Species and Genome Relationships in Arachis: A Molecular Phylogeny.

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The genus Arachis (Fabaceae) is comprised of 80 species restricted to South America. The existing monograph divided the genus into nine sections and provides an intuitive assessment of evolutionary relationships, but a comprehensive phylogenetic analysis of the genus is lacking.

To test the current systematic treatment of the genus, we reconstructed a phylogeny for Arachis using nuclear ITS and plastid trnT-trnF sequences from a total of 48 species representing all nine sections. ITS cloning of the allotetraploid species of section Arachis indicated the presence of A and B genome alleles and chimeric sequences. Our study also showed species from section Extranervosae as the first emerging lineage in the genus, followed by sections Triseminatae and Caulorrhizae, and two terminal major lineages, which we refer to as erectoides and arachis. Species in the arachis lineage formed two major clades, arachis I that includes the B and D genomes species and the aneuploids, and arachis II that includes the A genome species. Our results substantiated the sectional treatment of Caulorrhizae and Triseminatae, but demonstrated that five sections (Arachis, Erectoides, Procumbentes, and Trierectoides) are not monophyletic. A detailed study of the genus Arachis with denser taxon sampling, additional genomic regions, plus information from morphology and cytogenetics is needed for a comprehensive assessment of its systematics.