Mapping genetic loci associated with cassava mosaic disease (CMD)

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Introduction

Cassava (*Manihot esculenta* Crantz) - Euphorbiaceae

- Centre of origin - South America
- Food for 700 million people
- World production - 202 MT, Africa - 54% (FAO, 2005)
India

- Introduced to India by Portuguese – 17th century
- India: cultivated in Kerala, Tamil Nadu, Andhra Pradesh and Maharashtra
  - Productivity – 28 t/ha : ranks 1st
  - Production – 7 MT : ranks 7th
  - 5th important starchy food crop

Problem in cassava cultivation:
- Cultivated for starch and sago purpose
- According to WTO agreement, industries should produce more quantity of starch and sago, otherwise other countries will export to India very cheap rate
- All cultivated varieties are susceptible to CMD
- Production is low, so industries in India have to improve their production
- Industries are much interested in CMD resistant, high starch, high yielding varieties in their area
Cassava mosaic disease (CMD)

Important viral disease of cassava - ICMV

- First reported 1894 and India – 1956
- CMD caused by geminivirus and transmitted by whitefly (Vector transmitted disease)
- Yield loss ranging 20-90 per cent
Methods used for developing CMD resistance

- Resistance breeding - intervarietal
  - interspecific

Mapping genes using molecular markers

- For making selection at molecular level
- Method is quicker & more reliable

CMD resistant genes in cassava

Wild relative of Cassava

- *Manihot glaziovii* – ceara rubber


- >500 SSR markers in cassava genome
Objective of study

- Mapping the genetic loci associated with CMD resistance using SSR markers in segregating population of CO2 x MNga-1

Breeding material

<table>
<thead>
<tr>
<th>Parents</th>
<th>Resistant - IITA</th>
<th>Susceptible - TNAU</th>
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<tbody>
<tr>
<td></td>
<td>Leaf canopy of MNga-1</td>
<td>Tubers of MNga-1</td>
</tr>
<tr>
<td></td>
<td>Leaf canopy of CO2</td>
<td>Tubers of CO2</td>
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<tr>
<td>X</td>
<td>141 F₁ Progenies</td>
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Breeding material

Parents

Resistant: MNga-1 (TMS30001)

Susceptible: CO2

Pedigree of MNga-1
Screening for whitefly resistance

Parents

CO2

Mnga-1

Whiteflies feeding both susceptible and resistant parents

Virus diagnosis in parents

Geminivirus specific primers

Survey of resistant and susceptible parents for the presence of virus using ICMV and geminivirus coat protein specific primers
Nature of virus resistance in the parents

• Both the parents are susceptible to the vector
• Presence of virus detected in resistant and susceptible parents
• In MNga-1 virus spread & symptom expression blocked
• There by effect of virus in growth and physiological activity of the plant is nullified in MNga-1

Phenotypic scoring using symptom expression

Hahn et al. (1980)

• 6th month phenotypic scoring
• 7th month pruning
• 8th month phenotypic scoring
Phenotypic scoring using symptom expression

Hahn et al. (1980)

Severity of symptom expression

Phenotypic scoring

73

69
Parental screening

70 SSR primers – PCR amplification (Mba et al., 2001)

Genotyping with SSR primers

S - Susceptible parent  R – Resistant parent

Plate 9 Segregation pattern of SSRY40 and SSRY13 primers.
Genotyping with SSR primers

- S - Susceptible parent
- R - Resistant parent

Genotypic scoring

- Genotyping done as described by Wu et al. (1992)
- Single-dose Restriction Fragment – (SDFR)

DNA markers present in one parent and absent in another parent and segregate in a 1:1 ratio in progeny
Genotypic scoring - SDFR

SSRY28

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S - Susceptible parent  R - Resistant Parent

QTL mapping

QTL – Quantitative Trait Loci

- To identify SSR markers (genotypic data) associated with CMD resistance (phenotypic data)
- Single marker analysis – one way ANOVA
- A significant F-test indicates association of marker locus with phenotype
Associated linkage map-G

- SSRY28
- SSRY235d
- SSRY44b
- NS136d

CMD associated linkage map

- SSRY28a
- SSRY235d
**Associated linkage map-P**

- SSRY44\(^b\)
- NS136\(^d\)

**Marker associated with CMD**

SSR primers - SSRY28
Marker associated with CMD

**SSR primers - SSRY235**

MSR

T1 individuals

SSRY235

SRM

Marker associated with CMD

**SSR primers – NS136**

MSR

T1 individuals

NS136

SRM
Marker associated with CMD

SSR primers – SSRY44

Conclusion

• Virus present in both parents but expressed in susceptible parent alone

• Markers SSRY28a, SSRY44b, NS 136d and SSRY235d associated with CMD resistance

• Markers are present in different linkage group – polygenic nature of inheritance

• Based on these markers resistant lines were isolated which are being field evaluated in CTCRI
THANK YOU