

Phenotypic Diversity of Rice Landraces collected from Ayeyarwady Region, Myanmar, using Agro-morphological Characterization

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Rice is grown extensively in the countryside and rural areas of Myanmar, where it covers over 7.26 million ha. In 2017-2018, rice production was 28.1 million t with an average yield of 3.92 t ha⁻¹ (MoALI 2019). Myanmar has diverse landscapes and geographic variation ranging from the delta area of the Ayeyarwaddy River in the southern region, to the mountainous areas in the northern region. This landscape diversity resulted in the diverse agricultural system including deep water fields in the delta areas, irrigated or rain-fed paddy fields in plain areas and slash and burn fields in the mountain areas. Such a geographic diversity coupled with diverse traditional agricultural systems, contributes to the diversity of crop genetic resources in Myanmar (Garcia et al. 2003; San San Yi et al. 2008).

Results

Table 1. Diversity of 117 Myanmar rice accessions in 13qualitative traits

Descriptors	Predominant state	%	State Observed	H index
AC2	Very high (>25)	40.17	After harvest	0.84
FLA_E	Semi erect	62.39	Anthesis	0.83
LPC	Straw furrows	45.30	Ripening	0.81
СоА	None	50.43	After anthesis to hard dough stage	0.78
LPP	Short hairs	34.19	Ripening	0.78
PA_B	Spreading (open panicle)	53.85	Near maturity	0.77
AC1	Light green	57.26	Late vegetative	0.73
PA_M	Strongly drooping	49.57	Near maturity	0.72
FLA_L	Semi erect	50.43	Maturity	0.68
SC	Light green	58.12	Anthesis (between 09:00 and 14:00)	0.67
ЕТ	Cloudy and translucent	67.52	After polishing	0.66
AD	Awnless	78.63	Flowering to maturity	0.48
SLC	Straw	86.32	7 days after flowering	0.41
A	verage diversity			0.70





Local varieties of rice represent the main sources to undertake genetic improvement for the toleration of biotic and abiotic stress. Moreover, identifying the genetic diversity of local varieties compared with improved or introduced varieties will assist the breeding of elite varieties for use in sustainable agriculture. Well-characterized and evaluated germplasm collections would have greater chances of contributing to the development of new varieties, which can cope with changing climate and linked aggravation of rice cultivation problems and consequently greater realization of benefits for the resource-poor farmers (Prasanna 2010).

Objective

• To determine the agro-morphological characterization and relationship between rice accessions collected from the Ayeyarwady region for their utilization in breeding programs

Materials and Methods

Study area

Ayeyarwady region occupies the delta region of the Ayeyarwady river, which is the longest river in Myanmar. The total area of paddy in Ayeyarwady region was 2 million hectares, which is 28% of the total cultivated rice area in Myanmar. bubescence; PA_B:Panicle altitude of branches; AC1:Auricle color; PA_M:Panicle altitude of main axis; FLA_L:Flag leaf altitude (late observation); SC:Stigma color; ET:Endosperm type; AD:Awns distribution; SLC:Sterile lemma color



Fig. 4 Two dimensional principal coordinate axes for 117 Myanmar rice accessions based on 13 qualitative traits

Table 2 Diversity of 117 Myanmar rice accessions in 15quantitative traits

Descriptors	Range	Mean± SE	CV (%)	Skewness	Kurtosis
DTH	66.0-114.0	96.55±0.86	9.61	-0.37	0.01
CL	65.8-130.8	94.39±1.18	13.56	0.25	-0.11
PL	19.7-31.1	25.78±0.21	8.92	-0.08	-0.13
LSL	1.2-7.1	2.23±0.08	40.81	4.44	20.61
SSL	1.1-6.6	2.08±0.08	41.35	4.18	19.14
NTPP	10.0-36.0	20.64±0.51	26.55	0.84	0.37
NPP	6.0-33.0	16.42±0.37	24.54	0.65	1.82
NSPP	382.0-1510.0	827.39±20.00	26.15	0.42	-0.01
TGW	16.7-35.2	26.65±0.34	13.58	-0.49	-0.05
GL	6.6-11.2	8.18±0.08	10.88	0.90	0.42
GW	2.2-4.1	3.03±0.04	12.87	0.19	0.09
LWR	1.8-4.3	2.77±0.05	20.94	0.66	-0.41
FG%	44.6-95.8	87.92±0.71	8.75	-3.27	15.02
HI	0.1-0.9	0.51±0.01	27.45	-0.14	0.06
Y	0.0-0.5	0.21±0.01	14.29	0.40	1.64



Fig. 3 Dendrogram of 117 Myanmar rice accessions based on 13 qualitative traits

Table 3. Eigenvalue of six principal components andfactor loadings (eigenvectors) for 15 quantitative traits

	PC1	PC2	PC4	PC4	PC5	PC6
Eigenvalue	2.654	2.628	1.942	1.533	1.838	2.505
Percent variance	22.575	21.011	10.456	10.167	8.547	7.598
Cumulative percent of total variance	22.575	43.587	54.042	64.209	72.756	80.355
Eigenvectors						
Days to heading (days)		0.629				
Culm length (cm)					0.912	
Panicle length (cm)			0.589			
Long sterile lemma (mm)						0.963
Short sterile lemma (mm)						0.968
No. of tillers per plant				0.867		
No. of panicles per plant				0.868		
No. of spikelets per panicle					0.765	
Thousand grain weight (g)			0.916			
Grain length (mm)	-0.905					
GW: Grain width (mm)	0.696		0.443			
Length-width ratio	-0.931					
Filled grain %		0.607				
Harvest index		0.829				
Yield (kg)		0.730				
The scores lower than 0.5 are not shown.						

Plant materials

112 rice landraces

- 40 from agricultural fields in Ayeyarwady delta
- 72 from seed bank collected from the same areas
- 5 check (control) improved varieties

Experimental design

- two 3m x 30 m seedbeds
- transplanted 2-week old seedlings
- Augmented RCBD



Fig. 1 Field experiment in Myanmar

Data collection

5 mature plants in the center of a row were tagged at each entry for the data collection.

OTH: Days to heading (days); CL: Culm length (cm); PL: Panicle length (cm); LSL: Long sterile lemma (mm); SSL: Short sterile lemma (mm); NTPP: No. of tillers per plant; NPP: No. of spikelets per panicle; TGW: Thousand grain weight (g); GL: Grain length (mm); GW: Grain width (mm); LWR: Length-width ratio; FG% : Filled grain %; HI: Harvest index; Y: Yield (5 hills) kg

Table 4. Correlation coefficient matrix of the quantitative characters of 117 Myanmar rice accessions

DTH	CL	PL	LSL	SSL	NTPP	NPP	NSPP	TGW	GL	GW	LWR	FG	
.07													
.29**	.22*												
14	14	13											
04	12	12	.98**										
04	.01	01	07	06									
12	.02	1	.11	.1	.51**								
.15	.46**	.27**	30**	27**	.01	03							
.24**	.04	.45**	.16	.20*	03	•	25**						
13	.13	.08	12	13	02	.02	02	03					
.09	07	.04	.46**	.47**	03	•	26**	.62**	51**				
11	.07	.01	26**	27**	.01	•	.11	41**	.85**	87**			
.16	08	.26**	.06	.07	•	.03	.11	.18*	02	.02	01		
.47**	13	.32**	27**	22*	.03	07	.28**	.09	23*	.01	13	.21*	
.57**	.16	.43**	23*	16	.06	.04	.41**	.28**	28**	.17	27**	.22*	.73**

DTH: Days to heading (days); CL: Culm length (cm); PL: Panicle length (cm); LSL: Long sterile lemma (mm); SSL: Short sterile lemma (mm); NTPP: No. of tillers per plant; NSPP: No. of spikelets per panicle; TGW: Thousand grain weight (g); GL: Grain length (mm); GW: Grain width (mm); LWR: Length-width ratio; FG% : Filled grain %; HI: Harvest index; Y: Yield (5 hills) kg **n<.05: *n<.01

Summary

Shannon-Weaver diversity index ranged from 0.41 to 0.84 with a mean of 0.7 which is indicating a moderate diversity of qualitative characters exists in Myanmar traditional rice varieties. Several traits classified as low and moderate diversity might be prioritized in future collection to enhance their diversity. Cluster analysis separated the different varieties into various groups. Truncating the tree at the Euclidean distance of 1.18 resulted in 15 clusters. The principal coordinate analysis also showed the similar pattern of groupings as cluster analysis. For analysis of 15 quantitative traits, the coefficient of variation was more than 10 % for most of the characters, the highest one being the number of panicles per plant (24.54%). The presence of high variability suggests that this character can be improved either through selection/hybridization. Correlation analyses among quantitative traits showed a strong correlation in several traits. Trait correlations can be used to simultaneously improve correlated traits or reduce undesirable side effects when trying to improve only one of the correlated traits. Principal component analysis (PCA) was employed to reduce the complexity of the data set while retaining the variation within the data set as far as possible. PCA has revealed six major components, which altogether explained 80.4% of the total variation.

• 15 quantitative and 13 qualitative characters were collected on the particular stage for the rice plant by using IRRI rice descriptors.



Fig. 2 Morphological characters

References

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