

# **A Tale of two Markers**

**(Promising Story Sub Programme 1:  
Generation Challenge Program)**



# **Cassava in Sub-programme one**

- A pilot study to compare DArT and SSR Markers in structural characterization of 436 accessions

# Contributions to the cassava collections maintained at CIAT



**CIAT Hybrids:**  
**384 accessions**

**5,728 accessions as designated to FAO**

**Source: CIAT-GRU, 2003**

# A Pilot Study to Compare Marker Systems for Analyzing Structure of Diversity

## SSRs – 36 SSR Markers

- Codominant markers
- Highly polymorphic
- Development costs  
~US\$36000 per 36 markers
- Low Throughput
- Cost of getting genetic information /locus / genotype: US\$0.5/data point

## DArTs: Diversity Array of ~1000 clones

- Dominant markers
- Moderately polymorphic
- Development costs  
~ US\$ 20000 per chip  
(1000 polymorphic clones)
- High Throughput
- Cost of getting genetic information /locus / genotype: US\$0.025

# Pilot study: Strategy

## Random selection of accessions (436)

- 281 CIAT germplasm collection
- 155 IITA germplasm collection

## Molecular markers to detect structural diversity

- SSRs** (co-dominant and a modest number of loci)
  - 36, 2 from each of the 18 linkage groups that represent the 18 haploid chromosomes of cassava (high PIC value)
- DArTs** (dominant and a large number of loci)
  - 251 polymorphisms from a DArT array of 1000 clones

# Source of 436 Accessions

Landraces, Breeding lines, Resistant to drought

## Central

### America (77)

- Cuba (16)
- Guatemala (42)
- Mexico (9)
- Costa Rica (7)
- Puerto Rico (1)
- Panamá (2)

## South

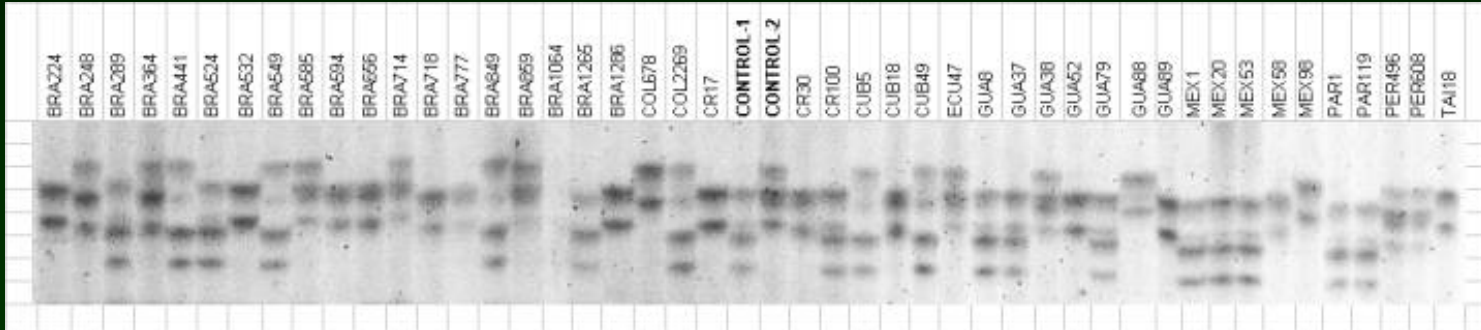
### America (149)

- Argentina (3)
- Brasil (65)
- Colombia (73)
- Venezuela (3)
- Ecuador (1)
- Peru (4)

## Africa (210)

- Sierra Leone (1)
- Cape Verde (12)
- Nigeria (112)
- Ghana (20)
- Cameroun (44)
- Gambia (2)
- Benin (6)
- Togo (2)
- Tanzania (11)

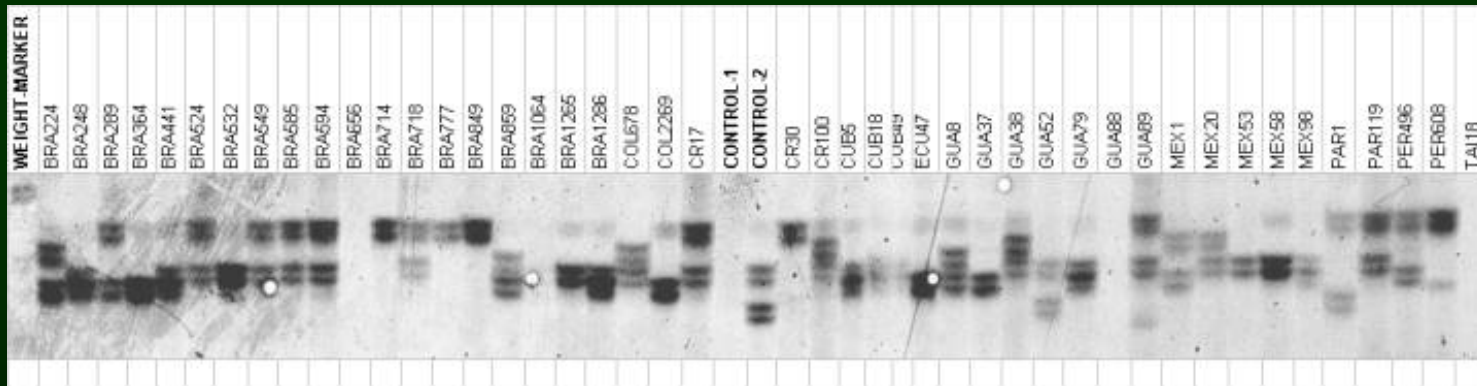
# Results – SSRs



SSRY135

35 22 46 13 18 33 33 33 22 46 47 13 33 26 14 36 56 44 55 24 24 55 23 14 11 11

Presence of alleles/locus/genotype



SSRY 4

22 67 13 18 23 24 56 57 26 25 13 33 25 15 26 56 36 55 23 14 11 12 11 45 11

Presence of alleles/locus/genotype



# Statistical analysis

- **Principal Coordinate Analysis (PCoA)**
  - Using the Jaccard's similarity index
- **Clustering analysis**
- **Similarity between and within the groups defined by PCoA**

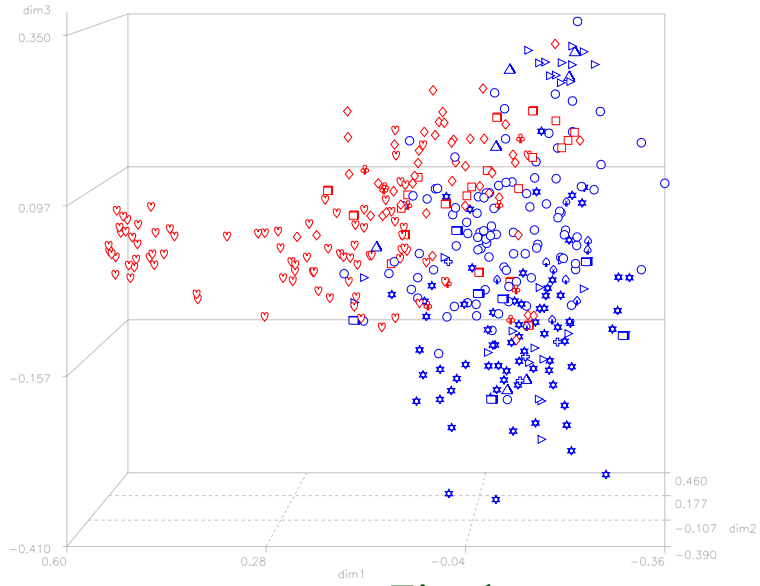


# AFRICA/AMERICA

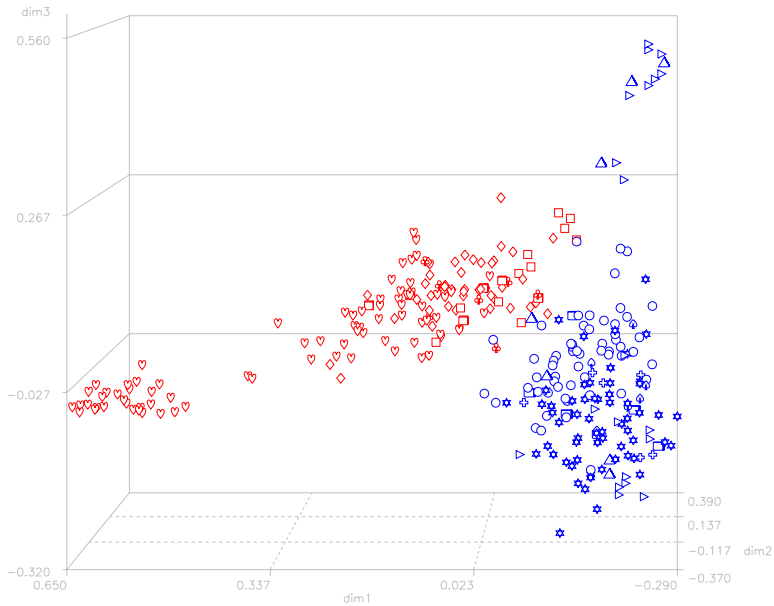
**SSR**

Preliminar

**3D**

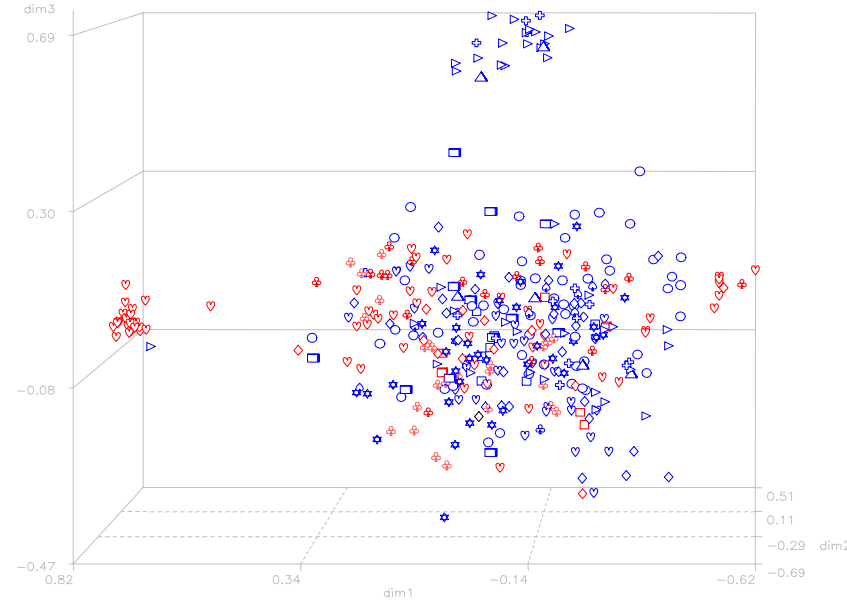


Final



**DArT**

Preliminar

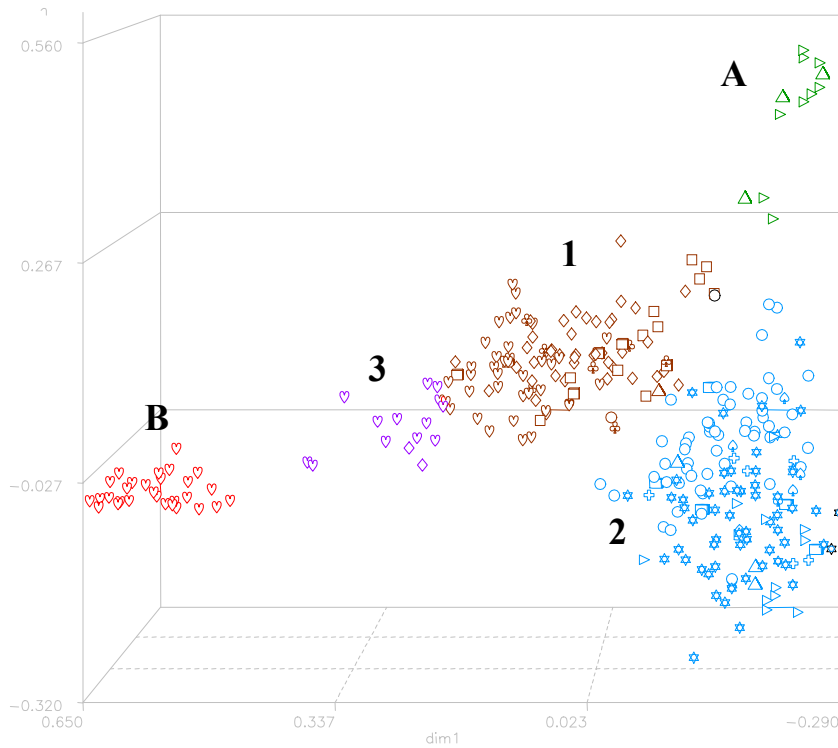


# Principal Coordinate Analysis

3D

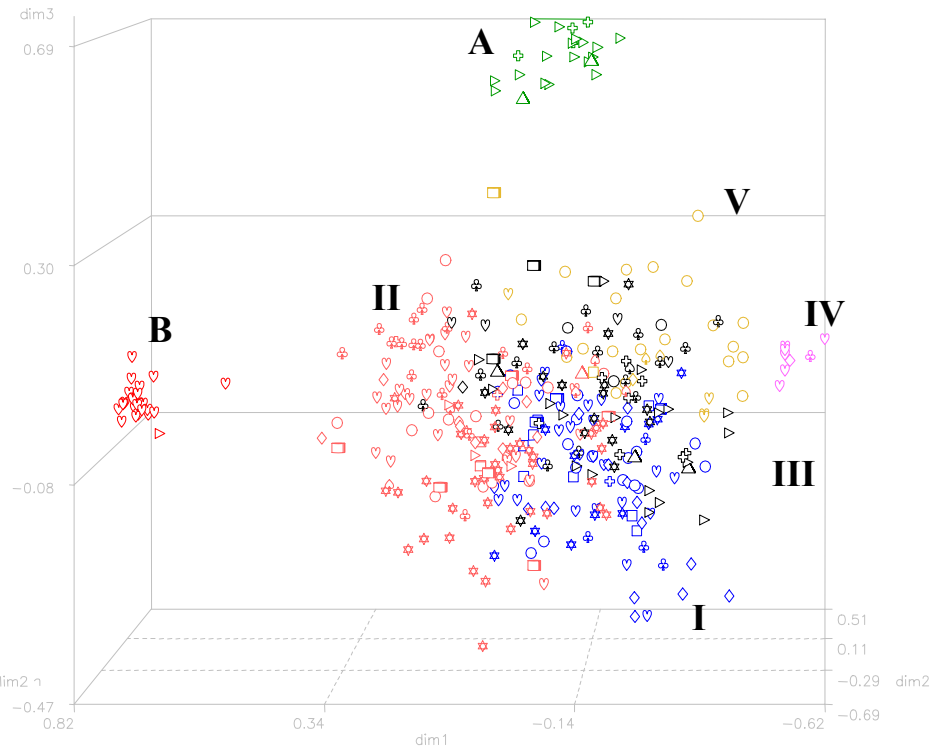
SSR

Final



DArT

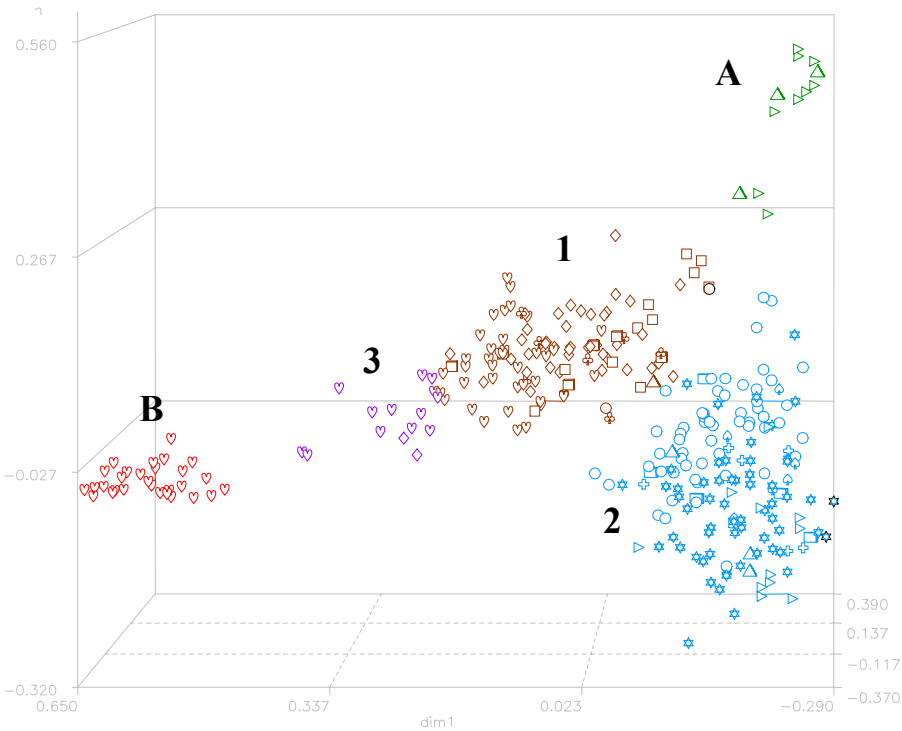
Preliminar



Up today

# SSR

**TOTAL SIMILARITY IN THE POPULATION : 0.29**



**Similarity **within** and between the groups defined by PCoA**

GROUP	1	<b>B</b>	<b>A</b>	2	3
<b>1</b>	<b>0.36</b>				
<b>B</b>	0.35	<b>0.78</b>			
<b>A</b>	0.25	0.25	<b>0.67</b>		
2	0.26	0.25	0.28	<b>0.28</b>	
3	0.35	0.50	0.24	0.25	<b>0.43</b>

**Country representation in the groups as defined by PCoA**

GROUP	COUNTRY	FREQUENCY (%)
1	CAMEROUN/ NIGERIA	37.1/37.9
<b>B</b>	<b>NIGERIA</b>	<b>100</b>
<b>A</b>	<b>GUATEMALA</b>	<b>80</b>
2	BRASIL	86.7
3	NIGERIA	86.6

# DArT

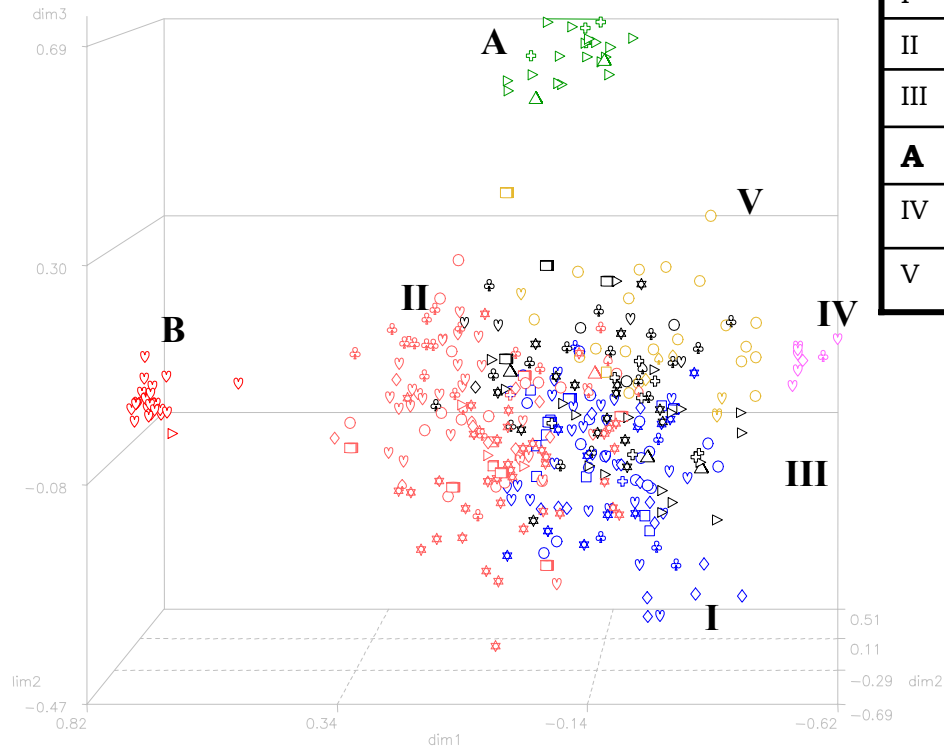
Similarity **within** and **between** the groups defined by PCoA

**TOTAL SIMILARITY IN THE POPULATION : 0.26**

GROUP	B	I	II	III	A	IV	V
<b>B</b>	<b>0.75</b>						
I	0.26	<b>0.32</b>					
II	0.28	0.27	<b>0.28</b>				
III	0.19	0.22	0.23	<b>0.26</b>			
<b>A</b>	0.24	0.27	0.26	0.23	<b>0.49</b>		
IV	0.19	0.27	0.23	0.24	0.22	<b>0.67</b>	
V	0.22	0.29	0.25	0.23	0.29	0.28	<b>0.32</b>

**Country representation in the groups as defined by PCoA**

GROUP	COUNTRY	FREQUENCY (%)
<b>B</b>	<b>NIGERIA</b>	<b>97</b>
I	BRASIL	23.6
II	COLOMBIA	31.6
III	GUATEMALA	24.3
<b>A</b>	<b>GUATEMALA</b>	<b>75</b>
IV	<b>NIGERIA</b>	<b>75</b>
V	BRASIL	70



# Conclusions

- **Both molecular marker systems gave broadly similar population structure when data files were in a preliminary stage**
- **That initial differentiation could be explained by the accession's origin**
- **A better group description requires phenotypic information about the accessions**
- **SSR markers analysis improved its resolution when amount of data/genotype were increased**
- **Structural diversity using 36 SSR markers separated Neo-tropical accessions from African ones**

# Conclusions

- **Because DArT data points can significantly increase up to 1000 (those offered by the microarray), it can be speculated that the level of resolution obtained with DArT could be higher**
- **The cost per assay (lots of data points in one single assay vs two data points per assay with SSR), would make DArT especially interesting for orphan crop species that do not have existing marker systems**

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