Applications of Molecular Markers in Sweetpotato
(I) **RFLPs Restriction Length Polymorphism**
non PCR (polymerase chain reaction), 1 loci per assay, 5g DNA, Co-dominant, 5 days per assay

(II) **RAPDs Random Amplified Polymorphic DNA**
PCR, 10 loci per assay, 0.2g DNA, Dominant, 5 hours per assay, unreliable

(III) **AFLPs Amplified Fragment Length Polymorphism**
PCR, 50 loci per assay, 0.2g DNA, Dominant, 1 day per assay,

(IV) **SSRs Simple Sequence Repeats**
PCR, 1 loci per assay, 0.2g DNA, Co-dominant, 5 hours per assay, large number of alleles per marker loci

(V) **DarTs Diversity Array Technology**
PCR, Applying bioarray chips to AFLPs, >100 loci per assay, 5ng DNA, Dominant, 1.5 to days per array
Application I - Germplasm

Identification of Duplicates
Verifying Distinct Accessions
Identifying Structures in Germplasm
Figure 1: Frequency distribution of pairwise SSR based similarity coefficients among 95 sweetpotato accessions.
Fig. 2 Dendrogam of the UPGMA cluster analysis of 92 sweetpotato cultivars (85 cultivar of African origin) on the basis of Jaccard's SSR based genetic similarities

(origin of clones: orange = Africa, green lines = South American germplasm, light blue = Pacific, deep blue = North America, and red = China; origin of East Africa farmer varieties: UG = Ugandan, cultivars, KE = Kenya, TZ = Tanzania, ZB = Zambia; □ = White fleshed clones, ∆ = Orange-fleshed clones)
Application II – Building Heterotic Genepools
Fig. Cluster analysis of 575 accessions of sweetpotato based on 20 SSR markers

(Central and North America in black, South America in green, Pacific including New Zealand, Austria and Papua New Guinea in blue, Asia in yellow and Sub Saharan Africa in red).
Fig. Cluster analysis of 575 accessions of sweetpotato based on 20 SSR markers

(farmer variety accessions in blue and accessions generated by breeding programs in green)
Marker Application for Heterosis and Genetic Distance

Heterosis increases with the Genetic Distance & decreases if the Genetic distance is too large.

Schematic representation of the relationship between mid-parent heterosis for yield and parental genetic distance based on unselected DNA markers (1) Crosses between related parents (2) intra-genepool crosses between unrelated lines (3) - (5) inter-genepool crosses (Lefort-Buson 1985, Melchinger 1999, modified)
Heterosis in Sweetpotato

Fig. Distribution of mid-offspring – mid parent heterosis in 231 families evaluated on basis of 30 clones per family and two plot replications for each clone across two locations.
Application III – Marker Assisted Selection
Markers and Sweetpotato virus disease (SPVD)

In experiments:
Yield reduction up to 90%

In practice:
Yield reduction up to 75%

Aphids

SPFMV+ SPCSV and / or Crinivirus other viruses

Whiteflies

Apparently healthy
SPFMV and / or other viruses

SPVD
SPCSV + SPFMV and / or Other viruses
Marker development

1) More SSR markers
   - Using unexploited set of EST available 48 new SSR loci were identified.
   - already available 64 SSR marker loci for sweetpotato.

2) Resistance groups formed from PJ parents & offspring
   (- -) 0 in SPCSVM and SPFMV ELISA scores
   A) - - (5 clones)
   B) - + (23 clones) inc. doubt full clones ↑SPFMV
   C) + - (31 clones)
   D) - - (763 clones)

   individual DNA -> CIP (AFLP) & Australia (DArT)

3) Extreme groups formed from PJ parents & offspring
   (-) 0 or very low in SPCSVM ELISA scores
   A) - 10 clones
   B) + 298 clones

   bulked DNA – CIP (AFLP)
Population PJ05.__ x DLP3163 + parents for AFLP marker screening

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<th>number</th>
<th>SFMV</th>
<th>SPCSV</th>
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<td>-</td>
</tr>
<tr>
<td>39</td>
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</tr>
<tr>
<td>28</td>
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<tr>
<td>747</td>
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10 clones

298 clones out of 747 (Highest ELISA titers)

Form the AFLP markers screened so far 4 markers have been selected

- **E33M49.187** Chi-Square 11.82 Prt. 0.0006
- **E35M36.293** Chi-Square 6.16 Prt. 0.0130
- **E35M36.267** Chi-Square 22.35 Prt. <.0001
- **E33M59.163** Chi-Square 11.04 Prt. 0.0009

For the combination 1\(^{st}\) E33M49.187, 2\(^{nd}\) E33M59.163, 3\(^{rd}\) E35M36.293, 4\(^{th}\) E35M36.267

- 2 wrong classifications of 10 resistant clones
- 8 wrong classifications of 298 susceptible clones

Note resistance group still too small for higher power of significance tests
Application IV – The Sweetpotato Map
**Sweetpotato AFLP & SSR markers**

**The Sweetpotato Map**
- Beauregard x Tanzania
- (SPK004 x Xushu18)
- Mapped: dry matter, starch, sucrose, ß-carotene

Work independently made at CIP and NCSU

All 90 chromosomes can be distinguished, not all chromosomes can be assigned to their homologous linkage group (15 homologous groups)
Thank you for your Attention