GENETIC DIVERSITY OF MAIZE INBRED LINES ASSESSED BY SSR MARKERS

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Introduction

Maize is one of the most important crops cultivated around the world. During the breeding programs, maize hybrids have narrowed the genetic basis, leeding to a significant reduction in diversity, so maize in commercial use contribute around 5% of the available germplasm. In order to prevent genetic erosion, i.e. loss of individual genes and their combinations, as well as further narrowing of maize diversity, it is necessary to characterize existing elite lines, modern varieties and hybrids. Many methodologies are used for the assessment of genetic diversity in maize such as pedigree data, morphological traits and molecular markers. Compared with morphological variation, molecular polymorphism is generally considered to be independent of the environment and they are able to detect differences on DNA level on different individuals. In the present work SSR fingerprinting of 23 maize inbred lines, that belong to diferent breeding programs was done for molecular identification and assessment of genetic diversity, as well as to compare their classification with their pedigree information.

Materials and Methods

A set of 23 maize inbred lines from the Maize Research Institute „Zemun Polje“ were analyzed with SSR 17 molecular markers (Table 1) to evaluate genetic diversity. DNA was isolated from kernel using the CTAB procedure according to Doyle and Doyle (1987). After amplifications PCR fragments were separated on 8% polyacrylamide gel, stained with ethidium bromide and photographed under UV light on BioDocAnalyse - Biometra. Based on presence or absence of alleles in each sample coefficient of similarity was calculated by Jaccard.
For marker data analyses statistical NTSYSpc2 program package (Rohlf FJ, 2000) was applied.

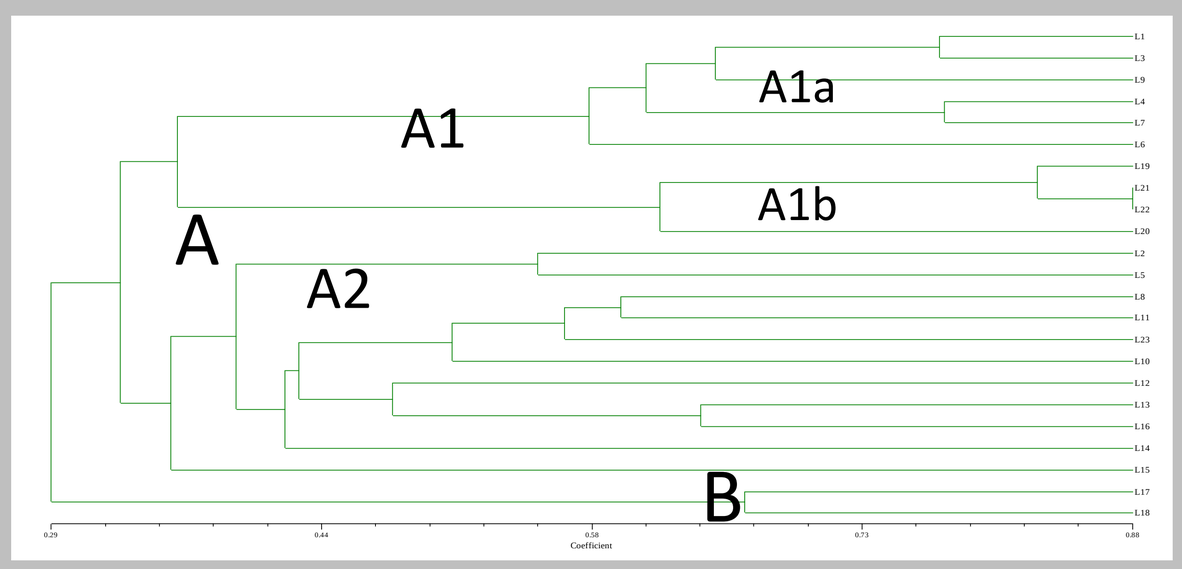

Figure 1. Dendrogram of 23 maize inbred lines constructed using UPGMA cluster analysis of genetic similarity values (Jaccard, 1908) obtained from SSR data.

Table 1. List of 17 informative primers, with their chromosome position, repeat motif, number of alleles within analyzed maize inbred lines

probe	bin	repeat motif	number of alleles
umc1282	1.00	(AT)6	8
phi109275	1.03	AGCT	3
bnlg1083	1.02	AG(29)	5
umc1122	1.06	(CGT)7	3
umc2047	1.09	(GACT)4	5
phi083	2.04	AGCT	4
umc1448	2.04	(GCT)5	4
nc133	2.05	GTGTC	2
bnlg1350	3.08	(AG)13	7
umc1109	4.10	(ACG)4	5
umc1153	5.09	(TCA)4	3
phi452693	6.04	AGCC	3
bnlg2235	8.02	AG(23)	5
phi080	8.08	AGGAG	8
umc1492	9.04	(GCT)4	4
umc1152	10.01	(ATAG)6	6
bnlg1526	10.04	AG(15)	3

Results and Discussion

Total of 78 alleles among 23 maize inbred lines were identified. The number of alleles obtained with different primers varied from two (nc133) to eight (umc1282 and phi080) with the average value of 4.6 per locus. The genetic similarities were in range from 0.18 for L3/L16 and L15/L20 to 0.88 between L21 and L22. The cluster analysis using UPGMA method, based on Jaccard similarities distributed genotypes into one large clusters (A) with 21 genotypes and one smaller cluster (B) with only two popcorn lines. The cluster A was devided to subclusters A1 (grouping sweet corn lines –A1b and maize lines from Lancaster Sure Crop germplasm –A1a) and A2 (eleven inbred lines with mixed background, mainly BSSS germplasm). In his study SSR analysis determined variability among maize inbred lines, as well as their grouping by genetic background. The genetic similarity ranging from 0.18 to 0.88 among analyzed maize inbred lines showed satisfying variability between them.

Conclusions

SSR markers is powerful tool for genetic characterization of maize inbred lines and their classification comparing with pedigree data. In this work 17 polymorphic SSR markers classified 23 maize hybrids into different groups in accordance to their pedigree data and breeding programs. Molecular marker could be successful and significant in evaluation of maize diversity and variability.