Genetic Diversity Analysis of Traditional Upland Rice Cultivars in Kihan, Malapatan, Sarangani Province, Philippines Using Morphometric Markers

Florence C. Lasalita-Zapico[1*], **Jaime A. Namocatcat**[1], and **Josephine L. Cariño-Turner**[2]

[1]Science Department, College of Natural Sciences and Mathematics,
Mindanao State University, Fatima, General Santos City 9500
[2]Indigenous Peoples Development Program, Office of the Provincial Governor,
Provincial Capitol, Alabel, Sarangani Province

In situ **characterization was carried out for thirty two traditional upland rice cultivars in Kihan, Malapatan, Sarangani Province using ten morpho-agronomic characters at the reproductive stage, as prelude to genetic diversity analysis of the Province's traditional rice gene pool. Cluster analysis revealed four groups, each group representing a distinct set of morpho-agronomic values, while Principal component analysis, which also sorted the cultivars into four clusters showed two principal components accounting for about 82.7% of total variance observed. Comparison of PCA and dendrogram groupings revealed generally similar trends, though slight inconsistencies were observed in terms of cluster composition. Pearson's correlation analysis of the morphological traits suggests that these traits are significantly and positively correlated with each other except for the flag leaf angle. Though inconclusive due to susceptibility of the evaluated morphological traits to environmental conditions, this study assessed the overall genetic diversity pattern of traditional upland rice cultivars based on morpho-agronomic variations that can be further subjected to more robust tests involving molecular markers.**

Key Words: Cluster Analysis, Morphometric markers, Upland rice

INTRODUCTION

Genetic uniformity among new rice varieties is an alarming situation confronting the rice industry (Morishima and Oka 1995) as it has increased the vulnerability of the rice crop to disease epidemics and insect infestation. Human selection for early maturing and high yielding rice varieties is identified as one factor that had resulted in the loss of genetic variability in farmers' fields.

Before the government introduced the Masagana '99 program in the early 70s promoting the use of genetically uniform modern hybrids, about 3,500 traditional rice cultivars were known. With the introduction of these modern, high yielding cultivars, farmers are now planting fewer traditional landraces in their fields (Salazar 1993).

Traditional rice cultivars still extant in upland ecosystems may provide the genetic diversity needed to diversify the depauperate gene pool of improved rice varieties. Owing to their adaptation to a wide range of agro-ecological conditions, traditional land races represent tremendous genetic variability not found in modern varieties. These cultivars can therefore be exploited to significantly enhance rice productivity in marginal upland areas.

This study assessed the orphological variability of upland rice cultivars in Barangay Kihan, Malapatan, Sarangani Province using uantitative morphological characters. This technique is a low-level yet powerful taxonomic tool that

*Corresponding author: florence_zapico@yahoo.com
florence_zapico@gmail.com

can be used for the preliminary grouping of cultivars prior to their characterization using more robust marker technologies.

MATERIALS AND METHODS

The Study Site
This study was conducted in Barangay Kihan, Malapatan, Sarangani Province. The barangay is located at the northeastern part of Barangay Poblacion and lies along the borders of Don Marcelino, Davao del Sur and the municipalities of Alabel and Malapatan in Sarangani Province. The place is inhabited predominantly by B'laan communities. Upland agriculture is the sole livelihood source though it is done at the subsistence level. This mountainous and river-enclosed region covers a total of 6,620 hectares with 3,529 people and 585 households distributed throughout the 26 sitios.

Morphological Characterization
Thirty two (32) upland rice cultivars were subjected to *in situ* characterization using ten (10) quantitative morphological traits - culm number, plant height, culm diameter, flag leaf angle, plant length, leaf length, leaf width, ligule length, leaf angle, and culm length, as described previously (Schlösser et. al. 2000; Thomas et. al. 2001). Characterization was done using rice plants actually growing in the farmers' fields and was limited to morphological traits during the reproductive phase prior to harvest. The experimental data was based on measurements of ten rice plants randomly chosen in the fields for each cultivar.

Pearson's Correlation Coefficient was computed and the data were analyzed using Unweighted Paired Group Method using Centroids (UPGMC). Cluster analysis was done to yield a dendrogram depicting the morphological relatedness of the upland rice cultivars. Principal component analysis was also used to detect underlying sources of morphological variability. PCA had been used to determine the optimum number of clusters (Thompson et. al. 1998), to complement cluster analysis (Lombard et. al. 2000), and to investigate patterns of genetic diversity (Mohammadi and Prasanna 2003). All analyses were done using the SPSS version 14 statistical package.

RESULTS AND DISCUSSION

Significant positive correlation among majority of the morphological characters evaluated was observed except for flag leaf angle (Table 1). All the characters, with the exception of culm number, were negatively correlated with flag leaf angle. It was also observed that in most cases, the morpho-agronomic traits studied showed significant correlation among themselves. A specific example is the very significant correlation of leaf width and culm number ($\alpha = 0.05$). Any of these morphological characters can be discarded to reduce the number of traits to characterize. This correlation can be used as basis for character discard if similar research is conducted in the future using additional morphological characters. Elimination of redundant characters will reduce the workload of the researcher and will render characterization less cumbersome and more efficient.

Principal components analysis of the morphological characters yielded two principal components accounting

Table 1. Pearson's Correlations of Ten Morphological Characteristics

	Culm number	Plant height	Culm diameter	Flag leaf angle	Panicle length	leaf length	leaf width	ligule length	leaf area	culm length
Culm number	1	.502(**)	.225	.197	.327	.528(**)	.422(*)	.094	.515(**)	.512(**)
Plant height		1	.641(**)	-.137	.856(**)	.876(**)	.850(**)	.052	.902(**)	.995(**)
Culm diameter			1	-.115	.636(**)	.693(**)	.765(**)	.066	.753(**)	.620(**)
Flag leaf angle				1	-.194	-.083	-.073	-.128	-.067	-.129
Panicle length					1	.832(**)	.810(**)	.092	.867(**)	.813(**)
leaf length						1	.818(**)	.168	.953(**)	.847(**)
leaf width							1	.188	.948(**)	.827(**)
ligule length								1	.174	.034
leaf area									1	.874(**)
culm length										1

**Correlation is significant at the 0.01 level (2-tailed).
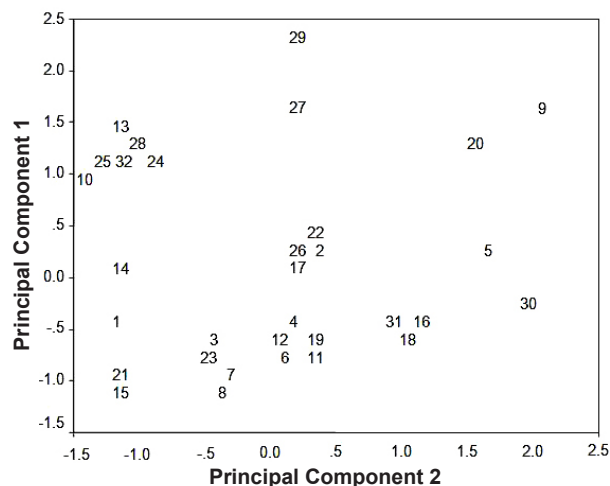*Correlation is significant at the 0.05 level (2-tailed).

Figure 1. Scatterplot of the first and second principal component scores of the rice cultivars based on 10 morpho-agronomic characters.

1. Mayaman
2. Muslim
3. Blanak
4. Bansalan
5. Azucena
6. Basag
7. Fungol
8. Fantig
9. Mlikat samlaka
10. Mlikat garong
11. Mlikat Linda
12. Mlikat balot
13. Mlikat mala
14. Mlikat bayad
15. Mlikat lagfisan
16. Mlikat tabe
17. Mlikat blawen
18. Bulabed
19. Samfang
20. Ubo
21. Kanone
22. Larangan
23. Fantilanon
24. Lumabet
25. Fanda bulaw
26. Fitamkwat
27. Tindah
28. Manabang
29. Fale bulaw
30. Buling
31. Magles
32. Mlang

for approximately 82.7% of total variance observed (Figure 1) Breakdown of this cumulative variance value revealed contributions of 66.9% and 15.87% for PCA 1 and PCA 2, respectively. The relative discriminating power of the two principal components, as inferred from PCA analysis, was high for PCA 1 (6.7) and quite low for PCA 2 (1.7). The first principal component was correlated with plant height, culm diameter, panicle length, leaf length, leaf width, leaf area, and culm length. Only flag leaf angle made substantial contribution to the second component.

The results obtained from PCA were further corroborated by cluster analysis using UPGMC (Unweighted Paired Group Method using Centroids). This clustering algorithm successfully classified the 32 rice cultivars characterized *in situ* into four morphologically distinct clusters (Figure 2). UPGMC proved to be useful in showing high internal
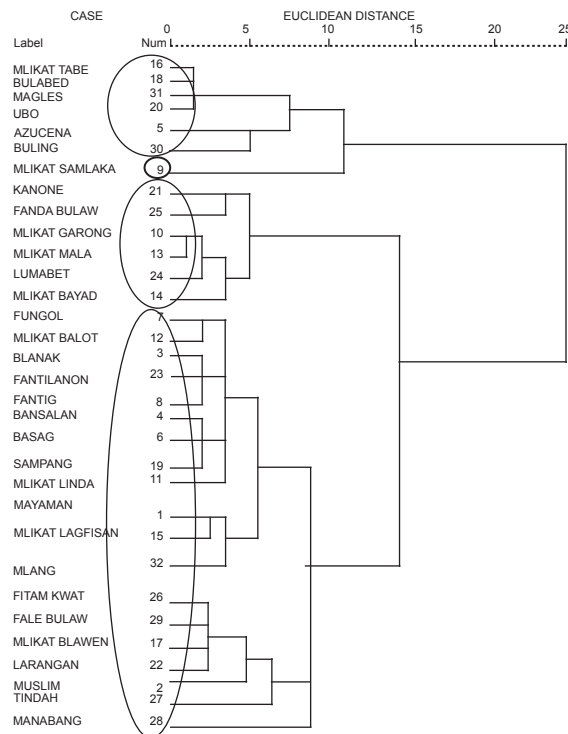

Figure 2. UPGMC Dendrogram Showing the Relationships of Upland Rice Cultivars in Kihan, Malapatan, Saranggani Province, Philippines as Revealed by Quantitative Morphological Characters.

(within cluster) homogeneity and external (between clusters) heterogeneity within cultivars, as previously ported (Mohammadi and Prasana 2003). The resulting four clusters were well resolved in terms of morphological characteristics. Cluster 1 cultivars were generally tall and high tillering (*Azucena*, *Mlikat*, *Samlaka*, *Buling*, etc.); Cluster 2 consisted of short cultivars such as Kanone, Lumabet, and Mlikat garong; Cluster 3 was composed of moderately tall but low tillering cultivars (*Fantilanen*, *Samfang*, and *Bansalan*) while the fourth cluster was dominated by *Larangan*, *Fitam kwat*, and *Tindah*. *Mlikat samlaka* emerged as the most distinct variety since it formed a separate cluster apart from the rest of the cultivars. This morphological divergence can be attributed to the high values scored for leaf length, leaf area, and culm length. Low variability for the three mentioned traits, however, was observed among cultivars making up the other three clusters.

The information gleaned from PCA and cluster analyses complemented each other with some slight inconsistencies in terms of cluster composition. Results of the study also revealed remarkable homogeneity among the upland rice cultivars for the quantitative agro-morphological characters evaluated. Similar results were reported by Ogunbayo et. al (2005) in assessing phylogenetic diversity and relationship among 40 rice accessions in

a field genebank in Nigeria using morphological values. It is to be noted that the discriminatory power of the cluster Analysis and principal components analysis is not conclusive owing to the small number of traits evaluated and their susceptibility to environmental conditions. These tests, however, allowed for preliminary groupings of cultivars based on cluster similarities 'and inter-cluster morphological variations. Li et al. (2002) reported that because of environmental effects, diversity analysis based on phenotypic values may not be the perfect representation of the natural groupings of cultivars. It is necessary to employ suitable genetic models or molecular markers such as SSR orAFLP to reduce environmental effects or experimental errors and allow the quantitative prediction of genotype values of the crop.

ACKNOWLEDGMENTS

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