

Editorial

Plant DNA barcoding in China

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Identification is the keystone of biology (Bell, 1986). However, to biologists and students of biology, the total numbers of species that must be identified far outnumber the names commonly used in English, Chinese, or other living languages. In addition, the identification cues vary greatly between different taxonomical groups. Even for the taxonomists with long training and experience, it is difficult to remember all specific terms for a given group, e.g., Orchidaceae or Poaceae, without help of floristic books or monographs. It takes much time and effort to train a taxonomist, at a time when fewer and fewer young students are interested in this “classical” and “out-of-style”, but extremely important, discipline. Many students elect to learn the more “advanced” and “modern” biological disciplines like molecular biology and biochemistry. Thus, in China and the rest of the world, taxonomists are themselves becoming “endangered”. The rise of the DNA barcoding is expected to mitigate, at least in part, this dilemma.

The concept of DNA barcoding was proposed to rapidly and accurately identify species by using short, standardized DNA markers (Arnot et al., 1993; Floyd et al., 2002; Hebert et al., 2003). In fact, the idea of species identification using molecular evidence dates back to 1982 for discerning the origin of fresh meats (Kang'ethe et al., 1982). Since 2003, the approach of DNA barcoding has been greatly promoted, mainly by zoologists, to provide tools for the recognition of species as an improvement on or supplement to traditional morphology-based taxonomy (Hebert et al., 2003;

Hebert & Gregory, 2005; Packer et al., 2009). It seems that a portion of the mitochondrial cytochrome oxidase subunit 1 (*COI*) fulfills almost all animal barcoding requirements (for birds, see Hebert et al., 2004a; for fish, see Ward et al., 2005; and for moths and butterflies, see Hebert et al., 2004b and Hajibabaei et al., 2006). Although great efforts have been made in plant barcoding (Kress et al., 2005; Chase et al., 2005; Cowan et al., 2006), progress has been hampered by three factors. First, it is difficult to design universal primers for the targeted homologous markers for all plants. Second, the proposed DNA markers can be easily amplified and sequenced in some families or genera but not in others. Finally, for a given DNA-barcoding marker, the genetic gaps between species are distinct in some plant groups but are lacking in others. Despite these problems, DNA barcoding is applicable in plants by combining two or three DNA markers to make a standardized plant barcode (Kress & Erickson, 2007; Pennisi, 2007; Fazekas et al., 2008; Hollingsworth et al., 2009). CBOL Plant Working Group (2009) proposed to use the combination of *rbcL* + *matK* as a core plant barcode. In November 2009, during the Third International Barcoding of Life Conference in Mexico City, both the plastid *trnH-psbA* and ITS (or ITS2) were suggested as complementary markers to the proposed core-barcode of *rbcL* + *matK*, to be further evaluated within 18 months.

The candidate DNA barcoding markers have proved useful in the diverse applications, such as uncovering cryptic species and delimiting closely related species (Bickford et al., 2006; Gao & Chen, 2009), establishing community phylogenies of diverse ecosystems (Kress et al., 2009), and discerning counterfeit plant materials for medicine or other uses

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(Liu et al., 2011). During recent years, plant DNA barcoding research in China has grown rapidly (Yao et al., 2009; Zhang et al., 2009; Chen et al., 2010; Gao et al., 2010; Liu et al., 2010; Ren et al., 2010; Yao et al., 2010; Liu et al., 2011). In August 2009, the Barcoding Chinese Plants Project associated with the Germplasm Bank of Wild Species (GBOWS), a Large-Scale Scientific Facility, was initiated with the support from the Chinese Academy of Sciences (CAS). A coordinated effort has been made among 60 research groups from 22 research institutes and universities to evaluate the candidate barcode markers, and to barcode around 6,000 species of plants in China, including the seed collection within the GBOWS facility (Li et al., 2011a).

This special issue of *Journal of Systematics and Evolution* includes 13 papers, mainly supported by the Barcoding Chinese Plants Project and reflecting the current status of plant barcoding research in China. Li et al. (2011c) examined the universality of the candidate *matK* primers for gymnosperms; they proposed one pair of *matK* primers exhibiting high success of amplification and sequencing for gymnosperms, and designed a specific *matK* primer for Ephedraceae. Meanwhile, Yu et al. (2011) developed a new pair of *matK* primers to barcode angiosperm species that resulted in success both for amplification and sequence analysis. Which barcode marker is most efficient and universal for delimiting closely related species? Wang et al. (2011) compared genetic delimitations between the only two species of *Pugionium* (Cruciferae) using sequences from ITS, three plastid markers, and five low-copy nuclear markers. Only ITS and one low-copy nuclear marker can discern the two species of this genus. Dong et al. (2011) used *rbcL*, *matK* and ITS to evaluate the five species of *Pterygiella* (Orabanchaceae) and found that only ITS could successfully identify all species of this genus. Similar conclusions were drawn when genetic gaps among species of *Hedyotis* (Rubiaceae) (Guo et al., 2011), *Ligustrum* (Oleaceae) (Gu et al., 2011), *Primula* (Primulaceae) (Yan et al., 2011) and *Tetrastigma* (Vitaceae) (Fu et al., 2011) were evaluated by the proposed plastid DNA markers and ITS. At the family level, Du et al. (2011), Xiang et al. (2011) and Shi et al. (2011) studied the application of the proposed DNA barcodes for the species identification of Potamogetonaceae, Juglandaceae and Zingiberaceae. Their studies indicate that ITS or its partial sequence, ITS2, has significant interspecific divergence. However, Xiang et al. (2011) also found that it is difficult to align ITS sequences in the Juglandaceae and suggested that a multi-locus tier method should be adopted for barcoding in this family. Xue & Li (2011) successfully used ITS sequences to distinguish the traditional Tibetan medic-

inal plant *Gentianopsis paludosa* from its adulterants. Finally, Li et al. (2011b) reviewed applications of the *rbcL*, *matK*, *trnH-psbA* and ITS in identifying herbal medicinal species and their imitations.

We hope this collection of papers will stimulate future plant DNA barcoding studies in China. We suggest that such research should be based on reliable, vouchered species identification for sampled materials, with multiple individuals collected for each of the species, if applicable, from the genus or family of interest. These studies will enhance the creation of a reference database for plant barcoding in China, towards the eventual goal of a digitalized encyclopedia of all of China's plant species.

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