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Selecting a Peruvian sweetpotato core collection on the basis of morphological, eco-geographical, and disease and pest reaction data

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Abstract Sweetpotato [*Ipomoea batatas* (L.) Lam.] ranks among the seven most important food crops of the world. The International Potato Center (CIP) holds one of the largest sweetpotato ($2n = 6x = 90$) genebanks with more than 5000 cultivated accessions from America, Africa, Asia and the Pacific. This collection is clonally maintained because it comprises farmer-selected cultivars that have been asexually propagated for many years. Because of this, numerous duplicate accessions of the same cultivar are to be expected. Considering that almost 30% of the sweetpotato accessions assembled in this collection were from Perú, the first step to select a sweetpotato core collection was to identify duplicates in this group. Duplicate identification, using detailed comparisons of morphological characters and electrophoretic banding patterns of total proteins and esterases, reduced the number of Peruvian accessions in the collection from 1939 to 673. The number of duplicates of the same cultivar ranged from 1 to 99 accessions. A Peruvian sweetpotato core collection was selected to enhance the utilization of this germplasm. A total of 21 morphological descriptors were scored in all the different Peruvian cultivars. The unweighted pair-group method using an arithmetic average (UPGMA) determined the pairwise distance for members of distinct clusters based on these morphological descriptors. A core subset was selected considering the square root of the number of accessions for each Peruvian department and respective cluster, as defined by UPGMA. The original core collection consists of 85 accessions (12.6%) from all Peruvian departments, except that of Madre de Dios, where sweetpotato was never collected, and from all agro-ecological zones except Paramo, which has only 0.5% of the accessions of the entire collection. The sampling for this core collection was appropriate as determined by comparisons of means and frequency distributions for all morphological descriptors. Furthermore, this sampling was validated by the partial assessment of this sweetpotato germplasm for resistance to diseases and pests, tolerance to salt, storage root dry matter content, and vegetative period.

Key words *Ipomoea batatas* · Duplicate accessions · Genebank · Genetic resources · Phenotypic diversity

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Introduction

The cultivated sweetpotato belongs to a single species, *Ipomoea batatas* (L.) Lam. (Austin and Huamán 1996). It ranks seventh among the most important food crops, after wheat, rice, maize, potato, barley, and cassava. World sweet potato production exceeds 134 million tons in an area of about 9.2 million ha (FAO 1997). Sweetpotato has been regarded as the 'potato' of the warm tropics due to its ability to grow under high temperatures and low inputs of water and fertilizer (Bohac et al. 1995).

Sweetpotato is a hexaploid ($2n = 6x = 90$) species that exhibits hexasomic or tetra-disomic inheritance as revealed by genetic analysis (Kumagai et al. 1990). This investigation suggested that cultivated sweetpotato is either a polysomic hexaploid or else has two identical genomes plus one genome that may be different. The crop was domesticated in tropical America. The primary center of diversity occurs in north-western South America (Colombia, Perú and Ecuador) (Huamán and

Zhang 1997), but the crop was spread following the migration routes of people in the New World Tropics (Bohac et al. 1995; Huamán and Zhang 1997). For example, the island of New Guinea has been considered as a secondary center of diversity for sweetpotato because of its range of isolated ecological niches and the large number of cultivars found within a small area (Zhang et al. 1998). Columbus took sweetpotato samples to Spain after his first voyage to America. Spanish and Portuguese explorers brought the crop to Africa and Asia (Vaughan and Geissler 1997), where it became an important staple food. Nowadays, China alone accounts for more than 85% of the total world production of sweetpotato.

A core collection is essential for rationalizing the management and enhancing the utilization of the genetic diversity available in the entire sweetpotato germplasm collection. A core collection contains a subset of accessions from the entire collection that captures most of the available genetic diversity of the species (Brown 1989). Core collections have been defined for many crops in the last decade (Ortiz et al. 1998 and references therein).

The International Potato Center (CIP) holds one of the largest collections of sweetpotato germplasm (Huamán and Zhang 1997). Since 1985 CIP has carried out collecting missions in tropical America and the Caribbean (Huamán and De La Puente 1988) to develop the sweetpotato genebank. In addition, accessions were donated from other genebanks to CIP, whose genebank currently contains 5526 cultivated accessions and 532 samples of ten wild species from all the world (Huamán and Zhang 1997).

Due to the asexual propagation of sweetpotato cultivars, numerous duplicate accessions of the same cultivar are to be expected in this collection. The same cultivar can be collected under different vernacular names along its area of cultivation. In addition, donations from national or institutional collections add further duplication because the same cultivar could have several different identification codes. Therefore, duplicate identification is the first step to rationalize the size of clonaly propagated collections. There is an ongoing effort to identify these duplicate accessions at CIP. Accessions that are morphologically identical and produce the same total protein and esterase electrophoretic banding patterns or DNA fingerprints are considered as duplicates (Huamán and Zhang 1997; Zhang et al. 1997). This paper reports on the selection of a Peruvian sweetpotato core collection based on morphological, eco-geographical, and disease and pest reaction data.

Materials and methods

The original number of hexaploid sweetpotato accessions collected in Perú and held in the genebank of CIP was 1939 (Huamán and Zhang 1997). These accessions were collected in 23 out of the 24 Peruvian departments and across eight agro-ecological zones ranging from sea level to 3800 m.

Morphological data were obtained at CIP's mid-elevation (800 m) tropical experimental station in San Ramón (Perú). These data were recorded using a 0–9 scale for 21 key sweetpotato descriptors selected from an internationally accepted list (Huamán 1988; CIP et al. 1991). Predominant storage root skin color was recorded by employing a color chart that combines the color and intensity that we developed to match the color diversity shown by sweetpotatoes. These colors were coded from 1 (white-cream) to 26 (dark purple). These morphological descriptors were found to provide an adequate description of sweetpotatoes and are widely used to identify duplicates in sweetpotato collections (Huamán 1992).

Cluster analysis of the morphological data was performed with NTSYS-pc, version 1.70 (Rohlf 1992) based on the simple matching coefficient and the unweighted pair-group method using an arithmetic average (UPGMA). All accessions with about 100% similarity were grown side by side in the field at San Ramon for more detailed morphological comparisons. Those accessions that were morphologically identical were also compared by polyacrylamide-gel electrophoresis of total proteins and esterases extracted from their storage roots. Accessions that were morphologically and electrophoretically identical were considered as duplicates. One accession of each duplicate group was selected to represent the group for further comparisons with other accessions in the collection.

The number of accessions to be selected for the core collection was based on the square root of the number of sweetpotato accessions for each Peruvian department of the remaining 673 accessions. Their corresponding agro-ecological zones were determined from a geographical information system (GIS) database, using ArcInfo and ArcView software according to the latitude and longitude data from these accessions. One accession representing a geographical origin was chosen from distant morphological clusters defined by the UPGMA method. If there were many accessions to choose from a cluster, more selection weight was given to those accessions with one or more desirable characteristics for sweetpotato breeding, e.g., resistance to diseases and pests, tolerance to salt, storage root dry matter content, and vegetative period.

The mean phenotypic diversity between the entire collection and the defined core subset was compared by *t*-tests for all descriptors. Similarly, the homogeneity of frequency distributions between entire and core collections was analyzed by chi-square tests as suggested by Ortiz et al. (1998).

Results

The original number of accessions (1939) from Perú was reduced to 673 after identifying duplicates. The number of duplicates of the same cultivar ranged from 1 to 99 accessions (Table 1) and the sweetpotato genebank maintained at CIP now holds 673 unique accessions from this cultivated Peruvian collection (Table 2).

The core collection has 85 accessions (12.6%) from all Peruvian departments in which sweetpotato was collected, and from seven out of the eight eco-regions (omitting Paramo with three accessions or $>0.5\%$) where farmers grow sweetpotato (Table 2). The core subset has unique accessions whose duplicates were eliminated earlier (Table 1). This subset also has accessions collected from all altitudes (Table 2) and belonging to most of the morphological clusters (data not shown). The frequency distributions of geographic

Table 1 Number of duplicated accessions detected in original sweetpotato collection of the International Potato Center

Duplicates	Accessions	Duplicates	Accessions	Duplicates	Accessions
None (or unique)	2	10	5	22	1
1	339	11	3	24	1
2	129	12	3	27	1
3	60	13	3	32	1
4	37	14	3	34	1
5	27	15	2	44	1
6	19	17	1	46	1
7	12	20	2	58	1
8	11	21	2	99	1
9	5				

Table 2 Accessions in entire (E) and core (C) collection of Peruvian sweetpotato according to geographic and agro-ecological data from their collecting site

Department	E	C	Agro-ecozone	E	C	Altitude (m)	E	C
Tumbes	12	3	Desert	207	24	<300	256	30
Piura	77	7	Dry forest	103	7	300–600	73	11
Lambayeque	16	3	Tropical forest	4	2	601–900	48	8
La Libertad	53	6	Mountains	86	10	901–1200	43	5
Cajamarca	103	8	Puna	39	5	1201–1500	31	2
Amazonas	35	5	Paramo	3	–	1501–1800	49	9
San Martín	28	4	Upper jungle	182	27	1801–2100	96	12
Loreto	9	2	Humid forest	49	10	2101–2400	59	5
Ucayali	1	1				2401–2700	15	1
Huánuco	21	4				2701–3000	1	1
Pasco	18	4				>3000	2	1
Ancash	72	7						
Junín	3	1						
Lima	119	8						
Ica	31	5						
Huancavelica	1	1						
Ayacucho	4	1						
Apurimac	3	1						
Cusco	21	4						
Puno	6	2						
Arequipa	25	4						
Moquegua	3	1						
Tacna	12	3						
Total	673	85						
χ^2	22.381				8.706			8.607
P	0.437				0.274			0.600

and agro-ecological data from their collecting site for the entire and core collections were homogeneous (Table 2). Similarly the means and frequency distributions for all morphological descriptors were statistically similar ($P > 0.05$) in both the entire and the core collections (Table 3). The analysis of means and frequency distributions based on data for resistance to diseases and pests, tolerance to salt, storage root dry matter content, and vegetative period, partially recorded in the entire collection and core subset, revealed similar results for four out of six characteristics (Table 4). Compared to the entire collection, the core collection was biased only towards lower susceptibility for host resistance to root knot nematode [*Meloidogyne incognita* (Kofoid & White) Chitwood] and West Indian sweetpotato weevil (*Euscepes postfasciatus* Fairmaire) (Fig. 1).

Discussion

An international genebank of a vegetatively propagated and highly heterozygous crop such as sweetpotato requires maintaining the collection in the field, in vitro, and as seed samples in cold storage (Huamán and Zhang 1997). Such an operation has become very expensive, especially in these days of short-funding for international agricultural research. Therefore, efforts to minimize redundancy in the genebank are very

Table 3 Means (± SE) and χ^2 tests of frequency distribution for morphological descriptors for the entire (673 accessions) and core collection (85 accessions) of Peruvian sweetpotato germplasm. The descriptor state was transformed into a 0–9 scale[a], except for predominant root skin color which combined color and intensity in a 2-digit score

Descriptor	Entire	Core	χ^2	*P*
Twining	0.66 ± 0.07	0.81 ± 0.20	2.289	0.683
Plant habit	6.82 ± 0.05	6.98 ± 0.15	1.123	0.772
Vine internode diameter	3.80 ± 0.04	3.58 ± 0.11	3.180	0.528
Vine internode length	2.83 ± 0.06	3.00 ± 0.17	3.819	0.431
Predominant vine color	4.61 ± 0.08	4.56 ± 0.22	1.147	0.887
Secondary vine color	2.00 ± 0.09	1.86 ± 0.25	0.729	0.866
General outline of the leaf	4.56 ± 0.05	4.52 ± 0.15	0.468	0.791
Leaf lobe type	3.70 ± 0.10	3.68 ± 0.30	0.837	0.933
Leaf lobe number	3.72 ± 0.06	3.56 ± 0.15	4.620	0.329
Shape of central leaf lobe	2.97 ± 0.07	3.01 ± 0.19	1.364	0.850
Mature leaf size	5.25 ± 0.03	5.21 ± 0.07	1.378	0.502
Abaxial leaf vein pigmentation	4.94 ± 0.08	5.09 ± 0.23	1.071	0.784
Mature leaf color	3.03 ± 0.06	2.93 ± 0.16	0.935	0.919
Immature leaf color	3.41 ± 0.06	3.56 ± 0.16	1.308	0.860
Petiole pigmentation	5.10 ± 0.11	5.05 ± 0.30	0.695	0.952
Petiole length	4.29 ± 0.05	4.22 ± 0.14	4.442	0.350
Predominant storage root skin color	13.16 ± 0.30	14.38 ± 0.83	5.395	0.715
Secondary storage root skin color	1.57 ± 0.11	1.52 ± 0.30	4.046	0.400
Primary storage root flesh color	3.76 ± 0.06	3.65 ± 0.16	5.838	0.212
Secondary storage root flesh color	2.65 ± 0.12	3.19 ± 0.37	2.867	0.580
Distribution of secondary root flesh color	1.48 ± 0.09	1.80 ± 0.28	2.238	0.692

[a] According to CIP et al. (1991)

Table 4 Means (x), standard errors (SE), and χ^2 tests of frequency disbribution for agronomic characteristics for the entire and core collection of Peruvian sweetpotato germplasm. The descriptor state was transformed into a 0 to 9 scale[a] except for root dry matter (%)

Characteristic	Entire			Core			χ^2	*P*
	N	x	SE	N	x	SE		
Resistance to root knot nematode	589	6.14	0.07	81	5.27	0.23	25.92	<0.001
Resistance to West Indian weevil	343	5.80	0.15	51	4.41	0.44	14.19	0.007
Resistance to Java black rot[b]	256	5.89	0.14	43	5.65	0.38	4.029	0.258
Tolerance to salt	221	5.71	0.10	50	5.60	0.19	1.676	0.642
Root dry matter (%)	651	34.19	0.22	83	35.51	0.70	12.117	0.097
Vine maturity	609	6.25	0.08	81	6.14	0.25	3.765	0.288

[a] According to CIP et al. (1991)
[b] *Diplodia gossypina* (Cke.)

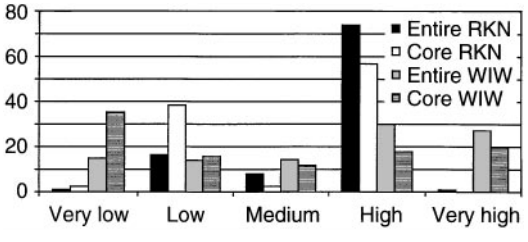

Fig. 1 Frequency distribution (%) of host susceptibility to root knot nematode (*RKN*) and West Indian weevil (*WIW*) in entire and core collection of Peruvian sweetpotato. Very low susceptibility indicates a resistant accession

important in order to lower operating costs. As suggested by Brown (1995), the core collection approach offers an alternative for deciding what accessions should be kept in field collections of vegetatively propagated crops.

The identification of duplicates was the first step for rationalizing the size of the entire collection and for developing a core collection of sweetpotato in the genebank maintained at CIP. The original number of cultivated accessions from Perú (1939) was reduced to 35% (or 673 unique samples) by comparisons of morphological characters, and electrophoretic banding patterns of proteins and esterases. Further cluster analysis based on data from 21 morphological descriptors of the 673 Peruvian unique accessions facilitated the selection of a core subset of 85 accessions (12.6%). We suggest the addition of one accession collected in Paramo to the original core collection of sweetpotato Peruvian germplasm, because no accession from this agro-ecological zone was selected in the original core collection. We also suggest to add to the core those accessions representing the largest duplicate groups because they are grown in a relatively large area of the country. By adding these extra accessions to the core subset, 94 samples (14%) of farmer-selected cultivars from Perú are considered in the new core subset.

The procedure for choosing accessions for the core collection was based on proportional sampling according to passport data and morphological clusters. The comparisons of means and frequency distributions for the morphological descriptors supported the sampling strategy. Furthermore, an independent assessment of the phenotypic diversity based on six desirable traits for breeding, partially recorded in accessions of both entire and core collections, validated this proportional sampling method. The excess of less-susceptible accessions to root knot nematodes and West Indian weevil in the core subset (Fig. 1) may be regarded as a bonus for sweetpotato breeders.

Core subsets of accessions collected in America, Asia and Africa, which are held at the genebank maintained at CIP, may be defined by a similar protocol. In this way, a comprehensive core collection of cultivated sweetpotato germplasm can be selected with accessions from both the primary and secondary centers of diversity of this crop. DNA markers have been used to assess genetic diversity in cultivated sweetpotato as well as to determine its systematic relationships with other wild *Ipomoea* species (Jarret et al. 1992; Jarret and Austin 1994; He et al. 1995; Zhang et al. 1998). Likewise, molecular markers such as RAPDs are useful tools to identify duplicates in sweetpotato germplasm (Zhang et al. 1997). Molecular-aided analysis may provide a means for investigating the structure of genetic diversity in different sweetpotato gene pools. Such investigations may facilitate the development of core subsets for other regions, which together with this Peruvian sweetpotato core collection could capture most of the world's genetic diversity of this crop. For example, stratified sampling with molecular markers may provide another genetic perspective for choosing accessions to be added to the core collection of sweetpotato germplasm. Such a worldwide sweetpotato core collection will make these genetic resources more accessible to breeders and other users.

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References

Austin DF, Huamán Z (1996) A synopsis of *Ipomoea* (Convolvulaceae) in the Americas. Taxon 45:3–38

Bohac JR, Dukes PD, Austin DF (1995) Sweet potato. In: Smart J, Simmonds NW (eds) Evolution of crop plants. Longman Scientific and Technical, Harlow, UK, pp 57–62

Brown AHD (1989) Core collections: a practical approach to genetic resource management. Genome 31:818–824

Brown AHD (1995) The core collection at the crossroads. In: Hodgkin T, Brown AHD, van Hintum ThJL, Morales EAV (eds) Core collections of plant genetic resources. John Wiley and Sons, Chichester, UK, pp 3–19

CIP, AVRDC, IBPGR (1991) Descriptors for sweet potato. Huamán Z (ed) International Board for Plant Genetic Resources, Rome, Italy

FAO (Food and Agriculture Organization of the United Nations) (1997) FAO production yearbook 1996. FAO, Rome, Italy

He G, Prakash CS, Jarret RL (1995) Analyses of genetic diversity in a sweetpotato (*Ipomoea batatas*) germplasm collection using DNA amplification fingerprinting. Genome 38:938–945

Huamán Z (1988) Descriptors for the characterization and evaluation of sweet potato genetic resources. In: Exploration, maintenance and utilization of sweet potato genetic resources. International Potato Center, Lima, Perú, pp 331–355

Huamán Z (1992) Morphologic identification of duplicates in collections of *Ipomoea batatas*. CIP Research Guide 36. International Potato Center, Lima, Perú

Huamán Z, De la Puente F (1988) Development of a sweet potato genebank at CIP. CIP Circular 16(2):1–7

Huamán Z, Zhang DP (1997) Sweetpotato. In: Fuccillo D, Sears L, Stapleton P (eds) Biodiversity in trust. Cambridge University Press, Cambridge, UK, pp 29–38

Jarret RL, Austin DF (1994) Genetic diversity and systematic relationships in sweetpotatoes [*Ipomoea batatas* (L.) Lam.] and related species as revealed by RAPD analysis. Genet Res Crop Evol 41:165–173

Jarret RL, Gawel N, Whittemore A (1992) Phylogenetic relationships of the sweetpotato [*Ipomoea batatas* (L.) Lam.]. J Am Soc Hort Sci 117:633–637

Kumagai T, Umemura Y, Baba T, Iwanaga M (1990) The inheritance of beta-amylase null in storage roots of sweet potato, *Ipomoea batatas* (L.) Lam. Theor Appl Genet 79:369–376

Ortiz R, Ruiz-Tapia EN, Mujica-Sanchez A (1998) Sampling strategy for a core collection of Peruvian quinoa germplasm. Theor Appl Genet 96:475–483

Rohlf FJ (1992) NTSYS-pc, numerical taxonomy and multivariate analysis system. Exeter Publishing Limited, New York

Vaughan JG, Geissler CA (1997) The new Oxford book of food plants. Oxford University Press, Oxford, UK

Zhang DP, Ghislain M, Huamán Z, Rodríguez F, Cervantes JC (1997) Identifying duplicates in sweetpotato germplasm using RAPD. In: CIP Program Report 1995–1996. International Potato Center, Lima, Perú, pp 90–96

Zhang DP, Ghislain M, Huamán Z, Golmirzaie A, Hijmans (1998) RAPD variation in sweetpotato [*Ipomoea batatas* (L.) Lam.] cultivars from South America and Papua New Guinea. Genetic Res Crop Evol 45:271–277