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Genetic Diversity of the Tropical Legume Genus *Stylosanthes* in Venezuela: An ongoing Project

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Abstract

Stylosanthes is a predominantly neotropical genus of legumes considered as most important for purposes other than grain production (*e.g.* feed, soil cover). Some species have been of particular importance in some regions of sub-Saharan Africa, tropical Asia, and Australia. In Venezuela, however, adoption of *Stylosanthes* species has been relatively low or nil. This is partly due to lack of commercial seed and to the fact that only small efforts have been undertaken to evaluate diversity at the local level. In previous research, a combined taxonomic and biogeographic study based on Venezuelan herbarium specimens and germplasm accessions was conducted. Based on morphological characters, 11 *Stylosanthes* species were identified, and their natural distribution was documented. Nevertheless, there were a number of differences among the populations that were not discernible using morphological analysis, only; a complementary technique is required to assess such differences.

The main objective of the research presented here is to measure intra-specific diversity of Venezuelan *Stylosanthes* species in order to assess whether variations among populations have a genetic basis. To ensure that the diversity evaluated is truly natural, the research concentrates on the variability that occurs in the wild, *i.e.* not considering germplasm conserved *ex situ*. In view of the need to make a compromise between solidity of data and economic feasibility of the collecting activities involved, for each of the 11 species three populations from contrasting environments, covering a large geographic range, were sampled in the dry seasons of 2007 and 2008 (seed and herbarium specimen). The collected seed will be used for molecular analysis of genetic diversity, applying the Simple Sequence Repeats marker (SSRs) technique, the collected herbarium specimens will be used for morphological studies.

As a result, we expect not only to have a better tool for delimiting the species within the genus, based on both, SSR and morphological analyses. In addition, we will have an indication whether the morphological differences among populations have a genetic basis. These results together with the ones we will obtain from further morpho-agronomic evaluations, may lead us to identify particularly promising populations.

Keywords: Molecular analysis, morphological analysis, SSRs markers, taxonomy