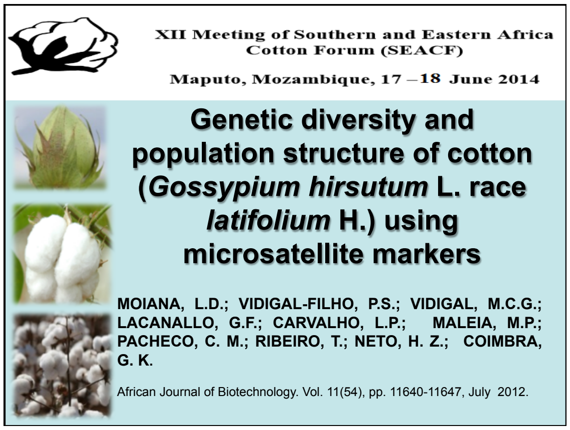


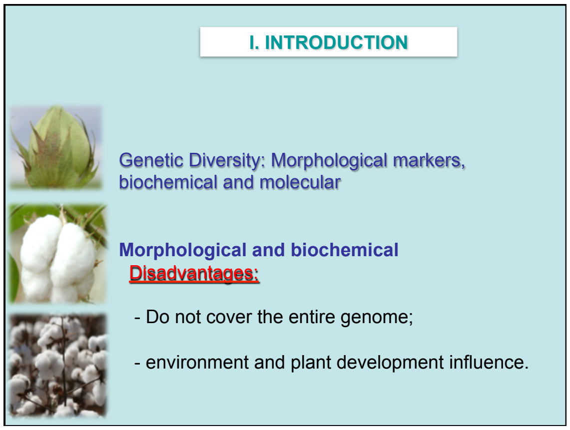
XII Meeting of Southern and Eastern Africa
Cotton Forum (SEACF)

Maputo, Mozambique, 17 – 18 June 2014

Genetic diversity and population structure of cotton (*Gossypium hirsutum* L. race *latifolium* H.) using microsatellite markers

MOIANA, L.D.; VIDIGAL-FILHO, P.S.; VIDIGAL, M.C.G.; LACANALLO, G.F.; CARVALHO, L.P.; MALEIA, M.P.; PACHECO, C. M.; RIBEIRO, T.; NETO, H. Z.; COIMBRA, G. K.

African Journal of Biotechnology. Vol. 11(54), pp. 11640-11647, July 2012.



I. INTRODUCTION

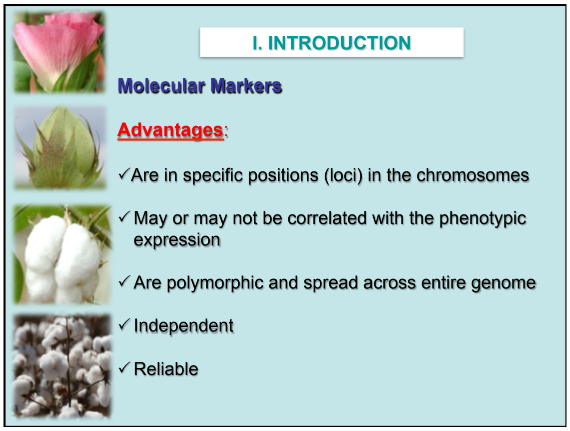
Genetic Diversity: Morphological markers, biochemical and molecular

Morphological and biochemical

Disadvantages:

- Do not cover the entire genome;

- environment and plant development influence.



I. INTRODUCTION

Molecular Markers

Advantages:

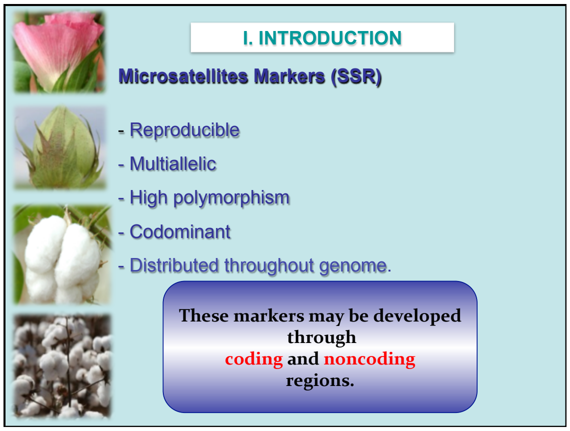
✓Are in specific positions (loci) in the chromosomes

✓ May or may not be correlated with the phenotypic expression

✓ Are polymorphic and spread across entire genome

✓ Independent

✓ Reliable

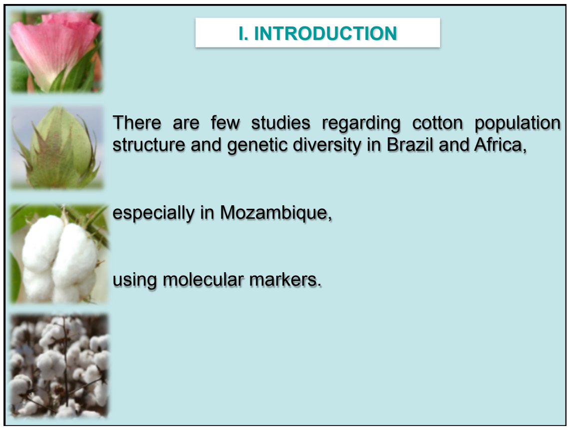


I. INTRODUCTION

Microsatellites Markers (SSR)

- Reproducible
- Multiallelic
- High polymorphism
- Codominant
- Distributed throughout genome.

These markers may be developed through coding and noncoding regions.

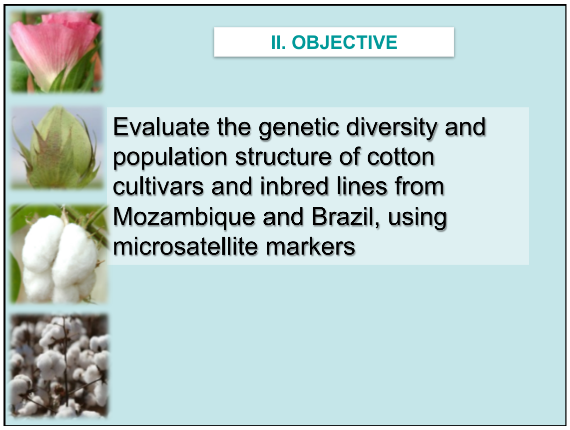


I. INTRODUCTION

There are few studies regarding cotton population structure and genetic diversity in Brazil and Africa,

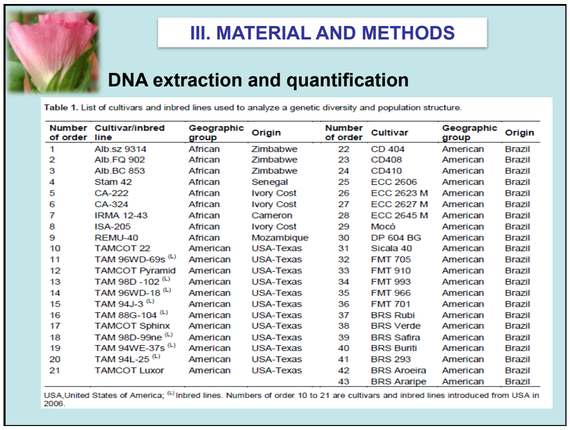
especially in Mozambique,

using molecular markers.



II. OBJECTIVE

Evaluate the genetic diversity and population structure of cotton cultivars and inbred lines from Mozambique and Brazil, using microsatellite markers



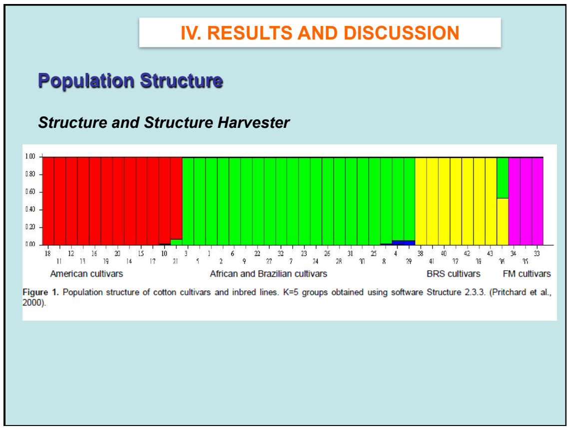
III. MATERIAL AND METHODS

DNA extraction and quantification

Table 1. List of cultivars and inbred lines used to analyze a genetic diversity and population structure.

Number of order	Cultivar/inbred line	Geographic group	Origin	Number of order	Cultivar	Geographic group	Origin
1	Alb.sz 9314	African	Zimbabwe	22	CD 404	American	Brazil
2	Alb.FQ 902	African	Zimbabwe	23	CD408	American	Brazil
3	Alb.BC 853	African	Zimbabwe	24	CD410	American	Brazil
4	Stam 42	African	Senegal	25	ECC 2606	American	Brazil
5	CA-222	African	Ivory Cost	26	ECC 2623 M	American	Brazil
6	CA-324	African	Ivory Cost	27	ECC 2627 M	American	Brazil
7	IRMA 12-43	African	Cameron	28	ECC 2645 M	American	Brazil
8	ISA-205	African	Ivory Cost	29	Mocó	American	Brazil
9	REMU-40	African	Mozambique	30	DP 604 BG	American	Brazil
10	TAMCOT 22	American	USA-Texas	31	Sicala 40	American	Brazil
11	TAM 96WD-69s $^{(L)}$	American	USA-Texas	32	FMT 705	American	Brazil
12	TAMCOT Pyramid	American	USA-Texas	33	FMT 910	American	Brazil
13	TAM 98D -102 $^{(L)}$	American	USA-Texas	34	FMT 993	American	Brazil
14	TAM 96WD-18 $^{(L)}$	American	USA-Texas	35	FMT 966	American	Brazil
15	TAM 94J-3 $^{(L)}$	American	USA-Texas	36	FMT 701	American	Brazil
16	TAM 88G-104 $^{(L)}$	American	USA-Texas	37	BRS Rubi	American	Brazil
17	TAMCOT Sphinx	American	USA-Texas	38	BRS Verde	American	Brazil
18	TAM 98D-99ne $^{(L)}$	American	USA-Texas	39	BRS Safira	American	Brazil
19	TAM 94WE-37s $^{(L)}$	American	USA-Texas	40	BRS Buriti	American	Brazil
20	TAM 94L-25 $^{(L)}$	American	USA-Texas	41	BRS 293	American	Brazil
21	TAMCOT Luxor	American	USA-Texas	42	BRS Aroeira	American	Brazil
				43	BRS Araripe	American	Brazil

USA,United States of America; $^{(L)}$ Inbred lines. Numbers of order 10 to 21 are cultivars and inbred lines introduced from USA in 2006.

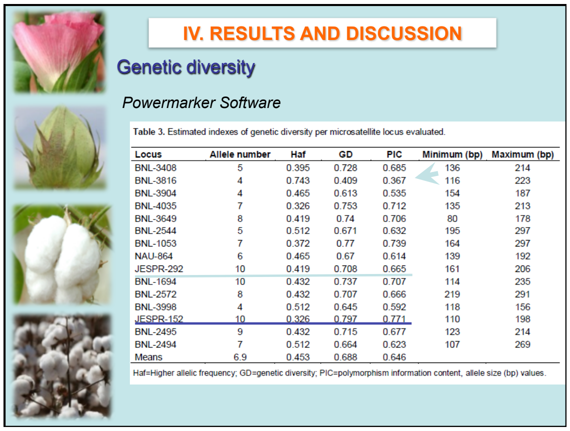


IV. RESULTS AND DISCUSSION

Population Structure

Structure and Structure Harvester

Figure 1. Population structure of cotton cultivars and inbred lines. K=5 groups obtained using software Structure 2.3.3. (Pritchard et al., 2000).



IV. RESULTS AND DISCUSSION

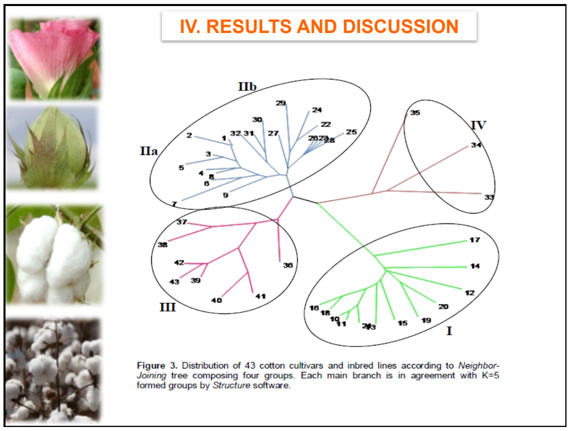
Genetic diversity

Powermarker Software

Table 3. Estimated indexes of genetic diversity per microsatellite locus evaluated.

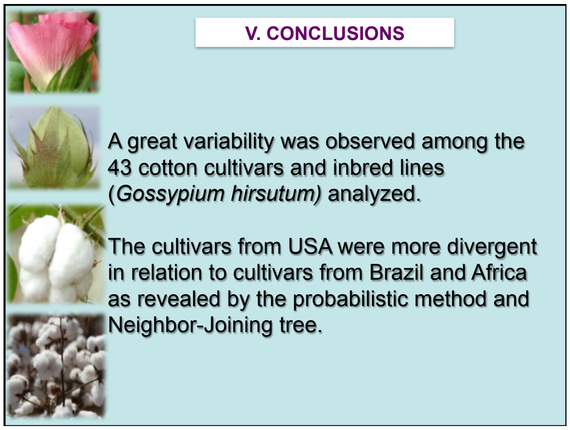
Locus	Allele number	Haf	GD	PIC	Minimum (bp)	Maximum (bp)
BNL-3408	5	0.395	0.728	0.685	136	214
BNL-3816	4	0.743	0.409	0.367	116	223
BNL-3904	4	0.465	0.613	0.535	154	187
BNL-4035	7	0.326	0.753	0.712	135	213
BNL-3649	8	0.419	0.74	0.706	80	178
BNL-2544	5	0.512	0.671	0.632	195	297
BNL-1053	7	0.372	0.77	0.739	164	297
NAU-864	6	0.465	0.67	0.614	139	192
JESPR-292	10	0.419	0.708	0.665	161	206
BNL-1694	10	0.432	0.737	0.707	114	235
BNL-2572	8	0.432	0.707	0.666	219	291
BNL-3998	4	0.512	0.645	0.592	118	156
JESPR-152	10	0.326	0.797	0.771	110	198
BNL-2495	9	0.432	0.715	0.677	123	214
BNL-2494	7	0.512	0.664	0.623	107	269
Means	6.9	0.453	0.688	0.646		

Haf=Higher allelic frequency; GD=genetic diversity; PIC=polymorphism information content, allele size (bp) values.



IV. RESULTS AND DISCUSSION

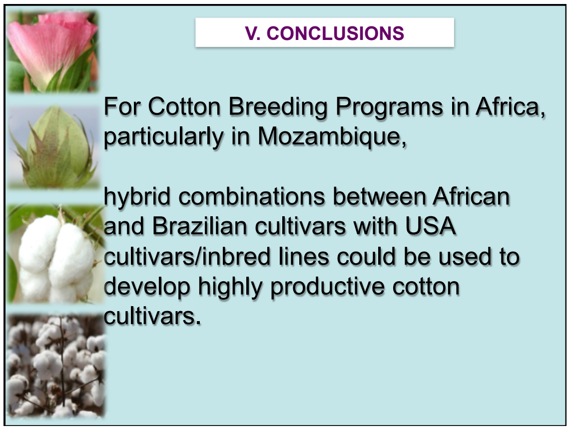
Figure 3. Distribution of 43 cotton cultivars and inbred lines according to *Neighbor-Joining* tree composing four groups. Each main branch is in agreement with K=5 formed groups by *Structure* software.



V. CONCLUSIONS

A great variability was observed among the 43 cotton cultivars and inbred lines (*Gossypium hirsutum)* analyzed.

The cultivars from USA were more divergent in relation to cultivars from Brazil and Africa as revealed by the probabilistic method and Neighbor-Joining tree.



V. CONCLUSIONS

For Cotton Breeding Programs in Africa, particularly in Mozambique,

hybrid combinations between African and Brazilian cultivars with USA cultivars/inbred lines could be used to develop highly productive cotton cultivars.

ACKNOWLEDGEMENT

PGM
PROGRAMA DE PÓS-GRADUAÇÃO EM GENÉTICA E MELHORAMENTO

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Republica de Mocambique
Ministério de Ciência e Tecnologia

IIAM
Instituto de Investigação Agrária de Moçambique

TEXAS TECH UNIVERSITY
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To all....

Khanimambo!!!

THANK YOU!!!

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