

Phenotyping and genotyping of cassava F1 population (CTS family) for mapping drought tolerance QTLs based on RAD Sequencing

María Alejandra Bedoya, Adriana Bohorquez-Chaux, Vianey Barrera-Enriquez & Xiaofei Zhang

Alliance of Bioversity International and CIAT – Palmira, Colombia

Email: m.bedoya@cgiar.org

The drought phenomenon is currently one of the main climatic problems that affects all types of crops around the world. Cassava is a crop of great importance in the tropics because it plays a relevant role in food security and in industrial processes; therefore, knowing the tolerance to abiotic phenomena such as drought allows generating breeding programs to obtain resistant genotypes. In addition to identifying traits that plants subjected to water deficit can develop and relating this type of results with genetic information.

The main objective of this research is to generate a phenotyping methodology for greenhouse plants subjected to drought.

METHODOLOGY

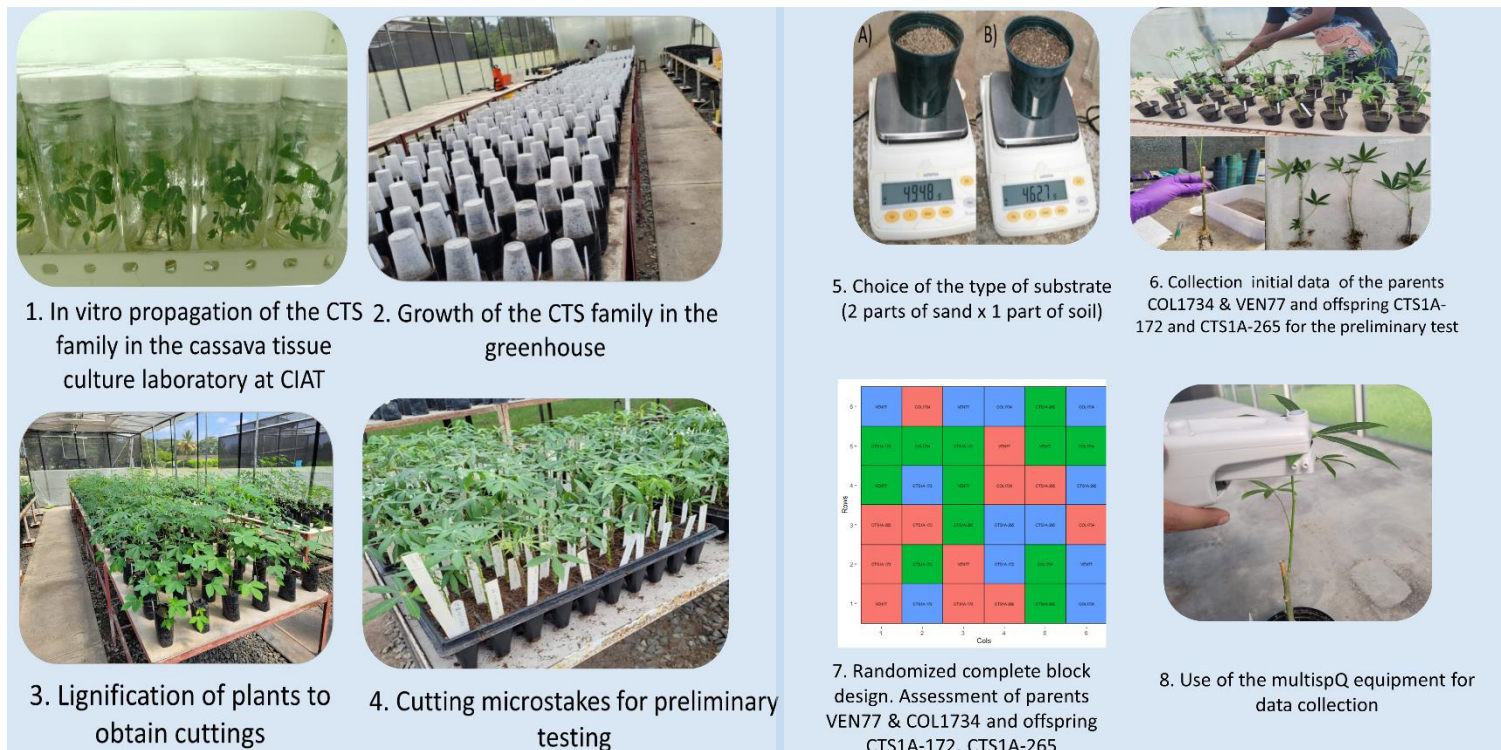


Fig 1. Phenotyping methodology for the CTS family

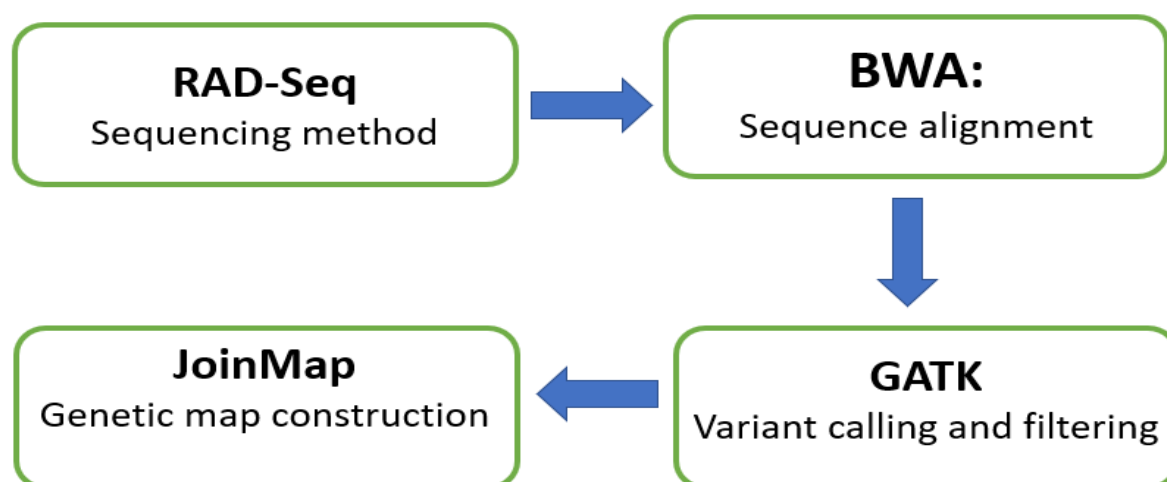


Fig 2. Methodology for genetic map construction of the CTS family, for Drought Tolerance

RESULTS AND DISCUSSION

Preliminary results were obtained from the greenhouse evaluation of four genotypes of family CTS (107 individuals), where plant growth could be observed for four weeks. This preliminary test was carried out in order to determine the effect of the treatments 10, 20 and 30 cc of water. Standardization of the greenhouse bioassays was carried out to determine the data collection time and general logistics.

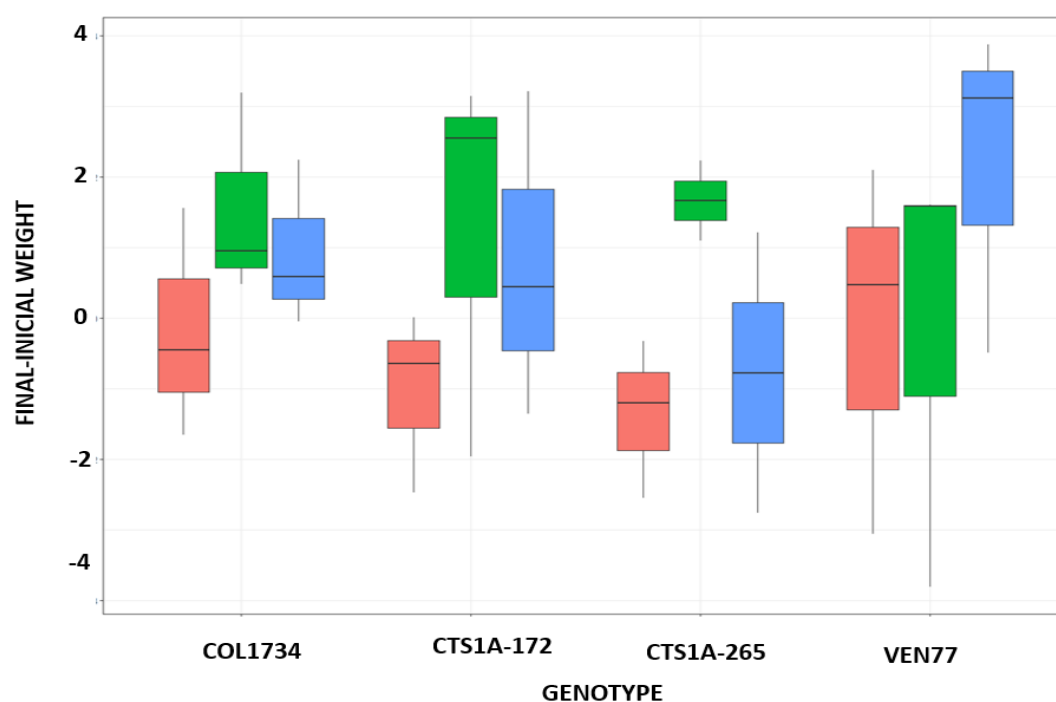


Fig 3. Weight of the evaluated genotypes vs treatments.

It was possible to determine that the growth for the COL1734 genotype was similar for the three treatments. In contrast, VEN77 which had a better growth with the 30-cc treatment. In the case of the offspring CTS1A-172 & CTS1A-265 they presented a better growth with the 20-cc treatment.

PERSPECTIVES

A complete phenotypic characterization of the family will be carried out, in order to make an association of genotypic and phenotypic data and to find genomic regions associated with Drought Tolerance trait. Activities for complete this objective are:

- Evaluate the whole CTS family (107 genotypes).
- Analysis of different morphological and physiological variables such as the activity of photosystems I & II using the MultispQ equipment.
- Construction of the genetic map.
- QTLs analysis.