

## Yield performance of Paw San rice (*Oryza sativa* L.) group: Paw San morphotype

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**Abstract:** Paw San group rice varieties are important for local adaptability, grain quality, market availability and premium price, and have been cultivated for long time in Myanmar. Undesirable negative effect of mutation and out-crossing with other local varieties or common wild rice may lead to inter-varietal variation, and limited seed flow system for Paw San rice may also lead to varietal degradation. In 2008, lower part of Myanmar was hit by Cyclone Nargis, and some of the local rice varieties in Paw San area may lose forever. This study was carried out to test yield performance of 5 genotypes of Paw San morphotype at Myaungmya and Yezin in 2009, and some genotypes which produced higher grain yields seemed to be promising for future varietal improvement for development of Paw San rice.

**Key words:** Genotype, morphotype, Paw San, yield and yield components.

### Introduction

Rice varietal groups in Myanmar have been standardized as *Emata*, *Letywezin*, *Ngasein*, *Meedon* and *Byat* in order to facilitate external and internal trade. Among them, Meedon rice area in 2007 was 449487 hectare, comprising 6.5% of total rice area in Myanmar, and mainly grown in rainfed lowland areas: Ayeyawady (52.1%), Yangon (27.9%), Yakhine (12.1%), Bago (4.5%), Mon (3.1%), and other Regions (0.3%) (MAS, 2008). Paw San rice varieties are included in *Meedon* group, and have been cultivated and maintained as on-farm conservation for centuries. Undesirable negative effect of mutation and out-crossing with other local varieties or common wild rice may lead to varietal variation, and since the possibility of the quality of some varieties show location specific, farmers in the areas used to grow their own seeds so that there was limited seed flow system for Paw San rice may lead to varietal degradation. On the other hand, the ability of low nitrogen tolerance, local adaptability, grain quality, market availability and premium price can extend the growing area for Paw San rice to the productive land such as favorable rainfed area and irrigated tract besides its native or marginal land of unpredictable flood in rainfed lowland. Therefore, Paw San rice varieties with high yield potential and wide adaptation may become essential.

Current national rice varietal improvement programs also focus on improving quality rice for regional and global rice trade competition. To improve rice varieties, breeding methods such as indigenous selection, selection of introduced entries, hybridization and mutation breeding can be used. By indigenous selection, varieties could be released in another adaptable area, and 13 local varieties had been released (Ohn Kyaw, 2002). Tin Tin Myint *et al.* (2004) also mentioned the indigenous selection and the release of 18 local varieties by this method. Small-scale, decentralized, farmer-participatory breeding and variety selection programs have been advocated to reduce genetic erosion by improving indigenous germplasm and exploiting local adaptation (Maurya *et al.*, 1988). In some cropping systems, such programs can increase crop genetic diversity when localized environmental constraints result in a failure of high-yield varieties to perform well (Witcombe *et al.*, 1996; Sthapit *et al.*, 1996).

With the advent of genetics and plant breeding, selection has been intensified for high yield potential with broader adaptation (Simmond, 1979). Although rice entries can be introduced through international evaluation nursery

program, utilization of local germplasm seemed to be suitable for greater adaptability to local special and temporal conditions. Genetic resources of Paw San rice were collected and conserved in Myanmar Seed Bank, and the study of Paw San rice germplasm showed a relatively high genetic diversity and elite accessions were identified (Min San Thein *et al.*, 2011).

In 2008 May 2, Myanmar was hit by Cyclone "Nargis", the largest storm of its history, and the Nargis hit the two major Paw San rice growing areas, Ayeyawady and Yangon Regions. By this natural disaster, many stores of rice have been swept, and some of the local rice varieties may lose forever (PoNJA, 2008). On the other hand, there was also limited varietal improvement program for Paw San rice. Therefore, this study was carried out to test yield performance of elite Paw San accessions to identify promising genotypes.

### Materials and Methods

**Material:** Five accessions viz. PS<sub>1</sub>, PS<sub>2</sub>, PS<sub>3</sub>, PS<sub>4</sub> AND PS<sub>5</sub> were identified as elite genotypes by indigenous selection based on evaluation test in 2008 (Min San Thein *et al.*, 2011). They were 5 genotypes of Paw San morphotype and those genotypes were used in yield performance trials. Local variety, Paw San Shwe War was used as check.

**Experimental sites and design:** Yield performance trials were conducted at the experimental fields of Myaungmya Agricultural Research Center, Ayeyawady Region and Seed Bank, DAR, Yezin, Nay Pyi Taw, Myanmar on 21 June 2009 and 27 June 2009, respectively. Yield trials were tested in RCB designs with four replications, and each plot was 4.0 m x 3.5 m. The seedlings were raised in nursery beds, and 30 days old seedlings were transplanted singly in each hill with a spacing of 25 cm between rows and 20 cm within row. Each plot consisted of 14 rows of 4.0 m long and 0.25 m apart. Each row consisted of 20 hills. Harvested area was 3.6 m x 3.0 m included 12 rows of 18 hills/row and total harvested hills were 216. A basal fertilizers application was 14:27:30 kg/ha of N: P<sub>2</sub>O<sub>5</sub>: K<sub>2</sub>O followed by top-dressing of 14 kg N/ha at 45 days after transplanting. Grain yield/plot, yield components and other traits such as biomass/hill, harvest index, days to heading, plant height, and panicle length were measured.

**Data analysis:** Individual and combined analyses of variance (ANOVA) for yield trials with 4 replications at Myaungmya and Yezin were computed using CropStat.Ver.7.2.2007.2, IRRRI, Manila, Philippines.

### Results and Discussion

Yield performance trials for Paw San genotypes: PS1, PS2, PS3, PS4 and PS5 with local check (Paw San Shwe War) were tested at two locations, Myaungmya and Yezin, and result of grain yield was shown in Table 1. The genotypes were not statistically significant at  $P \leq 0.05$  level for Yezin location. However, it was significantly different ( $P < 0.01$ ) for Myaungmya location.

Combined ANOVA was computed to determine the yield performance of genotypes across two locations. Genotype (G), location (L), and genotype - location interaction (G x L) were significantly different at  $P < 0.01$  level of probability. When genotype (G) and location (L) effects were observed, location effect was greater than genotype effect as shown in Table 2. The mean yield (ton/ha) of 5 Paw San genotypes under two locations was shown in Table 3. When yield performances of genotypes were compared, mean yields were not significantly different at Yezin location. However, genotypes PS3 and PS5 produced significantly ( $P < 0.01$ ) lower grain yield than

local check at Myaungmya location and by combined analysis. Genotypes PS2 (3.897 ton/ha) and PS4 (3.606 ton/ha) gave more yield than check (3.441 ton/ha) but not statistically significant at Yezin location as well as PS2 (3.469 ton/ha) gave more yield than check (3.385 ton/ha) by combined analysis. When yield performance under two locations was compared, mean grain yield (3.502 ton/ha) at Yezin location was significantly ( $P < 0.01$ ) higher than mean grain yield (2.788 ton/ha) at Myaungmya location.

Based on the results of ANOVA of grain yield for two locations, it was noted that test genotypes were not different at Yezin location while they were different at Myaungmya location. However, genotypes PS3 and PS5 produced significantly lower grain yield than local check at Myaungmya location (Table 4). It is suggested that there was more variable of environment in Myaungmya than in Yezin. Genotypes PS2 and PS4 produced more grain yield than check but not statistically significant at Yezin indicating the importance of those genotypes for conservation and use.

**Table 1.** Individual ANOVA of grain yield (ton/ha) for Paw San genotypes by locations

Source of variance	Degree of freedom	Sum of square	Mean square	P-value
<u>Yezin</u>				
Genotype	5	0.9426	0.1885 <sup>ns</sup>	0.1450
Replication	3	0.5113	0.1704 <sup>ns</sup>	0.1970
Residual	15	1.4506	0.0967	
Total	23	2.9046	0.1263	
<u>Myaungmya</u>				
Genotype	5	6.7653	1.3531 <sup>**</sup>	0.0010
Replication	3	3.429919	0.1433 <sup>ns</sup>	0.3220
Residual	15	1.6997	0.1133	
Total	23	8.8950	0.3867	

\*\* = significant at  $P < 0.01$  level, \* = significant at  $P < 0.05$  level, <sup>ns</sup> = not significant

Combined analysis of the two locations indicates the differences among genotypes (G), locations (L), and genotype-location interaction (G x L). The greater effect of location (L) indicating the variability of the two

locations that Yezin was irrigated tract where water requirement was controllable, whereas Myaungmya was rainfed lowland that unpredictable flood caused uncontrollable drainage or irrigation.

**Table 2.** Combined ANOVA of grain yield (ton/ha) for Paw San genotypes across two locations

Source of variance	Degree of freedom	Sum of square	Mean square	P-value
Genotype (G)	5	4.9504	0.9901 <sup>**</sup>	0.0000
Location (L)	1	6.1258	6.1258 <sup>**</sup>	0.0000
Replication (R)	3	0.4023	0.1341 <sup>ns</sup>	0.5104
Pooled error	38	6.4469	0.1697	
Total	47	17.9253	0.3814	
G x L	5	2.7575	0.5515 <sup>**</sup>	0.0020
G x R	15	2.6232	0.1749 <sup>ns</sup>	0.4440
L x R	3	0.9390	0.3130 <sup>ns</sup>	0.3780
G x L x R	15	0.5271	0.0351 <sup>ns</sup>	1.0000

**Table 3.** Mean yields (ton/ha) of Paw San genotypes tested in two locations

Genotype	Yezin	Myaungmya	Difference	Combined	Location
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PS1	3.375 <sup>ns</sup>	3.182 <sup>ns</sup>	0.193	3.278 <sup>ns</sup>	
PS2	3.897 <sup>ns</sup>	3.042 <sup>ns</sup>	0.855	3.469 <sup>ns</sup>	
PS3	3.322 <sup>ns</sup>	2.069 <sup>**</sup>	1.253	2.696 <sup>**</sup>	
PS4	3.606 <sup>ns</sup>	3.077 <sup>ns</sup>	0.529	3.341 <sup>ns</sup>	
PS5	3.373 <sup>ns</sup>	2.027 <sup>**</sup>	1.346	2.700 <sup>**</sup>	Yezin=3.502 <sup>**</sup>
Check	3.441	3.329	0.112	3.385	Myaungmya=2.788
Mean	3.502	2.788	0.714	3.145	3.145
SE	0.1555	0.1683		0.146	0.084
LSD <sub>(0.05)</sub>	0.4687	0.5074		0.417	0.241
P-value	0.1449	0.0010		0.0005	0.0000
CV (%)	8.9	12.1		13.1	13.1

SE=standard error, LSD<sub>(0.05)</sub>=least significant difference at P<0.05 probability level, CV=coefficient of variation

**Table 4.** Means of yield components of Paw San genotypes by two locations

Genotype	YLD	Gr/H	Gr/P	FGr/P	100W	ET	BIO	HI	DTH	PH	PNL
PS1	3540.5	17.4	3.42	114.1	2.71	6.4	78.7	0.235	140.9	147.7	28.0
PS2	3746.7	14.2	3.11	101.5	2.72	6.1	72.4	0.211	141.8	139.2	26.1
PS3	2911.3	13.7	2.57	88.9	2.60	7.4	84.0	0.165	145.8	148.6	27.0
PS4	3608.6	16.3	2.74	96.3	2.60	8.0	79.5	0.207	143.0	147.8	27.1
PS5	2916.2	13.0	2.42	87.8	2.55	7.2	74.1	0.195	145.3	147.1	27.5
Check	3655.9	26.0	2.92	113.4	2.56	9.9	80.8	0.329	139.9	132.2	25.8
Mean	3397.0	16.8	2.86	100.3	2.62	7.5	78.2	0.224	142.8	143.8	26.9
SE	157.3	1.091	0.167	6.102	0.029	0.436	3.991	0.015	0.432	1.269	0.386
LSD <sub>(0.05)</sub>	450.2	3.123	0.477	17.470	0.082	1.249	11.430	0.044	1.237	3.633	1.106
P- (G)	0.001	0.000	0.002	0.010	0.000	0.000	0.341	0.000	0.000	0.000	0.002
P- (L)	0.000	0.000	0.001	0.801	0.006	0.000	0.000	0.112	0.000	0.000	0.485
P- (G x L)	0.002	0.194	0.611	0.469	0.843	0.387	0.000	0.104	0.000	0.265	0.237
CV (%)	13.1	18.4	16.5	17.2	3.1	16.4	14.4	19.3	0.9	2.5	4.1

Yld=grain yield/plot (g), Gr/H=grain weight/hill (g), Gr/P=grain weight/panicle (g), FGr/P=no. of filled grain/panicle, 100GW=100-grain weight (g), ET=no. of effective tiller, BIO=biomass/hill (g), HI=harvest index, DTH=days to heading (day), PH= plant height (cm), PNL=panicle length (cm), SE=standard error, LSD<sub>(0.05)</sub>=least significant difference at P < 0.05 probability level, P=P-value, CV=coefficient of variation

The genotypes of three Paw San morphotypes were variable in grain yield and yield components, and some of the genotypes were important for yield potential and they

seemed to be promising genotypes for utilization in varietal improvement. Those genotypes were PS2 (Acc. 1139) and PS4 (Acc. 2501), respectively (Table 5).

**Table 5.** List of 15 potential genotypes of Paw San morphotypes

Sr. no.	YT code no.	Accession no.	Local name	State/ Region
1	PS1	ACC. 930	Paw San Hmwe	Bago
2	PS2	ACC. 1139	Paw San Hmwe	Bago
3	PS3	ACC. 3225	Mee Don Yoe Sein	Ayeyawady
4	PS4	ACC. 2501	Paw San Hmwe	Yangon
5	PS5	ACC. 2522	Paw San Hmwe	Ayeyawady

YT=Yield trial

### Conclusion

The two locations, Yezin and Myaungmya showed variation in terms of grain yield. Mean grain yields were generally greater in Yezin than in Myaungmya may be due to the favorable condition of water controllable irrigated tract of Yezin. Therefore, it could be concluded that most of the tested genotypes could produce higher grain yield in productive land of irrigated tract. Some of the tested accessions seemed to be promising genotypes, and they are important for their yield potential for conservation and use. Some accessions performed well in both locations although the locations differ substantially in rainfall, soil type and rice ecosystem. So, genotypes adapted to both locations were also important for conservation, and they

could be useful genotypes for wider adaptation for varietal improvement of morphotype of Paw San rice.

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