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.
(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 Hedysotis (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.

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


Workshop on DNA barcoding of plants and animals was conducted at Govt Science college Durg. In this 3 days power pack workshop around 50 students and faculties were participated. This workshop was arranged by Prof. Anil Kumar Shrivastav sir and Dr. Nikhil Mishra sir. 11th by ATG and it's a 2nd collaborative hand on workshop in Durg. Assisted by Research fellows, Dinesh Kumar, Motiram Sahu, Somendra Kumar and other faculties and research fellows. Following hands on training (with theory, calculations and troubleshooting) were transferred to Budding scientists; 1. PCR amplification 2. DN... DNA barcoding is a commonly used biotechnology in multiple disciplines including biology, environmental science, forensics and inspection, etc. Forest dynamic plots provide a unique opportunity to carry out large-scale, comparative, and multidisciplinary research for plant DNA barcoding. The paper concisely reviewed four previous progresses in China; specifically, species discrimination, community phylogenetic reconstruction, phylogenetic community structure exploration, and biodiversity index. CONTINUE READING.

DNA barcoding is a method of species identification using a short section of DNA from a specific gene or genes. The premise of DNA barcoding is that, by comparison with a reference library of such DNA sections (also called "sequences"), an individual sequence can be used to uniquely identify an organism to species, in the same way that a supermarket scanner uses the familiar black stripes of the UPC barcode to identify an item in its stock against its reference database. These "barcodes" are sometimes This shareable PDF can be hosted on any platform or network and is fully compliant with publisher copyright. Plant DNA barcoding in China. 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. Journal of Systematics and Evolution, May 2011, Wiley. DOI: 10.1111/j.1759-6831.2011.00137.x. The authors haven't finished explaining this publication. If you are the author, sign in to claim or explain your work. Read Publication. http://dx.doi.org/10.1111/j.1759-6831.2011.00137.x. The following have contributed to this page: Dr X During the last decade, DNA barcoding offers an accurate and efficient strategy that can identify existing species and discover unknown species via analysis of sequence variation in a standardized region of DNA. Recent studies have shown that DNA barcoding as well as minibarcoding and metabarcoding is capable of identifying animal species and discriminating the authentics from the adulterants in various types of traditional medicines, including raw materials, processed products, and complex preparations. G-Biosciences. Tissues from different species including animal, plant, bacteria, yeast and fungus. Together, these studies demonstrate the availability of DNA barcoding in trade supervision of threatened fish species used in TM.