

Phenotypic and Genetic Changes as a Result of Cassava Domestication

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Wilson Castelblanco^{1,2} and Anna Westerbergh¹



¹Department of Plant Biology and Forest Genetics, Swedish University of Agricultural Sciences (SLU), Uppsala, Sweden

²Centro Internacional de Agricultura Tropical (CIAT), Cali, Colombia

Wilson.Castelblanco@vbsg.slu.se

Anna.Westerbergh@vbsg.slu.se

Summary

- An F₂ population derived from a cross between cassava and its wild ancestor, *Manihot esculenta* spp. *flabellifolia*, is analyzed by quantitative trait loci (QTL) mapping to identify the genes that control trait differences between cassava and its ancestor.
- A linkage map based on SSR and EST-SSR markers is under construction in our lab at SLU.
- A phenotypic evaluation of cassava, *flabellifolia* and the F₂ population was conducted under controlled conditions in a greenhouse at SLU.
- Significant differences in root and stem traits between cassava and *flabellifolia* were found. Tuberous roots developed early during growth of cassava, while in *flabellifolia* the tuberous roots started to form when the shoot growth had ceased. The F₂ population showed large phenotypic variation and some F₂ genotypes showed higher tuberous root weight than cassava.
- This project will provide significant knowledge for the development of molecular marker tools for the introgression of favorable wild genes into cassava farmers' varieties.

Phenotypic changes

Cassava originates from South America and has been domesticated for more than 5000 years from its wild ancestor *Manihot esculenta* ssp. *flabellifolia* (1), which has resulted in phenotypic changes. We study phenotypic differences between cassava and *flabellifolia* and the genetic basis of these differences. Replicates of cassava, *flabellifolia* and F₂ plants have been grown in 3 blocks in a greenhouse and harvested after 6 and 10 months, respectively, and are also growing in an ongoing field study. Below we present some of the studied traits from the greenhouse trial.

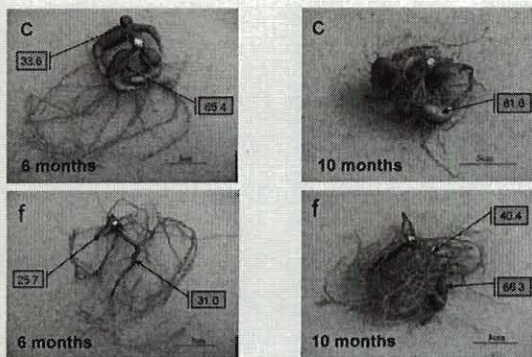
Stem and root traits differ between cassava and *flabellifolia*

Phenotypic mean and standard error at 6 months after planting of one parent genotype each of cassava and *flabellifolia* and the derived F₂ offspring.

| Trait | cassava | <i>flabellifolia</i> | F ₂ offspring |
|---|-------------|----------------------|--------------------------|
| Plant height after 6 months (cm)* | 220.2 ± 5.8 | 252.9 ± 12.4 | 193.4 ± 5.1 |
| Number of nodes* | 51.9 ± 1.8 | 42.7 ± 1.7 | 39.5 ± 0.7 |
| Mean internode length* | 8.1 ± 0.5 | 10.9 ± 0.6 | 9.0 ± 0.1 |
| Thickness of stem at the base (mm)* | 8.9 ± 0.2 | 6.8 ± 0.4 | 5.9 ± 0.1 |
| Thickness of stem in the middle (mm) | 6.9 ± 0.1 | 6.4 ± 0.4 | 5.3 ± 0.1 |
| Thickness of stem at the top (mm)* | 2.8 ± 0.1 | 3.6 ± 0.2 | 2.8 ± 0.1 |
| Weight of fibrous and tuberous roots (g)* | 35.8 ± 4.2 | 5.8 ± 0.9 | 16.4 ± 1.2 |
| Weight of tuberous roots (g)* | 30.7 ± 4.0 | 0.9 ± 0.5 | 12.4 ± 1.0 |
| Total number of tuberous roots* | 4.9 ± 0.5 | 1.6 ± 0.5 | 3.9 ± 0.3 |

*Significant difference between cassava and *flabellifolia* (ANOVA p<0.05). Number of cassava plants = 9, *flabellifolia* plants = 9 and F₂ genotypes = 183 with 3 replicates each.

Late formation of tuberous roots and synthesis of starch in *flabellifolia*



Root morphology and starch content (g/100g) in fibrous roots (green boxes) and tuberous roots (blue boxes) of cassava (c) and *flabellifolia* (f) at 6 and 10 months after planting.

Weight and number of tuberous roots at 6 and 10 months after planting.

| Trait | cassava | | <i>flabellifolia</i> | |
|--|------------|------------|----------------------|-------------|
| | 6 months | 10 months | 6 months | 10 months |
| Weight of fibrous and tuberous roots (g) | 35.8 ± 6.8 | 45.5 ± 8.0 | 5.8 ± 0.1 | 10.3 ± 1.5* |
| Weight of tuberous roots (g) | 30.7 ± 6.3 | 41.8 ± 7.7 | 0.8 ± 0.8 | 6.4 ± 1.3* |
| Total number of tuberous roots | 4.9 ± 0.8 | 4.8 ± 0.9 | 1.6 ± 0.8 | 5.8 ± 1.1* |

*Significant changes from 6 to 10 months (ANOVA p<0.05). Number of cassava plants at 6 months = 9, at 10 months = 6; *flabellifolia* plants at 6 months = 9 and at 10 months = 4.

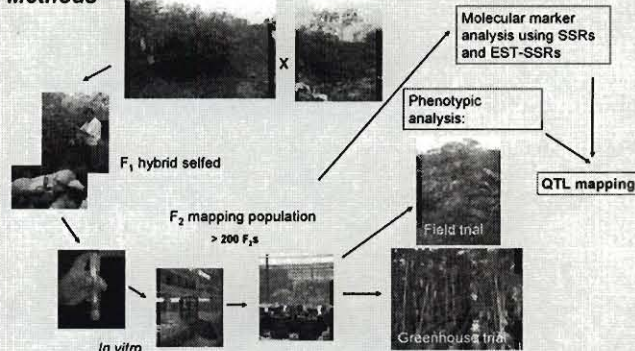
Goals

- Our specific goal is to understand the phenotypic and genetic changes that have occurred as a result of domestication, especially to identify the genes that control trait differences between cassava and its wild ancestor using QTL mapping, a method that combines molecular markers, trait and statistical analyses.
- Our long-term goal is to develop molecular markers for introgression of favorable wild genes into cassava. These markers will be used in marker-assisted selection where the breeders can take advantage of the linkage between a molecular marker allele and a QTL that controls the trait of interest.

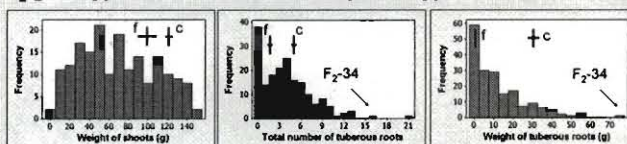
Genetic changes

The scientific breeding of cassava began relatively recently compared to other major crops. The small-scale farmers have been the engine behind the breeding for thousands of years. The farmers' needs vary a lot within different areas and they select different phenotypes. This is seen in a high heterozygosity level within cassava (2) and a high genetic variation within and between farmers' varieties (3). The less directed selection in cassava compared to many other crops may have resulted in contrasting patterns of genetic changes. Such difference has been found between maize and its wild relatives using the QTL mapping approach (4-6).

Methods



F₂ genotypes with more extreme phenotypes than cassava



F₂ population showing large phenotypic variation in stem and root traits at 6 months after planting and F₂ genotypes with considerable higher tuberous root weight than cassava were observed. The mean values and 95% confidence intervals for clones of the *flabellifolia* (f) and cassava (c) parents are indicated.



Fibrous and tuberous roots of cassava (c) and the F₂-34 genotype (F₂)

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