-diverse family. For example, Ge and Yang (2017) established a new monotypic genus, *Pseudolepiota* Z. W. Ge, based on its unique morphological characters and molecular data. In this work, *Pseudolepiota zangmui* Z. W. Ge was named in honor of the late Prof. Mu Zang, for his significant contribution to the knowledge of the larger fungi of China. Ge et al. (2018) proposed a new infrageneric classification for the genus *Chlorophyllum* Masee, based on the phylogeny inferred from DNA sequences and morphological differences. In this study, two new species, *Chlorophyllum africanum* Z. W. Ge & A. Jacobs and *Chlorophyllum palaeotropicum* Z. W. Ge & A. Jacobs, were also described. In addition to the above-mentioned important findings, at least 14 new species have been described from four genera, namely, *Hymenagaricus* Heinem. (1 sp., Ge et al., 2008a), *Lepiota* (Pers.: Fr.) S.F. Gray (3 spp., Liang and Yang, 2011, 2013; Liang et al., 2011), *Leucoagaricus* Locq. ex Singer (7 spp., Ge, 2010; Ge et al., 2015b; Liang et al., 2010) and *Macrolepiota* Singer (3 spp., Ge et al., 2010; Ge et al., 2012).

Amanitaceae, especially the genus *Amanita* Pers., has been a traditional subject of research by mycologists from KIB. Over the past ten years several studies have shown that species diversity within amanitas has been significantly underestimated, and as a consequence at least 23 new species have been described within *Amanita* (Cai et al., 2014, 2016c; Liu et al., 2017b; Tang et al., 2015a; Zhang et al., 2010).

Some important progress has also been made in the taxonomic studies of the family Physalacriaceae. A new genus for this family, *Cibaomyces* Zhu L. Yang, Y. J. Hao & J. Qin, was described using morphological and molecular evidence (Hao et al., 2014). Additionally, a number of new infra-generic taxa have been described and illustrated by various authors, e.g., *Cyptotrampa angustispora* Zhu L. Yang & J. Qin, *Cyptotrampa glabra* Zhu L. Yang & J. Qin, *Cyptotrampa shennongjia* Zhu L. Yang & J. Qin (Qin and Yang, 2016a), *Flammulina yunnanensis* Z. W. Ge & Zhu L. Yang (Ge et al., 2008b), *Flammulina velutipes* var. *filiformis* Z. W. Ge, X. B. Liu, & Zhu L. Yang, *F. velutipes* var. *himalayana* Z. W. Ge, Kuan Zhao & Zhu L. Yang (Ge et al., 2015a), *Paraxerula ellisospora* Zhu L. Yang & J. Qin (Qin et al., 2014), *Physalacria corneri* Zhu L. Yang & J. Qin, *Physalacria lacrymispora* Zhu L. Yang & J. Qin, *Physalacria sinensis* Zhu L. Yang & J. Qin (Qin and Yang, 2016b) and *Rhodotus asperior* L. P. Tang, Zhu L. Yang & B. Tollgor (Tang et al., 2014). Recently, the taxonomic position and phylogenetic relationships of “Heipijizong” (a radicate *Oudemansiella* species), which is widely cultivated in China, was clarified by Hao et al. (2016).

The family Russulaceae includes edible species, and species with high medicinal and ecological value. Taxonomists at KIB have made an important contribution to the understanding of species diversity and taxonomy within the family. A number of new species have been described for the genera *Lactarius* and *Russula* by using of molecular and morphological data (Wang, 2016, 2017a,b; Wang and Liu, 2009; Wang et al., 2015b; Wang et al., 2012b; Wang et al., 2009).

Tubercaceae, which include the edible ectomycorrhizal fungi known as truffles, is a family of great economic importance (Percudani et al., 1999). At least ten new species have been described by KIB taxonomists for the genus *Tuber*, namely, *Tuber badium* S. P. Wan, *Tuber depressum* S. P. Wan, *Tuber verrucosivolum*

S. P. Wan, *Tuber sinoaestivum* J. P. Zhang & P. G. Liu, *Tuber pan-zhihuanense* X. J. Deng & Y. Wang, *Tuber sinoniveum* S. P. Wan & F. Q. Yu, *Tuber shidianense* S. P. Wan, *Tuber calosporum* S. P. Wan, *Tuber polymorphosporum* S. P. Wan, and *Tuber baoshanense* S. P. Wan (Deng et al., 2013b; Wan et al., 2016, 2017a,b; Xu et al., 2017; Zhang et al., 2012a). Additionally, one new species, *Choioomyces helan-shanensis* Juan Chen & P.G. Liu, was described in Chen et al. (2016a).

For Cantharellaceae, three new species have been described in Shao et al. (2016) and Tian et al. (2012), namely, *Cantharellus zangii* X. F. Tian, P. G. Liu & Buyck, *Cantharellus phloginus* S. C. Shao & P. G. Liu, and *Cantharellus vaginatus* S. C. Shao, X. F. Tian & P. G. Liu. Within Suillaceae, four new species have been described in Shi et al. (2016) and Zhang et al. (2017b), namely, *Suillus phylopictus* R. Zhang, X. F. Shi, P. G. Liu & G. M. Mueller, *Suillus kwangtungensis* R. Zhang, X. F. Shi, P. G. Liu & G. M. Mueller, *Suillus alpinus* X. F. Shi & P. G. Liu, and *Suillus aurihymenius* X. F. Shi & P. G. Liu.

### 2.5. Lichen

The lichen collection at KUN (Herbarium, Kunming Institute of Botany) was established in 1981 by Prof. Lisong Wang, who focused on species diversity within the Hengduan Mountains in Southwest China. Much attention has subsequently been paid to this mountainous region from which more than 60,000 lichen specimens have now been collected.

Beginning in 2009, studies of Alectorioid lichens have been conducted, resulting in the illustration of many overlooked genera and species, e.g., *Alectoria spinosa* Li S. Wang & Xin Y. Wang (Parmeliaceae), *Bryoria yunnanensis* Li S. Wang & Xin Y. Wang, *Bryoria wuii* Li S. Wang, and *Bryoria divergescens* (Nyl.) Brodo & Hawksw. (Parmeliaceae) (Wang et al., 2012a, 2015a, 2017a). The integration of molecular phylogeny has greatly benefited lichen taxonomy. Combining morphological, chemical, and phylogenetic data, many cryptic species have been described and their phylogenetic relationships resolved, e.g., *Anzia rhabdorhiza* Li S. Wang & M. M. Liang, *Anzia pseudocolpota* Xin Y. Wang & Li S. Wang (Parmeliaceae), *Bulbothrix asiatica* Y. Y. Zhang & Li S. Wang (Parmeliaceae) and *Ophioparma pruinosa* Li S. Wang & Y. Y. Zhang (Ophioparmaceae) (Liang et al., 2012; Wang et al., 2015c; Zhang et al., 2014, 2018). This same approach has aided the phylogenetic study of Lepidostromatales (Liu et al., 2017a).

### 3. Future perspectives of taxonomy in KIB

During the past decade, taxonomists from KIB have taken a big step forward, combining new theories and approaches to identify new species, clarify phylogenetic relationships, establish new classifications, and reveal the evolutionary history for taxa at various taxonomic levels. Despite this progress, more efforts are required to pave the road for the future development of taxonomy at KIB.

Because of the increasing loss of biodiversity, there is an urgent need to explore and document species before they disappear from the planet. In spite of the publication of *Flora of China* and flora books for some regions or provinces, many problems remain to be resolved, especially at the species level (Ma, 2014; Yang, 2016). Recently, Cardoso et al. (2017) presented a taxonomically verified checklist of seed plants (14,003 species) from lowland Amazon rain forests, which advanced our understanding of the origin, evolution, and ecology of the exceptional biodiversity in this area. Taxonomists from KIB are encouraged to continually focus on the biodiversity of China, particularly the mountains of Southwest China and Himalayas, which are considered two of the world's biodiversity hotspots (Myers et al., 2000). Revision of the published floras and compilation of high-quality checklists or floras for specific

mountains or regions will contribute to a robust understanding of plant biodiversity in China and lay a solid foundation for the scientific research of various disciplines (Ma, 2014). Taxonomists at KIB are also encouraged to collaborate closely with the Herbarium (KUN) and the Germplasm Bank of Wild Species, as well as with other institutes and organizations. This will contribute to the iFlora project, construction of cyber-infrastructures and public databases, and scientific education for biodiversity protection.

Although traditional approaches remain important and useful, taxonomists from KIB should embrace new theories and acquire new skills to address taxonomic problems. Among these theories, phylogeny has become the foundation of evolutionary biology. A modern corollary to Dobzhansky's (1973) famous statement "nothing in biology makes sense except in the light of evolution" is that "things make a lot more sense in the light of a phylogeny." It was recently argued that taxonomists should avoid over-emphasizing phenotypic traits under local adaptation and ignoring a lack of phylogenetic signal in molecular markers (Liffield, 2015). Thus, conflicts between morphologists and molecular biologists should now subside (Padial et al., 2010), and the separation of classical and experimental taxonomy should not be over-emphasized (Yang, 2016). With the development and decreasing cost of next generation sequencing technology, genomic data has been efficiently used to resolve phylogenetic relationships (Gitzendanner et al., 2018), delineate species (Hu et al., 2016), trace the causes of phenotypic change (Rudman et al., 2018), and reveal mechanisms of speciation (Ma et al., 2018a), which greatly advances our knowledge of biodiversity and strongly benefits taxonomy. Furthermore, in this era of "big data," integrative biodiversity science, which combines phylogenetics with cyberinfrastructure and new data sources, enables us to investigate "next-generation" systematics, ecology, and evolution, and is crucial to the future of global biodiversity (Soltis and Soltis, 2016). Taxonomy is an unending synthetic science, and therefore, an ideal taxonomist must be very versatile (Stuessy, 2009).

A worrisome situation is that the overwhelming attention molecular phylogenetics has received from funding agencies, institutes, and journals has resulted in a lack of interest in general taxonomy, which often produces fewer, and lower-impact papers (Agnarsson and Kuntner, 2007; Wheeler, 2004; Yang, 2001). The new generation of systematists or taxonomists is becoming strongly specialized on gathering and analyzing molecular data, in lieu of basic taxonomic work, e.g., field investigation, identification, description of species, delimitation morphological characters, nomenclature (Sytsma and Pires, 2001). They often fail to identify the material collected from the wild accurately or just rely on the identification labels of herbarium specimens. Phylogeny divorced from taxonomy will erode the accuracy of research, limit the impact of phylogenetic knowledge, and slow down taxonomic work (Crisci, 2006; Wheeler, 2004). Thus, more funding and awards, and flexible assessment criteria are expected to recruit more Ph.D. students and systematists from KIB to engage in traditional taxonomy while pursuing cutting-edge technologies and theories. It is comforting that, increasingly, policymakers and funding agencies have realized that a shortage of trained taxonomists jeopardizes the protection of biodiversity. In response, measures (e.g., the special fund for classical taxonomy set up by the National Natural Science Foundation of China (NSFC)) have been taken to alleviate the taxonomic impediment.

Nowadays, few taxonomic studies are summarized into monographs, because writing a comprehensive and scholarly monograph is challenging and time-consuming, and may still be considered uncompetitive in terms of funding or permanent jobs. However, monographs are central to sorting out life forms into systems of valuable information for human society, and are crucial for dealing

with biodiversity challenges; furthermore, monographs serve as stimuli for other studies to be done, and provide important training opportunities for Ph.D. students (Stuessy and Lack, 2011). To go beyond basic biotic inventory and sporadic or serial taxonomic-related papers, more creative monographs are needed. Creativity means understanding relationships by observing population-level variation in the field; applying suitable species concepts by reading theoretical literature; detecting transitions between taxa by learning about evolutionary processes; gathering as much comparative data as possible in addition to morphology; and thoroughly documenting all aspects of the growing monograph (Stuessy and Lack, 2011). Creativity also means crossing over the regional limits and carrying out worldwide monographic work by cooperating with researchers from other countries. It is time the scientific community recognizes global monographic revisions as scientific products that are necessary, rigorous, and highly valuable, rather than old-fashioned, outdated, less exciting, and unattractive (Dayrat, 2015). The future development of creative monographic work at KIB requires more Ph.D. students to be trained as creative monographers and more financial support from institutions and funding agencies.

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### Further reading

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