Editorial

JSE IBC Special Issue on Frontiers in Plant Systematics and Evolution

The XIX International Botanical Congress (or IBC 2017), coorganized by Botanical Society of China and Shenzhen Municipal Government, will be held in Shenzhen City, China, from July 23 to 29, 2017, with the nomenclature session on July 17–21, 2017. It is the first time for such a high-level and prestigious botanical congress to be held in a developing country, which is of great significance to the plant science community for both China and the world. Plant systematics and evolution have been the major theme of IBC. It is thus timely for the community to highlight the advances and current perspectives with cutting-edge original research and reviews on advances in systematics and evolution. As a China-based international journal, Journal of Systematics and Evolution (JSE) is dedicated to the understanding of biodiversity and evolution. To celebrate the event of IBC 2017 in China, JSE is publishing this special issue on Frontiers in Plant Systematics and Evolution.

The current special issue includes 12 papers. Abbott (2017) provides a review on advances of plant hybrid zones between native species in the context of plant speciation. The author found that the total number of plant hybrid zones detected in a literature survey was only 137, which was surprisingly small. He also reports that plant hybrid zones may frequently move in response to climate changes. Renner et al. (2017) review the sex chromosomes of bryophytes and suggest that bryophyte sex chromosomes may have been gained and lost repeatedly. They explain how the sex chromosomes of haploid-dominant organisms are distinct from the X-Y and Z-W systems, and provide a summary on their distribution and genetic composition. Cai & Ge (2017) propose a pipeline for analyzing phytoliths based on machine learning algorithm, including data collection, morphometric analysis, model building, and taxon discrimination. Their methodology and pipeline are developed based on a case study on the rice tribe Oryzieae, but should be applied to studies across different groups of grasses and other plants that utilize phytoliths in evolutionary and ecology studies.

Constructing the plant tree of life (ToL) has been a major goal for plant systematics (Stuessy, 2009; Chen et al., 2016). This special issue includes three papers dealing with the advances on plant ToL using phylogenomics (Wen et al., 2015b; Zimmer & Wen, 2015). Fang et al. (2017) review the progress and the prospects on the chloroplast phylogenomics of the morphologically diverse algal clade Chlorophyta, which includes marine, freshwater, and terrestrial green algae, and ranges from planktonic unicellular organisms to colonial, multicellular, and siphonous algae. Mandel et al. (2017) employ the phylogenomic Hyb-Seq approach that use c. 1000 low-copy number nuclear markers, and partial plastome data to explore the evolutionary relationships of the sunflower family Compositae (or Asteraceae), the largest family of flowering plants. They present two phylogenies comprising nine subfamilies and 25 tribes using concatenated and coalescence-based analyses, and discuss future plans for incorporating high-quality reference genomes and transcriptomes to advance systematic and evolutionary studies in the Compositae with team efforts of global partnerships. Shahi Shavon et al. (2017) explore the utility of a large number of nuclear genes using the anchored hybrid enrichment approach for explosively radiating taxa using the diverse legume genus Oxytropis (Fabaceae) as a case study.

Another major goal of plant systematics is to organize biodiversity into predictive classifications. The development of an increasingly robust phylogenetic framework for lineages at various levels has resulted in refined and revised classifications for plants (e.g., APG IV, 2016; PPG I, 2016) and required numerous redefinitions of genera and higher taxa (Wen et al., 2017). Soreng et al. (2017) revised and updated their worldwide phylogenetic classification of the species-rich and economically and ecologically important grass family Poaceae (Gramineae) (also see Soreng et al., 2015). They classify the 11 506 grass species into 768 genera, 12 subfamilies, seven supertribes, 52 tribes, five supersubtribes, and 90 subtribes.

Polyplody or whole-genome duplication is a prominent feature of eukaryotic evolution and includes two main forms, autopolyploidy and allopolyploidy (Jiao et al., 2011; Wendel, 2015). Three papers in this special issue are dedicated to evolution of polyploidy in plants. Spoelhof et al. (2017) highlights recent research that has significantly increased scientific understanding of autopolyploidy. Sherman-Broyles et al. (2017) examined three allopolyploid and four diploid progenitor taxa of the soybean wild relatives Glycine using genome-wide single nucleotide polymorphisms or SNPs. They show previously unrecognized substructure within diploid taxa, and the likely subgroups, from which allopolyploids were derived. They also report that allopolyploids have evolved separately long enough from direct diploid progenitors for signals of genotypes to be obscured. Schneider et al. (2017) explore the evolution of polyploidy in the derived fern family Aspleniaceae, which has the highest frequency of polyploid taxa among all ferns. The authors used a comprehensive phylogenetic framework and mapped chromosome counts data onto the phylogeny to trace the evolution of polyploids. They report several whole genome duplication events within the family, and their phylogenetic evidence supports that
tetraploid Asplenium species may have replaced their diploid ancestors as the main evolutionary players in some clades of Aspleniaceae.

DNA barcodes have been widely used as a new tool by biologists in systematics, ecology, evolutionary biology and conservation. Kress (2017) reviews the utility of DNA barcodes in community assembly, species interaction networks, taxonomic discovery, and assessing priority areas for environmental protection, and calls for future development in building the global plant DNA barcode library (see Zhang et al., 2017) and adopting genomic sequencing technologies for a more efficient and cost-effective workflow.

Wen et al. (2017) argue for developing integrative systematics as the paradigm for charting the vast biosphere for discovery of biodiversity and exploring the patterns and processes of biodiversity evolution and its conservation. They also propose the establishment of a new global cyberinfrastructure or Biodiversity Cyberbank that will function as the main repository of many types of biodiversity data to ensure the long-term sustainability of the vast and growing amount of systematic data (also see Wen et al., 2015a). This Biodiversity Cyberbank will contain new and efficient analytical pipelines for systematics research, especially for efficiently generating taxonomic treatments (e.g., revisions, e-monographs and floras).

JSE will continue to publish a series of special issues on Frontiers in Plant Systematics and Evolution in 2018 to celebrate IBC 2017. All articles published in the special issues will have free open access, and all publication charges (page and color) will be waived by the journal.

Interested authors may submit their outstanding research at http://mc.manuscriptcentral.com/jose! We now open the Biodiversity Cyberbank will contain new and efficient analytical pipelines for systematics research, especially for efficiently generating taxonomic treatments (e.g., revisions, e-monographs and floras).

References


