DNA Marker-based Study of Genetic Relatedness in United States Sweetpotato Cultivars

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Abstract. The polymerase chain reaction (PCR)-based DNA amplification fingerprinting (DAF) approach was used to investigate genetic relationships among 30 U.S. sweetpotato (Ipomoea batatas L. Lam.) genotypes including heirloom cultivars and recent releases. Phenogram, pairwise similarity matrix, and principal coordinate plots were developed based on Jaccard’s coefficients using band-sharing data generated by seven octamer primers. All cultivars showed unique fingerprint patterns indicating the utility of DAF in cultivar identification. Many heirloom cultivars such as ‘Creole’ and ‘Porto Rico’ were readily differentiated from recently developed cultivars. Modern cultivars such as ‘Jewel’, ‘Carver’, ‘Nugget’, and ‘Scarlet’ exhibited a high degree of similarity reflecting ancestral relatedness. ‘Regal’ and ‘Excel’, recently developed using a population-based breeding approach, showed greater divergence from all other cultivars. Those cultivars, developed as a result of somatic mutations, exhibited high levels of genetic similarity to their normal-type parents and yet had distinct fingerprint profiles. With few exceptions, genetic relationships derived from DAF data appear to be consistent with available pedigree information.

Sweetpotato (Ipomoea batatas) has been grown in the United States for more than 300 years since its introduction from South America, its presumed primary center of origin and domestication (Bohac et al., 1995) While cultivars grown in the United States before 1920 were direct introductions, modern cultivars are products of open-pollinated polycrosses and somatic selections of mutants (Jones et al., 1986). Sweetpotato is an outcross species that is vegetatively propagated, and each cultivar is a clone. More than 100 sweetpotato cultivars have been grown in the United States, although currently sweetpotato culture in this country is dominated by two or three cultivars (Dukes et al., 1992).

Traditionally, phenotypic markers have been used to provide descriptors for identifying sweetpotato cultivars (Huanan et al., 1991), but they are unreliable due to their paucity and because of their vulnerability to environmental influence. In addition, they provide no data on patterns of crop origin or domestication (Gepts, 1993). Protein-based markers such as isozymes and SDS-PAGE (Kennedy and Thompson, 1991; Stegemann et al., 1992) have been used with limited success in sweetpotato genetic studies primarily because of low levels of polymorphism. A reliable approach to identify sweetpotato genotypes will facilitate better germplasm management and improvement (Huanan et al., 1991; Stegemann et al., 1992). The polymerase chain reaction (PCR)-based approaches, including random amplified polymorphic DNA (RAPD) and DNA amplification fingerprinting (DAF), have proved useful in genetic and germplasm studies (Caetano-Anollés, 1994; Williams et al., 1990). DNA markers have been used to fingerprint crop cultivars and to gain insight into the organization of genetic diversity in many crop species (Caetano-Anollés, 1994; Tingey and del Tufo, 1993) including sweetpotato and related *Ipomoea* species (Connolly et al., 1994; He et al., 1995; Jarret and Austin, 1994).

This study evaluated the genetic relatedness among U.S. sweetpotato cultivars based on DNA markers and examined the validity of this information in light of the known pedigree history of the cultivars.

Materials and Methods

Plant material. Thirty U.S. sweetpotato genotypes representing a cross-section of heirloom and recently released cultivars were obtained as in vitro plants from the U.S. Dept. of Agriculture–Plant Introduction Service, Griffin, Ga. (Jarret, 1989).

DNA amplification. Total genomic DNA was isolated as described by Wilson et al. (1992). Twenty-eight oligonucleotide (octamer) primers of arbitrary sequence were initially used to screen eight sweetpotato genotypes. Among these, the following seven primers were selected for further study based on their ability to detect high levels of polymorphism: CGCACACC, GTAACGCC, GAACGGGT, GCGGACAG, GGAGACC, GTGGAGCT, and CCTTGAGT (G. He and C.S. Prakash, unpublished). Reaction mixtures (25 µL) contained 26 ng·µL⁻¹ template DNA, 7.7 µM primer, 5 mM MgCl₂, 5 units of Stoffel fragment Taq polymerase (Perkin Elmer, Norwalk, Conn.), 200 µM each of dNTPs and 10 mM KCl, and 10 mM Tris-HCl buffer. Mixtures were overlaid with 2 drops of mineral oil and amplified in a thermal cycler (Hybaid; National Labnet, Woodbridge, N.J.) for 35 cycles after an initial denaturation at 96 °C for 10 min. Each amplification

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cycle consisted of 5 s at 96 °C, 20 s at 45 °C, and 30 s at 72 °C, with a final extension step of 5 min at 72 °C.

**DNA electrophoresis and visualization.** Amplification products were separated on a polyacrylamide-based vinyl polymer (PCR Purity Plus; AT Biochem, Malvern, Pa.) gel (0.7 mm thick) prepared in TBE. Electrophoresis was performed in a vertical gel apparatus (Mini-Protean; Bio Rad) at 25 v/cm (He et al., 1994). Gels were silver-stained using the procedure of Bassam et al. (1991), which was modified to include an oxidation step using an oxidizer solution (Bio-Rad #161-0444) for 5 min at room temperature. Gels were backed with a plastic film (GelBond; FMC BioProducts, Rockland, Maine) and air-dried at room temperature.

**Data analysis.** Bands that were highly stained and 300 to 1500 bp in size were scored. Bands in this size range were selected because of their high degree of reproducibility with minimal artifacts as determined in our preliminary experiments. Gels were scored visually for the presence (1) or absence (0) of bands using photographs enlarged via a PC-video image analyzer. An NTSYS-pc software (version 1.7) was used to compute Jaccard’s similarity coefficients, construct phenograms using the unweighted pair group method with arithmetic averages (UPGMA), and develop a triangular matrix of percent similarity (Rholf, 1992).

**Results**

High DNA polymorphism was observed among 30 U.S. sweetpotato cultivars tested with all seven octamer primers, and a total of

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Table 1. Pairwise matrix of genetic distances among the 30 sweetpotato cultivars obtained using the DNA amplification fingerprinting data.

|        | Creole | Camarone | Continental | Centennial | Nugget | Jewel | Porto Rico | E. Processor | Cover | Oblong | Caragold | Cherokee | Goldrush | Pelican Processor | White Triumph | White Star | Bunch Porto Rico | Ecora | Eureca | Codmar | Goldrush | Gori | Hapet | Regal | Fleist | Negrin | Porto Rico | Cherokeee |
|--------|--------|----------|-------------|------------|--------|-------|------------|--------------|-------|--------|----------|----------|----------|-----------------|--------------|------------|-------------|--------|--------|--------|----------|------|-------|--------|--------|--------|--------|--------|----------|
| Creole | 1.00   | 1.00     | 1.00        | 1.00       | 1.00   | 1.00  | 1.00       | 1.00         | 1.00  | 1.00   | 1.00     | 1.00     | 1.00     | 1.00            | 1.00         | 1.00      | 1.00        | 1.00  | 1.00  | 1.00  | 1.00     | 1.00 | 1.00  | 1.00  | 1.00  | 1.00  | 1.00  | 1.00  |
| Camarone| 1.00   | 1.00     | 1.00        | 1.00       | 1.00   | 1.00  | 1.00       | 1.00         | 1.00  | 1.00   | 1.00     | 1.00     | 1.00     | 1.00            | 1.00         | 1.00      | 1.00        | 1.00  | 1.00  | 1.00  | 1.00     | 1.00 | 1.00  | 1.00  | 1.00  | 1.00  | 1.00  | 1.00  |
| Continental | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| Centennial | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| Nugget | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| Jewel | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| Porto Rico | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| E. Processor | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| Cover | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| Oblong | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| Caragold | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| Cherokee | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |

Fig. 1. Phenogram of 30 U.S. sweetpotato cultivars based on Jaccard’s coefficient derived from the DNA fingerprinting analysis data.
144 bands were scored. Detectable DNA fragments ranged between 100 to 2500 bp in size. The level of variation among these cultivars was large enough to permit the development of cultivar-specific profiles from the fingerprint data. For example, primer CCGGGAGCT or GAACGGGT. The study was repeated once and the degree of reproducibility was high as the patterns obtained were identical.

Based on the binary band-share data generated by a matrix of 30 cultivars and 144 fragments, Jaccard’s coefficients of relationships were computed and used to generate a pairwise matrix of genetic distances (Table 1) and a phenogram depicting relationships among the cultivars (Fig. 1). Several clusters of genotypes were observed in the phenogram (Fig. 1). ‘Creole’, ‘Caromex’, ‘Kandee’, ‘Bunch Porto Rico’, ‘Porto Rico’, and ‘Cherokee’ were grouped together. The closest relationships were observed between ‘Resisto’ and ‘Copper Resisto’ (similarity index of 0.85) and between ‘Redmar’ and ‘Goldmar’ (0.84) (Table 1). ‘Jewel’ and ‘Nugget’ also clustered closely together (0.83) and ‘Carver’ was closely linked to both (0.79 and 0.75). In the principal component analysis (Fig. 2), the first three coordinates accounted for 99% of the variation among cultivars. Two distinct groups were observed between the first and second coordinates. One group consisted of ‘Resisto’, ‘Copper Resisto’, ‘Regal’, ‘Excel’, and ‘Hop’, while the other consisted of all remaining cultivars. ‘Creole’, ‘Porto Rico’, ‘Bunch Porto Rico’, and ‘Nancy Hall’ were also distinct from all others along the third coordinate. ‘Nugget’, ‘Carver’, ‘Jewel’, and ‘Scarlet’ were on the opposite extreme of the third coordinate (Fig. 2).

Discussion

The U.S. sweetpotato cultivars exhibited substantial genetic diversity as discerned by the DNA polymorphism data. In an earlier study of 73 sweetpotato genotypes from around the world, a sample of few cultivars from United States clustered together indicating a close genetic affinity within this group (He et al., 1995). The present study shows that U.S. cultivars, despite their close relatedness, possess sufficient variation enabling us to distinguish clearly all the cultivars based on their DNA fingerprints. High genetic diversity in sweetpotato is evident also from other studies (Connolly et al. 1994; He et al., 1995; Jarret and Austin, 1994). The present study tests the usefulness of the DNA-marker approach in predicting the genetic relationships among U.S. sweetpotato cultivars.

Many heirloom sweetpotato cultivars such as ‘Creole’, ‘Porto Rico’, ‘Bunch Porto Rico’, and ‘Nancy Hall’, which have been introduced in the United States during the 19th and early 20th centuries (Harmon et al., 1970; Thompson and Beattie, 1922), showed a moderate degree of relatedness to recent cultivars, although heirloom cultivars were distinctly placed along the vertical axis of the principal coordinate plot (Fig. 1). ‘Porto Rico’ and ‘Centennial’ have been used as parents in the development of many U.S. cultivars; thus, it is not surprising that they appear related to many cultivars in our study. ‘Regal’, ‘Excel’, ‘Resisto’, and ‘Copper Resisto’ are more recently developed cultivars and were separated from other cultivars (Jones et al., 1983, 1985, 1989). These four cultivars are products of a population-based breeding program and were developed using a large number of genetically diverse lines as parents in the base population. All four lines are characterized by high levels of resistance to nematodes and other soil insects, and their genetic similarity may have been partly influenced by the selection for these traits. Our results indicate that these new cultivars have a broader genetic base and exhibit considerable divergence from other popular cultivars, including ‘Jewel’ (Dukes et al., 1992). Interestingly, ‘Hopi’, an early cultivar (Hsi et al., 1966), did not group with newer cultivars, but rather with ‘Excel’, ‘Regal’, ‘Resisto’, and ‘Copper Resisto’. ‘Hop’ was used in polycross breeding of these four cultivars (A. Jones, personal communication), and our data suggests that ‘Hopi’ might have contributed substantially to their genetic makeup.

Reliable pedigree information is not available for many U.S. cultivars either because they are early introductions or they are open-pollinated selections. Nevertheless, in those instances where pedigree information is available, the DAF data appears to support these pedigrees. For example, ‘Redmar’ is a mutant selection from ‘Goldmar’, while ‘Copper Resisto’ is a mutant of ‘Resisto’ (American Society for Horticultural Science, 1972; Jones et al., 1983; A. Jones, personal communication). Close genetic relationships between these pairs of cultivars were also evident in our DAF data. ‘Excel’, an open-pollinated selection of ‘Regal’, was shown to be similar to ‘Regal’ (Jones et al., 1989).

‘Jewel’ and ‘Carver’ are derived from ‘Nugget’ and ‘Centennial’ (Pope et al., 1971; Whatley and Phillips, 1977), and ‘Scarlet’ is
a somaclonal variant of ‘Jewel’ (Moyer and Collins, 1983). The observed high degree of similarity among these cultivars reflects known ancestral interrelationships, although ‘Scarlet’ has shown only 68% similarity to ‘Jewel’. ‘Caromex’ clustered with ‘Kandee’, and ‘Gem’ clustered with ‘Tinian’, their respective progenitors (Collins et al., 1979; Pope et al., 1964). ‘Rose Centennial’ and ‘Bunch Porto Rico’ are suspected to be somatic mutants of ‘Centennial’ and ‘Porto Rico’, respectively (A. Jones, personal communication). However, these two mutants have shown lower than expected similarity to their respective normal types. Overall, clustering of parents with progeny, and mutant selections with their normal types suggests that DAF may reliably elucidate genetic relationships among sweetpotato accessions.

In the United States, sweetpotatoes are grown mostly in the southeastern states. North Carolina and Louisiana are the leading producers. Although there is considerable diversity among cultivars tested, only two to three closely related cultivars are widely grown in this country. For instance, in 1989, ‘Jewel’ accounted for about 80% of sweetpotato acreage in the United States (Dukes et al., 1992). The use of DNA-based markers in conjunction with traditional phenotypic markers may be useful in selecting appropriate parents to broaden the genetic base of this crop. Breeders depend on polycross nurseries where only the female parent is known; however, DAF studies may help identify the parents of elite cultivars from those nurseries.

Frequent occurrence of somatic mutations and the plasticity of morphological traits due to environmental factors are problems in sweetpotato plantings (Hernandez et al., 1964). Farmers in North Carolina have developed a detailed brochure to facilitate identification of off-types or cultivar run-offs (Wilson et al., 1980). There is evidence that changes in RAPD markers are associated with clonal variation (Villordon and LaBonte, 1995). Sweetpotato accessions maintained as in vitro cultures in gene banks may be subject to somaclonal variation as these cultures are propagated via axillary buds, while in the field these are propagated via adventitious roots (Jarret and Florkowski, 1990). As DAF can distinguish among very closely related genotypes, it may be useful in determining clonal purity of genotypes.

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