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Assessment of diversity using agro-morphological traits for selecting a core sample of Papua New Guinea taro (*Colocasia esculenta* (L.) Schott) collection

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Abstract

Agro-morphological variation in the taro germplasm of Papua New Guinea was estimated using 18 polymorphic descriptor states to aid in the selection of a core sample for the formation of a regional core collection currently being assembled under the Taro Network for Southeast Asia and Oceania. A total of 276 accessions were stratified into five homogenous groups by using a hierarchical approach according to botanical variety (dasheen or eddoe), altitude (high or low) and stolon formation (present or absent). In selecting the core sample, the eddoe group were directly included because of their rarity in the germplasm collection. While, a ten per cent sample fraction within each group of the dasheen types were selected based on principal component scores. A total of 31 accessions were selected for the core sample. Multivariate analysis of the core sample revealed wide variation, which was mainly influenced by botanical variety, plant height, lamina colour and variegation, petiole colour, corm shape, corm weight and palatability. Cluster analysis identified two homogeneous clusters based on predominant characters that should be useful to breeders. The results obtained in this study provide useful background information for further development of a national core collection.

Introduction

Taro (*Colocasia esculenta* (L.) Schott) is an edible aroid belonging to the family Araceae. It is an antique staple root crop in Papua New Guinea (PNG), where its cultivation has been dated to 9, 000 B.P. (Golson 1977). The beginning of taro cultivation may be closely associated with its genetic improvement. New varieties may have been selected from progenies of wild and/or cultivated parents. Considering such practice as rare, genetic advancement of the crop, in general, has been kept in abeyance over the centuries because of continuous vegetative propagation and rare flowering and seedling development in nature.

Genetic improvement of taro has the potential to overcome production constraints, particularly resistance to pests and diseases. The success of genetic improvement of a crop, however, depends on the availability of genetic resources and their diversity. Numerous varieties exist in village gardens in PNG. In attempts to capture this diversity, a large number of accessions were collected in the past (Aburu 1980; Akus et al. 1989) and maintained *ex situ*. However, most collected accessions were lost before even being characterised and evaluated, raising serious concerns over the management and utilisation of field genebanks.

The need to rationalise collections for efficient conservation and utilisation of genetic diversity has led to the development of core (representative) collections. A core collection consists of a limited set of accessions derived from an existing germplasm collection and chosen to represent the genetic spectrum of the whole collection. In such an attempt, the Taro

Network for Southeast Asia and Oceania (TANSAO), supported by the European Union INCO-DC programme, is assembling a regional core collection (RCC) of taro from five Southeast Asian countries (Vietnam, Philippines, Malaysia, Thailand and Indonesia) and two South Pacific countries (PNG and Vanuatu). A core sample representing 10 % of the total number of accessions from each country will be amalgamated into an RCC (TANSAO 1998). The aim of this study was to establish a core sample of maximal diversity based on variation within the national taro germplasm collection for inclusion in the RCC.

Materials and methods

Field planting and layout

A total of 279 cultivated taro accessions were collected from nine provinces in PNG (Figure 1). All accessions were maintained in an *ex situ* gene bank at the Wet Lowland-Mainland Programme, Bubia (146°4′E, 6°41′S), of the National Agricultural Research Institute (NARI). Bubia is situated at 20 m a.s.l. and receives a mean annual rainfall of 2870 mm. Individual accessions were planted in single rows of eight plants spaced at 0.5 m between plants and 1.0 m between rows. An application of 50 kg N/ha in the form of Urea was applied at three months to boost growth. Weeds were controlled manually as required.

Characterisation

The accessions were characterised using 18 major agro-morphological descriptors standardised for use in the TANSAO project (TANSAO 1998). Characterisation of aboveground traits was carried out at five months after planting. Underground traits were characterised at six months during harvest.

Statistical analysis

A total of 276 accessions having complete data were classified using a hierarchical approach according to botanical variety (dasheen or eddoe), altitude (high or low) and stolon formation (present or absent). Five homogenous groups were identified (Figure 2). Cluster analysis of each diversity group, except for group E where the data set was unanalysable, was performed based on Euclidean distance coefficients and the unweigthed pair-group method analysis, UPGMA, (Sokal and Michener 1958) using the software NTSYS-pc®, version 2.202i (Rohlf 1998). This allowed rationalisation of accessions within each diversity group. In selecting the core sample, a ten per cent sample fraction within each group, except for group E where ordination of the data set was impossible, were selected based on principal component (PC) scores strategy using the software S-Plus 2000® (MathSoft Inc.). A further ordination of the core sample was performed to estimate variability. Those PCs with eigen values > 1.0 were selected, as proposed by Jeffers (1967). Correlations between the original traits and the respective PCs were obtained. Characters with correlation values $\approx$ 0.6 were considered as relevant for that PC as recommended by Matus et al. (1996). In addition, cluster analysis was also performed to assess the level of dissimilarity within the core sample. A dissimilarity matrix based on Euclidean distance coefficients was generated and clustered using UPGMA. A dendrogram was created using the TREE sub-programme of NTSYS-pc®.

Results

The characterised data indicated wide variation for the 18 traits considered in this study (Table 1). Most accessions were dasheen types (99.28 %) with medium (50 – 100 cm) height (89.25 %) and semi-erect growth habit (77.78 %). In the majority of the accessions, the leaves were predominantly non-variegated, dark green, cup-shaped with semi-erect orientation and undulating margins. Accessions with light green petioles out-numbered those that expressed other pigments. The corms of the majority of the accessions were small (0.25 – 0.59 kg), unbranched, conical, white-fleshed and had acceptable palatability. Maturity periods ranged from six to eight months.

The initial hierarchical classification separated the 276 accessions into five homogeneous (similar) diversity groups (Figure 2). The eddoe types constituted less than 1 % of the collection and were directly included into the core sample because of their rarity. Further stratification according to altitude and stolon formation allowed segregation of the dasheen types into another four groups. Cluster analysis performed within each of these groups revealed four duplicate accessions and the extras were discarded prior to ordination and selection of core samples. A total of thirty-one accessions were selected for the core sample (Table 2).

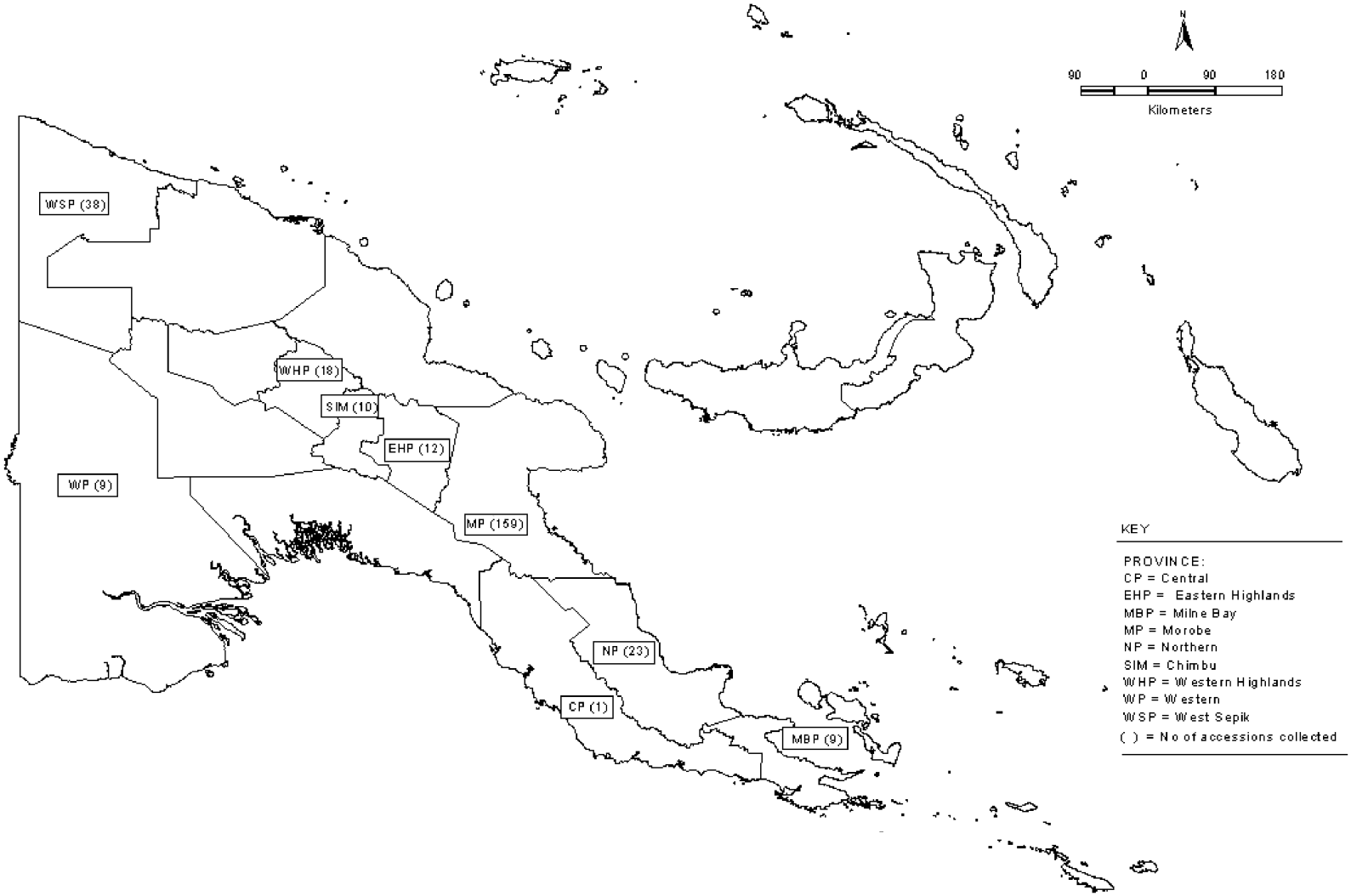

Figure 1. Map of Papua New Guinea showing the provincial origin of collected taro germplasm in the whole collection. The map was produced using Mapping Agricultural Systems Project database (Bourke et al. 1998).

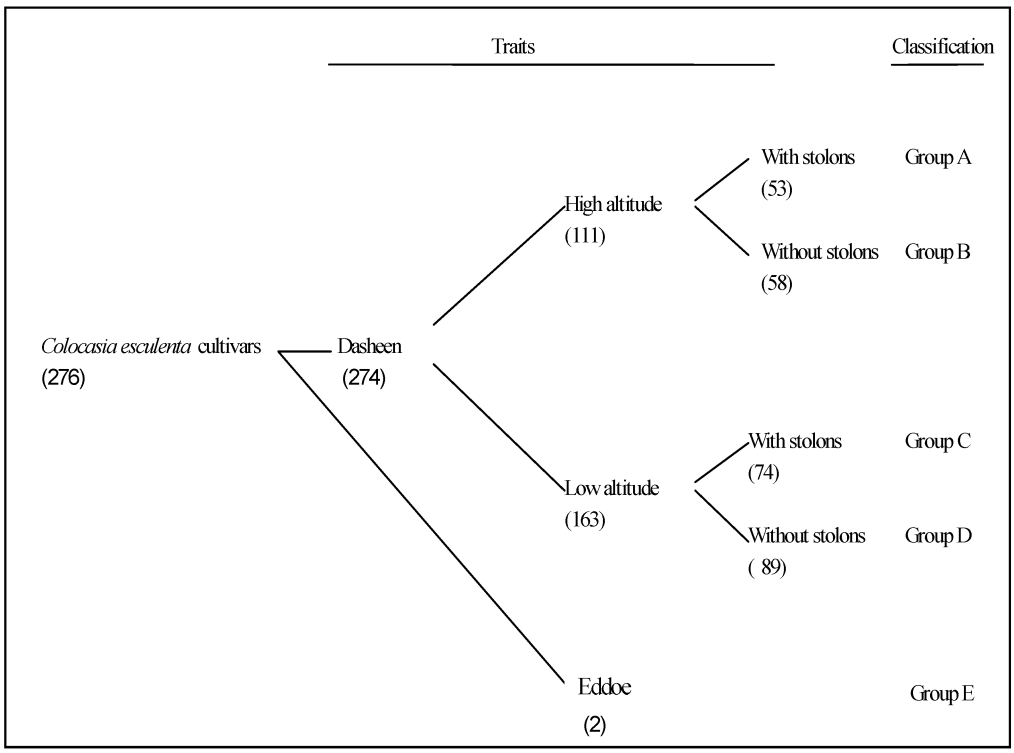

Figure 2. Hierarchical classification of the Papua New Guinea taro collection using major agro-morphological traits (figures in parenthesis indicate the number of accessionsM38).

Multivariate analysis of the core sample revealed that the first six PCs (PC1 to PC6) gave Eigen-values > 1.0 and cumulatively accounted for 72.66 % of the total variation (Table 3). Correlation coefficients of considered traits were determined to estimate their association with specific PCs (Table 4). The variation in PC1 was mainly associated with corm shape, lamina colour and corm weight, PC2 with plant height, petiole colour and palatability, and PC3 with botanical variety. PC4 had minimal influence from all traits although correlation coefficients were relatively higher for altitude, growth habit, leaf shape, and petiole colour variations. PC5 and PC6 were mainly associated with lamina variegation and plant height, respectively.

The dendrogram (Figure 3) constructed showed Euclidean distance coefficient ranging from 6.93 to 2.30 with two clusters formed at 5.26.

Discussion

Since taro cultivars are vegetatively propagated, low intraspecific variability is expected. However, in the present study, high morphological variation in PNG germplasm was demonstrated using 18 agro-morphological descriptor states. Various studies have also reported wide variation among PNG taro accessions (Lebot et al. 2000; Godwin et al. 2001). This variability may be attributed to sexual recombination, migration and perhaps mutation, with subsequent selection by farmers in geographical isolation for adaptability under various agro-ecological regimes and cropping systems, and culinary qualities preferences. In order to rationalise the collection by removing duplicates and to use the diversity efficiently in breeding programmes, it was considered important to establish a core sample of manageable size.

Cluster analysis performed directly on the entire data matrix did not produce dendrograms and clusters of meaningful value. However, the hierarchical classification approach based on three major characters (botanical variety – dasheen or eddoe, altitude – high or low, and stolon – present or absent) produced useful morphological and ecological groups. This method of stratified sampling ensured that maximum diversity, relative to the genetic variation of the whole collection, was represented in the core sample. This

Table 1. Proportion of descriptors in the entire taro collection.

Descriptor State	Proportion (%)
1. Altitude	
Low (<800 m)	59.78
High (>800 m)	41.62
2. Botanical variety	
Dasheen	99.28
Eddoe	0.72
Intermediate	0.00
3. Growth Habit	
Erect	1.08
Semi-erect	77.78
Semi-prostrate	18.64
Prostrate	1.78
Not determined	0.72
4. Stolon	
Absent	18.64
Present	79.92
Not determined	1.44
5. Plant height	
Dwarf (<50 cm)	4.30
Medium (50–100 cm)	89.25
Tall (100–150 cm)	5.73
Not determined	0.72
6. Leaf Shape	
Plain (flat)	13.62
Drooping edges	0.72
Cup-shaped	84.94
Not determined	0.72
7. Leaf lamina orientation	
Semi-erect, apex down	99.64
Not determined	0.36
8. Leaf lamina margin	
Entire	0.36
Sinuate	0.36
Undulate	98.56
Not determined	0.72
9. Leaf lamina colour	
Yellow	0.36
Normal green	36.92
Dark green	62.00
Not determined	0.72
10. Lamina variegation	
Absent	80.64
Present	18.64
Not determined	0.72
11. Sinus outline	
Pointed, narrow (<450)	8.24
Pointed, wide (>450)	12.18
Rounded, narrow	23.30
Rounded, broad	55.56
Not determined	0.72
12. Vein junction colour	
White	0.36
Light green	28.67
Dark green	28.32

Table 1. Continued.

Descriptor State	Proportion (%)
Light purple	28.32
Dark purple	11.11
Red	2.50
Not determined	0.72
13. Primary petiole colour	
Light green	45.88
Dark green	33.69
Red	1.08
Light purple	3.58
Dark purple	6.09
Brown or brown-purple	8.24
Not determined	1.44
14. Petiole colour variation	
No variation	49.82
Upper part darker	9.32
Light green lines/stripes	17.56
Dark green lines/stripes	10.04
Purple lines/stripes	5.02
Brown lines/stripes	2.16
Light blotches	1.79
Dark blotches	1.79
15. Corm Shape	
Unbranched, round	16.85
Unbranched, dumb-bell	5.02
Unbranched, conical	38.71
Unbranched, elliptical	15.05
Unbranched, cylindrical	10.75
branched	1.08
Branched, head	1.43
Extremely elongated	2.15
Not determined	8.96
16. Corm weight	
Very small (<0.25 kg)	17.20
Small (0.25–0.5 kg)	39.78
Medium (0.5.–2.0 kg)	28.68
Large (2.0–4.0 kg)	3.94
Very large (>4.0 kg)	1.44
Not determined	8.96
17. Corm flesh colour	
White	44.09
Yellow	6.09
Orange	1.79
Pink	23.30
Purple	13.98
Colour not uniform	1.79
Not determined	8.96
18. Culinary quality of corm	
Poor quality	0.72
Acceptable	84.23
Good	1.43
Very good	2.87
Excellent	1.79
Not determined	8.96

Table 2. Accession numbers and origin of the core sample on the basis of provinces.

Province of origin	Accession Numbers[1,2]
Milne Bay	BC 749 (11)
Western	BC 894 (30)
Eastern Highland	BC 643 (1), BC 646 (2)
Chimbu	BC 656 (3) BC 661 (4)
Western Highland	BC 674 5), BC 677 (6)
Northern	BC 680 (7), BC 691 (8)
West Sepik	BC 734 (9), BC 740 (10)
Morobe	BC 759 (12), BC 769 (13), BC 770 (14), BC 773 (15), BC 786 (16), BC 793 (17), BC 798 (18), BC 810 (19), BC 813 (20), BC 818 (21), BC 835 (22), BC 844 (23), BC 846 (24), BC 853 (25), BC 859 (26), BC 874 (27), BC 885 (28), BC 887 (29), BC 902 (31)

[1]BC = Bubia Collection number; [2]Serial numbers are given in parenthesesM38.

Table 3. Variation accounted for by each principal component (PC).

PC	Eigen-value	Variability (%)	Accumulated variability (%)
1	3.33	20.86	20.86
2	2.49	15.57	36.43
3	1.71	10.68	47.11
4	1.47	9.17	56.28
5	1.36	8.51	64.79
6	1.25	7.87	72.66

can also provide useful information to breeders on existing diversity and available genotypes that can be immediately used. The dasheen and the eddoe types are cross compatible (T. Okpul, personal observation), but the possible benefit of such hybridisation does not appear to be significant considering the variation available in the germplasm. The eddoe types have lower yield and no real market value, although they are staples in some parts of the country. Further, PNG is characterised by diverse agro-ecological regimes, partly determined by the ruggedly undulating landform with altitude up to 4,000 m. Stratification of accessions into eco-geographic classes, like altitude as in this case, provides useful information for ecotype development. Additionally, formation of stolons is usually associated with wild or primitive traits such as high oxalate content and small corms (Ivancic and Okpul 1997). Although the genetics of this trait is yet to be elucidated, its separation enables breeders to avoid introgression of wild traits into breeding programmes.

The cluster analysis of the core sample identified homogeneous clusters at a high level of variability. Most of the variation (over 72 %) was associated with traits such as lamina colour and variegation, corm weight, petiole colour, botanical variety, palatability and plant height. Noticeably, botanical variety, stolon formation, plant height, corm shape and corm weight are important agronomic traits and their grouping, as in the two clusters, will indeed be useful for future cultivar development.

Colours or pigmentations, and their patterns on leaf petioles and corm flesh, also influenced the observed variation. The inheritance of pigments in taro is not clear and should be considered with some reservation in diversity assessment, as it seems to be influenced by different methods of vegetative propagation.

Comparisons of genetic variability among germplasm between and within provinces cannot be made due to the limited sample sizes. However, indications of wide variation in the collected germplasm are obvious. In conclusion, the results obtained in this study provide useful background information for further development of a national taro core collection. The sample can serve the objectives of efficient germplasm management and utilisation. For more effective utilization, the material is being characterized by RAPD markers in collaboration with Wageningen Agricultural University, Netherlands.

Table 4. Correlation coefficients of each trait with respect to each principal component.

Trait	Principal component (PC)					
	PC1	PC2	PC3	PC4	PC5	PC6
Botanical variety	0.28	–0.15	–0.79†	0.20	–0.01	0.06
Altitude	–0.28	–0.43	0.23	0.51	0.28	–0.13
Stolon	–0.53	0.26	0.25	–0.32	–0.17	–0.16
Corm shape	0.68†	–0.16	–0.11	–0.11	0.10	–0.45
Growth habit	–0.44	0.14	–0.15	0.48	0.50	–0.33
Plant height	0.11	0.61†	–0.01	0.13	–0.10	0.65†
Leaf shape	0.43	–0.31	–0.32	–0.54	0.10	–0.05
Leaf colour	0.64†	0.06	0.25	0.18	–0.07	0.19
Leaf variegation	0.31	–0.20	0.30	0.29	–0.58†	–0.18
Sinus outline	0.38	–0.45	0.48	0.27	0.17	0.03
Vein junction	0.54	0.48	0.15	0.05	–0.15	–0.43
Petiole colour	–0.18	0.75†	0.16	0.27	0.01	–0.03
Petiole colour variation	–0.44	0.27	0.51	–0.47	0.33	–0.19
Corm weight	0.67†	0.44	–0.31	0.16	0.05	–0.20
Flesh colour	0.45	–0.30	0.23	–0.07	0.48	0.40
Palatability	0.45	0.56†	–0.10	–0.06	0.49	0.01

† relevant traits when explaining the component (based on Matus et al. 1996).

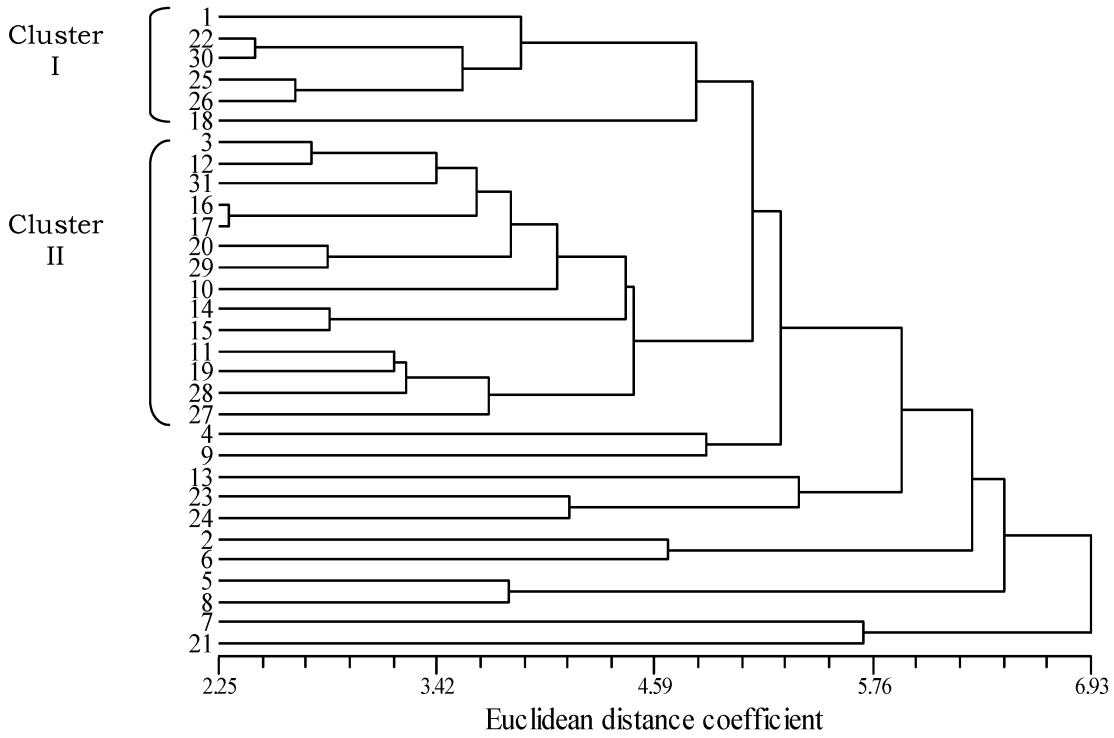

Figure 3. A dendrogram illustrating dissimilarity based on Euclidean distance coefficient and the UPGMA clustering technique for 31 taro accessions (refer to Table 2) selected as the core sample based on 18 agro-morphological descriptor states.

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