Novel Iterative Methodologies in the Search for a Universally-Functional DNA Barcode for Plants

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Much biological research depends upon species diagnoses of sample organisms. The advent of DNA barcoding has made this process fast, inexpensive, and highly accurate. In place of the morphological markers used in conventional species identification systems, DNA barcoding employs a molecular marker—a short, standardized sequence of DNA—to identify species. Although there exists an effective barcode for identification of animals, there is no universally-successful equivalent for plants. In an attempt to find one, we devised a novel methodology in which whole plant chloroplast genomes are iteratively and systematically analyzed in successive 500 base pair brackets. Two 500bp barcodes (out of the 2950 tested) were found to have unprecedented, near-perfect accuracy in plant species identifications. Additional testing on extraneous genomes confirmed 100% accuracy. Using these barcodes, erroneous identifications that have afflicted environmental and ecological research will be resolved. Moreover, these barcodes will aid in the rapid discovery of new plant life, urgent due to the current crisis of biodiversity loss. New plant species are also of tremendous medicinal value. However, the computer program we designed to perform the iterative screening took over 125 hours to run to completion. In order to optimize the process, therefore, we devised an algorithm that iteratively analyzed shorter 1-2 base pair segments, only later resolving them into the larger functional barcode. The algorithm required only 40 minutes for the entire genome screening, a 170-fold reduction in time-consumption. Our iterative methodology can now be utilized rapidly and practically, potentially to uncover exceptionally accurate barcodes (like those found in this study) for other kingdoms of life.

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