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DNA-Based Identification of Pigweed Species from Six Tennessee Regions

Abstract

Accurately identifying plant species at the genetic level is essential for understanding biodiversity, managing invasive species, and advancing agricultural research. This study focuses on the DNA-based identification of pigweed species in Tennessee, utilizing molecular techniques such as DNA extraction and Polymerase Chain Reaction (PCR). The primary objective was to develop and refine methodologies for extracting and analyzing plant DNA to identify pigweed species based on PCR amplified genetic markers. Pigweed leaf samples were collected from different counties across Tennessee during summers of years 2022-2024. To ensure comprehensive representation, three distinct samples were procured from separate locations within each selected Tennessee county. In total, 51 out of 92 counties, comprising nine from Northwestern Tennessee, 10 from Southwestern Tennessee, six from Northeastern Tennessee, seven from Southeastern Tennessee, 12 from Northcentral Tennessee and seven from the Middle Tennessee regions were covered. DNA extractions were conducted on various pigweed samples, ensuring high-yield and high-purity DNAs for subsequent analysis. PCR techniques were employed to amplify specific conserved genomic regions, which were then visualized using gel electrophoresis. Thus, DNA barcoding methods enabled species identification and preliminary findings revealed that even minimal leaf tissue provided sufficient genetic material for identification, emphasizing the efficiency of modern molecular approaches in plant taxonomy. Furthermore, variations in DNA extraction efficiency among pigweed populations highlighted the need for species-specific protocol adjustments to optimize genetic recovery. Collaborating within the research group allowed sample collection and refining analytical and technical approaches per molecular biology tools and experimental design. Observing genetic similarities among species towards phylogenetics and evolutionary biology are crucial for a future in plant genetics and biotechnology. This research provided pathways towards exploration of plant genetic manipulations such as incorporating genome-editing technologies (CRISPR) to enhance plant traits.

Keywords: DNA extraction, pigweed species, genetic sequencing, PCR, phylogenetics, molecular biology, plant biotechnology, CRISPR, DNA barcoding, species identification