

Abstract

Rapid and accurate identification of endangered species is a critical component of bio-surveillance and conservation management, and potentially policing illegal trades. However, this is often not possible using traditional taxonomy, especially where only small or pre-processed parts of plants are available. Reliable identification can be achieved via a comprehensive DNA barcode reference library, accompanied by precise distribution data. However, these require extensive sampling at spatial and taxonomic scales, which has rarely been achieved for cosmopolitan taxa. Here we construct a comprehensive DNA barcode reference library, and generate distribution maps using species distribution modeling (SDM), for all 15 *Taxus* species worldwide. We find that trnL-trnF is the ideal barcode for *Taxus*: it can distinguish all *Taxus* species, and in combination with ITS identify hybrids. Among five analysis methods tested, NJ was the most effective. Among 4151 individuals screened for trnL-trnF, 73 haplotypes were detected, all species-specific and some population private. Taxonomical, geographical and genetic dimensions of sampling strategy were all found to affect the comprehensiveness of the resulting DNA barcode library. Maps from SDM showed that most species had allopatric distributions, except three in the Sino-Himalayan region. Using the barcode library and distribution map data, two unknown forensic samples were identified to species (and in one case, population) level, and another was determined as a putative interspecific hybrid. This integrated species identification system for *Taxus* can be used for bio-surveillance, conservation management and to monitor and prosecute illegal trade. Similar identification systems are recommended for other IUCN- and -CITES listed taxa. This article is protected by copyright. All rights reserved.