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# Genetic diversity in sweetpotato [*Ipomoea batatas* (L.) Lam.] in relationship to geographic sources as assessed with RAPD markers

Simon Templar Gichuki[1,*], Maria Berenyi[2], Dapeng Zhang[3], Michael Hermann[3], Josef Schmidt[2], Josef Glössl[4] and Kornel Burg[2,*]

*[1]Biotechnology Centre, Kenya Agricultural Research Institute, P.O Box 57811, Nairobi, Kenya; [2]Dept. of Life Sciences/Biotechnology, ARC Seibersdorf research GmbH, A-2444 Seibersdorf, Austria; [3]International Potato Center, Apartado 1558, Lima 12, Peru; [4]Centre for Applied genetics, University of Agricultural Sciences, Muthgasse 18, A-1190 Vienna, Austria; [*]Author for correspondence (e-mail: s.gichuki@cgiar.org; phone: +254 (2) 440113; fax: +254 (2) 440113); (e-mail: kornel.burg@arcs.ac.at; phone: ++43 (0) 50550 3530; fax: ++43 (0) 50550 3653)*

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**Abstract**

Available evidence shows that sweetpotato originated from either Central or South American lowlands with subsequent dispersal to North America, Europe, Africa, Asia and the pacific islands. A total of 71 polymorphic RAPD molecular markers were used to assess the genetic relationships amongst 74 sweetpotato varieties originating from a total of 23 sweetpotato producing countries within six geographical regions, namely, South America, Central America/Caribbean, United States of America (USA), East Africa, Asia and Oceania. An Analysis of Molecular Variance (AMOVA) indicated that 93.4% of the total variance was due to the differences between genotypes within regions. The difference between regions was significant ($P < 0.001$) but only contributed 6.6% to the variance. Genetic distance (PhiST) calculated with AMOVA and multidimensional scaling (MDS) revealed that the South American and the Central American/Caribbean genotypes formed two separate clusters. East African varieties, which have unique characteristics from other traditional varieties, were distinct from other traditional varieties from South America and Oceania. These results support the reported hypothesis of the origin and dispersal of the sweetpotato and indicate that the primary centre of diversity probably has two distinct genepools. It is proposed that the dispersal of the sweetpotato from its origin may have mainly involved varieties from Central America/Caribbean as opposed to varieties from South America. There is an indication that new genepools may be evolving in Africa and Asia due to hybridisation and adaptation to the local environments.

## Introduction

Sweetpotato is an important food crop particularly in developing countries where most of it is grown (Scott et al. 2000). Sweetpotato is produced in Asia, Africa, Oceania (Australia, New Zealand and the Pacific Islands), the United States of America, South and Central America with China being the largest producer in the world. Out of an approximate 1,5 million hectares of sweetpotato grown in Sub-Sahara Africa, East and Central Africa accounts for about 80% (FAO 1997).

Archaeological, linguistic and historical evidences establish that the sweetpotato originated either in the Central or South American lowlands with subsequent dispersal to North America, Europe, Africa, Asia and the Pacific (O'Brien 1972). The high level of genetic diversity of related *Ipomoea* spp. in this area supports this hypothesis (Austin 1988). Immigrant Europeans probably introduced the plant in North America be-

tween the seventeenth and eighteenth century (O'Brien 1972). It appears that the sweetpotato was unknown in the Far East until the Spanish introduced it to the Philippines, Guam and Malaysia with its Mexican name *camote* by the mid sixteenth century from where it spread to China and Japan. Introduction to India was most likely by the Portuguese with a later spread to South East Asia and parts of China with the name *batata*. Linguistic evidence in the frequency of use of the words *batata*, *tata and mbatata* and other close variations in sweetpotato names in Africa support the theory of introduction of sweetpotato to Africa by the Portuguese. Kapinga et al. (1995) reports sweetpotato varieties in Southern Tanzanian named *Mbatata white* and *Mbatata red* which supports this hypothesis but may also indicate the influence of Portuguese speaking Mozambique in the Southern Tanzania. However, it is suggested that the frequency of the names *bombe*, *bambai*, *bambaira* or *bangbe* in possible reference to the Indian port of Bombay, colonised by the British in 1662, suggests the possibility of a two pronged introduction to Africa, with an early introduction by the Portuguese via Mozambique and Angola and a later introduction by the British colonialists and missionaries either as early as the seventeenth century or as late as the nineteenth century. The introduction of the sweetpotato to the Pacific islands was probably prior to the era of European exploration possibly by early Polynesian travellers or chance spread of seeds by ocean currents (Williams et al. 1990).

Over time, natural hybridisation and selection have resulted in evolvement of hundreds of native sweetpotato cultivars in South and Central America, Africa, Asia and Oceania. Central and South America has been identified as the primary centre of diversity of sweetpotato with East Africa, Asia and Oceania suggested as secondary centres of diversity. The International Potato Center (CIP) holds one of the largest sweetpotato gene banks with more than 5,000 cultivated varieties from America, Africa, Asia and Oceania (Huamán et al. 1999). This includes over 1671 accessions from over 30 countries of Asia and the Pacific transferred from the Asian Vegetable Research and Development Centre (AVRDC) after 1991 (Asian Vegetable Research and Development Centre 1992). Several national programs in the major sweetpotato producing countries hold smaller germplasm collections. Characterisation of this germplasm in terms of determination of amount and distribution of genetic diversity is necessary for proper utilisation and conservation.

Different genetic markers have been used by sweetpotato scientists to characterise sweetpotato and its close relatives including morphological and agronomic characters (Huamán 1991), chloroplast restriction site variation (McDonald and Mabry 1992) and Restriction Fragment Length Polymorphism (RFLP) (Jarret et al. 1992). With the advent of Polymerase Chain Reaction (PCR) and development of fingerprinting methods using arbitrary primers like Random Amplified Polymorphic DNA (RAPD; (Williams et al. 1990)), DNA Amplification Fingerprinting (DAF; Caetano-Annollés et al. (1991)) and more recently Amplified Fragment Length Polymorphism (AFLP (Vos et al. 1995)) there has been an increase in use of molecular markers in characterisation of sweetpotato varieties (Connolly et al. 1994; Villordon and LaBonte 1995; Zhang et al. 1998; Huamán et al. 1999).

Despite of its importance, East African sweetpotato genetic resources have neither been characterised nor related to sweetpotato genotypes from other regions. The objective of this study was to assess the level of genetic diversity in sweetpotato and determine the relationships between sweetpotato genotypes from the different centres of primary and secondary diversity. This paper presents an analysis of 74 sweetpotato varieties using RAPDs from the primary and secondary centres of diversity.

## Materials and methods

### *Plant material*

A total of 74 sweetpotato genotypes originating from a total of 23 countries within six geographical regions of South America, Central America, United States of America (USA), East Africa, Asia, and Oceania were used in this study (Table 1). Oceania was represented by varieties from Tonga and Papua New Guinea. All the samples were acquired from the joint Kenya Agricultural Research Institute (KARI) and the International Potato Center (CIP) field genebank at the University of Nairobi Kabete campus field station. Genotypes with CIP code numbers originally came from CIP's international germplasm collection in Lima, Peru. The Ugandan, Tanzanian and Kenyan National Sweetpotato Research programmes provided the East African varieties. From each geographic region, genotypes were selected with wide variation in morphological characteristics (growth habit, colour of leaves, vine pigmentation, storage root skin and

flesh colour) as well as agronomic characteristics (fresh yield and dry matter content of storage root, fresh foliage yield) variation. The genotypes were classified into three broad categories as landraces (farmers varieties), advanced varieties (released varieties), and breeding lines based on the classification by Huamán (1988) foliage yield.

From vigorously growing plants, 5–7 young leaves were cut, immediately dipped in liquid nitrogen, kept in cool boxes with dry ice during transfer from field to laboratory and lyophilised. Freeze dried leaves were stored at 4 °C until DNA was isolated.

*DNA isolation*

About 20 mg of freeze dried plant material in liquid nitrogen was ground in a bead mill (Retsch) for 5 min. Total DNA was isolated and purified with a 'Dneasy plant minikit' (QIAGEN) following the original protocol. After extraction, 4 $\mu$l of 10 mg/ml RNase A was added and the sample incubated at 37 °C for one hour. DNA was quantified with a 'TKO 100' Minifluorimeter (Hoefer scientific instruments) and quality assessed on a 0.8% agarose gel in a 1X TBE buffer and stained with 0.5 $\mu$g/ml ethidium bromide.

*RAPD reaction and analysis*

Screening of about 100 random primers (Operon 10-mer Kits A, B, E, F, H and J from Operon technologies, California, USA) resulted in 52 primers which produced scorable amplification products fragments (data not shown). Eleven primers that generated 71 polymorphic markers were selected for this study (Table 2). Only distinct and reproducible bands were selected for analysis.

A 25 $\mu$l PCR reaction was set up as follows: 0.2 $\mu$M RAPD primer; 0.2 mM for each dNTP; 0.5 U Dynazyme™ Thermostable DNA Polymerase (Finzymes); 2.5 $\mu$l 10X PCR buffer (10 mM Tris-HCl pH: 8.8, 1.5 mM $MgCl_2$, 50 mM KCl, 0.1% Triton X-100); 5 $\mu$l genomic DNA template (5 ng/$\mu$l) and $dH_2O$. The reaction was overlaid with one drop of mineral oil. Amplification was done in 96-well microtest plates using a PTC-100™ programmable thermal cycler (M.J. Research). The amplification conditions were 46 cycles of: denaturation at 94 °C for 1 min; annealing at 36 °C for 1 min and polymerisation at 72 °C for 2 min and a final extension step of 72 °C for 8 min. Amplification products were analysed by electrophoresis of 10 $\mu$l PCR product with 1X loading buffer (0.25% Bromophenol blue, 0.25% Xylene Cyanol and 40% sucrose in water) on a 1.5% agarose gel in 1X TBE and stained with ethidium bromide (0.5 $\mu$g/ml). The gel was run for $4\frac{1}{2}$ h at 100 V in 1X TBE buffer. A 100 bp DNA ladder molecular weight marker (Gibcol) was used to determine the size of the amplified products.

*Data analysis*

Gel analysis and band scoring was done using RFLPSCAN (SCANALYTICS) computer programme. All varieties were scored for presence (1) or absence (0) of a fragment for each selected band of the amplified products. Only distinct and polymorphic bands were scored. Faint bands were omitted from the score. An analysis of molecular variance (AMOVA) was performed using Euclidean distances with AMOVA programme to estimate variance components between regions and between individuals within regions (Excoffier et al. 1992; Excoffier and Smouse 1994). Genetic relationships were analysed by multidimensional scaling (MDS) using simple matching binary dichotomy coefficients distance matrix with SYSTAT (SPSS-SCIENCE) assigning a point in two dimensional space to each variety. These coefficients are metric and produce symmetric positive semidefinite matrices, which makes them suitable for MDS, factoring or clustering.

## Results

*Analysis of Molecular Variance (AMOVA)*

AMOVA of all the sweetpotato genotypes showed that the largest contribution to the variance was due to differences amongst varieties within regions (93.4% of the total variance). The difference between regions was significant ($P < 0.001$) but only contributed 6.6% to the total variance. This indicated that there were significant differences between some regions. Genetic distance (PhiST) generated by AMOVA similarly showed significant differences between regions (Table 3). Genetic distance between South America and all the other regions was significant except with U.S.A ($p = 0.0649$). Africa was also significantly distanced from all the other regions. The genetic distance between Oceania with Africa, South America and Central America/Caribbean was significant, but was not significant with U.S.A ($P = 0.0699$) and Asia. Central America/Caribbean was not significantly different from Asia and U.S.A. Similarly, the

*Table 1.* Sweetpotato accessions used in RAPD analysis showing their original source by region and country.

| Region | Country | No | Name | Clone code | Type |
|---|---|---|---|---|---|
| SOUTH AMERICA | PERU | 1 | CAMOTE ROSITA | CIP 420048 | Landrace |
| | PERU | 2 | CAMOTE TALLO | CIP 420026 | Landrace |
| | PERU | 3 | JAP. TRES. SELECTO | CIP 420009 | Landrace |
| | PERU | 4 | MARIA ANGOLA | CIP 420008 | Landrace |
| | PERU | 5 | ZAPALLO | CIP 420027 | Landrace |
| | BRASIL | 6 | SANTO AMARO | CIP 400011 | Landrace |
| | COLOMBIA | 7 | CAMOTE AMARILLO | CIP 400014 | Landrace |
| | ECUADOR | 8 | MORADO MARAVI | CIP 400002 | Landrace |
| CA & CARIBBEAN | CUBA | 1 | CEMSA 74-228 | CIP 400004 | Breeding line |
| | CUBA | 2 | CEMSA 78-326 | CIP 400005 | Breeding line |
| | MEXICO | 3 | No.221 | CIP 400009 | Landrace |
| | PUERTO RICO | 4 | BLANQUITA | CIP 440206 | Advanced cv. |
| | PUERTO RICO | 5 | IVOIRE | CIP 440056 | Advanced cv. |
| | PUERTO RICO | 6 | SNEAKY | CIP 440220 | Advanced cv. |
| | PUERTO RICO | 7 | VIOLA | CIP 440046 | Advanced cv. |
| | PUERTO RICO | 8 | WART | CIP 420039 | Advanced cv. |
| USA | USA | 1 | LO-323 | CIP 440185 | Breeding line |
| | USA | 2 | NC196-20 | CIP 440086 | Breeding line |
| | USA | 3 | REGAL | CIP 440002 | Advanced cv. |
| | USA | 4 | SOUTHERN DELITE | CIP 440111 | Advanced cv. |
| | USA | 5 | W-228A | CIP 440023 | Breeding line |
| | USA | 6 | W-228B | CIP 440023 | Breeding line |
| EAST AFRICA | KENYA | 1 | GIKANDA | KEMB 23 | Landrace |
| | KENYA | 2 | GLUCOSE | K149 | Landrace |
| | KENYA | 3 | JAYALO | | Landrace |
| | KENYA | 4 | SPK 004 | | Landrace |
| | KENYA | 5 | SPK 013 | | Landrace |
| | KENYA | 6 | MAFUTA | | Landrace |
| | KENYA | 7 | MUIBAI | KEMB 36 | Landrace |
| | KENYA | 8 | OGURO IWE | | Landrace |
| | KENYA | 9 | SIMAMA | KEMB 10 | Landrace |
| | RWANDA | 10 | K 51/3251 | CIP 440164 | Landrace |
| | RWANDA | 11 | MUGANDE | CIP 440163 | Landrace |
| | TANZANIA | 12 | BUDAGALA | | Landrace |
| | TANZANIA | 13 | IBOJA | | Landrace |
| | UGANDA | 14 | KYEBANDULA | EAI 56702 | Landrace |
| | UGANDA | 15 | NEW KAWOGO | EAI 56681 | Landrace |
| | UGANDA | 16 | TORORO 3 | EAI 56683 | Landrace |
| | UGANDA | 17 | WAGABOLIGE | CIP 440167 | Landrace |
| ASIA | BANGLANDESH | 1 | KAMARA SUNDARI | CIP 440254 | Landrace |
| | BANGLANDESH | 2 | SP-094 | CIP 440255 | Landrace |
| | LKA | 3 | CARI 9 | CIP 440228 | Landrace |
| | INDIA | 4 | BIS 50 | CIP 440283 | ? |
| | TAIWAN | 5 | CN 1280-3 | CIP 440178 | Breeding line |
| | TAIWAN | 6 | CN 1367-2 | CIP 440223 | Breeding line |
| | TAIWAN | 7 | CN 1747-2 | CIP 440226 | Breeding line |
| | TAIWAN | 8 | TAINAN No 15 | CIP 440186 | Landrace |
| | TAIWAN | 9 | YI LANG RED | CIP 440241 | Landrace |
| | CHINA | 10 | GISHU 2 | CIP 440388 | Breeding line |
| | CHINA | 11 | LAIO SHU 44 | CIP 440151 | Breeding line |
| | CHINA | 12 | XUSHU 18 | CIP 440025 | Advanced cv. |
| | CHINA | 13 | YAN SHU 1 | CIP 440024 | Advanced cv. |
| | JAPAN | 14 | BENIAZUMA | CIP 440114 | Advanced cv. |
| | JAPAN | 15 | KOKEI No 14 | CIP 440240 | Breeding line |

*Table 1.* (*continued*)

| Region | Country | No | Name | Clone code | Type |
|---|---|---|---|---|---|
| | JAPAN | 16 | KURIKOGANE | CIP 440174 | Advanced cv. |
| | JAPAN | 17 | KYUSHU No 100 | CIP 440173 | Breeding line |
| | MALASIA | 18 | PURPLE | CIP 440257 | ? |
| | PHILLIPINES | 19 | BNAS 1 | CIP 440285 | Landrace |
| | PHILLIPINES | 20 | KINANG KONG | CIP 440187 | Landrace |
| | THAILAND | 21 | I01264 | CIP 440192 | Landrace |
| | THAILAND | 22 | I01275 | CIP 440194 | Landrace |
| | THAILAND | 23 | I01291 | CIP 440196 | Landrace |
| | THAILAND | 24 | PM-04-4 | CIP 440333 | Landrace |
| OCEANIA | PNG | 1 | BOIANAI No 3 | CIP 440303 | Landrace |
| | PNG | 2 | DAKASUM | CIP 440200 | Landrace |
| | PNG | 3 | HABARE 127 | CIP 440380 | Landrace |
| | PNG | 4 | KUMANI | CIP 440381 | Landrace |
| | PNG | 5 | MA'ALUA | CIP 440129 | Landrace |
| | PNG | 6 | MERIKAN | CIP 440296 | Landrace |
| | PNG | 7 | MUNDUENA | CIP 440130 | Landrace |
| | PNG | 8 | NAVETO | CIP 440131 | Landrace |
| | PNG | 9 | NG 7570 | CIP 440377 | Landrace |
| | PNG | 10 | SERENETA | CIP 440208 | Landrace |
| | TONGA | 11 | AMELIKA | CIP 440384 | Landrace |

*CA – Central America; ** Jap.Tres. – Japonese Tresimesino; **PNG – Papua New Guinea

*Table 2.* List of Operon 10-mer primers used in the RAPD analysis of 74 sweetpotato varieties, their oligonucleotide sequences and number of polymorphic fragments scored per primer.

| Primer | Oligonucleotide sequence (5′–3′) | Polymorphic fragments scored |
|---|---|---|
| OPA-04 | AATCGGGCTG | 5 |
| OPA-07 | GAAACGGGTG | 6 |
| OPA-11 | CAATCGCCGT | 5 |
| OPA-17 | GACCGCTTGT | 5 |
| OPA-18 | AGGTGACCGT | 7 |
| OPA-19 | CAAACGTCGG | 10 |
| OPB-13 | TTCCCCCGCT | 11 |
| OPE-13 | CCCGATTCGG | 6 |
| OPF-19 | CCTCTAGACC | 4 |
| OPH-09 | TGTAGCTGGG | 7 |
| OPH-19 | CTGACCAGCC | 5 |
| Total | | 71 |

distance between Asia with U.S.A was not significant. The greatest genetic distance between two regions was between South America and Oceania (0.2033) followed by distance between South America and Africa (0.1809). The smallest pair wise genetic distance was between Asia and U.S.A (0.0035) followed by distance between Asia and Oceania (0.0087). South America had the highest mean distance from all the other regions (0.1460) followed by Africa (0.0871) and Oceania (0.0736). Asia had the shortest mean distance to all the other regions (0.0386).

According to available records, all the genotypes from South America, Africa and Oceania used in this study are traditional varieties while most of those from Central America and the Caribbean, Asia and the U.S.A are either breeding lines or advanced

*Table 3.* Genetic distance (PhiST) between sweetpotato genotypes from six geographic regions generated by AMOVA.

| | SA | CA/Caribbean | U.S.A. | Africa | Asia | Oceania |
|---|---|---|---|---|---|---|
| SA | 0.0000 | 0.0000 | 0.0649 | 0.0000 | 0.0000 | 0.0000 |
| CA/Caribbean | 0.1462* | 0.0000 | 0.0639 | 0.0320 | 0.1848 | 0.0000 |
| U.S.A. | 0.0726 ns | 0.0367 ns | 0.0000 | 0.0000 | 0.3986 | 0.0699 |
| Africa | 0.1809* | 0.0551* | 0.0891* | 0.0000 | 0.0000 | 0.0000 |
| Asia | 0.1268* | 0.0166 ns | 0.0035 ns | 0.0375* | 0.0000 | 0.2468 |
| Oceania | 0.2033* | 0.0286* | 0.0545 ns | 0.0729* | 0.0087 ns | 0.0000 |
| Mean distance to other regions | 0.1460 | 0.0566 | 0.0513 | 0.0871 | 0.0386 | 0.0736 |

Distances = PhiST between pairs of populations; Above diagonal = Probability random distance (PhiST) > than observed distance with 1000 iterations; * Significant difference between regions ($P < 0.05$), ns – No significant difference between regions; SA: South America; CA: Central America; U.S.A.: United States of America

varieties (Table 1). An AMOVA including only landraces from South America, Africa and Oceania plus all the genotypes from Central America/Caribbean was also done. This was to minimise the confounding effects of the breeding materials. The resultant contribution to variance due to differences between genotypes was 88.9% and a significant contribution due to differences between regions of 11.1% at $P < 0.001$. Genetic distance between South America and the other three regions was significant, as was that between Africa and the other regions. It was barely significant between Oceania and Central America/Caribbean ($P = 0.0639$). The longest distance between two regions still was between South America and Oceania and between South America and Africa with similar values as in the analysis involving all the varieties (Table 3).

*Genetic relationships amongst sweetpotato genotypes within regions*

Genetic analysis of the traditional varieties by MDS revealed clustering patterns between different varieties within regions. All the varieties from South America formed one cluster that was distinct from almost all the other varieties (Figure 1A). Similarly the African and Oceania varieties generally formed separate clusters except for some varieties which could not be grouped within the cluster of their source region. Almost half of the Central America/Caribbean genotypes were grouped with the African cluster. The other four were grouped within the Oceania cluster. Only one genotype from Central America/Caribbean (CEMSA 78-323) was grouped within the South American cluster. Regardless of type, genotypes from the primary centre of diversity of the sweetpotato clearly formed two separate groups. Most traditional varieties from Africa and Oceania were more genetically related to the Central American/Caribbean group than with the South American. Since South and Central America is the accepted centre of origin of the sweetpotato, formation of these two clusters means there are possibly two genepools in the primary centre of diversity, South American and Central American/Caribbean. Due to its importance as the primary centre of diversity, genetic analysis of genotypes from other regions of the world may then be related to these two groups.

A second MDS shows the relationship between genotypes from U.S.A and Asia with those from the primary centre of diversity (Figure 1B). Here also the South American group was clearly distinct from the other groups including the Central America/Caribbean group. Genotypes from Asia predominantly grouped with the Central America/Caribbean group. On the other hand the U.S.A. genotypes were associated with both South American and the Central America/Caribbean groups (Figure 1B). A small group of Asian genotypes formed a sub-cluster between the two clusters from the primary centre of diversity.

## Discussion

Though documented evidence show dispersal of sweetpotato to Asia and Africa to be recent, these results indicate a high level of variation amongst sweetpotato varieties within and between regions. The AMOVA results showed high level of diversity between genotypes, within the traditional cultivars as well as within all the genotypes studied.

South American varieties were found to be significantly different from genotypes from all the other regions by both statistical evaluation using AMOVA and by clustering methods with MDS. But within traditional varieties they had the highest mean similarity within regions (data not shown). Of particular interest is the significant genetic distance between South American cultivars and the Central American/Caribbean genotypes. It is quite informative that the two groups form distinctly separate clusters. The only two traditional varieties within the Central American/Caribbean genotypes (No 221. from Mexico and Blanquita from Puerto Rico) were the most distanced from the South American group. The highest diversity of the sweetpotato and its wild relatives is found in Central and South America (Austin 1988). The results suggest that this primary centre of diversity probably consist of two genepools, a South American genepool and a Central American/Caribbean one. This supports the findings of Zhang et al. (2000) who found Peruvian-Ecuadorian genotypes to be quite distinct from other cultivars from tropical America.

The Central American/Caribbean genotypes demonstrate a close relationship with sweetpotato genotypes from all the regions outside the Americas. This relationship is evident in traditional varieties, advanced varieties and breeding lines. The genotypes from this region also had the highest level of within region. The data suggests that the dispersal of the sweetpotato from its origin to the rest of the world

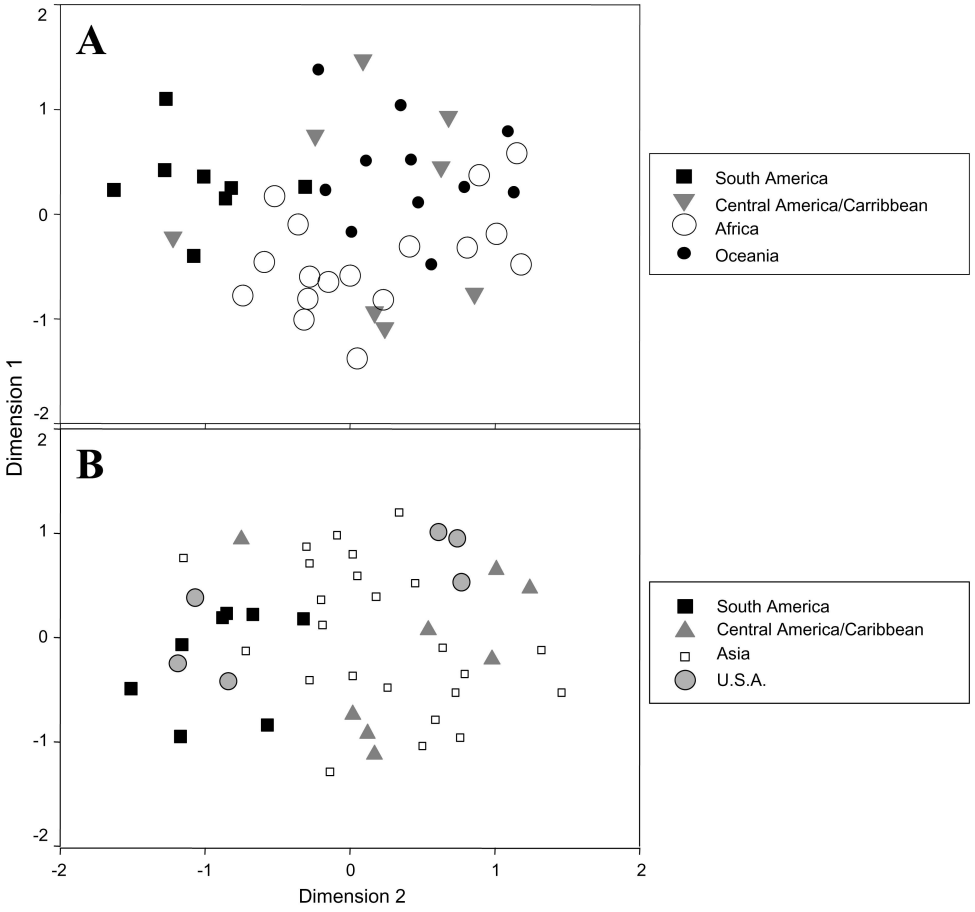


*Figure 1.* Relationship of sweetpotato genotypes as revealed by 71 RAPD loci. A. Relationship between landrace varieties from Africa, Asia, South and Central America/Caribbean including advanced varieties and breeding lines from Central America/Caribbean. B. Relationship among sweetpotato genotypes from South America, Central America/Caribbean, U.S.A. and Asia

mainly involved the Central American/Caribbean genepool. The historic perspective would support this view since the major spread of the Sweetpotato particularly to Asia and probably also to the Pacific region occurred during the peak of the Spanish empire. Spain initially established colonies in the Caribbean Islands before defeating the Aztec Empire in Mexico by 1521 and the Inca Empire in Peru by 1530. From Peru the Spaniards spread northwards to Ecuador and Colombia and southwards to Chile. It is possible that the introduction of sweetpotato to the Philippines by 1524 came from the Caribbean and Mexico since resistance to Spanish rule in Peru continued for several years.

Recent evidence has shown that there is high diversity of cultivated sweetpotato in Central America compared to other Latin American regions (Zhang et al. 2000) and the region is rich in wild *Ipomoea* sp. closely related to the sweetpotato. This strongly suggests that Central America may be the actual centre of origin of the sweetpotato and our results further supports this view.

The East African germplasm is also shown to be different from the germplasm from other regions. The lowest genetic distance from Africa to other regions is with Asia, which may be due to the hypothesised later introduction from India. The MDS shows that part of the African cluster is separate from the South American, Central American/Caribbean and Oceania groups. The East African sweetpotato has been found to be quite unique in several important characteristics. It has a high occurrence of certain desirable characteristics, which includes, high storage root dry matter content, high resistance to virus diseases and vigorous foliage growth and ground cover. Similarly some other important characteristics have been found to

have a low occurrence in East African genotypes including storage root ß-carotene content and early maturity.

Oceania varieties, though distanced from South America genotypes seem closely related to Asian genotypes. This is quite likely due to the several hundred years of sea trade links between these two regions. The Asian and the U.S.A. genepool are quite confounded with the high level of breeding activities. This diversified nature is reflected in the results from Asia and the U.S.A.

Within the short period since the sweetpotato's introduction into Africa and Asia, mutations and other evolutionary processes (few introduced genotypes, local inbreeding) have resulted in genetic drift as evident by the presence of distinct genepools within these two regions. It is evident that evolutionary and germplasm exchange processes have been going on between the three regions of Africa, Asia and the Pacific for centuries. Introductions to India by the Portuguese and the Philippines by the Spanish must have spread to many parts of Asia and the pacific islands. Part of this genepool might have been introduced to East Africa by the British imperialists between the seventeenth and nineteenth centuries. Hybridisation between the two genepools and adaptation to the local environment within East Africa and Asia may explain the formation of these separate clusters observed between the South American and Central American/Caribbean genepools.

Despite these arguments it is important to note that there has been extensive exchange of germplasm mediated by breeders and agronomists in recent times. Examples are the Asian Vegetable Research and Development centre (AVRDC) and the International Institute of Tropical agriculture (IITA). These two institutions carried out extensive germplasm activities in Asia and Africa prior to the mid-eighties, when the sweetpotato world collection was transferred and reorganised in Lima, Peru. This included collection, characterisation, breeding, selection and dissemination of elite Sweetpotato genotypes to many countries in the three regions of Asia, African and Oceania. By 1986 AVRDC had distributed a total of 3850 sweetpotato samples of breeding lines and accessions to Asia, Oceania, South America, North America, Africa and other unspecified regions (Fernandez and Lu 1988). Introductions and exchange between countries within regions have also been going on for decades. Introduced varieties are often given new names in the new areas where they are grown which partially contribute to similarities amongst genotypes from different regions and failure of certain genotypes to group within their source region. This demonstrates the complex nature of sweetpotato genetic resources and the difficult task of trying to characterise them.

From these results we may conclude that the primary centre of diversity of the sweetpotato probably consists of two genepools and that the dispersal of the sweetpotato probably involved mainly the Central American/Caribbean genepool. We can also conclude that within the regions of Asia, Oceania and Africa there is evidence of new genepools evolving, possibly through hybridisation of the two groups.

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