Strengthening Smallholders' Capacity to Adapt to Agro-climatic Changes: Optimization of Root Crops Germplasm Management and Use

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Abstract

Since their domestication, root crops have been clonally distributed over wide geographical distances. The bottle necks induced by the introduction process often resulted in varieties with narrow genetic bases, now increasing smallholders' vulnerability to forthcoming agro-climatic changes. The question is: how can we develop adapted varieties, considering climatic uncertainties, the constraints in developing countries and the characteristics of the root crop species involved? These species share common biological traits: they are asexually propagated in farmers' fields, flowering ability of varieties is erratic, they have variable ploidy levels but are predominantly allogamous and highly heterozygous. Breeding is a slow process conducted on research stations even though it is widely accepted that G x E interactions are highly significant. The distribution of selected clones is then constrained by their low multiplication rate, the large number of smallholders, their geographical isolation, the absence of a 'seed' industry and strict international regulations. This paper presents a review of studies on root crops genetic diversity, their germplasm management systems and breeding constraints. It attempts to propose a new approach to strengthen smallholders' capacity to adapt to forthcoming changes. Suggestions are made for future research to address adaptation, taking into consideration improvement program needs at the national level. The geographical distribution of allelic diversity appears as a practical and cost-efficient approach.

Key words: Adaptation, distribution of allelic diversity (DAD), participatory plant breeding

Introduction

During the last decades, successful international collaborations for germplasm collections of root crops (cassava, sweet potato, yams and aroids) have been implemented with fantastic results. Thousands of accessions are now maintained *ex situ*, in the field or *in vitro*. Because of the complexity of this operation and the costs involved, the germplasm management and characterisation system is centralised in well equipped research stations. Breeding programmes are adjacent to these germplasm collections and, in most cases, local farmers are the direct beneficiaries of the research station's improved varieties. Unfortunately, quite often, the number of beneficiaries decreases with the distance from these research stations.

Root crop species share common biological traits: they are vegetatively propagated, flowering of varieties is erratic, ploidy levels are variable, they are allogamous and highly heterozygous. Breeding starts with the selection of parents based on their individual value. Hybrids are evaluated for a few traits and undesirable genotypes are discarded as soon as possible. Due to the limited means available, this process is conducted on a few research stations even though it is widely accepted that G x E interactions are highly significant. The distribution of a few clones is then constrained by their

low multiplication rate, the large number of smallholders, their geographical isolation, the absence of a 'seed' industry and strict international regulations.

Now that climatic changes are accelerating farmers' demand for diversely adapted plants, there is a need to develop an alternative approach which could strengthen the existing system. The problem is that in order to prepare for such changes, we need to know what to prepare for (Jarvis et al., 2009). Because of climatic uncertainties, it is quite difficult to develop long term breeding strategies, although the need to breed varieties for future conditions is recognized. The situation is quite complex because most of the World's farming population relies on traditional varieties (Mercer and Perales, 2010) and not on organized breeding and seed systems similar to those existing in for sexually propagated crops. Most smallholders are, therefore, left to themselves. This is especially true for farmers cultivating root crop species in tropical countries who are still relying on their local, sometimes very ancient varieties. Considering their socio-economic situation, and the fact that in many countries these species are not national priorities, it is likely that this situation will remain the same for the forthcoming decades.

The urgent questions are: how can we improve smallholders' capacity to adapt to climatic change? Can we propose an alternative to strengthen, not to replace, the existing centralized system? How could we develop this alternative to correspond to existing traditional germplasm management practices and plant material exchange networks? Also, what can we learn from the most recent studies combining molecular data with surveys in farmers' fields?

This paper presents a review of the research on root crops genetic diversity (for cassava, sweet potato, yams and aroids), and on their germplasm management systems and breeding constraints. It then attempts to propose a new approach to strengthen smallholders' capacity to adapt to forthcoming changes. The focus is on smallholders cultivating root crops for food security and local markets, rather than on farmers involved in cash cropping for the starch industry. Suggestions are made for taking into consideration national improvement program needs. The geographical distribution of allelic diversity appears as a practical and cost-efficient approach.

Farmers' traditional management practices of root crops genetic diversity

Cassava (*Manihot esculenta*)

Cassava genetic diversity is well distributed geographically. Core collections have been made by selecting about 10% of the accessions on the basis of diversity of origin, morphology, isozyme patterns and specific agronomic criteria. Using molecular markers, this approach has been shown to be highly effective for selecting unique genotypes. It appears that the allelic diversity is fairly well distributed within the area of origin, with Colombia and Brazil having the largest number of different alleles across all loci, followed by Costa Rica, Venezuela, Peru and Mexico, unique alleles being present in each of these six countries (Chavarriaga-Aguirre et al., 1999). Tropical Africa is considered to be a secondary centre of diversity and when compared with South America, there is sufficient genetic distance to separate African from American accessions. This suggests that the forces shaping allele frequencies (at SSR loci), probably involved spontaneous recombination and farmers' selection for local adaptation during centuries after its introduction from South America (Fregene et al., 2003).

Farmers' selection of spontaneous volunteers resulting from recombination and true seeds germinating in their plots has been well documented in South America (Elias et al., 2001), Africa (Manu et al., 2005) and Oceania (Sardos et al., 2008). The process is fairly simple: farmers intercrop different cassava varieties, these varieties exchange pollen, sometimes with wild forms nearby (Duputié et al., 2007), seeds germinate spontaneously and the most vigorous, and/or attractive, plants are selected and cloned (Pujol et al., 2005). In some cases, farmers can even select spontaneous triploids with outstanding characteristics (Sardos et al., 2009). This selection process can lead to significant genetic diversity in a fairly short time, even when the crop is clonally introduced on oceanic islands (Sardos et al., 2008).

In most cases, the genetic diversity is concentrated within the regions but often, migration of human populations and the clonal introduction of new cassava varieties, is one of the possible reasons for closer resemblance or greater disparity among varieties from various regions (Siqueira et al., 2009; Delêtre et al., 2011). Farmers often focus on the physico-chemical characteristics of

the underground organs, attempting to reduce the levels of anti-nutritional factors while improving the quality of the roots (Kombo et al., 2012). If the selection focuses on a remarkable trait, such as orange flesh, rich in pro Vitamin A, for example, the divergence between American and African genepools (measured with SSR markers) can be quite significant (Esuma et al., 2012).

Sweet potato (*Ipomoea batatas*)

Sweet potato is a hexaploid, but this high ploidy level is not a constraint for farmers' traditional management practices, which are very similar to what cassava growers are doing. Sweet potato varieties produce flowers when the days are getting short and these are visited by many pollinators, often bees. Because of the self incompatibility mechanisms, crosses result in seeds which represent each, a unique heterozygous genotype. The seedlings are cloned in farmers' fields and if their characteristics are interesting, they can be transported across very long distances (Roullier et al., 2012). Tremendous genetic diversity exists in the area of origin where two distinct genepools indicate, most likely, two independent domestication processes, one in southern America (Peru-Ecuador region) and the other one in Central America (Roullier et al., 2011).

The large island of New Guinea is being considered as a secondary centre of diversity with almost 5000 varieties being cultivated (Ballard et al., 2005). In Papua New Guinea and Irian Jaya, farmers traditionally adopt volunteer plants resulting from the spontaneous germination of the numerous self-sown seeds the crop produces. This is especially remarkable in the Highlands (Schneider, 1995; Yaku and Widsyastuti, 2002), where different varieties are planted together in the same large hills, made to improve drainage. The fact that genotypes originating from different genepools have been introduced into New Guinea (the so called *batata*, *camote* and *kumara* lines), and have inter-crossed in farmers' fields, is a possible explanation for such diversity (Roullier et al., 2013). The same process occurred in Africa (Gibson et al., 2008) and Brazil (Veasey et al., 2008), where farmers sometimes select unconsciously volunteers with interesting characteristics. The exchange of clones and the introduction of new genotypes, contribute to the diversification of farmers' portfolios. Because of the high variability of the major compounds of the roots,

especially total sugars, the focus of traditional selection is often on the chemotype (Gibson et al., 2008).

Yams (*Dioscorea* spp.)

With not less than ten cultivated species originating from different geographic continents, yam domestication is a fairly ancient but straight forward process which occurred independently in different locations, probably at different times and from different genepools. Clones have been distributed over very large distances in very ancient times. However, some traditional varieties have been shown, with co-dominant markers, to be the result of cross pollinations (Tostain et al., 2007). The domestication process is still going on, not only in the yam belt of West Africa (Dumont et al., 2006) but also in Melanesia where spontaneous inter specific hybrids might exist (Malapa et al., 2005). The process is straight forward: an edible wild form is vegetatively propagated and cultivated. Tubers' physico-chemical characteristics are the useful traits that are selected. Cultivated and wild forms are not very different morphologically but have significant chemical differences. Molecular marker studies have confirmed this process (Mignouna and Dansi, 2003).

The fact that *Dioscorea* spp. are dioecious with different ploidy levels, does not seem to be a constraint to farmers' management of genetic diversity. In West Africa, the traditional practice involves the introduction of naturally occurring wild yams, probably *D. abyssinica* and *D. praehensilis*, in cultivated varieties of the *D. cayenensis-rotundata* species complex. Through this practice farmers increase the genetic diversity within their portfolios by using sexual reproduction of wild and possibly cultivated genotypes and their hybrids. Unconsciously, farmers create varieties with new genetic combinations and ensure cultivation of the best genotypes while preserving potential for adaptation (Chaïr et al., 2010; Scarcelli et al., 2006). Wild relatives are, therefore, an interesting potential source of genetic diversity and deserve to be protected (Chaïr et al., 2011).

Aroids (*Colocasia esculenta, Xanthosoma sagittifolium, Alocasia* spp. *Amorphophallus* spp.)

Thousands of varieties of taro exist. The genetic diversity is organized following a remarkable geographical structure and within one country most varieties share a common genetic base. There are two gene pools, an Asian and a Pacific, for cultivated taro, with Indonesia hosting

the greatest diversity (Kreike et al., 2004). Valuable germplasm exists in different geographical regions, and it is of utmost importance to explore its agronomic potential. If more studies have been conducted in the India-Bangladesh region and/or in southern China, other genepools would have been probably identified (Matsuda, 2002). A high morphological variation between varieties is not a guarantee for a high genetic variation. Wild taro, although morphologically not very variable, is highly diverse. Farmers select their own varieties from seedlings and/or mutants and traditional exchange networks contribute to the introduction of new genetic combinations into the system (Sardos et al., 2012). Farmers' focus is always on the quality of the corm, with emphasis on high dry matter and starch contents and low acridity.

The other aroids are not well documented at the molecular level. However, considering their traditional cropping practices, favoring the association of different varieties within the same plot and the cross-pollination systems of most species, there is no reason why the diversity should not be managed in a way similar to that of taro and the same approach is also valid for other root crop species.

How can we strengthen smallholders' capacity to adapt to climatic changes?

Over the last three decades, molecular marker studies have greatly contributed to upgradation of our knowledge, not only on the allelic diversity existing within genepools, but also within and between cultivated and wild forms. For most root crop species, we now have a better understanding of the traditional system for germplasm maintenance and use:

- The genetic diversity is distributed geographically with different countries hosting unique alleles. Geographic distances correlate with genetic distances resulting in patterns of isolation by distance.

- Different genepools exist and they often correspond to different domestication events.

- Farmers are continuing the domestication process. They keep on selecting new genotypes resulting from sexual recombination occurring in their fields. They capture volunteers and clone them if they satisfy their taste requirements.

- Clones, when interesting, can be easily exchanged and are distributed over large geographical distances,

introducing new alleles in sometimes very isolated places.

- Therefore, there is some sort of ongoing recurrent selection process being conducted in farmers' fields. Even if its pace is very slow, it does occur and needs to be encouraged.

If we accept that genetic variation is the most important source of adaptive variation, we should then attempt to increase genetic variation within smallholders' portfolios. We can expect farmers to use it in order to adapt to climatic changes. The question is therefore: how can we strengthen farmers' capacity to adapt to climatic changes while attempting to contribute to what they already do rather than disturbing their traditional germplasm management system?

The constraints of the present centralized system

Fundamental problems of root crops breeding have been studied (Bradshaw, 2010). Breeding programmes have produced clonal material with good performances when measured on station. Clonal selections may have local potential, but are unlikely to suit most countries where environments are highly variable and G x E interactions precludes the widespread adaptations of a few varieties. Especially in smallholders' plots where environmental factors are highly significant. Also, because of the low multiplication rate of the planting material, it takes several years before multilocation trials can be concluded. The consequence is that the selection process is affected by the absence of replications in different environments. So far, except for cassava, very few improved varieties have been widely distributed.

The present institutional system for germplasm management and use preserves a significant proportion of the genetic diversity. Major important breeding efforts are made but the centralised aspect is a real constraint. Breeding for adaptability to specific environments requires detailed evaluations of the existing germplasm, not only within one country, but also worldwide, across the entire genepool. The genetic variation which is required to suit the present agro-ecological conditions, never mind a future influenced by climatic changes, can only be obtained from segregating populations of parents of diverse origins.

Such work is presently done in very few research stations although the demand is likely to increase drastically with the forthcoming changes.

Obviously, if the present system does not benefit from a complementary approach, smallholders' capacity to adapt will not be strengthened. Changes will occur but the improved material delivery time will not be reduced. The impact in smallholders' plots will be slow. This is not due to the breeding programmes efficiency but rather to the planting materials constraints. Participatory plant breeding has already been identified as a way of collaborating with farmers to develop varieties adapted to their needs (Witcombe et al., 1996; Cleveland et al., 2000). However, in the case of root crops species, if allelic diversity is needed to develop new varieties, it is also the first constraint in farmers' fields.

The geographic distribution of allelic diversity: old wine in a new bottle?

The geographic distribution of allelic diversity (DAD) has been proposed as a practical approach for conserving germplasm for minor root crop species (Lebot et al., 2005). In practice, this is done by:

- Assembling a core sample representing the useful diversity of the species

- Distributing genotypes for direct use or for breeding

- Distributing genes as clones in segregating progenies

- Selecting clones with local adaptation

Core sample: The easiest way to distribute allelic diversity is to identify useful genotypes (a core sample) and to exchange them internationally for direct distribution to farmers. To make the most of the genetic resources inherent in a core sample, it is necessary to have access to DNA data and to distant geographic origins. However, farmers often give priority to taste rather than yield, especially when the crop is grown for domestic use. Quality in terms of dry matter content, cooking texture and taste, is also an important trait for the core sample. An understanding of how properties are influenced by variety is of critical importance in assessing the potential of genotypes.

Distribution of genotypes: Root crop species are, unfortunately, the host of a number of viruses and international transfers of germplasm need to be indexed to ensure that they are healthy. The core sample has to go through a transit centre, where viruses can be detected, and where therapy can take place if they are infected. Once the core sample has been distributed *in vitro*, field multiplication allows direct distribution to farmers. When this is done over a wide geographical area and when genotypes satisfy farmers' needs, farmers insert the exotic germplasm into their portfolios and this increases allelic diversity. As these genotypes are clonally propagated, farmers can exchange and distribute them further.

Distribution of genes: To be useful for breeders, the core sample genotypes need to have sexual reproductive potential, which means that their ploidy levels, and other factors involved in genetic compatibility, must be understood. Selected genotypes of the core sample are then intercrossed, and the F_1s raised for distribution as C_1 clonal stock to farmers. Visual tools are used at an early stage to screen progenies so that only hybrid plants in their first clonal generation (C_1s) with some form of potential are distributed. Also, for breeding purposes, there is a need to use germplasm from different genepools to broaden the base of the existing programmes (Kawano, 2011). Seeds can be generated in large quantities, with thousands of seedlings grown in small nurseries with minimum efforts. This has the advantage of maintaining genetic diversity, in contrast to the selection of a relatively small number of clones, whose diversity is fixed by vegetative propagation (Rajendran et al., 2005).

Clonal selection for local adaptation: Greater farmer involvement in the C_1 screening process is used to exploit G × E interactions through decentralised evaluation and selection. The selected C_1 clones are divided into small batches, each going to a different farmer. On station, assessment of chemotype is difficult when hundreds or thousands of progenies have to be tested, but if C_1s are distributed to farmers, participatory evaluation of clonal material is feasible. There are some risks of distributing clones which have not been evaluated for appropriate chemical composition, but farmers will automatically discard them early in their selection process. Farmers will select varieties which satisfy their cooking and/or processing requirements, which are quite variable, and adopt them if they show potential. Additionally, if a farmer selects an outstanding genotype, it is likely that he or she will soon be in a position to exchange it with others.

Testing the DAD

The practical implementation of the DAD concept described above has been tested *in situ* with different root crop species. Two years after the introduction of new varieties, a survey was conducted with 449 farmers located in ten different villages of Vanuatu and Oceanic archipelago. Qualitative and quantitative investigations were conducted and data were analyzed. It appeared that farmers do enrich their varietal portfolios with introduced exotic genotypes thus broadening the narrow genetic bases of some species. Nevertheless, no local varieties were lost. Significant geographic distribution of clones of new varieties throughout the archipelago also took place via spontaneous, informal distribution to farmers' relatives (Camus and Lebot, 2010). A survey of taro genetic resources was then conducted in the same set of ten villages. A sample of 344 varieties referred as the National Sample (NS) was collected and its genetic diversity assessed using nine microsatellite markers and then compared with an International Core Sample (ICS) previously distributed in the ten villages. The ICS was composed of 41 varieties, including 23 originating from South-East Asia and included 52 new alleles. The genetic diversity of taro in Vanuatu was, therefore, expanded from 89 alleles to a total of 141 alleles, based on the set of SSR markers used in this study. This suggests that the distribution of clones genetically different and sexually fertile could lead to the incorporation of new and useful alleles in the local genepool (Sardos et al., 2012).

These two experiments, the on-farm assessment of clonal introductions and the molecular evaluation of the diversity therein, indicate that DAD is a practical approach for taro. Also, the approach was proven successful for base broadening and allelic diversity introduction, increasing genetic variation in farmer's portfolios, and therefore strengthening their capacity to adapt. The fact that taro shares a common biological trait with other root crop species, but also is grown by smallholders with similar constraints, indicate that the approach could be used for other species.

Conclusion

Producing crops ready for change - changes to climate or pest and disease outbreaks – is particularly difficult for those that are vegetatively propagated. Genetic diversity is constrained by geographical isolation; it is based on a few chance mutations or the occasional result of sexual reproduction; either way, genetic diversity is narrow, and this limits their usefulness as environments change rapidly. To create the diversity required, the genetic base of the crops needs to be broadened. To do that successfully, requires cooperation between countries, the use of modern biotechnologies, and development of a network of scientists exchanging information and germplasm under the auspices of international treaties.

The INEA (International Network for Edible Aroids) is now attempting to test the DAD approach on a global scale. The target groups are the plant breeders and other scientists working on cocoyam and taro worldwide, who do so in isolation. Although taro is extensively cultivated, it remains outside the remit of the international agriculture research system. Scientists and farmers cannot easily access new genotypes. Breeding of taro demands considerable expertise as well as the safe distribution and preservation of germplasm. There is an urgent need to train breeders. The intended beneficiaries of INEA are growers throughout the world, those that grow the crop both for subsistence and commercial use. They are smallholders who require access to improved germplasm to overcome production constraints. Women are the primary target in on-farm activities, as they have the greatest knowledge of varieties, and are the custodians of the genetic resources.

Acknowledgement

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