

# ***ABSTRACTS***

*from oral and poster presentations  
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# Seed Identification from ITS DNA Sequencing

Robert Price

## ABSTRACT

The ITS (internal transcribed spacer of 18S-26S nuclear ribosomal DNA) region was amplified and sequenced from our samples of individual or small numbers of seed, from a diversity of flowering plant families, including Acanthaceae, Apiaceae, Asteraceae, Chenopodiaceae, Convolvulaceae, Euphorbiaceae, Fabaceae, Lamiaceae, Meliaceae, Plantaginaceae, Poaceae, Primulaceae and Ranunculaceae. Seeds or seedlike fruits were decoated and the embryo plus endosperm/perisperm thinly sliced then transferred to a microcentrifuge tube with indicator silica gel and a magnetic ceramic bead used to pulverize the seed material for DNA extraction. Hard coated seeds (e.g., of Fabaceae) were soaked in water overnight to facilitate decoating and slicing. PCR amplification was successful in 21 out of 25 samples, with the failed amplifications due to seeds with very hard storage tissue and/or very small and possibly poorly developed embryos. Resulting sequences were identified by comparison to GenBank database sequences by BLAST search, and only unique matches of 99–100% identity were treated as probable identifications to individual species. All 21 samples with successful amplification were placed in the correct family by the sequence analysis, as judged by morphological analysis of the seed or fruit material. Eighteen of the 21 samples (86%) were identified successfully to a plausible individual genus by the best sequence match, with the three samples identified only to tribe either representing large or subtropical to tropical groups with limited sequence sampling (Asteraceae tribes Gnaphalieae and Vernonieae, and Meliaceae). Eleven of the 21 samples (52%) were successfully identified to a likely individual species or species-pair by the sequence analyses. Identifications were only made to the genus level in cases where the maximum sequence match was below 99% [a tropical *Astripomoea* A. Meeuse (Convolvulaceae) and a tropical *Ocimum* L. (Lamiaceae)], when multiple species gave the same percentage matches in identity (found in the large genera *Anthemis* L. (Asteraceae), *Ruellia* L. (Acanthaceae) and *Vicia* L. (Fabaceae), or when seed or spikelet morphology suggested that the sample may represent a related species that may not have been present in the GenBank database. Results suggest that ITS sequencing from individual seeds may be a very valuable approach for identifying unusual seed contaminants that are difficult to identify morphologically due to nonrepresentation in reference collections, atypical appearance, or loss of characters in seed conditioning. It is likely to be particularly helpful in identifying contaminants such as infrequently encountered native species or unfamiliar taxa in globally sourced seeds.

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# Forages: the Seeds of Sustainability

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## ABSTRACT

The world needs high quality seeds and the food systems they support. Those working in agriculture and natural resources management have a great purpose: improving food production systems and sustaining the resources that make them possible. The Food and Agriculture Organization of the United Nations (FAO) projects needing 70% more food for an additional 2.3 billion people by 2050. Accomplishing this while combating poverty and hunger, using scarce natural resources more efficiently, and adapting to climate change will require improved management of grasslands based on research-based information and improved seed resources. The grassland biome covers  $\frac{2}{3}$  of the land masses of the world and makes up  $\frac{1}{4}$  of the earth's surface. This land must be used more effectively to produce food since much of the earth's land surface is incapable of producing annual cereal, vegetable, or fruit crops. Although grasslands contain mostly grass, they are areas of great diversity of plant and animal species. Domestic and wild ruminant animals convert grasses, legumes, and other forbs to high quality human food. Ruminant animal digestive tract microorganisms produce enzymes that degrade cellulose and hemicellulose in fibrous plant materials. High quality forage seeds provide the foundation for the uniquely sustainable forage-livestock systems that link soil, plant, animal, and human components in a "circle of life." Multiple scientific disciplines are involved in managing this continuum to ensure a healthy, sustainable system and global food security. Improving, producing, testing, and wisely utilizing high quality seeds is central to creating economically and environmentally sustainable agriculture, and enhancing the quality of life for farmers and society as a whole.

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