

International network for cassava genetic resources

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DEFINITION OF A CORE COLLECTION FOR CASSAVA

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ABSTRACT

The main responsibility of CIAT as a curator of the world's cassava germplasm is to assure long-term conservation at low risk of genetic loss and to facilitate access to genetic variability. The present collection of 5477 accessions is maintained both in the field and *in vitro* at CIAT headquarters in Cali, Colombia. For purposes of improving the efficiency and effectiveness of collecting, conservation and evaluation, a core collection of 630 accessions has been selected to represent the total diversity of the species. The theoretical basis of core collections is discussed and procedures for the definition of a cassava core collection are presented. Short-, medium- and long-term implications of this strategy for global germplasm management are reviewed.

INTRODUCTION

Crop germplasm collections are the basic source of genetic variability for breeding programmes. Exploiting this variability for sustained human benefit depends on effective long-term management. A logical setting of priorities for different accessions can aid in designing conservation and evaluation strategies which most effectively utilize resources, while at the same time making the most appropriate material available to the users. Conservation of vegetatively propagated crops can be especially costly, bringing additional urgency to the need for prioritization.

The concept of 'core collections' grew out of the need to solve these problems. Originally conceived by Frankel (1984), a core collection would represent, 'with a minimum of repetitiveness, the genetic diversity of a crop species and its wild relatives.' According to IBPGR studies, by the end of 1989 there were over 20 projects directly concerned with setting up core collections. Four established core collections were identified (Hodgkins, 1990). This paper presents the procedure followed for the development of a cassava core collection at CIAT. A balance was sought between the principal theoretical ideals of definition of a core collection and the practical needs and existing realities in the specific case of cassava.

CASSAVA GERMPLASM COLLECTION AT CIAT

CIAT has accepted global responsibility for the conservation of cassava germplasm, within the CGIAR system. In late 1993, the collection consisted of 5477 accessions, whose origin is described in Table 1. The collection was established in 1969, essentially as the first activity of the Cassava Programme. It is maintained as both field-grown plants with annual renewal, and *in vitro* under slow growth conditions.

While the cassava collection is not large compared to those of some other major crops, conservation is costly because of the need for vegetative propagation to conserve not only genes but genotypes. The mode or modes of conservation need to take into account security of maintenance, mutation rate, resource requirements, and accessibility for evaluation and utilization.

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Table 1. Descriptive information available on the CIAT cassava germplasm collection

| Origin | No. of accessions | % with passport data ¹ | | % with agronomic evaluation ² | % with isozyme character. | % with morphological character. |
|---------------|-------------------|-----------------------------------|----------|--|---------------------------|---------------------------------|
| | | Basic | Complete | | | |
| Argentina | 16 | 0 | 0 | 100 | 100 | 94 |
| Bolivia | 3 | 0 | 0 | 100 | 67 | 67 |
| Brazil | 1637 | 28 | 0 | 84 | 65 | 65 |
| China | 2 | 0 | 0 | 100 | 50 | 50 |
| Colombia | 1907 | 50 | 30 | 92 | 84 | 98 |
| Costa Rica | 147 | 0 | 0 | 100 | 93 | 94 |
| Cuba | 74 | 0 | 0 | 100 | 100 | 100 |
| Dom. Rep. | 5 | 0 | 0 | 100 | 100 | 100 |
| Ecuador | 117 | 90 | 0 | 100 | 98 | 100 |
| Fiji | 6 | 0 | 0 | 100 | 100 | 100 |
| Guatemala | 91 | 0 | 0 | 100 | 96 | 94 |
| Indonesia | 51 | 0 | 0 | 100 | 100 | 100 |
| Malaysia | 68 | 0 | 0 | 100 | 98 | 100 |
| Mexico | 100 | 70 | 0 | 100 | 94 | 98 |
| Panama | 42 | 50 | 0 | 100 | 95 | 100 |
| Paraguay | 192 | 10 | 90 | 95 | 89 | 94 |
| Peru | 405 | 40 | 0 | 98 | 93 | 92 |
| Philippines | 6 | 0 | 0 | 100 | 100 | 100 |
| Puerto Rico | 15 | 100 | 0 | 100 | 100 | 100 |
| Thailand | 8 | 100 | 0 | 100 | 100 | 100 |
| United States | 9 | 0 | 0 | 100 | 89 | 89 |
| Venezuela | 240 | 50 | 0 | 100 | 98 | 100 |
| CIAT clones | 324 | - | - | 100 | 84 | 76 |
| IITA clones | 19 | - | - | 100 | 84 | 84 |
| Total | 5477 | 40 ³ | 17 | 92 | 87 | 89 |

¹ Basic: origin; date of collecting; complete: origin; date of collecting; site description; qualities and uses. ² Evaluation in at least one major ecosystem. ³ Excluding clones.

This hierarchy of needs suggests that it would be useful to have criteria established for defining a management strategy for distinct subsets of the collection. A core collection would contribute significantly to this end. Specifically, it is anticipated that the core collection would define the part of the collection first to be duplicated outside of Colombia, to be placed in cryopreservation, and to be evaluated intensively for identification of duplicate accessions.

The desirability of having a better understanding of, and more effective access to, the variability within the cassava germplasm has been highlighted in recent years by the growing interest in searching for specific new traits, such as photosynthetic rate, presence of C4 photosynthetic enzymes, root amylose/amylopectin ratios, nutrient use efficiency, HCN levels in roots and leaves, daylength sensitivity, resistance to pests and diseases not yet evaluated, and others. Several of these characters require highly specific and expensive

evaluations, and may be difficult to apply to the entire germplasm collection. The main interest for cassava genetic improvement purposes is to determine the variability which exists within cassava, and where to search more intensively within the collection if promising preliminary results are obtained. These objectives can be better met with a prioritization based on a core collection.

DESCRIPTIVE INFORMATION ON CIAT'S CASSAVA COLLECTION

The appropriate definition of a core collection depends on the availability of substantial information from which assumptions about genetic diversity can be derived. Ideally, the definition of a core collection for a cultivated species should be made within a collection which:

- covers the total range of the crop's genetic variability;
- consists mainly of landrace cultivars having complete passport data;
- has no duplication of accessions;
- is characterized for molecular and morphological traits; and
- is well evaluated for agronomic, physiological, quality and resistance traits.

Further, good knowledge of the crop evolution and genetic diversity should be available.

The documentation for CIAT's cassava collection includes passport data, morphological descriptors, isozyme characterization and agronomic evaluation. There are particular deficiencies in the knowledge of the crop's evolution. Estimates of availability of this information for accessions of different origins are given in Table 1, and described in more detail below.

Passport data

Most of the early collections sponsored by CIAT obtained only basic information on collecting site and altitude. These collections account for most of what is presently available from Mexico, Panama, Colombia, Venezuela and Ecuador. By 1983, IBPGR had developed a standard collection format, and most collections from that point onward include more complete passport data. The principal collection among this group is that of Paraguay. Guatemala, Peru and Colombia also have a substantial number of accessions with complete passport data. For most other countries, the availability and the quality of the data are highly variable. Most of the accessions from Brazil and Peru can be traced at least to a state or department of origin, but most have little other passport data attached. The Asian accessions have essentially no passport data except for country of origin. There is some possibility of obtaining more information from original sources, but for most countries, this information is impossible to retrieve.

Agronomic evaluation

The cassava breeding section has given priority to evaluating the germplasm collection under a range of edaphoclimatic conditions in Colombia. This has provided the basis for selection of promising clones for direct recommendation to national programmes, and for use as parents in breeding. Although evaluation sites have changed somewhat over time, most emphasis has been placed on the subhumid lowlands (north coast); acid soil lowland savannas (Llanos Orientales); mid-altitude tropics (CIAT headquarters, Palmira); and highland tropics (Cauca

Department). Priority among these sites has been based on the worldwide importance of the zone, with the subhumid and acid soil savannas receiving highest priority.

Biochemical characterization

Work begun in the mid-1980s demonstrated a high degree of polymorphism for the α,β -esterase isozyme system for cassava. A concentrated effort was then made to characterize the entire collection for esterase banding patterns produced from root tip extracts separated on polyacrylamide gels. By now, 4260 accessions (78% of the collection) have been characterized for esterase, and the processing of remaining accessions is expected to be completed by the end of 1992.

Morphological characterization

Approximately 90% of the collection has been evaluated for the IBPGR-defined morphological descriptors. While some of these data are still incomplete, the amount of effort required to finish these evaluations is not great. Since these descriptors have been evaluated over time in different plantings of the germplasm collection, there is likely to be some variability due to environmental factors for some of the less stable descriptors.

DEFINITION OF A CORE COLLECTION

Species included

The core collection focuses only on the cultivated species, *M. esculenta*, as there is still too little information on the wild species of the genus. It is envisaged that at least 4-5 years will be required to obtain sufficient background information on these species to incorporate them into a core collection.

Number of accessions

Brown (1989a) suggests an average core collection size of 5% of accessions in a large collection, and 10% in a small one as a reasonable target. Given this guideline, considerations of conservation, and the limits for easily managing evaluations for a range of characters, a core collection of approximately 600-650 accessions was initially proposed.

Core collection composition: dynamic or fixed?

For most crops, and especially for cassava, where basic information on genetic diversity is limited, we can expect that the theoretical basis for selection of components of the core collection will become increasingly better understood. The question arises as to how flexible should be the structure of the core, i.e. to what degree should accessions be discarded or new ones added? Certainly, it would be counterproductive in terms of investment in resources for extensive evaluation if the core collection were excessively dynamic. The majority of accessions of the core should be sufficiently stable so that a long term accumulation of evaluation and other information can be achieved on a set of 'reference' accessions. On the other hand, the actual structure of the core should conform to new information, and introduction of new accessions into the total collection. In practical terms, it may be reasonable to expect that on the order of 70-80% of the originally defined core collection would remain unchanged as part of the core, while 20-30% would be subject to entry or removal based on an improved information base.

National programme core collections and implications for CIAT

Only a handful of national programmes worldwide have a sufficient number of cassava accessions in germplasm collections to warrant establishing a core collection. In Latin America, only Brazil, with 1226 accessions at CNPMF (Cruz das Almas, Bahia), and an estimated 2 700 nationally, is considering the establishment of a core collection. In Asia, the CTCRI (Trivandrum, India), maintains 1327 accessions and SRIFC (Sukamandi, Subang, West Java), holds 954 accessions (Lawrence *et al.*, 1986). Given that at present CIAT has no accessions from India and only a few landrace varieties from Indonesia, the collection of principal concern to CIAT with regard to defining a core is that of Brazil. CENARGEN has expressed interest in coordinating with CIAT the definition of a core collection for the Brazilian germplasm.

There would be several advantages to coordinating with Brazilian scientists (CENARGEN and CNPMF) for the selection of a common core of Brazilian clones. First, it would provide extensive information, well beyond that which any individual institution could gather, on a defined set of clones, which would represent the total genetic diversity of Brazil. Secondly, it would be an additional incentive for close collaboration between CIAT and EMBRAPA in the area of genetic resources management. Nevertheless, in order not to delay the definition of a core collection at CIAT, the Brazilian accessions for the core were initially selected solely on the basis of CIAT criteria. It is hoped that some future coordination can be achieved, possibly requiring some modification in this subsection of the core.

Definition of parameters

Since direct measures of genetic diversity are almost entirely lacking, criteria must be chosen which can be expected to reflect or influence genetic variability, in some way. Criteria for inclusion in the cassava core collection were defined in four major groups:

- geographic origin, where the number of accessions per country is determined by a series of weighting factors;
- diversity of morphological characters;
- diversity of α,β -esterase banding patterns;
- *a priori* selection of accessions based on predetermined criteria of specific interest. Highest importance was given to geographic origin, as a more appropriate way to sample genetic diversity. Approximately two-thirds of accessions for the core were chosen in this manner, and one-third selected based on the other criteria.

Clones selected by geographic origin

Geographic origin has a fundamental influence on genetic diversity, because of differences in physical, biological and cultural influences. While not necessarily the best measure of geographic entities for purposes of defining genetic diversity, country boundaries are certainly the most convenient starting point. To determine a tentative number of clones to include from each country, the following criteria were considered:

- proportion of a given country's accessions which are believed to be local landrace varieties;
- importance as a centre of diversity;

- proportion of the country's total diversity represented in CIAT's collection; and
 - the diversity of cassava-growing ecosystems which that country represents.
- The estimates and the weights for these factors are given in Table 2.

Table 2. Description of parameters used in determining number of accessions to be chosen from each country of origin

| Origin | No. access. | Local land race var. (%) | Est. level of dupl. (%) | Base No. of landrace accessions | Importance | | Country's total div. in CIAT collection | | Diversity of ecosystems | | Correct factor for coll. size ¹ | Sum of wts. ² | No. of clones for distinct parameters | | | | |
|---------------------|-------------|--------------------------|-------------------------|---------------------------------|------------|------|---|------|-------------------------|------|--|--------------------------|---------------------------------------|----------------------------|------------------|---------------------------------|--------------------------------|
| | | | | | Scale | Wt | % | Wt | Scale | Wt | | | Geog. orig. ³ | Morphol. div. ⁴ | Div. of esterase | A priori selection ⁵ | Final No. in core ⁶ |
| | | | | | | | | | | | | | | | | | |
| Argentina | 16 | 40 | 10 | 6 | 1 | 1.00 | 25 | 0.75 | 2 | 0.40 | 1.00 | 2.15 | 2 | 4 | 0 | 3 | 8 |
| Bolivia | 3 | 100 | 0 | 3 | 1 | 1.00 | 5 | 0.95 | 2 | 0.40 | 1.00 | 2.35 | 1 | 2 | 0 | 3 | 3 |
| Brazil ⁷ | 1637 | 95 | 20 | 1244 | 1 | 1.00 | 40 | 0.60 | 5 | 1.00 | 0.20 | 0.52 | 110 ⁸ | 13 | 15 | 20 | 101 |
| China | 2 | 100 | 0 | 2 | 3 | 0.50 | 25 | 0.75 | 3 | 0.60 | 1.00 | 1.85 | 1 | 0 | 0 | 2 | 2 |
| Colombia | 1907 | 95 | 20 | 1449 | 1 | 1.00 | 75 | 0.25 | 5 | 1.00 | 0.20 | 0.45 | 111 | 15 | 13 | 14 | 14 |
| Costa Rica | 147 | 40 | 20 | 47 | 2 | 0.75 | 80 | 0.20 | 2 | 0.40 | 0.80 | 1.08 | 9 | 7 | 5 | 4 | 23 |
| Cuba | 74 | 90 | 20 | 53 | 2 | 0.75 | 80 | 0.20 | 2 | 0.40 | 0.80 | 1.08 | 10 | 5 | 1 | 2 | 18 |
| Dom. Rep. | 5 | 100 | 10 | 5 | 2 | 0.75 | 10 | 0.90 | 3 | 0.60 | 1.00 | 2.25 | 2 | 2 | 0 | 4 | 5 |
| Ecuador | 117 | 100 | 25 | 88 | 1 | 1.00 | 50 | 0.50 | 3 | 0.60 | 0.80 | 1.68 | 25 | 6 | 0 | 4 | 32 |
| Fiji | 6 | 100 | 10 | 5 | 3 | 0.50 | 50 | 0.50 | 1 | 0.20 | 1.00 | 1.20 | 1 | 0 | 0 | 2 | 2 |
| Guatemala | 91 | 100 | 50 | 46 | 2 | 0.75 | 80 | 0.20 | 2 | 0.40 | 0.80 | 1.08 | 8 | 6 | 0 | 2 | 15 |
| Indonesia | 51 | 10 | 15 | 4 | 3 | 0.50 | 10 | 0.90 | 3 | 0.60 | 0.80 | 1.60 | 1 | 0 | 2 | 5 | 7 |
| Malaysia | 68 | 70 | 15 | 40 | 3 | 0.50 | 50 | 0.50 | 2 | 0.40 | 0.80 | 1.12 | 8 | 0 | 1 | 6 | 15 |
| Mexico | 100 | 95 | 30 | 67 | 2 | 0.75 | 75 | 0.25 | 3 | 0.60 | 0.80 | 1.28 | 14 | 6 | 0 | 2 | 20 |
| Panama | 42 | 100 | 20 | 34 | 2 | 0.75 | 75 | 0.25 | 2 | 0.40 | 0.80 | 1.12 | 6 | 2 | 0 | 2 | 9 |
| Paraguay | 192 | 100 | 20 | 154 | 1 | 1.00 | 80 | 0.20 | 2 | 0.40 | 0.60 | 0.96 | 25 | 8 | 3 | 7 | 40 |
| Peru | 405 | 95 | 20 | 308 | 1 | 1.00 | 60 | 0.40 | 2 | 0.60 | 0.60 | 1.20 | 63 | 10 | 3 | 2 | 76 |
| Philippines | 6 | 30 | 0 | 2 | 3 | 0.50 | 5 | 0.95 | 2 | 0.40 | 1.00 | 1.85 | 1 | 0 | 0 | 2 | 2 |
| Puerto Rico | 15 | 40 | 15 | 5 | 2 | 0.75 | 60 | 0.40 | 2 | 0.40 | 1.00 | 1.55 | 1 | 2 | 0 | 4 | 7 |
| Thailand | 8 | 10 | 0 | 1 | 3 | 0.50 | 75 | 0.25 | 2 | 0.40 | 1.00 | 1.15 | 0 | 0 | 0 | 4 | 4 |
| USA | 9 | 0 | 0 | 0 | 3 | 0.50 | 100 | 0.00 | 1 | 0.20 | 1.00 | 0.70 | 0 | 0 | 0 | 4 | 4 |
| Venezuela | 240 | 95 | 20 | 182 | 1 | 1.00 | 60 | 0.40 | 4 | 0.80 | 0.60 | 1.32 | 41 | 9 | 3 | 3 | 55 |
| CIAT hybrids | 317 | 0 | 0 | 0 | | | | | | | | | 0 | 3 | 5 | 27 | 33 |
| IITA hybrids | 19 | 09 | 0 | 0 | | | | | | | | | 0 | 0 | 0 | 3 | 3 |
| Totals | 5477 | | | 3744 | | | | | | | | | 440 | 100 | 51 | 121 | 630 ⁹ |

¹ Correction factor for collection size: >1000 = 0.2; >400-1000 = 0.4; >100-400 = 0.6; >20-100 = 0.8; 1-20 = 1.0. ² Sum of weights 1, 2 and 3 x correction factor for collection size. ³ Number of accessions for core = (sum of weights x base no. of landrace accessions x constant), where constant = 0.17. ⁴ Clones included in CIAT/IBPGR *in vitro* Pilot Genebank (IVAG). ⁵ Selected by three criteria: a = Included in CBN studies on basis of diversity of geographic origin and agronomic value. b = Common landrace cultivars. c = Elite clones from CIAT and IITA. ⁶ Final number may be less than the sum of columns, since the same clone may be repeated for different criteria. ⁷ Including 800 accessions to be introduced in 1991/92. ⁸ 60 accessions to be included prior to introduction of 800 new accessions. ⁹ Actual total will likely be lower after testing for, and elimination of, duplicates within the core.

Clones for the core were randomly chosen from among the landrace cultivars of each country. Although additional weighting within countries could have been considered, this was probably not justified for the existing cassava collection. For the intermediate and larger sized collections, the existing accessions are rather well distributed from across the cassava-growing areas of the country, and therefore random selection can adequately represent the variability in a balanced way.

Base number of landrace accessions

Based on available passport information, the proportion of accessions from each country which are likely to be local landraces was estimated. This ranges from 0 to 100%, with most countries being highly represented by landrace varieties.

Since there are a significant number of duplicates among accessions, this needed to be taken into account in order to define a base number of landrace accessions; i.e. base number = (total number of accessions) × (proportion of these which are local landraces) × (proportion which are not duplicates). These calculations provide an estimate of 3744 non-duplicated landrace accessions in the collection.

Importance as centre of diversity

Each country was classified as high (1), intermediate (2) or low (3) in importance as a centre of diversity. Latin American countries were classified either high or intermediate and Asian countries as low. The following weights were assigned: 1 = 1.00; 2 = 0.75; and 3 = 0.50.

Country's total diversity in CIAT collection

A very subjective estimate was made of the total diversity of each country which is represented in CIAT's collection (in terms of number of distinct genotypes). The higher the degree of a country's total diversity which is represented at CIAT, the lower need be the proportion of genotypes which enter the core collection. It is assumed that many genotypes in a given region are derived from related backgrounds, and that a smaller proportion can be sampled to represent the total genetic diversity than if only a small part of the total number of clones have been collected. Therefore, weights are assigned which are inversely proportional to percentage representation in CIAT's collection. For example, a country with an estimated 20% of its landrace varieties in CIAT's collection is given a weight of 0.80, and with 90%, a weight of 0.10.

Diversity of ecosystems

A third weighting factor was based on an estimate of edaphoclimatic diversity in the cassava-growing regions of the country, and assigned a 1-5 scale, which was converted directly to proportional weights of 0.20 to 1.00. The assumption behind this weighting was that diversity of agroecosystems directly influences crop genetic diversity under conditions of both natural and farmer selection.

Correction factor for collection size

Mainly in order to avoid very low representation in the case of countries with few accessions in the CIAT collection, a 'correction factor' was applied in inverse proportion to collection size, as follows:

| No. accessions | Correction factor |
|----------------|-------------------|
| > 1000 | 0.2 |
| 400 - 1000 | 0.4 |
| 100 - 400 | 0.6 |
| 20 - 100 | 0.8 |
| 1 - 20 | 1.0 |

Calculation of the contribution of each country

Final calculation of the contribution of each country to the geographic subset of the core was made by adding the weights described in the preceding sections,

multiplying by the estimated base number of landrace accessions, multiplying by the correction factor for collection size, and finally, multiplying by a constant which would give a core collection size of about 450 accessions from this subset.

Clones selected for biochemical diversity

The estimates of biochemical diversity were from the α,β -esterase studies of 3270 accessions. Given that this is only one of many possible measures of biochemical diversity, it is suggested to include only 50 accessions representing the range of variation of isozyme patterns. For this, a cluster analysis was performed on the esterase banding patterns (where three classes are recognized: absent, questionable (very light band), and present). Fifty clusters were formed *a priori* using the FASTCLUS procedure of SAS (SAS Institute Inc.), and within each cluster an accession randomly chosen. In this procedure, no clone was selected which showed band No. 17, a rare band, and therefore MBra 315 was added to the list. The representation from each country is given in Table 2.

Clones selected for morphological diversity

Given that morphological diversity was one of the principal criteria for definition of the clones to be included in the IBPGR-funded *in vitro* Pilot Genebank project (IVAG), and that this group of 100 accessions has been intensively studied for a range of traits, these were included as representative of the range of morphological diversity of cultivated cassava.

Clones selected for *a priori* inclusion

Clones included in studies within the Cassava Biotechnology Network (CBN)

A base group of clones has been selected for a few studies within the CBN (primarily DNA fingerprinting and HCN studies), based on diverse origins and/or agronomic value. Given that important biochemical information is being obtained on these clones, and that their selection was based on some indication of genetic diversity, it was considered advantageous to include this group of 74 clones in the core collection.

Common landrace cultivars

While information has not been well compiled on the area planted to different cultivars worldwide, it is logical to use the best information available to include the world's most commonly grown clones in the core collection. These clones represent some of the most important genetic diversity of the species from an agronomic viewpoint. The large majority of these are landrace varieties. Approximately 40 such clones were included in the core collection.

Elite clones from breeding programmes

Elite clones from breeding programmes represent genotypes with favorable genes in high frequency for a number of traits. Their inclusion is important for breeding.

Elimination of duplicates

It is assumed that the initially defined core collection will have a certain number of duplicate accessions. Given that this is a subset of germplasm derived by specific criteria, the level of duplication should, however, be less than in the total collection. One of the first procedures after tentative selection of the clones for the core should be the elimination of duplicates based on morphological and

biochemical descriptors. Those identified as tentative duplicates on this basis will be planted side by side in the field for further confirmation of morphological similarity (see Hershey *et al.*, 1991, for more complete description of methodology). Duplicates should have only one representative in the core, with others moved to the reserve collection. The identification and management of duplicates in the reserve collection is still in the process of definition, but this will not affect the definition or the management of the core.

MANAGEMENT IMPLICATIONS

The structuring of a core collection has a series of implications for management of the cassava collection at CIAT. Some of the issues are relatively straightforward, and others require further study and discussion. The following sections delineate some of the alternatives and provide concrete suggestions as a basis for discussion.

Collection

Some of the gaps in the collection are highlighted by the criteria by which a core collection is defined. For example, for several countries of moderate to high importance for cassava production, even the most common landrace cultivars have not been incorporated into the collection. This is the case for the Dominican Republic, Haiti, Nicaragua, Bolivia, Indonesia and the Philippines, as well as all of India and Africa.

Introduction from southeast Asian and Latin American countries is relatively straightforward. From Africa and India there are severe quarantine restrictions. IITA is in the process of compiling information on germplasm available in national collections, with the goal to eventually consolidate an Africa-wide collection at IITA. Ideally, they should then define a core collection for Africa, which could be incorporated into CIAT's global core collection. Likewise, if quarantine regulations begin to permit introduction of *in vitro* germplasm from Latin America to Africa, based on improved indexing techniques, the Latin American and Asian components of the global core collection could be introduced to Africa.

Conservation

Definition of a core collection has broad implications for germplasm conservation. The main issues are form(s) of conservation for core and reserve accessions, and the duplication of the collection in another institution.

At present, CIAT's collection is maintained continuously in the field, and *in vitro* under slow growth conditions. Probably only about half the accessions are duplicated in national programme collections. The principal deficiency is the case of Colombia (40% of the total collection), where very few of the accessions are maintained by the national programme.

The primary obligation of CIAT as curator of the world cassava germplasm is to maintain, in a high degree of security, the genetic variability of the species. This responsibility can be viewed in hierarchical form, with different conservation strategies assigned to different categories of germplasm. The scheme presented in Table 3 is proposed, taking into account the special importance of the core collection in a conservation strategy.

In the short term (1-2 years) it is visualized that both the core and reserve part of the collection will be maintained both in the field and *in vitro*. During this time,

seed and/ or pollen will be collected from the reserve collection as a backup reserve of genetic diversity. With this additional security of conservation, by the medium term (3-5 years) the reserve collection will be maintained in the field but with reduced plot size, as a source of planting material for research purposes. Also in the medium term, it is anticipated that cryopreservation techniques could become routine; an African core collection will be defined and introduced to CIAT; and another institution will be identified for duplication of the core collection, either as *in vitro* or cryopreserved cultures.

Table 3. Proposed strategy for conservation of *Manihot esculenta* genetic diversity

| Implementation ¹ | Description of germplasm | Institution ² | Type of conservation | Estimated No. of accessions |
|-----------------------------|---------------------------------|--------------------------|----------------------|-----------------------------|
| Actual | Total (LA and Asia) | CIAT | Field | 5477 |
| | | CIAT | <i>in vitro</i> | 5254 |
| Short-term | Reserve (LA and Asia) | CIAT | Field | 4000 |
| | | CIAT | <i>in vitro</i> | 4000 |
| | Core (LA and Asia) | CIAT | Field | 630 |
| | | CIAT | <i>in vitro</i> | 630 |
| Medium-term | Reserve (LA and Asia) | CIAT | Cryopreserv. | 3500 |
| | | CIAT | Seed/pollen | 2000 |
| | Core (global) | CIAT | Cryopreserv. | 700 |
| | | CIAT | <i>in vitro</i> | 700 |
| | | CIAT | Seed/pollen | 500 |
| | | CIAT | Field | 700 |
| Other | <i>in vitro</i> or cryopreserv. | 700 | | |
| Long-term | Reserve (global) | CIAT | Cryopreserv. | 4500 |
| | | CIAT | Seed/pollen | 2500 |
| | | Other | Seed/pollen | 2500 |
| | Core (global) | CIAT | Cryopreserv. | 700 |
| | | CIAT | <i>in vitro</i> | 700 |
| | | CIAT | Seed/pollen | 500 |
| | | CIAT | Field | 700 |
| | | Other | Cryopreserv. | 700 |

¹Short term = 2-3 years; medium-term = 4-8 years; long-term = >8 years. ²Excludes conservation activities in Africa related to core and non-core collections.

In the longer term (>5 years), a comprehensive conservation strategy would hopefully include the elimination of the field collection and its conservation *in vitro* and cryopreservation at CIAT (including African accessions). A sample of the reserve collection will also be duplicated in other institution and maintained by cryopreservation. The core collection would continue to be managed as in the previous, medium-term phase.

Characterization and evaluation

A core collection allows a better understanding of genetic diversity in the whole collection, through more efficient use of resources for evaluation. While CIAT's

collection has been evaluated fairly extensively for agronomic traits in distinct ecosystems, a more thorough evaluation is needed due to important effects of genotype by environment interaction. The number of traits which could be measured on a core collection is virtually limitless, and therefore it is useful to plan, at least in a general way, the priorities. Several areas can be suggested; the following list is not comprehensive.

Root and leaf quality traits are increasingly recognized as critical for both traditional and new markets. Recently, the defined core collection was evaluated for cyanide content in leaves, root peel and parenchyma. Results showed that it is possible to select accessions with extremely low levels of cyanide in root parenchyma, while retaining considerable accumulation in root peel and leaves (CIAT, 1992). The majority of the low cyanide genotypes (less than 10 ppm) came from the highlands of Colombia, indicating that if further genetic diversity is required, accessions from that region should be given priority for future screening. Starch quality and suitability for processing into various products are also being evaluated in the core collection, as well as leaf quality, which has not previously been evaluated across a wide range of genetic diversity.

Physiological traits related to productivity and yield stability often cannot be evaluated in large samples of genotypes due to the time and cost of screening. Traits like efficiency of photosynthesis, tolerance to drought stress, leaf life, shading tolerance, photoperiod sensitivity, and others, could be evaluated in the core collection.

Reaction to several of the major pests and diseases have been evaluated in the germplasm collection, but several have yet to be done. Systematic evaluation for variability for resistance to mealybug, lacebug, burrowing bug, and several root rotting species should have priority.

The rapidly growing Cassava Biotechnology Network will rely heavily on CIAT as a source of germplasm for a wide range of projects. The core collection can provide a manageable sample size for measuring the genetic diversity for such traits as: isozymes and RFLPs; ability for regeneration from individual cells, callus or somatic embryos; haploid production from anther culture; somaclonal variation; and many others.

OTHER COLLECTION SUBSETS

Apart from the core collection, which constitutes the principal subset of the collection for purposes of conservation and evaluation, it is anticipated that the definition of other collection subsets will be advantageous. These will be defined on the basis of specific needs, and the form of management of each may vary accordingly. Already within the collection there are subsets defined for high expression of pest and disease resistance, a marker gene subset, and an elite clone subset. Rare or geographically restricted alleles that may not be represented in the core collection can be allocated to other collection subsets.

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