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ON FARM CONSERVATION OF *MUSA* DIVERSITY IN THE GREAT LAKES REGION OF EAST AFRICA

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ABSTRACT

Banana (*Musa* spp.) cultivar diversity in the Great Lakes region of East Africa has been on the decline for the last several decades. A number of abiotic, biotic and socio-economic factors are thought to be responsible for this decline. In spite of low variation with respect to stress resistance, a number of farmers have continued to maintain a diversity of the local landrace highland banana cultivars in small plots. Studies to assess diversity on farm were carried out in four benchmark sites in Uganda and Tanzania. The objectives of the study were to estimate levels of *Musa* diversity within and between benchmark sites; understand diversity trends over time in respect to changes in diversity within national genebanks and finally assess the usefulness of numerical methods in diversity assessment of a wider *Musa* genepool. Cultivar diversity per farm per site was assessed in 135 households and then compared with cultivar diversity in the national collections. Morphometric data was then taken from 135 sampled farms. Altogether, 257 accessions were studied; 125 from the national collection, and 132 from on farm. A total of 60 characters were used to measure diversity in the sampled household farms and the national collections. Two coefficients were used to measure diversity; group average clustering and principal component analyses were used to analyse similarity or dissimilarity among different groups of bananas and between different cultivars of the East African highland bananas. There was variation in cultivar diversity per site. The percentage variation explained by the first major components did not exceed 20% and these were able to separate genome groups. Within the highland bananas, clusters corresponding to clone sets were not very distinct in the first run of the analyses due to overlap. Thus, distinct clusters of the East African highland bananas were only observed in the second run of the analyses. Diversity varied in sites, and also between sites and national *Musa* collections due to different selection criteria and needs of different stakeholders. The level of viability between groups is demonstrated to be great but small within subgroups and this morphological diversity can be linked to utility of these traits by the farmers.

Key Words: Cluster analysis, cultivars, morphometric data, principal component analysis

RÉSUMÉ

La diversité des variétés des bananes dans la région des grands lacs de l'Afrique de l'est a été en déclin pour plusieurs dernières décennies. Un nombre des facteurs abiotiques, biotiques et socio économiques sont pensés être responsables pour ce déclin. Malgré la faible variation avec respect a la stresse de résistance, un nombre des fermiers a continué à maintenir une diversité des variétés locales des races de terre de banane des régions de montagne dans les petites parcelles. Les études pour évaluer la diversité sur ferme étaient conduites dans quatre sites de référence en Ouganda et Tanzanie. Les objectives de cette étude étaient d'estimer les niveaux de diversité de *Musa* dans et entre les sites de référence; comprendre les tendances de diversité tout au long du temps en respect aux changements dans la diversité dans les banques nationales des gènes et finalement évaluer l'utilité des méthodes numériques dans l'évaluation de diversité d'une large gène commune. La diversité des variétés par ferme et par site était évaluée dans 135 ménages et ainsi comparée avec la diversité des variétés dans les collections nationales. La donnée morphométrique était alors prise à partir de 135 fermes échantillonnées. Ensemble, 257 accessions étaient étudiées ; 125 de la collection nationale, et 132 à partir de la ferme. Un total de 60 caractères était utilisé pour mesurer la diversité, le groupe moyen de bouquet et les analyses des composants principaux étaient utilisés pour analyser la similarité ou la dissimilarite parmi les différents groupes des bananes et entre les différentes variétés de bananes de région de montagne de l'Afrique de l'est. Il y avait une variation dans la diversité des variétés par site. La variation du pourcentage expliquée par les premiers composants majeurs n'a pas excèdé 20% et ceux ci étaient capables de séparer les groupes de génomes. Dans les bananes de région de montagne, bouquets correspondant aux groupes de clones n'étaient pas distincts dans les premiers essais des analyses dues à l'empiétement. Ainsi, les bouquets distincts des bananes de région de montagne de l'Afrique de l'est étaient seulement observés dans le second essai des analyses. La diversité variée dans les sites, et aussi entre les sites et les collections nationales *Musa* due au différent critère de sélection et les besoins des différents participants. Le niveau de viabilité entre les groupes est démontré être grand mais petit dans les sous groupes et cette diversité morphologique peut être liée a l'utilité de ces traits par les fermiers.

Mots Clés: Analyse de bouquet, variétés, donnée morphologique, analyse du principal composant

INTRODUCTION

The *Musa* diversity in the region is of three categories. The East African coastal cultivars of different genome groups including the edible AA, various AAA, AB and ABB (De Langhe *et al.*, 1994). The coastal cultivars are limited in number per genome group and none of these groups is being used as a staple food along the coast or inland. The second category is the African plantains (AAB), growing in backyard gardens or intercropped with other banana types. Plantains are less relatively important above 800 meters in East Africa than they are in the humid lowlands of west and central Africa. The third category is the East African highland bananas which is unique to the East African highland plateau. The East African highland bananas are the green-cooking and beer cultivars different from the *Musa acuminata* triploid dessert types. Since their introduction into the Great Lakes region, the highland bananas have diversified through mutations, natural and farmer selections giving rise to the large number of distinct clones found today (Simmonds, 1959; De Langhe *et al.*, 1994). These bananas are grown in large plantations, that traditionally exist for more than 30 years(Tothill, 1940). Since the 1970s, traditional East African banana farming systems have rapidly declined in productivity, and in cultivar diversity and this has threatened the livelihood of the different communities growing the crop.

A number of factors have been responsible for reductions in the diversity of bananas in the East African region among which are soil infertility, and various diseases and pests. Bananas in the East African region have low variation for resistance to pests, diseases, drought and many other stressing conditions. In spite of this low variation for resistance, a number of farmers have continued to maintain traditional East African banana cultivars in small plots in areas of high disease and pest pressure. These farmers believe that land races are well adapted to their growing conditions, and they are averse to the risk of planting new unknown cultivars. The diversity on farm is maintained in a mixture of land-race, farmer selected cultivars. This same diversity is in proportions equivalent to farmer's needs and it can increase if it targets farmer's needs. The success of any on- farm conservation scheme will therefore depend upon understanding farmers' perceptions of the East African traditional *Musa* diversity.

The identification and classification of banana landraces in the East African great Lakes region is complicated by the fact that morphological characters are greatly influenced by the environment in which the bananas are grown and by the relatively high incidence of somatic mutations in many of the clones. The farmers who have been growing these cultvars are usually acutely aware of the differences affecting either the appearance or the quality of these cultivars. Several studies have examined diversity in the East African highland bananas. These studies can be divided into two categories; surveys of farmer perceptions and measurement of quantitative variation. Surveys have determined that farmers select specific cultivars for special end use attributes, for adaptation to specific environments, and for resistance to diseases and pests (Davies, 1995). Surveys have also helped to determine the areas of greatest cultivar diversity (Karamura *et al.*, 1996).

Different attempts to look at quantitative variation in bananas growing in East Africa has been done by several people (Rossel and Mbwana, 1991; Karamura, 1999). Quantitative variation in the East African highland bananas grown in Uganda has been assessed by Karamura (1999) to show that each clone can be assigned unambiguously to one of five groups of clones by multivariate methods. Discriminant analysis with a reduced set of characters, selected using principle component analysis can maximise the differences between groups as defined by cluster analysis. By using a reduced set of these diagnostic characters, banana researchers can now classify the Ugandan East African highland banana landraces into the five groups which have been also called clone sets. The clone sets are considered to be a category above the level of clone or cultivar but below the level of genome group (the highland bananas are distinct sub-group within the genome group comprised by the AAA triploids). It is however, important to expand this characterisation process to determine whether the classification will prove workable through out the range of the East African highland bananas. The following study was carried out at Maruku National Collection in Tanzania and at the four on farm *Musa* conservation sites, two in Tanzania, Kagera region and two in Uganda, Masaka and Bushenyi districts. The purpose of the study was to apply the clone set classification to yet another large sample of the East African bananas in the Great Lakes region and see whether it is workable through out the range of the crop in these areas. The objectives of the study were to estimate levels of *Musa* diversity within and between benchmark sites; understand diversity trends over time in respect to changes in diversity within national genebanks and finally assess the usefulness of numerical methods in diversity assessment of a wider *Musa* genepool.

MATERIALS AND METHODS

One hundred and thirty five farms from Tanzania and Uganda *Musa In situ* conservation research sites were selected to determine cultivar diversity on each. The first task was to determine diversity found at each site and compare it with that of the on-station (*Ex-situ*) collections in order to estimate the representativeness of the collections to the diversity on farm. At the same time information on the total number of accessions accessed in different years was also recorded. The second task was to sample cultivars to use in estimating levels of diversity both on sites and in the national collection. The plants sampled were those in the third year ratoon cycle. For each cultivar 3 to 5 plants were used.

Two hundred and fifty seven accessions were sampled from Maruku National Collection, in Tanzania and from 135 farms of Tanzania and Uganda. An investigation into the morphological variation among the 257 accessions of the East African highland bananas was carried out. One hundred and twenty five accessions were sampled from the national collection of Tanzania at Maruku Agricultural Research and Development Institute, and one hundred and thirty two were sampled from four on farm conservation sites, two from Tanzania and two from Uganda (Table 1). All accessions which were sampled were provided with labels based on their genomic groups and local highland bananas were provided with labels indicating their subjective clone sets using the diagnostic characters of the previous study of the Ugandan bananas. Data was taken on 257 accessions based on 60 characters (20 quantitative and 40 qualitative). Preliminary analyses of all accessions belonging to different genome groups was carried out to confirm that categories resulting from these analyses agree with the existing and widely accepted classification (Simmonds and Shepherd, 1955; Simmonds, 1959; Simmonds and Weatherup, 1990a,b). The analyses included all 125 accessions from Maruku National Collection, 35 from Ibwera and 25 from Chanika, in Tanzania; 49 from Masaka and 23 from Bushenyi in Uganda. The analyses were carried out separately according to the sampled accessions per site. The accessions per site were used to calculate the correlation matrices which were then subjected to principal component and cluster analyses as appropriate using the numerical taxonomic package Ntsys-pc by Rohlf (2000). The second task was to separate the local endemic East African highland bananas from each site and carry out similar analyses to determine how applicable the clone set classification was, in relation to the whole range of the crop in the region.

RESULTS

Cultivar diversity varied between farms and sites (Table 2) while the distribution and proportion of each cultivar also varied with sites and country. A few cultivars were in all sites. The national collections have a higher cultivar diversity than farms although cultivars on farm are not necessarily the ones in the collection. In different years, accessions from the collections have been generally reducing (Table 3). The phenograms resulting from the preliminary analyses displayed more or less well defined clusters corresponding to genomic groups and accounting for a correlation coeffient of 20 which was higher than that within groups. The main clusters were those of plantains (AAB), the bluggoes (ABB), the Ney Poovan (AB), the dessert acuminata triploids (AAA) and the East African highland (AAA-EA) which separated further by sub-clusters corresponding to clone sets. The Ibwera scatter plot (Fig.1) has been represented to demonstrate this classification. Results from the second analyses where the East African highland bananas were separated out from other groups demonstrated that the classification of clone sets is still viable although few clones remain intermediate due to sharing characters between clone sets as shown by the phenogram of the Maruku National Collection (Fig. 2). One big cluster consisted entirely of beer bananas. Nfuuka and Nakabululu clone sets were more heterogeneuos than other three clone sets and overlapped with others (Karamura, 1999). The characters which were found useful in separating clone sets are given in Table 4 and these had loadings above 0.5 (Karamura, 1999).

DISCUSSION

There was variation in cultivar diversity between sites and among the different farms. The distribution and proportion of each cultivar also varied with sites and country, while a few cultivars were found in all sites. The selection criteria and cultivar preferences within different communities probably account for the observed differences. Preliminary observations from ethnobotanical studies (Davis, 1995) suggest that farmers perceive different clones as having strengths and weaknesses. Farmers have a variety of criteria for determining the proportion of each cultivar to be planted. The different proportions of cultivars grown by the farmers allows farmers to balance various needs and limit risks. Just like in most national collections, diversity in the national collections was larger than that on on-farm sites, although not all cultivars on farm were found to be represented in the national collection. National

TABLE 1. Sites and number of accessions used in the analyses

Cultivar groups	Tanzania			Uganda	
	Maruku collection	Chanika	Ibwera	Bushenyi	Masaka
AA	1	0	0	0	0
AB	1	2	2	1	2
AAB	8	0	3	2	2
ABB	2	1	2	1	2
AAA	3	0	3	1	2
AAA-EAH	110	22	24	18	41
Tetraploids		0	1	0	0
Total	125	25	35	23	49

collections continuously access new germplasm from international breeding centres and genebanks. Most of these materials are not passed on to farmers as fast as they are required and since they had been selected for resistance to diverse environment stresses in the first place, they tend to stay long in field gene-banks.

In addition, national collections also acquire materials for research purposes (e.g. breeding) which are not suitable for use on farm. These too are kept in *Ex-situ* collections. When National Agricutural Research Institutes carry out collecting missions, they tend to cover the entire country, thus diversity in *Ex situ* collections is representative

TABLE 2. Comparison between cultivar diversity and genome composition on farm and that in the national collections of Tanzania and Uganda

Country	Project/Collection site	Total number of cultivars	Genome composition
Tanzania	Chanika	60	AB=2, AAA=3, AAB=2, ABB=2, AAA-EAB=9, AAA-EAC=39, Tetraploids=3
	Ibwera	46	AA=1, AB=2, AAA=5, AAB=4, ABB=2, AA-EAB=5, AAA-EAC=24, Tetraploids=3
	Maruku collection	135	AB=1, AA=2, ABB=2, AAB=8, AAA=7, AAA EAB = 23, AAA-EAC=89, Tetraploids=3
Uganda	Bushenyi	29	AB=1, AAA=1, AAB=3 ABB=1, AAA-EAB*=4 AAA-EAC*=19
	Masaka	54	AB=2, AAA=2, AAB=4, ABB=3, AAA-EAB=9 AAA-EAC=34
	Kawanda collection	253	AA=10 , AB=2, BB=2, SS=2 AAA=12, AAB=12, ABB=17, AAA-EAB=31, AAA-EAC=113 Tetraploids=52

TABLE 3. Genome composition and cultivar diversity in the national *ex situ* collections over the last 30 years

Period	No. of cultivars	
	Maruku Collection, Tanzania	Kawanda Collection, Uganda
1970	300	227
1989	153	400
2000	135	253
Current genome composition	AB=1, AA=2, ABB=2 AAB=8, AAA=7 AAA EAB = 23, AAA-EAC=89 Tetraploids=3	AA=10 AB=2, BB=2, SS=2 AAA=12, AAB=12 ABB=17, AAA-EAB=31 AAA-EAC=113 Tetraploids=52

• Numbers may include synonymous materials among East African highland cultivars, except for Kawanda 2000 figure.

of national diversity, not just diversity from a single site. It is no wonder therefore that diversity on-farm is less than that on station.

In general, over the last 30 years, the overall trend has been one of continuous loss of *Musa* genetic diversity in the Great Lakes region of East Africa. In Uganda for instance, the entire banana germplasm collection which was first established at Bukalasa Agricultural College in the 1960s was lost by 1985. It was not until 1987 that efforts were made to collect and set up another national collection at Kawanda Agricultural Research Institute, with a duplicate at Makerere University Agricultural Research Institute Kabanyolo (MUARIK). The Kabanyolo collection has since been lost. At Kawanda over the last 10 years, loss

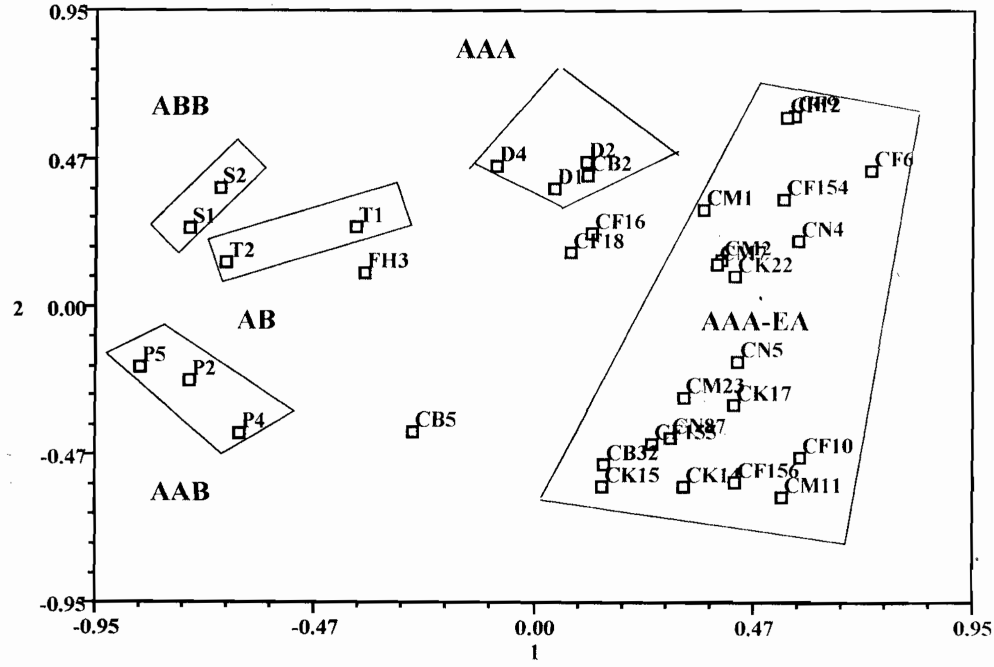

Figure 1. Positions of banana cultivar groups of Ibwera *Musa In situ* conservation site in Tanzania with respect to 1st and 2nd principal component.

TABLE 4. Characters with loadings greater than 0.5 (in bold) on principal component one, two and three

Character	PC 1	PC2	PC3
Plant girth	**-0.5228**	0.2078	-0.0058
Leaf width	**-0.6482**	0.3938	0.2039
Male inflorescence rachis position	**-0.5320**	-0.0977	-0.3129
Persistent floral remains on rachis	-0.2870	0.2209	**-0.5528**
Male bud imbrication	-0.1735	0.1977	**-0.5075**
Bunch position	**-0.6448**	-0.1379	-0.1080
Fruit positions within the bunch	**0.5406**	0.3386	0.1254
Fruit base insertion	**-0.5631**	-0.1785	0.1161
Persistent style on tip of fruits	0.2244	**0.5414**	-0.0158
Pulp with brown sticky excretions	-0.2116	**0.8324**	-0.0136
Pulp taste	-0.2116	**0.8324**	-0.0136
Fruit length	**-0.5174**	-0.1483	-0.3249
Bunch weights	**-0.6201**	0.1721	0.0342

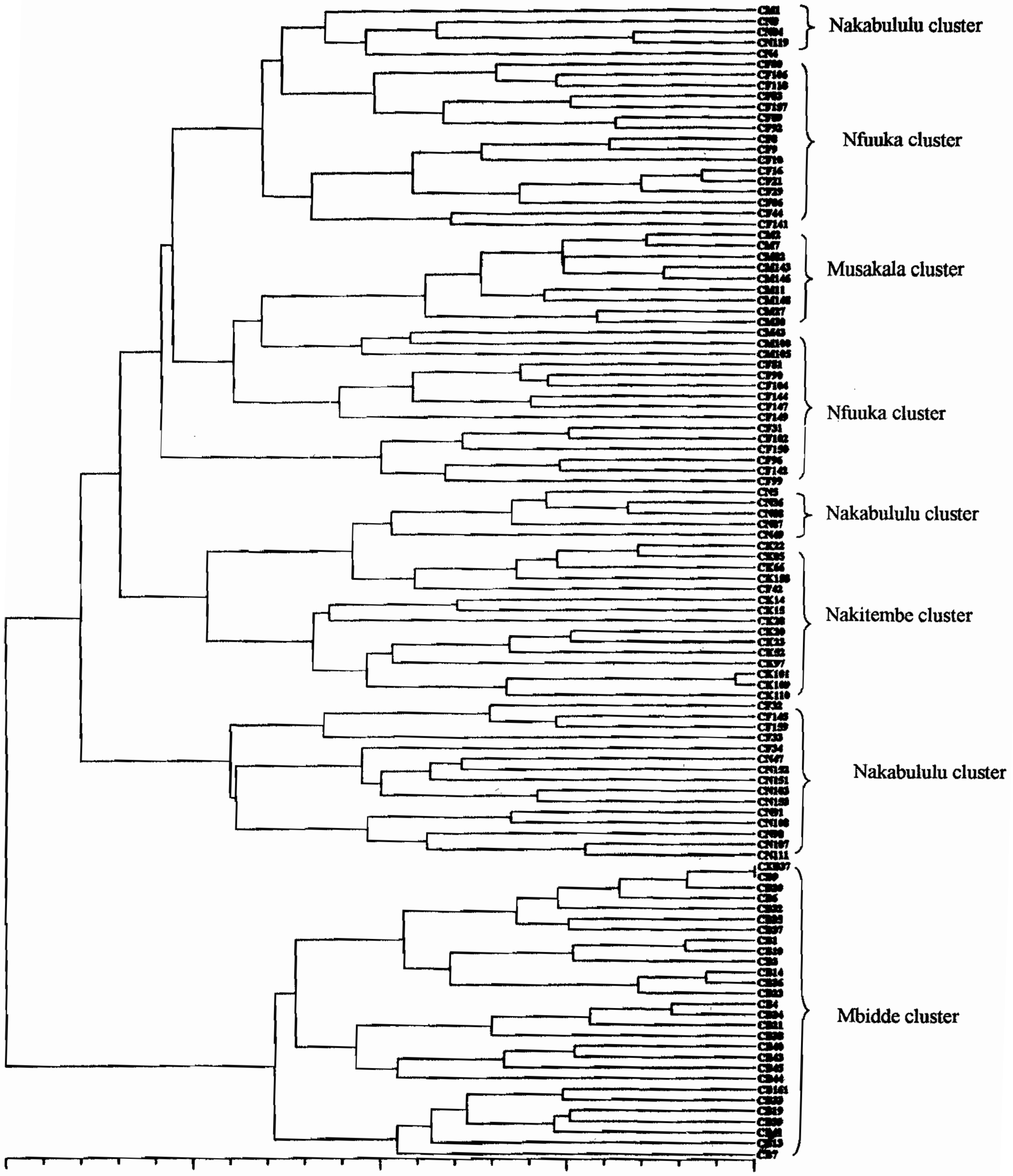

Figure 2. Group average clustering of 125 accessions being held at Maruku National collection.

of accessions in the collection up to 37% has been observed. In Tanzania, the rate of accession loss has been lower but very steady, mounting up to 55% over the last 30 years.

It is more difficult to understand the picture in farmers' fields. Farmers in the Great Lakes region have been reported to grow a complex mixture of cultivars for many years, but the changes in this diversity that have occurred over time have not been recorded. Various types of cultivars are accumulated through the process of planting material exchange, which allows farmers to access desired cultivars in the quest to meet household as well as community needs. Therefore, understanding both household and community needs with respect to a crop like banana is necessary in order to appreciate their importance in farming systems.

Group average clustering and principal component analysis are useful methods in analysing similarity by grouping similar clones and providing a measure of diversity.

It was important to determine whether cultivars grown by farmers and also those represented in the national collection in Tanzania, another area within the range of the East African highland bananas could be placed in the five clone sets already proposed (Karamura, 1999). One of the phenogram resulting from cluster analysis of data from the Maruku National Collection shown in Figure 2 has indicated that majority of accessions have been assigned to clusters corresponding to the five clone sets. Musakala, Nakitembe and Mbidde clone sets were more homogeneous than the other two clone sets. The Mbidde clone set forms a coherent clone set that probably has been evolving separately from the cooking bananas for some considerable time. Musakala clone set contains clones with large lax bunches and long fruits. These include the highest yielding clones grown on a commercial scale to supply the urban markets. This clone set has been evolving through farmers' selections year after year and hence it is also quite distinct. The Nakitembe clone set sucker profusely, matures very fast and produce soft-textured fruits. The clones are also characterised by imbricated male buds and persistent floral remains on rachis and fruits. These have also been selected by farmers for quite a long time and they are believed to have been among the first highland bananas introduced. Hence, the associations between morphological or trait diversity and the utility of these trait to farmers is gradually being understood. It is hypothesised that phenotypic distance or phenotypic dissimilarity and clustering are related to genetic and evolutionary distances between clones. The shorter the phenotypic distance or the lower the percentage dissimilarity between two cultivars or cultivar groups, the more genetically related they would be ruling out convergence in different phenotypes. This classification system is currently our best means of prioritising East African highland banana landraces for conservation. As stated earlier, although there has been a reduction in diversity of bananas in the East African region, significant diversity still exists in some Great Lakes communities. These communities provide the most logical sites for an *In situ* conservation program. Farmers who have maintained diversity must value that diversity and hence a project directed at *In situ* conservation must support those farmers who value diversity. The advantages of *In situ* conservation have been outlined by others (Bush, 1995). A great advantage of using this approach with particularly the local highland races in the Great Lakes region is that both cultivar and the farmers' knowledge associated with the cultivars are maintained.

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