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## Contribution to the Systematics of the Genus *Centrosema* (Leguminosae) through Molecular Analyses: An Ongoing Project in Venezuela

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## Abstract

*Centrosema* is an economically important Neotropical genus which, together with *Desmodium* and *Stylosanthes*, is regarded as a genus with particularly high potential as a forage legume in the tropics and sub-tropics. Several *Centrosema* species are currently being used not only as forage but also for soil cover and soil improvement. Some species are well adapted to prolonged drought and the acid, low-fertility soils that prevail in the tropics, thus making *Centrosema* species particularly important for low-input agricultural production systems.

There are some uncertainties regarding species delimitation and evolutionary relationships within the genus, due to the morphological plasticity of the species. Consequently, there is a number of differences between species which are not discernable using only morphological analysis. Therefore, the main objective of this research is to assess species delimitation and phylogenetic relationships among Venezuelan *Centrosema* species, using molecular data, as a complement of morphological studies. Molecular analyses are based on polymorphism of intergenic sequences of cpDNA  $atp\beta$ -rbcL and trnK/matK, Internal Transcribed Spacer (ITS) of rDNA, Random Amplification of Polymorphic DNA (RAPD), and Simple Sequence Repeats (SSRs).

Preliminary results of the intergenic sequences trnK/matK (trnK685F/matK1932) and  $atp\beta$ -rbcL (R7/S11) show, on the one hand, that Centrosema has a monophyletic origin, *i.e.*, the species have a common ancestor. On the other hand, the grouping of species (clades) obtained by these molecular markers differs, in some cases, from the classification proposed by Williams and Clements (1990) where the Centrosema species were classified in 11 sub-generic groups based on morphological similarities. More conclusive results are expected when further data are obtained.

Keywords: Centrosema, introns, ITS, phylogenetics, RAPD, SSRs

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