

## Editorial

## The Tree of Life: China project

The knowledge of evolutionary relationships is fundamental to all disciplines of biology, yielding novel and profound insights across plant sciences, from comparative genomics, molecular evolution, and plant development, to the study of adaptation, speciation, community assembly, and ecosystem functioning (Forest et al., 2007; Donoghue, 2008; Gehrke & Linder, 2011). Phylogeny (the Tree of Life, TOL) has become the foundation of evolutionary biology. It is accurate to say “Evolutionary biology makes much more sense in the light of phylogeny”, as a corollary to Dobzhansky’s (1973) famous statement “Nothing in biology makes sense except in the light of evolution.”

China harbors 31 362 species, 3328 genera, and 312 families of vascular plants (Wu et al., 1994–2013) and has the richest flora of the Northern Hemisphere (Wu et al., 2003). A well-resolved phylogeny of vascular plants of China has many potential uses in various areas of biology—ecology, conservation genetics, and agriculture—as well as stimulates new research at the interface of evolutionary ecology, phylogenetics, and biogeography, thus clarifying processes that shaped patterns of distribution and diversity of such a rich flora of the Northern Hemisphere (Qian & Ricklefs, 2000; Wang et al., 2009; López-Pujol et al., 2011). Understanding the phylogeny of vascular plants and phylogenetic diversity at this scale will help elucidate fundamental processes underlying plant/animal associations and the assembly of entire ecosystems, and help manage the impact of global challenges to biodiversity and the maintenance of natural resources to humankind.

In June 2007, an international symposium on the TOL was held in Beijing, China. *Journal of Systematics and Evolution* (JSE) organized and published the symposium special issue: Patterns of Evolution and the Tree of Life (JSE vol. 46, no. 3, 2008). Since then, the Chinese botanical community has continued to make contributions to TOL studies. The present special issue aims to present recent progress in reconstructing TOL of the vascular plant genera in China, including the assembly of DNA materials, establishment of co-operation, data generation, tree reconstruction, on how to use the China TOL as a framework to further examine the origin and evolution of major clades in vascular plants, and the floristic relationship between China and other regions of the world as all vascular plants share a common ancestor (Wen et al., 2010; Xiang et al., 2015).

This special issue consists of 11 papers all related to the “giant” phylogeny of the Chinese vascular plants. Chen et al. (2016) sampled 6098 species representing 3114 genera of vascular plants and five genera of bryophytes as out-groups to reconstruct the TOL of the Chinese vascular plants at the generic level. To facilitate further application of such a large-scale phylogeny to other biology fields, the SoTree software

was introduced to enable the efficient generation of the phylogenetic trees by providing sub-datasets with interested species lists for studies concerning the origin, ecology, and biogeography of the local flora in China. Using DNA sequences of three plastid genes, Liu (2016) presents a phylogenetic analysis of 259 genera of pteridophytes, which provided evidence documenting the impact of Ren-Chang Ching’s integrative classification of pteridophytes. Ten out of 11 orders in Ching’s system are consistent with the modern DNA-based phylogeny, whereas four new orders were introduced to avoid paraphyletic orders in the leptosporangiate ferns. Wang et al. (2016) integrated *Leefructus mirus*—one of the earliest eudicot macrofossils—in an exhaustive morphological dataset of extant Ranunculales to improve our understanding of the diversification of this lineage in eudicots. As a result of the integration of this fossil, the authors recovered that basal eudicots experienced an accelerated diversification during the onset of the angiosperm radiation in the Early Cretaceous. Du et al. (2016) sampled 139 genera (in 43 families) representing most families of the aquatic plants worldwide. Their results suggested that aquatic habitats were colonized at least three times during the early radiation of angiosperms, namely by Nymphaeales, Ceratophyllales, and the monocots.

Three of the papers address the phylogeny of angiosperms at the ordinal level or above. Special attention is given to the rosids (*Rosidae*) because the clade contributes not only one-quarter of the extant diversity of angiosperms, including considerable economically important crops and most dominant forest trees, but is also recognized as a major contributor to the angiosperm diversity of China. Using a supermatrix approach, Sun et al. (2016) resolved the phylogeny of *Rosidae* world-wide with a dense sampling scheme (four genes, a total of 9300 taxa representing 2775 genera, 138 families, and 17 orders). They discovered several novel relationships and recognized two families and 467 genera as non-monophyletic. As part of the rosids, the N-fixing clade is one of the largest clades of the angiosperms, containing over 1300 genera, approximately 30 000 species, which are important components of extant temperate and tropical forest. Li et al. (2016a) constructed the most comprehensive and robust global tree of the N-fixing clade to date with a supermatrix to compare with the local tree from the TOL of the Chinese vascular plants. Topologies of the global tree and the local tree are generally congruent and most of the internal supports are greatly improved with dense sampling. Yang et al. (2016) used eight chloroplast markers and one mitochondrial gene, and assembled a matrix of 11 951 characters of 649 genera, covering ca. 54% of the genera of Gentianales, to reconstruct the phylogeny of Gentianales. Topologies of the global Gentianales tree and the Chinese Gentianales tree are largely

congruent. The Gentianales and each family within the order are strongly supported as monophyletic. Relationships among some deep nodes are newly resolved.

This special issue also includes the phylogenetic analyses of four families, of which Asteraceae and Orchidaceae are the first and fourth largest families of the Chinese flora, respectively. Fu et al. (2016) used three plastid markers (*rbcl*, *ndhF*, and *matK*) to reconstruct the phylogeny of 506 genera, approximately one-third of all the genera of the Asteraceae, with a total of 200 Chinese Asteraceae genera included in the analysis. The results are largely congruent with those of earlier studies. A systematic arrangement of all the genera of the Chinese Asteraceae was presented, in which 255 genera (48 introduced), 22 tribes, and 7 subfamilies were recognized. Orchidaceae have ca. 200 genera in China. Li et al. (2016b) investigated the molecular phylogenetic relationships of the higher-level Chinese orchids with 175 genera sampled. The subfamilies, tribes, and subtribes *sensu* Genera Orchidacearum are supported as monophyletic, except that the paraphyletic Disteioidae, Calyposeae, Vandeeae, and Eriinae, and the relationships of Epidendroideae are weakly supported. Five faster-evolving genes (*rbcl*, *matK*, *psaB*, *ycf1*, and *Xdh*) were used to further reconstruct the phylogenies of the perplexing Epidendroideae. Li & Wen (2016) sampled 96 accessions representing all 20 genera and 50 species of Chinese Araliaceae and 45 closely related taxa to assess the evolutionary relationships of Araliaceae and their biogeographic diversification in China. Their results supported that the Chinese members of Araliaceae were scattered within the Asian Palmate group and the *Aralia*–*Panax* group with *Osmoxylon* at the base of core Araliaceae. The Chinese Araliaceae have originated in Asia and the distribution pattern of the phylogenetic diversity of Araliaceae corresponds with its taxonomic diversity across the entire region. Cai & Ma (2016) present a case study of phylogeny at the generic and specific levels with nuclear genes, using Brassicaceae taxa as examples. They used three protein-coding nuclear genes, *MLH1*, *SMC2*, and *MCM5*, with up to 10 200 base pairs (in both exons and introns) to reconstruct a phylogeny with multiple species in each of five genera within Brassicaceae for a total of 65 taxa. The combined data revealed high resolution at various phylogenetic depths and their results provided a robust species-level phylogeny for a number of Brassicaceae members and supported an optimistic perspective on the phylogenetic utility of conserved nuclear data for relatively recent clades.

The TOL China project has been carried out as a long-term collaboration among several institutions since March 2009. The State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences (Beijing, China) organized the project and has closely collaborated with the following institutions: Fairy Lake Botanical Garden (Shenzhen), Computer Network Information Center, Chinese Academy of Sciences (Beijing), Wuhan Botanical Garden, Chinese Academy of Sciences (Wuhan), the Orchid Conservation and Research Center of Shenzhen (Shenzhen), and University of Florida, Gainesville (USA) in the last 7 years. This project was financially supported by grants from the National Natural Science Foundation of China (Grant Nos. 31590822, 31270268, and 31270269), the National Key Basic Research Program of China (Grant No. 2014CB954100),

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The project has arguably achieved now its main goal, a phylogeny comprising almost all genera of vascular plants native in China. However, this is only the first step towards an exhaustive understanding of the phylogeny of Chinese plants. In the future, the trees need to be expanded to cover not only other land plant lineages, such as liverworts and mosses, but especially to be expanded to include at least one representative of each plant species occurring in China. These efforts will allow the merging of efforts of the TOL project with those of the DNA barcoding of land plants. The importance of this next step forward was well illustrated by the unique insights provided by the studies published in this special issue of JSE.

Finally, we want to briefly discuss the plurality and singularity of the family names in Latin as there are two different writing ways that coexist. According to Stearn's Botanical Latin (1992), families are female plural nouns and they should be treated as plural nouns in English. However, it is common to find that writers consider a family name in Latin as singular and use the plural noun in combination with a singular verb. This common usage may be consistent in the context that families are considered to correspond to monophyla in contrast to their grammatical status; families are therefore individuals instead of classes in the context of ontology (Minelli, 2012). We prefer using the family names as plural nouns and have consistently used them this way in this special issue.

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Appendix.

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## Appendix

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