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VARIABILITY WITHIN MAIZE INBRED LINES
DETERMINED WITH SSRS

prepared by experts from Germany and the United States of America

VARIABILITY WITHIN MAIZE INBRED LINES DETERMINED WITH SSRS

M. Bohn, M. Heckenberger, J.S. Ziegle, L.K. Joe and J.D. Hauser, A.E. Melchinger

Celera AgGen, 1756 Picasso Avenue, Davis CA 95616 - USA
Institute of Plant Breeding, Seed Science, and Population Genetics
University of Hohenheim, 70593 Stuttgart, Germany

ABSTRACT

Molecular markers are assumed to be an important tool for identifying essentially-derived varieties (EDVs). In order to determine accurate thresholds for defining EDVs in maize, information is essential on the variability within maize lines that can be observed with molecular markers. The objective of this study was to determine the variability observed within maize inbred lines. Using a set of nine maize lines, two to five different accessions per line were selected. The accessions were taken from different multiplication generations, multiplication programs performed by different breeders, or different breeding generations (Tab. 1). Each accession was genotyped with 100 SSR markers. The fluorescent SSR analysis was performed by Celera AgGen (Davis, USA) using a sequencer (ABI377). The SSR markers were selected based on their even distribution across the maize genome. In total, 392 SSR fragments were identified. The number of fragments found for each SSR marker ranged from 1 to 8 with a mean number of alleles per locus of 4. The polymorphic information content (PIC) of the SSRs varied between 0.03 and 0.77 with an average PIC value of 0.54. Only one SSR marker was monomorphic for the genotyped set of maize lines. One third of the SSR markers revealed heterozygosity for at least one accession. The number of heterozygote accessions per SSR ranged from 0 to 14. Per accession an average number of 2.6 heterozygote marker loci was observed. The highest level of heterozygosity was revealed for line 5113 (average number of heterozygote SSRs: 5.7), whereas line 1105 showed the lowest number of heterozygote SSR marker loci (average number of heterozygote SSRs: 0.5). The average genetic similarity within the accession sets varied between 0.91 for line 5113 and 0.99 for lines 1721 and 2065 (Fig. 1). The observed genetic variability within accession sets was mainly caused by heterozygosity of single accessions detected with SSR markers (Tab. 2). In addition, SSR fragments with small size differences (1 to 3 bp differences) were detected for all accession sets except for line 2065. In order to determine the amount of diversity within maize lines caused by the SSR technique itself a set of doubled haploid maize lines will be SSR genotyped.

Table 1 Maize inbred lines used in this study. All maize lines were developed at the University of Hohenheim.

Maize line	Heterotic pool	Number of accession or breeding generations
1721	Dent	5
5113	Flint	3
5248	Flint	4
5271	Flint	4
2065	Flint	2
1105	Flint	4
F012	Flint	F_6, F_{10}
S002	Dent	F_6, F_{10}
P006	Dent	F_6, F_{10}

Table 2 Number and category of observed differences between accessions of the same maize line.

Line	Accessions	Fragment size differences				Heterozygosity
		1bp[1]	2bp	3bp	≥ 4bp	
	---------- No. ----------					
1721	5		1		1	2
5113	3	4	1	1	2	10
5248	4		1			8
5271	4			1	1	4
2065	2					1
1105	4	4			3	3
F012	3					5
S002	3	1			1	4
P006					1	3

[1] bp = base pair

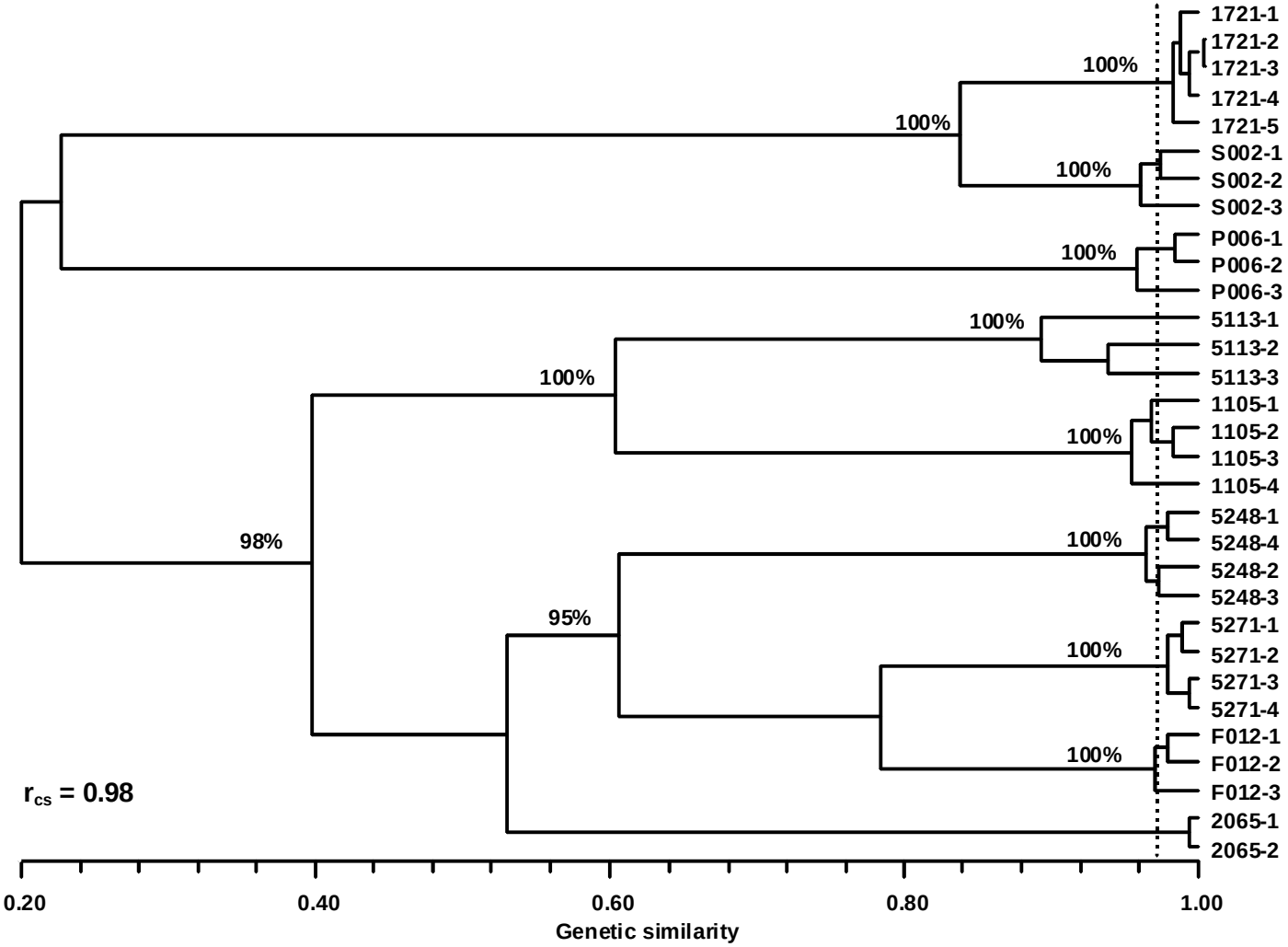

Figure 1 Dendrogram and cophenetic value (r_{cs}) of 31 maize inbred line accessions revealed by UPGMA cluster analysis based on genetic similarity estimates calculated from SSR marker data. The number at the forks show the percentage of times the group consisting of the accessions, which are on the right of the fork, occurred. Only percentages ≥95% are shown. The dashed line indicates the mean genetic similarity accross all accession sets.

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