

Using DNA to assess errors in tropical tree identifications: How often are ecologists wrong and when does it matter?

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Abstract

Ecological surveys of tropical tree communities have provided an important source of data to study the forces that generate and maintain tropical diversity. Accurate species identification is central to these studies. Incorrect lumping or splitting of species will distort results, which may in turn affect conclusions. Although ecologists often work with taxonomists, they likely make some identification errors. This is because most trees encountered in the field are not reproductive and must be identified using vegetative characters, while most species descriptions rely on fruit and flower characters. Because every tree has DNA, ecological surveys can incorporate molecular approaches to enhance accuracy. This study reports an extensive ecological and molecular survey of nearly 4000 trees belonging to 55 species in the tree genus *Inga* (Fabaceae). These trees were sampled in 25 community surveys in the southwestern Amazon. In a process of reciprocal illumination, trees were first identified to species using vegetative characters, and these identifications were revised using phylogenies derived from nuclear and chloroplast DNA sequences.

We next evaluated the effects of these revised species counts upon analyses often used to assess ecological neutral theory. The most common morphological identification errors involved incorrectly splitting rare morphological variants of common species and incorrectly lumping geographically segregated, morphologically similar species. Total error rates were significant (6.8–7.6% of all individuals) and had a measurable impact on ecological analyses. The revised identifications increased support for spatially autocorrelated, potentially neutral factors in determining community composition. Nevertheless, the general conclusions of community-level ecological analyses were robust to misidentifications. Ecological factors, such as soil composition, and potentially neutral factors, such as dispersal limitation, both play important roles in the assembly of *Inga* communities. In contrast, species-level analyses of neutrality with respect to habitat were strongly impacted by identification errors. Although this study found errors in morphological identifications, there was also strong evidence that a purely molecular approach to species identification, such as DNA barcoding, would be prone to substantial errors. The greatest accuracy in ecological surveys will be obtained through a synthesis of traditional, morphological and modern, molecular approaches.

Supporting Information

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