Phylogenetic relationships in the genus Manihot P. Mill. (Euphorbiaceae): Biogeography and comparative ecology of the species from the Andes and the Amazon regions

Juliana Chacón and Santiago Madriñán

ABSTRACT

The genus *Manihot* P. Mill. (Euphorbiaceae) comprises 98 species of herbs, shrubs, and vines, which grow in semi-arid zones of tropical regions, from southern North America to Argentina and the West Indies. The geographical range of the genus extends to Africa and Asia, where cassava (*Manihot esculenta* Crantz subsp. *esculenta*) grows as a cultivated plant. Its socioeconomic importance lies in the high content of starch accumulated in its tuberous roots—one of the primary sources of carbohydrates for people in the tropics. Wild *Manihot* species, however, are not such a valuable resource, because of the presence of slender roots, and high contents of latex and cyanogenic glycosides.

Genetic variability in cultivated cassava has been decreasing because of artificial selection over the last few centuries. This loss has resulted in plants that are vulnerable to tropical diseases, insect attacks, or severe climatic conditions, such as drought. Hybridization with wild Manihot species has been proposed as a mechanism for recovering such variability. This is based on the fact that alleles lost during the cassava domestication process are present in its wild ancestors, which are more variable, but less productive.

Identification of cassava's wild ancestors has been a matter of debate since 1973, when Rogers and Appan proposed that *Manihot aesculifolia* (Kunth) Pohl, from Central America, was its closest wild relative. In the last few years, molecular techniques such as RAPD, AFLP, and microsatellites, have suggested that *M. esculenta* is most closely related with some recently discovered populations of *M. esculenta* subsp. *flabellifolia*, from the Brazilian Cerrado. Phylogeographic studies of nuclear genes confirmed this result, although little is known about the populations of cassava distributed in the northern end of South America. Phylogenetic relationships with other species in the genus are still unclear, and often obscured by the high plasticity of morphological characters and by the limited sampling.

Direct DNA sequencing of several genes will be used to build a molecular phylogeny of *Manihot*, serving as an evolutionary context for previous analyses. The resulting cladogram from the Maximum Parsimony, Maximum Likelihood, and Bayesian analyses will be used to elucidate biogeographic patterns in the genus. Nested Cladistic Analyses (NCA) of populations of *M. esculenta* from the north of Colombia will be analyzed also. Using the "independent contrast" method, we will study the evolution of ecological characters (habitat preferences, pollination systems, etc.) in a phylogenetic context to understand the adaptation process in the genus.

Ginés-Mera Memorial Fellowship