

MOLECULAR CHARACTERIZATION OF ELITE MAIZE INBRED LINES FOR DROUGHT TOLERANCE

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INTRODUCTION

The development of drought tolerant maize has been limited by the influence of the environments on drought traits. Fortunately, molecular markers that are linked to drought tolerance QTLs have been discovered in maize (Sserumaga *et al.*, 2014). However, the extensive use of these markers requires validation before they can be deployed to assisted breeding efforts.

This study validated 19 selected SSR markers linked to drought tolerance in maize and determine the genetic diversity of elite maize inbred lines for drought tolerance.

MATERIALS & METHODS

DNA extraction: Genomic DNA was extracted from 68 maize inbred lines using the CTAB method at the Biotechnology Laboratory of the Makerere University of Agricultural Research Institute, Kabanyolo (MUARIK), Uganda.

Markers: 19 SSRs markers were chosen from the Maize GDB (Maize Genetics and Genomics Database, 2016) based on repeat unit and bin location to provide uniform coverage of the entire maize genome.

PCR & Visualization: PCR was performed based on the common method for microsatellite markers. PCR products were separated using 3% Agarose Gel. Auto radiogram was visually scored for the presence (1) or absence (0) of polymorphic bands for the establishment of data matrix. The polymorphism information content (PIC) value was obtained as the mean of the calculated PIC of all loci. The PIC for SSR was calculated as $PIC = 1 - \sum f_i^2$.

Data Analysis: The generated data matrices were subjected to statistical analysis using R statistical software to determine the genetic diversity among the genotypes by cluster analysis.

RESULTS & DISCUSSION

Under the experimental conditions of this study, ten (10) primers showed polymorphism among the maize inbred lines, while 6 showed monomorphic bands (Fig. 1) and the remaining 3 did not amplified. (Table 1).



Fig. 1: Polymorphic and monomorphic gels of PCR products generated by markers umc 2214 (A) and p-bnlg434 (B) respectively on maize inbred lines 20-36 on a 3% Metaphor agarose gel.

REFERENCES

- Maize Genetics and Genomics Database 2016. <http://www.maizegdb.org>.
- Sserumaga J. P., D. Makumbi, H. Ji, K. Njoroge, J. W. Muthomi, G. N. Chemining'wa, L. Si-myung, G. Asea, H. Kim 2014. Molecular characterization of tropical maize inbred lines using microsatellite DNA markers. *Maydica* : 59:267-274

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Table1:The types of bands obtained

Primers	Type of Bands
p - bnlg 238	Polymorphic
umc 2038	
p-bnlg 1014	
Umc 2214	
p-umc 2189	
Phi 037	
P-bnlg 434	
p-bnlg 1179	
Umc 1545	
Bnlg 2190	
Umc 1447	Monomorphic
Umc 1862	
Phi 115	
Umc 1719	
Umc 1432	
Umc 2359	
Phi 034	No bands
Umc 1542	
Bnlg1074	

Four distinct clusters (of 2, 24, 16, and 26 closely related lines) were found indicating a considerable genetic diversity among the maize inbred lines (Fig. 2).

The lines CKLMARS1F60677 from CIMMYT and NML88 from NACCRI had the highest genetic distance on the dendrogram.

A total of 33 alleles ranging from 2 to 5 per locus. Primer UMC2214 had the highest number of alleles (Table 2).

The PIC values ranged from 0.13 to 0.76 with a mean of 0.47 (Table 2). Seven SSR loci showed PIC values greater than 0.4 indicating their potential ability to detect differences among the inbred lines.

Table 2: Bin location, Allele numbers and PIC of the primers

Primer	Bin Location	Number of alleles	PIC
P-bnlg238	6.00	4	0.76
UMC2038	4.07	4	0.43
P-bnlg1014	1.01	3	0.49
UMC2214	2.1	5	0.60
P-UMC2189	1.00	3	0.19
Phi037	1.08	3	0.70
P-bnlg434	7.01	3	0.13
P-bnlg1179	1.00	3	0.64
UMC 1545	7.00	2	0.20
Bnlg2190	10.06	3	0.59
Mean		3.3	0.47

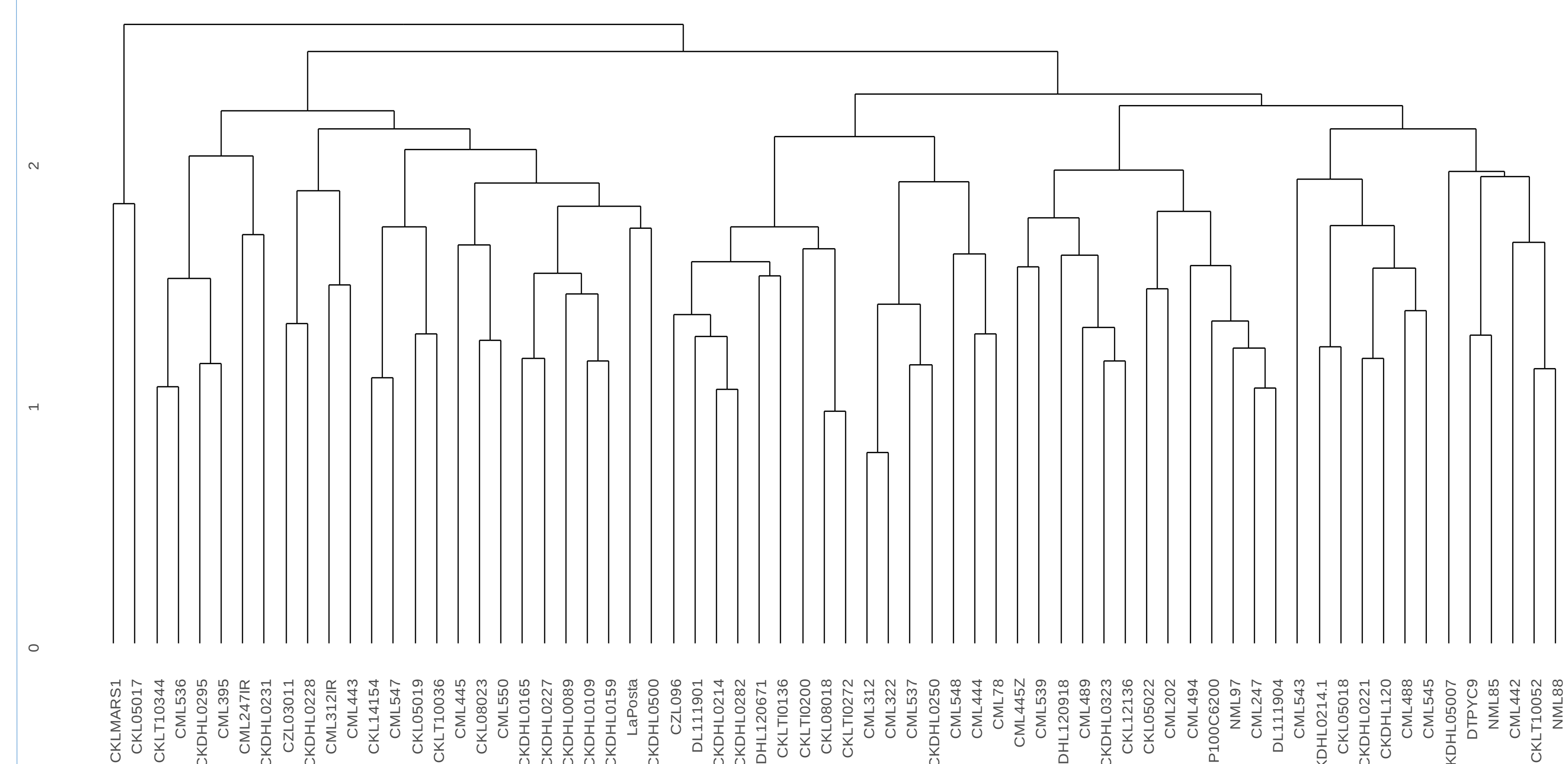


Fig. 2: Dendrogram showing strength of relationship among the 68 elite maize inbred lines.

CONCLUSION

Markers P-bnlg 238, Phi037, P-bnlg 1179 and UMC 2214 were among the informative markers that significantly differentiated the maize inbred lines into groups.

There was considerable genetic diversity among the sixty-eight elite maize inbred lines that can be exploited for the development of drought tolerant maize hybrids.