

Genetics of traits selected upon in the domestication of cassava

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Introduction

Loss of genetic diversity during domestication

During domestication strong selection on specific traits has gradually decreased the genetic variability in crops. This has led to accumulation of some genotypes and traits, whereas others have been lost. Some of the lost traits (such as pathogen resistance) are of importance for cultivation of modern crops. However, these traits and genotypes are preserved in the wild relatives.

QTL mapping

A useful approach to identify the genetic changes that have occurred during domestication is quantitative trait loci (QTL) mapping. For that we need detailed genetic maps and advanced statistical methods.

Using this method we can determine

- i) the minimum number of genes or group of genes (QTLs) controlling a trait
- ii) how large effect a single QTL has on a trait
- iii) where these QTLs are located in the genome

Experiences from QTL mapping in maize and its wild relatives

QTL mapping studies of maize⁽¹⁾ and other major crops such as rice⁽²⁾, sorghum⁽³⁾ and tomato⁽⁴⁾ have shown that the morphological differences between the crops and their wild relatives are often controlled by:

- a small number of genes
- some of these having a large effect

However, in our QTL mapping studies of the morphological differences between perennial and annual teosinte, wild relatives of maize, we found a different pattern of genetic changes.

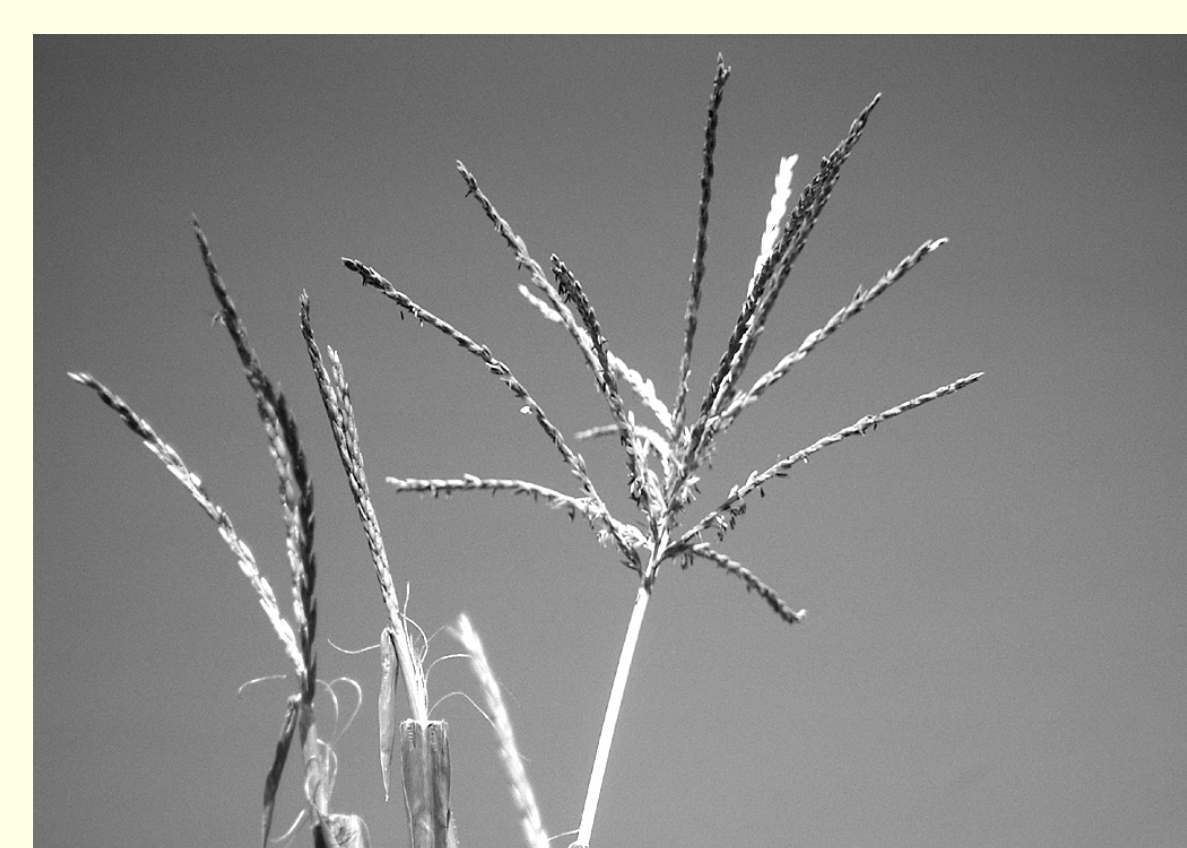
Zea diploperennis



Z. mays ssp. parviglumis



The perennial *Zea diploperennis* and the annual *Z. mays ssp. parviglumis* differ in a number of traits. Among the most striking differences is that *Z. diploperennis* forms rhizomes (yellow arrows), while *Z. mays ssp. parviglumis* lacks these over-wintering underground stems⁽⁵⁾.



They also differ in tassel (male inflorescence) morphology. The tassels of *Zea diploperennis* possess few branches and large male spiklets, while the tassels of *Z. mays ssp. parviglumis* branch much more abundantly and bear small spiklets⁽⁶⁾.

We found that the evolution of tassel and perennial traits under natural selection has, in contrast to crop domestication, only involved genes of small to moderate effects^(5,6).

References

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QTL mapping in Cassava

A major part of the cassava breeding takes place in the farmer's villages. This local breeding has resulted in a less directed selection in cassava than in maize and other crops grown in the industrial world. The difference in the selection regime between cassava and many other crops may have resulted in contrasting patterns of genetic changes.

Relatively few DNA-based studies have been carried out on cassava and very little is known about the genetics of domestication. The characterization of QTLs controlling trait differences between cassava and its wild relatives will make it possible to reintroduce genes from the wild relatives with marker-assisted breeding in an effective and directed way.

Main goals:

- i) to elucidate the genetic changes that have occurred during domestication
- to test whether the pattern of genetic changes involving major genes applies to cassava
- iii) to provide tools for reintroducing genes for desirable traits from the wild relatives into cassava cultivars

The origin of cassava

A close genetic relationship has been found between the wild *Manihot esculenta ssp. flabellifolia* and the cultivated cassava. *M. esculenta ssp. flabellifolia* is therefore suggested to be the ancestor of cassava⁽⁷⁾.



M. esculenta ssp. flabellifolia



M. esculenta ssp. esculenta
cassava

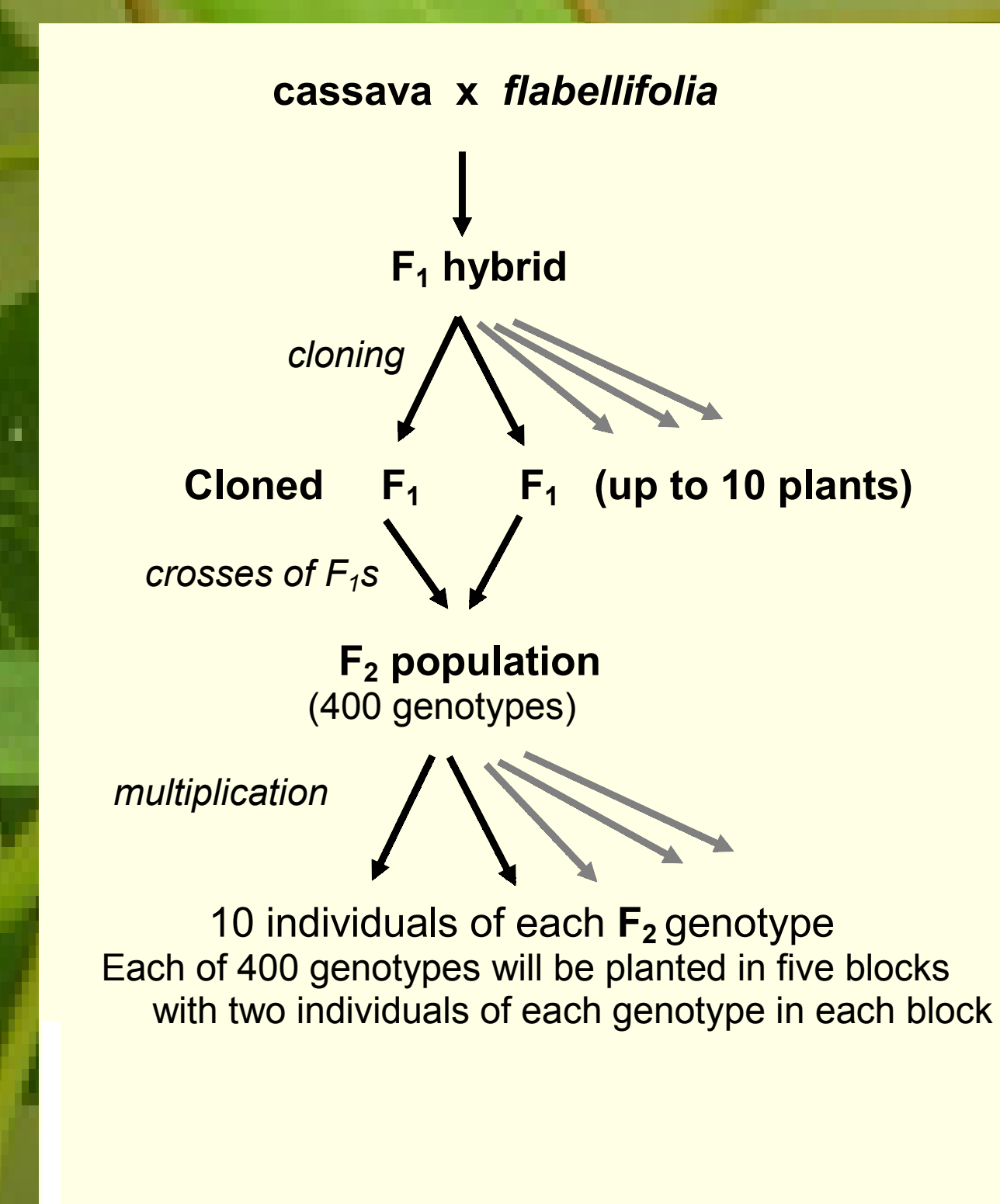
A QTL mapping approach will be used for identifying and estimating the effect of individual QTLs controlling trait differences between cassava and *M. esculenta ssp. flabellifolia*.

Traits of interest:

Four groups of traits are of major interest in the domestication of cassava:

- Morphological traits – roots, stem and leaves
- Contents of cyanogenic glucosides
- Contents of nutrients – iron, zinc and β -carotene
- Resistance to pathogens

Experimental design:



Analyses:

- i) Phenotypic analysis of 4 000 F_2 individuals
- ii) Molecular analysis of the 400 F_2 genotypes using 150 SSR and RFLP markers
- iii) Statistical analysis using composite interval mapping