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USO DE MARCADORES MOLECULARES (RAPD) PARA AVALIAÇÃO DE PUREZA GENÉTICA EM MILHO (*Zea mays* L.).

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A produção de sementes de milho híbrido (*Zea mays* L.) requer a remoção completa de pendões do parental fêmea antes da polinização. O despendoamento incompleto deste parental produz "selfs" e "sibs" que na próxima geração resultam em plantas menos vigorosas e de baixa produtividade, diminuindo os ganhos genéticos. Este estudo objetivou avaliar o potencial da técnica de reação em cadeia da polimerase com "primers" aleatórios (RAPD) para determinação de pureza genética em milho. Os materiais genéticos utilizados foram os híbridos simples fêmea (HS 200) e macho (HS-201M) parentais do híbrido duplo BR-201. Foram empregados seis tratamentos que consistiam em diferentes níveis de contaminação (0, 1, 3, 5, 8 e 10%) do parental fêmea HS 200. O DNA utilizado para amplificação por RAPD, foi obtido de folhas de um conjunto de 100 plântulas de cada tratamento. Foram testados 480 "primers" (OPERON, Alameda. CA). De todos os "primers" utilizados somente o CCC-33 originou uma banda de aproximadamente 1.584 pb que apresentou variação de intensidade em relação ao nível de contaminação. Esta banda permitiu detectar com clareza níveis de contaminação acima de 10%.

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CASSAVA (*Manihot esculenta* CRANTZ) PHENETIC RELATIONSHIPS AND GENETIC DIVERSITY REVEALED BY MORPHOLOGICAL DESCRIPTORS AND RAPD MARKERS.1 Luiz J.C. B. Carvalho2, Barbara A. Schaal3*, Wania M.G. Fukuda 4. CENARGEN/EMBRAPA Brasilia-DF. Department of Biology - Washington University St Louis-MO, USA. CNPMF/EMBRAPA, Cruz das Almas-Ba.

Morphological descriptors and Random Amplified Polymorphic DNA (RAPD) marker were used to assess the genetic variability of cassava (Manihot esculenta Crantz). Ninety four cassava accessions, three majo morphological descriptors (determined by PCA) and 96 polymorphic bands were analyzed by the mean of phenetic relationship. Cluster groups generated with Jaccard similarity index by UPMGA method were further analyzed by the consensus tree method to assess the distinctness of the clusters identified by UPGMA-derived phenogram. Genetic diversity o the morphological groups was assessed by the meaning of the estimated value of nucleotide diversity. The grouping pattern implied by the phenogram generated with UPGMA method showed different degree o resolution (truly bifurcated phenogram), different levels of tree imbalance, and no group correspondence between the two markers. A consensus fork index (CIc) value of 0.41 and 0.22 as well as the Mickevich's index (CIm) values of 0.03 and 0.01 were observed for morphological and RAPD markers respectively. Morphological descriptors revealed 22 distinct clusters of accessions with high resolution, while the RAPD markers revealed 18 distinct clusters with low resolution and high group imbalance. None of the cultivars clustered by one kind of marker was clustered the same way by the other marker. The correlation between the cluster groups obtained by the two markers was very low (r=0.077) and not statistically significant. The genetic diversity among accessions in the morphological distinct clusters revealed by nucleotide diversity showed a nucleotide variation per site varying from 0.326 to 2.779 percent. These results indicate that RAPD marker provides means for discriminating genetic.variation in cassava germplasm, specially when used in concert with morphological diagnoses.

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GENETIC DIVERSITY OF CASSAVA (MANIHOT ESCULENTA CRANTZ) IN A GERMPLASM COLLECTION ASSESSED BY RAPD ASSAY1. Luiz J.C.B. Carvalho2, Barbara A. Schaal3*, Wania M.A. Fukuda 4. CENARGEN/EMBRAPA Brasilia-DF. Department of Biology - Washington University St Louis-MO, USA. CNPMF/EMBRAPA, Cruz das Almas-Ba.

Geographic population structure of cassava germplasm collection was assessed by RAPD markers. Fifty nine cassava accessions represeting the World Core Collection and seven geographic regions in one of the center of diversity of cassava were used. Phenetic analysis discriminated nine distinct clusters, two clusters from Colombia, two clusters from Brazil and five clusters of distinct regions in Brazil. None of the other representative individuals from the other countries showed distinct clusters. This population structure represents the genetic diversity of cassava germplasm in the World Core Collection, and confirms the high genetic diversity in different regions in Brazil. It is also inferred that accessions originated from Cerrados, Litoral, and Sub Tropics are well represented in the World Core Collection, but not the other regions. Degree of genetic diversity within individuals indicated higher values for nucleotide diversity (2.7%) in the Brazilian collection than in the World Core Collection (2.1%). From the geographic regions of Brazil, it is possible to distinguish three major source of genetic diversity. One region, the Cerrados area, with limited diversity (0.6% of nucleotide diversity per site in the genome), a second source of variation with high genetic diversity in Caatinga and Humid Tropics regions, and a third source of variation with intermedian genetic diversity in Sub Tropics, Litoral, and Semi Arid regions. Divergence between the different geographic regions varied from 0.3% between Brazil and Cuba, but 0.6% between Brazil and Malaysia. Accessions from Cuba are more close to accessions from Colombia then the other countries. The highest divergence between populations is observed between Wide Occurrence population in Brazil and the population from Malaysia, and between Litoral and Malaysia. This indicates that the germplasm in Malaysia shows substantial differences from the one in Brazil, and may be provenance from different region in South America.

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PHENETIC RELATIONSHIPS AND GENETIC DIVERSITY AMONG GEOGRAPHIC LANDRACES OF CASSAVA (*Manihot esculenta* CRANTZ) REVEALED BY PCR-BASED ASSAYS1. Luiz J.C.B. Carvalho2, Barbara A. Schaal3*, Wania M.G. Fukuda4. CENARGEN/ EMBRAPA Brasilia-DF. Department of Biology - Washington University St Louis-MO, USA. CNPMF/EMBRAPA, Cruz das Almas-Ba.

Two PCR-based molecular genetic markers were used to examine the distribution of genetic variation among cassava accessions representing seven geographical regions in Brazil. RAPD assay, and Microsatellite-primed PCR assay, together with phenetic analysis and nucleotide diversitey and divergence were used to understand the genetic structure of the geographic representative accessions and to assess genetic diversity within and between the accessions from geographic regions sampled. The level of band polymorphism among cassava accessions varies with the kind of marker, being high in RAPD than in microsatellite-primed PCR. The distinctness of clusters identified by UPGMA-derived phenogram was higher for the microsatellite-primed PCR than for RAPD analysis as indicated by the matrix correlation and consensus tree analysis. This observation was reflected on the grouping pattern differentiation obtained by the two markers. The RAPD polymorphism showed resolution to form distinct groups of individuals for accessions from Cerrados (CE) and Caatinga (CA), but not from other regions. While the microsatellite-primed PCR formed distinct groups of individuals for accessions from Humid Tropics (HT), Sub Tropics (ST), Cerrados (CE), Semi Arid (SA) and Littoral (LI). The polymorphism of both techniques did not show resolution to resolve individuals for geographic regions from Wide Occurrence. Overall, the nucleotide diversity (pi values) were 0.3% higher in RAPD markers than in microsatellite-primed PCR. This indicate that the two markers hits different regions in the genome of cassava.

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