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Meeting the Challenges
of the
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Multilocal evaluation of the cassava core collection from CIAT

CIAT hosts in trust (on FAO's behalf) the world collection of cassava and related species. The collection includes 5184 landraces and 400 improved Manihot esculenta clones and 883 accessions from 33 different Manihot wild relative species. A subset of this large collection (the core collection) was chosen to represent as much as 95% of all the genetic variability present in M. esculenta gene pool. Plants from entire core collection (630 accessions) were as recovered from the in vitro status and grown in three contrasting environments of Colombia (mid-altitude vallevs, sub-humid environment and acid-soil savannas) in three consecutive years (one evaluation per year). Evaluation was conducted in single ñ row plots with 8 plants per plot. Not all the accessions could be evaluated because some eventually got infected with frog skin disease or simply failed to produce enough planting material for the following evaluation. No replications could be used given the scarcity of planting material and the size of the evaluation. Contrasts with improved germplasm suggest that for some traits considerable gains have been made to improve cassava (for example to increase dry matter content in the root). As expected. considerable genotype - by - environment affected the performance of these accessions. This work is also important to understand the stability of different traits for proper phenotypic characterization of cassava germplasm, to avoid duplications and to prevent contaminations or mistakes that once they are committed tend to be perpetuated.

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Gene flow in cassava: the case of Manihot esculenta and Manihot leptophylla in Ecuador

In Ecuador, cassava is produced principally in the Amazon Basin (where Amerindian farmers cultivate many varieties) and in coastal regions, where it is cultivated both commercially and for subsistence. Throughout Ecuador, only sweet varieties are grown. Of cassava's two wild congeners in Ecuador, M. brachyloba occurs only east of the Andes and M. leptophylla exclusively in coastal provinces. Allem (2002) tentatively placed M. leptophylla within the complex including cassava (M. esculenta ssp. esculenta) and its closest wild relatives, M. esculenta ssp. flabellifolia and M. esculenta ssp. peruviana. However, we previously reported that M. leptophylla was genetically distant from the species in cassava's primary genepool. We evaluated whether gene flow occurred between a population of M. leptophylla (N = 48 individuals sampled) and a nearby population of domesticated cassava (N = 16), using 35 microsatellite markers. The two species were strongly differentiated; many alleles found in M. leptophylla were restricted to this species. However, population structure analysis revealed three genetically distinct groups: i) domesticated cassava; ii) the wild species; and iii) one intermediate individual. Our a priori classification of individuals as wild or domesticated was only partially supported: seven individuals classified a priori as M leptophylla in fact grouped with domesticated cassava. Of these, four were from disturbed areas (rural roadsides) and are likely feral individuals. The single intermediate individual showed a 1:1 proportion of alleles from the wild and domesticated genepools. Despite small sample sizes, our results suggest that some gene flow occurs between cassava and this distant wild species.