

Short communication

Phenotypic variability of Manila hemp (*Musa textilis* L. Nee) genotypes in southern Mindanao Island, Philippines

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Abstract

In situ morphological characterization using 25 qualitative and six quantitative morphological traits was carried out to determine the phenotypic variability of 110 Manila hemp (*abaca*) varieties in Southern Mindanao, Philippines. Principal Component Analysis (PCA) revealed the divergence of varieties *Wago/Lyl2-dv* and the *MDG1-tb/MDG2-tb/Lud2-tb* groups and the morphological homogeneity of the rest of the *abaca* genotypes. Pseudostem and leaf characters were identified as chief discriminatory characters in assigning *abaca* varieties into distinct functional groups. Despite the uncertainties relating to environmental factors, morphological grouping of *abaca* may provide a useful tool for genetic improvement of this crop.

Keywords: Morphological characterization, Phenotypic variability.

Abaca (*Musa textilis* L. Nee), known worldwide as Manila hemp, closely resembles its more famous relative, banana (Lacuna-Richman, 2002). Its endemic nature and the superior quality of the fibre have evoked worldwide interest (Gonzal, 2005). In Southern Mindanao (Philippines), *abaca* is mostly planted by the smallholders and information about its genetic diversity is virtually non-existent there. Many wild *abaca* populations also remain largely unexplored and it is probable that the remaining wild stocks may be depleted since habitat degradation is rampant in the poverty-stricken upland areas of this region (Lacuna-Richman, 2002). This study aimed to assess the morphological variability of *abaca* germplasm from different areas in Southern Mindanao, Philippines.

Locations with existing *abaca* plantations and *abaca* germplasm collections in field genebanks *viz.* Maitum, and Kiamba in Sarangani Province, T'boli and Lake Sebu in South Cotabato, Makilala in North Cotabato Province (7°21' N; 126°1' E) were selected for this *in*

situ morphological characterization. Both wild and cultivated *abaca* varieties and hybrids were included in the study. Six quantitative traits (pseudostem height, plant diameter, petiole length and margin width, and leaf blade length, and width) and 25 qualitative morpho-agronomic (leaf habit; petiole canal leaf; pseudostem colour, appearance, and blotching; petiole margin corrugation; sap colour; anthocyanin pigment at pseudostem base, leaf midrib, and leaf base; wax on leaf sheaths; petiole margin colour; blotches at the petiole base; petiole blotches colour; edge of petiole margin; lamina-attitude, tip shape, tip bending, base equality, base shape, and base handedness; colour of leaf upper and lower surfaces; and appearance of leaf upper and lower surfaces) descriptor states were used. The morphological parameters for evaluating different *abaca* accessions were based on modified morpho-taxonomic descriptors for *abaca* (IPGRI-INIBAP/CIRAD, 1996). The morphological data were subjected to Principal component analysis (PCA) using the SAS-JMP v. 6 software.

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The PCA reduced the original 31 morpho-agronomic characters to 10 principal components, which accounted for approximately 72.5% of total variance (Table 1). Prin 1 was the most important component with a latent root (eigen value) of 5.37 and explained 17.0% of the total variance. Variables with the highest loadings on Prin 1 were leaf blade length, pseudostem height, plant diameter, leaf blade width, and petiole length (absolute values >0.7). Petiole margin width and the colour of leaf upper and lower surfaces (>0.6) also made substantial contributions to Prin 1. Appearance of leaf upper surface and lamina base shape (>0.5) correlated moderately well with Prin 2 and Prin 3 respectively.

The PCA scatterplot showed 10 groups varying mainly in quantitative pseudostem stem and leaf characters (Fig. 1). *Laylay2-Davao* (92) and *Wago* (13) were isolated from the rest of the *abaca* varieties due to low

Table 1. Eigen values and % variation of 31 morpho-agronomic characters of 110 Manila hemp (*abaca*) varieties in Southern Mindanao, Philippines.

Principal Component	Eigen values	% of variance	Cumulative variance
1	5.279	17.029	17.029
2	3.350	10.808	27.837
3	2.671	8.615	36.452
4	2.182	7.039	43.491
5	2.075	6.694	50.185
6	1.736	5.599	55.784
7	1.532	4.943	60.727
8	1.353	4.365	65.092
9	1.183	3.816	68.908
10	1.122	3.621	72.529

or negative Prin 1 values. The positions of *Maguindanaon1-Tboli*, *Maguindanaon2-Tboli*, and *Ludon2-Tboli* at the upper right hand corner of the PCA

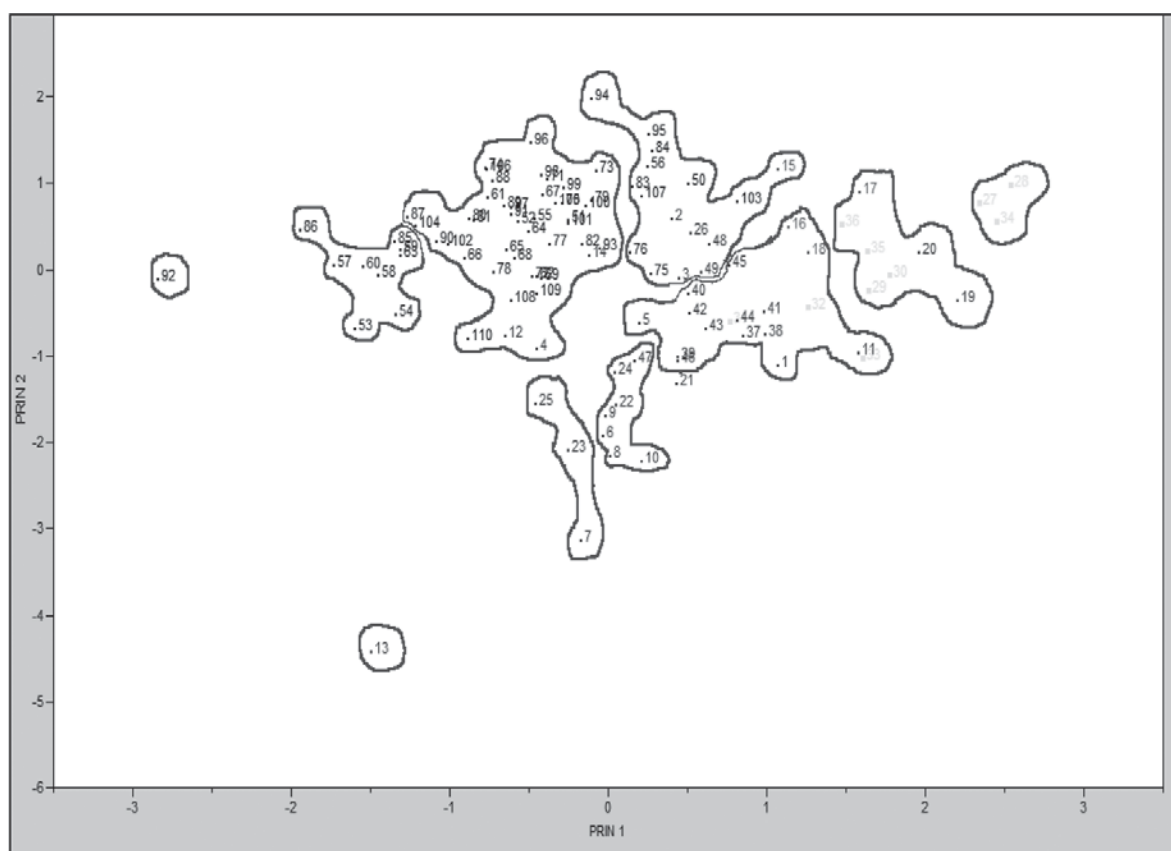


Figure 1. Scatterplot of PC scores of PRIN 1 and PRIN 2 based on 31 morpho-agronomic characters of 110 Manila hemp (*abaca*) varieties in Southern Mindanao, Philippines.

quadrant can be attributed to the highest values they exhibited for all measured pseudostem and leaf parameters. The big groups occupying the middle portion of the quadrant manifested intermediate to slightly low values for the mentioned traits. These groupings formed in the PCA scatterplot can aid in the selection of genotypes for future improvement programmes and in the identification of suitable parents for the production of hybrids with heterotic traits. The remarkably high loadings of pseudostem characters (height and diameter) imply that they contribute significantly to phenotypic variability and can thus be exploited for increased fibre yield. Although the varieties/populations formed separate groups (*WGOmt/LYL2dv* and *MGD1tb/MGD2tb/LUD2tb*), relatively low level of morphological diversity was noted within the major clusters, implying a narrow genetic base for Southern Mindanao *abaca* cultivars.

Despite its cultivation in many provinces of Philippines, *abaca* genetics is relatively unknown and there is a paucity of literature on the genetic diversity of this crop. Variations due to differences in phenotypic expression in the field and the subjective nature of morphological characterization schemes (Jarret and Gawel, 1995) further complicate the matter. Nonetheless, morphological characterization is effective in low level taxonomy as it provides initial groupings which can subsequently be subjected to more robust marker analyses.

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