Journal of Systematics and Evolution 49 (3): 165–168 (2011) doi: 10.1111/j.1759-6831.2011.00137.x

Editorial

Plant DNA barcoding in China

[1]De-Zhu LI* [2]Jian-Quan LIU [3]Zhi-Duan CHEN [1]Hong WANG [4]Xue-Jun GE
[3]Shi-Liang ZHOU [1]Lian-Ming GAO [5]Cheng-Xin FU [6]Shi-Lin CHEN

[1](*Plant Germplasm and Genomics Centre, Germplasm Bank of Wild Species in Southwest China; Key Laboratory of Biodiversity and Biogeography, Kunming Institute of Botany, Chinese Academy of Sciences,* Kunming 650204, China)
[2](*Key Laboratory of Arid and Grassland Ecology, College of Life Sciences, Lanzhou University,* Lanzhou 730000, China)
[3](*State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences,* Beijing 100093, China)
[4](*Key Laboratory of Plant Resources Conservation and Sustainable Utilization, South China Botanical Garden, Chinese Academy of Sciences,* Guangzhou 510650, China)
[5](*Key Laboratory of Conservation Biology for Endangered Wildlife of the Ministry of Education, College of Life Sciences, Zhejiang University,* Hangzhou 310058, China)
[6](*Institute of Medicinal Plant Development, Chinese Academy of Medical Sciences, Peking Union Medical College,* Beijing 100193, China)

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 disciples 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 (*CO1*) 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

* Author for correspondence. E-mail: dzl@mail.kib.ac.cn; Tel.: 86-871-5223503; Fax: 86-871-5217791.

(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 *mat*K 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 medicinal 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.

Acknowledgements This study is supported by a grant from the Large-Scale Scientific Facilities of the Chinese Academy of Sciences (No. 2009-LSF-GBOWS-01). Dr. Zachary Larson-Rabin (CAS Kunming Institute of Botany) critically read the manuscript. We greatly appreciate the staff of JSE, particularly the Managing Editor, Yan LIANG for the support of the making of this special issue.

References

Arnot DE, Roper C, Bayoumi RAL. 1993. Digital codes from hypervariable tandemly repeated DNA sequences in the *Plasmodium falciparum* circumsporozoite gene can genetically barcode isolates. Molecular and Biochemical Parasitology 61: 15–24.

Bell EA. 1986. Preface. In: Clayton WD, Renvoize SA eds. Genera Graminum, grasses of the world. London: Her Majesty's Stationary Office.

Bickford D, Lohman DJ, Sodhi NS, Ng PKL, Meier R, Winker K, Ingram KK, Das I. 2006. Cryptic species as a window on diversity and conservation. Trends in Ecology and Evolution 22: 148–155.

CBOL Plant Working Group. 2009. A DNA barcode for land plants. Proceedings of the National Academy of Sciences USA 106: 12794–12797.

Chase MW, Salamin N, Wilkinson M, Dunwell JM, Kesanakurthi RP, Haidar N, Savolainen V. 2005. Land plants and DNA barcodes: short-term and long-term goals. Philosophical Transactions of the Royal Society of London, B: Biological Sciences 360: 1889–1895.

Chen SL, Yao H, Han JP, Liu C, Song JY, Shi LC, Zhu YJ, Ma XY, Gao T, Pang XH, Luo K, Li Y, Li XW, Jia XC, Lin YL, Leon C. 2010. Validation of the ITS2 region as a novel DNA barcode for identifying medicinal plant species. PLoS ONE 5: e8613.

Cowan RS, Chase MW, Kress WJ, Savolainen V. 2006. 300,000 species to identify: problems, progress, and prospects in DNA barcoding of land plants. Taxon 55: 611–616.

Dong LN, Wortley AH, Wang H, Li DZ, Lu L. 2011. Efficiency of DNA barcodes for species delimitation: a case in *Pterygiella* Oliv. (Orobanchaceae). Journal of Systematics and Evolution 49: 189–202.

Du ZY, Qimike A, Yang CF, Chen JM, Wang QF. 2011. Testing four barcoding markers for species identification of Potamogetonaceae. Journal of Systematics and Evolution 49: 246–251.

Fazekas AJ, Burgess KS, Kesanakurti PR, Graham SW, Newmaster SG, Husband BC, Percy DM, Hajibabaei M, Barrett SCH. 2008. Multiple multilocus DNA barcodes from the plastid genome discriminate plant species equally well. PLoS ONE 3: e2802.

Floyd R, Abebe E, Papert A, Blaxter M. 2002. Molecular barcodes for soil nematode identification. Molecular Ecology 11: 839–850.

Fu YM, Jiang WM, Fu CX. 2011. Identification of species within *Tetrastigma* (Miq.) Planch. (Vitaceae) based on DNA barcoding techniques. Journal of Systematics and Evolution 49: 237–245.

Gao T, Chen SL. 2009. Authentication of the medicinal plants in Fabaceae by DNA barcoding technique. Planta Medica 75: 417.

Gao T, Yao H, Song JY, Liu C, Zhu YJ, Ma XY, Pang XH, Xu HX, Chen SL. 2010. Identification of medicinal plants in the family Fabaceae using a potential DNA barcode ITS2. Journal of Ethnopharmacology 130: 116–121.

Gu J, Su JX, Lin RZ, Li RQ, Xiao PG. 2011. Testing four proposed barcoding markers for the identification of species within *Ligustrum* L. (Oleaceae). Journal of Systematics and Evolution 49: 213–224.

Guo X, Simmons MP, But PPH, Shaw PC, Wang RJ. 2011. Application of DNA barcodes in *Hedyotis* L. (Spermacoceae, Rubiaceae). Journal of Systematics and Evolution 49: 203–212.

Hajibabaei M, Janzen DH, Burns JM, Hallwachs W, Hebert PDN. 2006. DNA barcodes distinguish species of tropical Lepidoptera. Proceedings of the National Academy of Sciences USA 103: 968–971.

Hebert PDN, Cywinska A, Ball SL, deWaard JR. 2003. Biological identifications through DNA barcodes. Proceedings of the Royal Society of London, B: Biological Sciences 270: 313–321.

Hebert PDN, Stoeckle MY, Zemlak TS, Francis CM. 2004a. Identification of birds through DNA barcodes. PLoS Biology 2: e312.

Hebert PDN, Penton EH, Burns JM, Janzen DH, Hallwachs W. 2004b. Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly *Astraptes fulgerator*. Proceedings of the National Academy of Sciences USA 101: 14812–14817.

Hebert PDN, Gregory TR. 2005. The promise of DNA barcoding for taxonomy. Systematic Biology 54: 852–859.

Hollingsworth ML, Clark A, Forrest LL, Richardson J, Pennington RT, Long DG, Cowan R, Chase MW, Daudeul M, Hollingsworth P. 2009. Selecting barcoding loci for plants: evaluation of seven candidate loci with species-level sampling in three divergent groups of land plants. Molecular Ecology Resources 9: 439–457.

Kang'ethe EK, Jones SJ, Patterson RLS. 1982. Identification of the species of origin of fresh meat using as enzyme-linked immunoabsorbent assay procedure. Meat Science 7: 229–240.

Kress WJ, Wurdack KJ, Zimmer EA, Weigt LA, Janzen DH. 2005. Use of DNA barcodes to identify flowering plants. Proceedings of the National Academy of Sciences USA 102: 8369–8374.

Kress WJ, Erickson DL. 2007. A two-locus global DNA barcode for land plants: the coding *rbcL* gene complements the non-coding *trnH-psbA* spacer region. PLoS ONE 2: e508.

Kress WJ, Erickson DL, Jones FA, Swenson NG, Perez R, Sanjur O, Bermingham E. 2009. Plant DNA barcodes and a community phylogeny of a tropical forest dynamics plot in Panama. Proceedings of the National Academy of Sciences USA 106: 18621–18626.

Li DZ, Yang XY, Pritchard HW. 2011a. Strategies and challenges in plant germplasm conservation. Plant Diversity and Resources 23: 11–18.

Li M, Cao H, But PPH, Shaw PC. 2011b. Identification of herbal medicinal materials using DNA barcodes. Journal of Systematics and Evolution 49: 271–283.

Li Y, Gao LM, Poudel RC, Li DZ, Forrest A. 2011c. High universality of *matK* primers for barcoding gymnosperms. Journal of Systematics and Evolution 49: 169–175.

Liu Y, Yan HF, Cao T, Ge XJ. 2010. Evaluation of ten plant barcodes in Bryophyta (mosses). Journal of Systematics and Evolution 48: 36–46.

Liu J, Moller M, Gao LM, Zhang DQ, Li DZ. 2011. DNA barcoding for the discrimination of Eurasian yews (*Taxus* L., Taxaceae) and the discovery of cryptic species. Molecular Ecology Resources 11: 89–100.

Packer L, Gibbs J, Sheffield C, Hanner R. 2009. DNA barcoding and the mediocrity of morphology. Molecular Ecology Resources 9: 42–50.

Pennisi E. 2007. Taxonomy. Wanted: A barcode for plants. Science 318: 190–191.

Ren BQ, Xiang XG, Chen ZD. 2010. Species identification of *Alnus* (Betulaceae) using nrDNA and cpDNA genetic markers. Molecular Ecology Resources 10: 594–605.

Shi LC, Zhang J, Han JP, Song JY, Yao H, Zhu YJ, Li JC, Wang ZZ, Xiao W, Lin YL, Xie CX, Qian ZZ, Chen SL. 2011. Testing the potential of proposed DNA barcodes for species identification of Zingiberaceae. Journal of Systematics and Evolution 49: 261–266.

Wang Q, Yu QH, Liu JQ. 2011. Are nuclear loci ideal for barcoding plants? A case study of genetic delimitation of two sister species using multiple loci and multiple intraspecific individuals. Journal of Systematics and Evolution 49: 182–188.

Ward RD, Zemlak TS, Innes BH, Last PR, Hebert PDN. 2005. DNA barcoding Australia's fish species. Philosophical Transactions of the Royal Society of London, B: Biological Sciences 360: 1847–1857.

Xiang XG, Zhang JB, Lu AM, Li RQ. 2011. Molecular identification of species in Juglandaceae: A tiered method. Journal of Systematics and Evolution 49: 252–260.

Xue CY, Li DZ. 2011. Use of DNA barcode *sensu lato* to identify traditional Tibetan medicinal plant *Gentianopsis paludosa*

(Gentianaceae). Journal of Systematics and Evolution 49: 267–270.

Yan HF, Hao G, Hu CM, Ge XJ. 2011. DNA barcoding in closely related species: A case study of *Primula* L. sect. *Proliferae* Pax (Primulaceae) in China. Journal of Systematics and Evolution 49: 225–236.

Yao H, Song JY, Ma XY, Liu C, Li Y, Yu HX, Han JP, Duan LS, Chen SL. 2009. Identification of *Dendrobium* species by a candidate DNA barcode sequence: the chloroplast *psbA-trnH* intergenic region. Planta Medica 75: 667–669.

Yao H, Song JY, Liu C, Luo K, Han JP, Li Y, Pang XH, Xu HX, Zhu YJ, Xiao PG, Chen SL. 2010. Use of ITS2 region as the universal DNA barcode for plants and animals. PLoS One 5: e13102.

Yu J, Xue JH, Zhou SL. 2011. New universal *matK* primers for DNA barcoding angiosperms. Journal of Systematics and Evolution 49: 176–181.

Zhang JM, Wang JX, Xia T, Zhou SL. 2009. DNA barcoding: species delimitation in tree peonies. Science in China Series C: Life Sciences 52: 568–578.

Plant DNA barcoding in China

作者： De-Zhu LI， Jian-Quan LIU， Zhi-Duan CHEN， Hong WANG， Xue-Jun GE， Shi-Liang ZHOU， Lian-Ming GAO， Cheng-Xin FU， Shi-Lin CHEN

作者单位： De-Zhu LI,Hong WANG,Lian-Ming GAO(Plant Germplasm and Genomics Centre, Germplasm Bank of Wild Species in Southwest China; Key Laboratory of Biodiversity and Biogeography, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650204, China)， Jian-Quan LIU(Key Laboratory of Arid and Grassland Ecology, College of Life Sciences, Lanzhou University, Lanzhou 730000, China)， Zhi-Duan CHEN,Shi-Liang ZHOU(State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, Beijing 100093, China)， Xue-Jun GE(Key Laboratory of Plant Resources Conservation and Sustainable Utilization, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou 510650, China)， Cheng-Xin FU(Key Laboratory of Conservation Biology for Endangered Wildlife of the Ministry of Education, College of Life Sciences, Zhejiang University, Hangzhou 310058, China)， Shi-Lin CHEN(Institute of Medicinal Plant Development, Chinese Academy of Medical Sciences, Peking Union Medical College, Beijing 100193, China)

刊名： 植物分类学报 ISTIC SCI PKU

英文刊名： JOURNAL OF SYSTEMATICS AND EVOLUTION

年，卷(期)： 2011,49(3)