

Progress in determining the genetic basis and genetic linkage mapping of Cassava Brown Streak Disease tolerance in Tanzania

Kulembeka, H.P.^{1,2,4}; Ferguson, M²; Kanju¹ E³; Labuschagne, M⁴; Herselman, L⁴; Mkamilo, G¹ and Fregene, M⁵

Introduction

A major biotic constraint of cassava in Tanzania is cassava brown streak disease (CBSD). Using sources of field tolerance available, experiments were initiated with the objectives to study the genetics for resistance to the disease and search for molecular markers associated with the field tolerance.

Cassava brown streak disease: a problem to address

Cassava brown streak disease is a devastating viral disease that was first reported at Amani in Tanzania in 1936 (Nichols, 1950). It is caused by a virus, *Ipomovirus* of the family Potyviridae and transmitted by a whitefly vector, *Bemisia tabaci* (Hillocks and Thresh, 1998, Maruthi et al 2005). Yield losses ranging from 49–74% have been reported in some coastal districts of Tanzania (Muhanna and Mtund, 2002) but in severely affected fields, losses up to 100% to root production and quality have been observed. Symptoms appear on all parts of the plant, leaves, stem and roots.

CBSD Foliar symptoms

CBSD symptoms



CBSD Root necrosis



Identification of parents

From fifteen tolerant and susceptible potential parental varieties four— Namikonga and Kalolo (tolerant) and Albert and Kibaha (susceptible) were selected for diallel genetic crosses and development of mapping population. Selection was based on the extent of flowering and molecular diversity at 27 SSR loci.

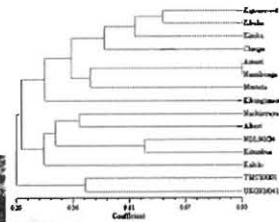
Strategies and approaches

Parents for genetic crosses



Namikonga (tolerant)

Albert (susceptible)



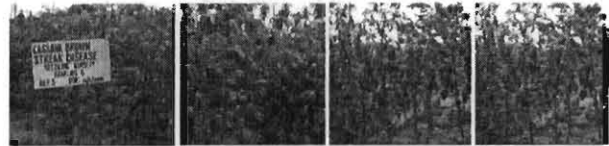
Genetic crosses



Evaluation of progenies in diallel and mapping population

Symptom expression of CBSD appear both in the leaves/stem and roots. Disease reaction of the segregating progenies in the diallel and mapping evaluations showed variations between and within families with respect to foliar symptoms and root necrosis.

Segregating progenies showing variations in CBSD reaction in the shoot



Chopping of roots to assess root necrosis and segregating progenies showing variation in reaction to CBSD in the roots

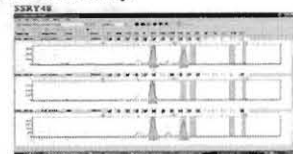


Genotyping

Parental screen of 188 SSR loci was done at the BeCA Platform in collaboration with IITA-Nairobi. 139 and 135 SSR loci were found to be polymorphic in Namikonga x Albert and Kalolo x Kibaha respectively. Genotyping of Namikonga x Albert population using polymorphic markers is underway.



DNA extraction



ABI 3730 Prisms polymorphism profiling

Prospects

- Identification of parents for use in the breeding programs for CBSD resistance and genetic studies
- Generation of information on gene actions and combining ability for CBSD resistance
- Identification of QTL associated with CBSD resistance
- Identification of CBSD tolerant genotypes

References

1. FAO. 2001. Cassava production statistics. <http://www.fao.org>
2. FAO. 2006. Cassava production statistics. <http://www.fao.org>
3. Hillocks R. J and Thresh, J. M. 1998. Cassava mosaic and cassava brown streak virus diseases in Africa: A comparative guide to Symptoms and Aetiology. Natural Resource Institute, UK
4. Maruthi et al 2005. Transmission of cassava brown streak virus by *Bemisia tabaci* (Gennadius). *Phytopathology* 153: 307 - 312
5. Nichols, R.F.W. 1950. The brown streak disease of cassava: distribution, climate effects and diagnostic symptoms. *E. African Agric Journal*, 15:154 - 160.

Acknowledgement

We acknowledge support from the Rockefeller Foundation.

¹Ministry of Agriculture and Cooperatives, Dar es Salaam, Tanzania; ²International Institute of Tropical Agriculture, Nairobi, Kenya; ³International Institute of Tropical Agriculture, Dar es Salaam, Tanzania; ⁴University of Free State, Bloemfontein, South Africa, ⁵International Center for Tropical Agriculture, Cali, Colombia.

