

# Evaluation Of Recombinant Inbred Lines Derived From Bulk Population Method Of Selection In Rice (*Oryza sativa* L.)

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**Abstract:** Current climate shocks in Myanmar reduce the rice productivity and production stability that already have high levels of food insecurity. To attend local self-sufficiency, plant breeders have to develop high yielding cultivars with desirable agronomic traits. In order to evaluate genetic variability of recombinant inbred lines based on agro-morphological traits and also determine the correlation between these traits, 49 F7 recombinant inbred lines (RILs), their parents and a check variety were grown in the research field of Yezin Agricultural University during January to May, 2016. A field experiment was conducted using Randomized Complete Block design with three replications. All tested genotypes showed wide range of variability for population uniformity, flag leaf altitude and leaf pubescence. YAU 1215-B-B-B-138-3, YAU 1215-B-B-B-123-3 and YAU 1215-B-B-B-91-3 were identified as the early maturity promising lines. The best yields were shown in YAU 1214-B-B-B-51-2 and YAU 1215-B-B-B-156-1. Phenotypic coefficients of variance were higher than genotypic coefficients of variance in all the characters. Progeny selection will be effective to improve plant height, total grains plant<sup>-1</sup>, no. of filled grains panicle<sup>-1</sup> and 1000 seed weight indicating high heritability and high genetic advance. In rice seed production, panicle length, number of total grains panicle<sup>-1</sup> and number of filled grains panicle<sup>-1</sup> were found to be the main yield contributing traits. In cluster analysis, 2 RILs in cluster VI had medium number of panicle plant<sup>-1</sup>, longest panicle length, largest number of total grains plant<sup>-1</sup>, medium 1000 seed weight and highest seed yield were identified as highly valuable sources to be incorporated in rice breeding programs.

**Key words:** RILs, heritability, genetic advance, correlation, cluster

## 1. Introduction

Rice is the major stable food for billions of people in Asia, Africa and Latin America. Asia is a major producer and consumer of rice which accounts for 90 to 92% of world's rice area and productivity, respectively. Rice is the main leading cereal crop of Myanmar with 7.2 million hectares area planted and 28.19 million MT productions with the national average yield of 3.97 MT ha<sup>-1</sup> in 2013-2014 (MOAI 2015). The world population is expected to reach 9.8 billion by 2050. With an alarming increase in the population throughout the world, the demand for rice will continue to increase in near future. On the other hand, the area under rice cultivation has decreased with increased development and industrialization, hence increasing the grain yield per unit area is the only way to meet the target of increasing crop yield (Ashfaq et al. 2012). Current climate shocks (drought and high temperature) in Myanmar are now threatening agricultural crops including rice germplasm. Climate shocks reduce the rice productivity and production stability that already have high levels of food insecurity. In Myanmar, plan for the increase in sown area and yield per hectare of rice and plant breeding program is needed to support local sufficiency policy. Most research in rice breeding in Myanmar was focused on breeding for high yields, resistance to biotic factors and tolerance to abiotic stresses. Recently, the trend has changed to the life-span of the crop due to the limited water resource. To meet this demand and attend rice self-sufficiency, plant breeders have to develop high yielding cultivars with desirable agronomic traits. The development of new genotypes requires some

knowledge about the genetic variability presents in the germplasm of the crop to build efficient breeding programme. The magnitude of variation due to heritable component is very important because, it would be a guide for selection of parents for crop improvement. Therefore, selection for high yield requires knowledge about genetic variability and good understanding of correlation between yield and yield components regarding to the genetic material that is on hand. Genetic variability for agronomic traits is the key component of breeding programme for broadening the gene pool of rice (Dutta et al. 2013). Estimate heritability along with genetic advance conjointly are reliable helpful in predicting the gain under selection than heritability alone. Consequently, selection for yield may not be satisfying without taking into consideration yield component traits (Ogunbayo et al. 2014). Therefore, to fulfill these requirements, this study was carried out with the following objectives: (1) to evaluate genetic variability of rice recombinant inbred lines based on agro-morphological traits and (2) to analyse the relationships between yield and its components.

## 2. Materials and Methods

The experiments were conducted in the research field of Department of Plant Breeding, Physiology and Ecology, Yezin Agricultural University from January 2016 to May 2016. The experimental material consisted of 36 recombinant inbred lines derived from a cross of agronomically superior line, Shwe Thwe Yin which is a semi-dwarf, early maturing and high yielding rice variety

with Long 8, a tall, medium maturing and high yielding variety, and 13 RIL derived from a cross of Shwe Thwe Yin with Long 6, a tall, medium maturing and high yielding variety. The RIL population which comprised of 49 individuals was developed using bulk population method. The fifty-three rice genotypes which consisted of forty-nine RILs, their parents (Long 6, Long 8, and Shwe Thwe Yin) and one check variety (Manawthukha) were used as experimental materials in this study. The genotypes of rice were raised in a randomized complete block (RCB) design with three replications. Seven morphological characters and ten yield and yield component characters were recorded by referencing with Standard Evaluation System for Rice (IRRI 2002) in this study. The data were statistically analyzed for simple analysis of variances according to Star, Version 2.0.1. Correlation coefficient and cluster analyses, were performed with the XLSTAT (2014). The phenotypic and genotypic coefficients of variation, and heritability in broad sense ( $H_{bs}$ ) were computed by the formula suggested by Singh and Chaudhary (1985). The expected genetic advance (GA) with 5% selection intensity and the genetic advance as percent of mean (GA %) was calculated as the formula given by Johnson et al. (1955).

### 3. Results and Discussion

#### 3.1 The morphological characters of recombinant inbred lines

The forty-nine recombinant inbred lines showed wide range of variability for population uniformity, ligule shape and flag leaf altitude studied (Table 1). Among these genotypes, 41.51% of the genotypes showed homogenous and 58.49% were heterogenous in population uniformity. Based on the ligule shape character, the genotypes were grouped as acute to acuminate and 2-cleft. Among the genotypes studied, 11.32% of the genotypes showed acute to acuminate and 88.68% were 2-cleft for ligule shape character. For flag leaf altitude, the genotypes were grouped into three categories as erect, semi-erect and horizontal based on the altitude of flag leaf on the main culm. Among the genotypes, 39.62% of the genotypes were erect, 58.49% semi-erect and 1.89% horizontal.

**Table 1.** Predominance of morphological characters for recombinant inbred lines

Character	Percent of genotypes		
Population uniformity	41.51% Homogenous		58.49% Heterogenous
Basal leaf sheath colour	100% Green		
Auricle colour	100% Yellowish green		
Collar colour	100% Light green		
Ligule shap	11.32% Acute to acuminate		88.68% 2-cleft
Flag leaf altitude	39.62% Erect	58.49% Semi-erect	1.89% Horizontal
Leaf blade pubescence	100% Pubescence		

#### 3.2 Analysis of variances for yield and yield components of recombinant inbred lines

The analysis of variance (ANOVA) revealed statistically significant differences at 0.1% probability level among the 53 RILs for yield and yield component characters in Table

2. It was indicated that there were much genetic variation among genotypes in all characters.

**Table 2** Analysis of variance for quantitative characters in recombinant inbred lines

Character	Mean square			
	Genotype	Block	Error	CV(%)
Days to first flowering	57.50**	2.00 <sup>ns</sup>	9.65	3.29
Days to 50% flowering	58.43**	34.32 <sup>ns</sup>	14.43	3.62
Days to 100% flowering	54.26**	1.02 <sup>ns</sup>	1.83	1.26
Days to maturity	54.26**	1.02 <sup>ns</sup>	1.83	1.12
Plant height	392.36**	0.88 <sup>ns</sup>	2.79	1.55
Panicles plant <sup>-1</sup>	9.63**	4.94 <sup>ns</sup>	4.30	15.01
Panicle length	18.56**	6.06 <sup>ns</sup>	6.07	10.10
Total grains panicle <sup>-1</sup>	2031.22**	103.78 <sup>ns</sup>	317.08	11.69
Filled grains panicle <sup>-1</sup>	943.01**	2.76 <sup>ns</sup>	265.18	13.36
1000 seed weight	12.00**	3.97 <sup>ns</sup>	2.35	5.59
Effective yield plant <sup>-1</sup>	131.27**	55.32 <sup>ns</sup>	65.85	17.91

"\*\*" Significant at 1% probability level

"ns" Non-significant

#### 3.3 Mean performances of yield and yield component characters of rice genotypes

The mean values of fifty-three rice genotypes for different characters are described in Table 3 (a) and (b).

**Table 3 (a).** Mean performances for yield and yield components of fifty-three rice genotypes

Genotypes	DTF (days)	DTFP (days)	HPF (days)	DTM (days)	PH (cm)
Long 6	94.5	104.5	107.5	121.5	110
Manaw Thu Kha	89.5	95	104	118	137.9
long 8	98.5	110.5	120	134	123.3
Shwe Thwe Yin	92	91	93	107	78.05
YAU 1214-B-B-B-105-2	103.5	111.5	113	127	98.46
YAU 1214-B-B-B-1-1	90.5	103.5	107.5	121.5	105.3
YAU 1214-B-B-B-1-2	98	102.5	111.5	125.5	109.6
YAU 1214-B-B-B-122-1	102	109.5	112	126	111.04
YAU 1214-B-B-B-123-1	92.5	105	109.5	123.50	109.27
YAU 1214-B-B-B-33-1	100.5	103.5	108.5	122.50	110.60
YAU 1214-B-B-B-33-3	93.5	102	106.5	120.5	123.84
YAU 1214-B-B-B-51-1	102.5	115	118	132	119.305
YAU 1214-B-B-B-51-2	102.5	113.5	115	129	115.355
YAU 1214-B-B-B-53-1	102	113	114	128	126.8
YAU 1214-B-B-B-53-2	105.5	113	116.5	130.5	129.89
YAU 1214-B-B-B-67-1	98.5	110	113	127	105.16
YAU 1214-B-B-B-67-2	92	101	103.5	117.5	90.555
YAU 1215-B-B-B-10-1	90	104	106	120	99.59
YAU 1215-B-B-B-1-1	96.5	99	117	131	102.79
YAU 1215-B-B-B-110-1	87	94.5	101.5	115.5	131.25
YAU 1215-B-B-B-113-1	87.5	110	112.5	126.5	92.49
YAU 1215-B-B-B-123-1	91	103.5	108	122	96.115
YAU 1215-B-B-B-123-3	90	96	98.5	112.5	90.035
YAU 1215-B-B-B-124-1	91.5	104	107	121	93.205

YAU 1215-B-B-B-133-1	91.5	99.5	104	118	100.00
YAU 1215-B-B-B-134-1	94.5	99.5	101.5	115.5	103.965
YAU 1215-B-B-B-135-3	99.5	104.5	107	121	133.545
YAU 1215-B-B-B-137-3	99.5	109.5	112	126	107.15
YAU 1215-B-B-B-138-3	88.5	95.5	98	112	140.85
YAU 1215-B-B-B-139-1	88	99.5	102.5	116.5	107.21
YAU 1215-B-B-B-139-3	89	100.5	105.5	119.5	107.915
YAU 1215-B-B-B-140-1	93.5	100.5	105	119	112.045
YAU 1215-B-B-B-141-3	91	103.5	103	117	147.7
YAU 1215-B-B-B-153-1	89	101	103.5	117.5	91.91
YAU 1215-B-B-B-156-1	95.5	108.5	114	128	102.32
YAU 1215-B-B-B-168-1	90	102.5	108	122	113.485
YAU 1215-B-B-B-181-1	99	105	108	122	90.885
YAU 1215-B-B-B-193-3	89.5	97	102.5	116.5	105.39
YAU 1215-B-B-B-197-1	95.5	106.5	104	118	99.255
YAU 1215-B-B-B-197-2	104	110.5	114	128	100.98
YAU 1215-B-B-B-197-3	102.5	110	114	128	97.11
YAU 1215-B-B-B-52-2	91.5	99.5	104	118	98.95
YAU 1215-B-B-B-53-1	91	96.5	101	115	115.4
YAU 1215-B-B-B-55-1	91	101.5	105	119	94.595
YAU 1215-B-B-B-63-1	92.5	109	111.5	125.5	103.9
YAU 1215-B-B-B-66-1	101.00	108.50	111.00	125.00	104.12
YAU 1215-B-B-B-67-1	92.00	102.00	104.00	118.00	102.06
YAU 1215-B-B-B-67-2	95.50	104.00	105.00	119.00	99.77
YAU 1215-B-B-B-73-3	90.50	96.00	101.50	115.50	114.7
YAU 1215-B-B-B-76-1	97.50	103.50	110.00	124.00	80.21
YAU 1215-B-B-B-77-3	85.50	96.50	103.00	117.00	121.50
YAU 1215-B-B-B-78-1	89.50	100.00	102.00	116.00	99.45
YAU 1215-B-B-B-91-3	89.50	96.50	99.50	113.50	123.50

DTFF=Days to first flowering, DTFFP=Days to 50% flowering, HPF=Days to 100% flowering, DTM=Days to maturity, PH=Plant height Among the tested RILs, for days to 50% flowering, the maximum performance (115 days) was observed in YAU 1214-B-B-B-51-1 while the minimum performance was found in YAU 1215-B-B-B-110-1 (94.5 days). The days to 50% flowering of these line was later than that of Shwe Thwe Yin (91 days). The maximum performance (132 days) was observed in YAU 1214-B-B-B-51-1 while the minimum performance (112 days) was observed in YAU 1215-B-B-B-138-3 for days to maturity.

**Table 3(b).** Mean performances for yield and yield components of fifty-three rice genotypes

Genotypes	PPP (no.)	PL (cm)	TGPP (no.)	FGPP (no.)	TSW (g)	EYPP (g)
Long 6	11.3	24.68	175.24	153.35	31.20	55.79
Manaw Thu Kha	8.80	24.84	191.5	150.65	23.02	30.39
long 8	15.7	20.97	110.61	96.05	24.08	36.29
Shwe Thwe Yin	19.4	17.58	75.09	66.18	21.27	27.28
YAU 1214-B-B-B-105-2	14.5	24.63	154.46	131.96	25.645	46.09
YAU 1214-B-B-B-1-1	10.2	22.88	196.17	160.74	27.06	44.37
YAU 1214-B-B-B-1-2	9.20	23.25	227.35	175.00	27.11	43.58
YAU 1214-B-B-B-122-1	9.40	26.86	183.35	134.90	14.705	37.16
YAU 1214-B-B-B-123-1	15.6	24.33	164.75	131.17	13.67	56.14
YAU 1214-B-B-B-33-1	11.2	28.42	150.50	121.80	29.00	41.15
YAU 1214-B-B-B-33-3	11.4	31.07	151.30	116.56	30.37	40.15
YAU 1214-B-B-B-51-1	12	29.19	201.55	135.60	30.53	55.36
YAU 1214-B-B-B-51-2	13.5	30.81	235.35	165.75	27.98	66.16
YAU 1214-B-B-B-53-1	11.7	24.49	174.58	133.90	12.60	37.26
YAU 1214-B-B-B-53-2	12.9	24.32	186.18	150.06	24.24	53.82
YAU 1214-B-B-B-67-1	12.2	23.55	169.71	133.61	26.09	42.52
YAU 1214-B-B-B-67-2	13.9	18.08	75.74	68.75	27.98	26.70
YAU 1215-B-B-B-10-1	14.3	21.95	146.66	107.34	28.335	49.64
YAU 1215-B-B-B-1-1	17.9	23.24	161.17	129.8	22.11	51.28
YAU 1215-B-B-B-110-1	15.2	23.21	140.31	114.66	27.575	47.97
YAU 1215-B-B-B-113-1	16.6	22.99	136.76	109.87	12.605	44.26
YAU 1215-B-B-B-123-1	14	24.95	166.18	124.38	26.92	46.81
YAU 1215-B-B-B-123-3	13.2	24.71	150.19	119.17	26.08	49.49
YAU 1215-B-B-B-124-1	13.9	24.45	148.14	128.78	26.36	47.18
YAU 1215-B-B-B-133-1	11	22.29	137.10	116.4	30.68	39.32
YAU 1215-B-B-B-134-1	12.1	37.3	168.41	138.59	29.575	48.72
YAU 1215-B-B-B-135-3	11.4	26.47	161.08	133.62	27.605	42.13
YAU 1215-B-B-B-137-3	12.6	23.7	182.45	149.65	26.52	50.01
YAU 1215-B-B-B-138-3	14.0	21.77	106.90	95.635	27.115	36.00
YAU 1215-B-B-B-139-1	13.6	25.91	115.96	96.075	30.545	39.87
YAU 1215-B-B-B-139-3	14.6	22.97	117.84	89.24	27	34.52
YAU 1215-B-B-B-140-1	14.9	25.95	116.66	98.45	30.865	45.23
YAU 1215-B-B-B-141-3	15.5	24.15	101.54	88.435	31.515	43.64
YAU 1215-B-B-B-153-1	13.9	24.79	167.59	131.90	26.08	46.64
YAU 1215-B-B-B-156-1	19.2	23.90	147.15	114.24	14.195	62.30
YAU 1215-B-B-B-168-1	13.7	27.04	146.47	118.17	33.44	54.06

YAU 1215-B-B-B-181-1	17.1	22.3 9	125.3 8	105.8 2	30.00 5	54.62
YAU 1215-B-B-B-193-3	11.5	25.1 4	191.0 8	147.5 5	26.29	44.34
YAU 1215-B-B-B-197-1	11.8	23.2 1	174.5 8	147.0 1	30.56 5	53.36
YAU 1215-B-B-B-197-2	16.2	24.1	147.1 5	116.7	12.70 5	47.63
YAU 1215-B-B-B-197-3	14.8	22.9 9	130.0 4	103.8 9	24.98 5	38.45
YAU 1215-B-B-B-52-2	12.9	24.6 3	132.5 5	105.8	31.82 5	44.55
YAU 1215-B-B-B-53-1	17.7	23.7 5	146.7 8	110.7 9	24.41	47.74
YAU 1215-B-B-B-55-1	10.6	22.9 2	167.0 7	133.6 8	25.16	35.61
YAU 1215-B-B-B-63-1	14.1	23.1 5	176.9 7	114.0 9	23.83 5	38.30
YAU 1215-B-B-B-66-1	15.3	20.9 3	112.8 9	95.69	25.97	37.98
YAU 1215-B-B-B-67-1	16.1	22.9 2	149.9 7	123.8 7	25.37	50.80
YAU 1215-B-B-B-67-2	14.0	24.6 7	155.3 4	129.4 3	27.61 5	49.96
YAU 1215-B-B-B-73-3	12.4	20.4 8	123.2 9	101.9 7	27.12	34.47
YAU 1215-B-B-B-76-1	14.0	22.3 0	125.3 3	109.3 1	27.05	41.19
YAU 1215-B-B-B-77-3	13.8	23.6 1	149.5 5	133.4 6	27.35	49.17
YAU 1215-B-B-B-78-1	15.5	24.3 9	140.6 9	127.3 7	28.41	56.60
YAU 1215-B-B-B-91-3	12.8	20.4 6	95.54	85.25	23.24	25.65

PPP=No. of panicles plant<sup>-1</sup>, PL=Panicle length, TGPP=No. of total grains panicle<sup>-1</sup>, FGPP=No. of filled grains panicle<sup>-1</sup>, TSW=1000 seed weight, EYPP=Effective yield plant<sup>-1</sup>

The life span of YAU 1215-B-B-B-138-3 was longer than that of Shwe Thwe Yin (107 days), the early maturity variety in Myanmar. The earliest day to maturity character is preferred to double cropping pattern. Among the tested genotypes, YAU 1215-B-B-B-76-1 possessed the lowest plant height (80.21 cm) but this line was higher than Shwe Thwe Yin (78.05 days). The maximum value (19.20) was found in YAU 1215-B-B-B-156-1 although Shwe Thwe Yin showed more panicles than the latter. For panicle length, YAU 1215-B-B-B-134-1 possessed the best performance (37.30 cm). The panicle length of twelve RILs including YAU 1215-B-B-B-134-1 showed longer than that of Manaw Thu Kha (24.84 cm) possessing the longest panicle length among the checks. YAU 1214-B-B-B-51-2 possessed the highest value (235.35) for grains panicle<sup>-1</sup>. YAU 1214-B-B-B-67-2 showed the lowest value (75.74) which possessed more grains than Shwe Thwe Yin (75.09). For filled grain panicle<sup>-1</sup>, the highest value (175) was found in YAU 1214-B-B-B-1-2 showing more filled grains than Long 6 (153.35), the highest filled grain among tested checks. The maximum value (33.44 g) was found in YAU 1215-B-B-B-168-1 which was heavier seed weight than Long 6, the heaviest seed weight among checks. YAU 1214-B-B-B-51-2 gave the highest yield (66.16 g) for effective yield plant<sup>-1</sup> followed by YAU 1215-B-B-B-156-1 (62.30 g), YAU 1215-B-B-B-78-1 (56.6 g) and YAU 1214-B-B-B-123-1 (56.14 g).

### 3.4. Range, mean, coefficients of variation, heritability and genetic advance for quantitative traits in recombinant inbred lines

The phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all

characters in Table 4. This indicated that the environment had an important role in the expression of these characters. The estimates of PCV were slightly higher than the corresponding GCV estimates for plant height, days to first flowering, days to 100% flowering, days to maturity, 1000 seed weight indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

**Table 4. Parameters estimation of variability for yield and yield components in RILs**

Character	Mean	Min.	Max.	PCV (%)	GCV (%)	H <sub>bs</sub> (%)	GA (%)
Days to first flowering	94.31	85.50	105.5	5.69	5.19	83.22	9.75
Days to 50% flowering	103.43	91.00	115.0	5.23	4.53	75.30	8.11
Days to 100% flowering	107.31	93.00	120.0	4.85	4.77	96.63	9.66
Days to maturity	121.31	107.0	134.0	4.29	4.22	96.63	8.55
Plant height	106.22	78.05	147.7	13.19	13.14	99.29	26.97
Panicles plant <sup>-1</sup>	13.68	8.80	19.40	16.04	11.93	55.35	18.29
Panicle length	24.22	17.58	37.30	12.58	10.32	67.30	17.44
Total grains panicle <sup>-1</sup>	150.68	75.09	235.3	21.15	19.43	84.39	36.77
Filled grains panicle <sup>-1</sup>	121.17	66.18	175.0	17.92	15.19	71.88	26.54
1000 seed weight	25.73	12.60	33.44	9.52	8.54	80.42	15.77
Effective yield plant <sup>-1</sup>	44.71	25.65	66.16	18.12	12.79	49.84	18.60

The traits, number of total grains plant<sup>-1</sup>, number of filled grains plant<sup>-1</sup> and effective yield plant<sup>-1</sup> showed high PCV and GCV estimates that suggested the possibility of yield improvement through selection of these traits in confirmation with earlier report of Padmaja (2008) and Sinha et al. (2004). The broad sense heritability estimates obtained were high for all the characters studied except number of panicle plant<sup>-1</sup>, panicle length and effective yield plant<sup>-1</sup> which recorded medium heritability. High heritability combined with high genetic advance observed for plant height, total grains plant<sup>-1</sup>, no. of filled grains panicle<sup>-1</sup> and 1000 seed weight. Similar result was reported by Padmaja (2008). These characters were controlled by additive gene effects and phenotypic selection for these characters would likely to be effective. Days to first flowering, days to 50% flowering, days to 100% flowering and days to maturity showed high heritability with low genetic advance. These characters may be governed by non-additive gene action. Similar result was reported by Samadia (2005). The characters showing high heritability along with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding.

### 3.5. Correlation coefficient between yield and yield component characters in RILs

Correlation coefficient analysis measures the mutual relationship between various characters and is used to determine the component character on which selection can be done for improvement in yield (Table 5).

**Table 5** Correlation Coefficients between yield and yield component characters in RILs

Cha.	DTFP F	HPF	DT M	PH	PPP	PL	TGPP	FGPP	TSW	EYPP
DFFF	0.74**	0.73**	0.73**	0.01	-0.06	0.17	0.31*	0.29*	-0.14	0.16
DFFPF		0.85**	0.85**	0.0	0.03	0.15	0.35*	0.29*	-0.19	0.27
DTHP F			1.00**	0.03	0.04	0.13	0.38**	0.31*	-0.31*	0.22
DTM				0.03	0.04	0.13	0.38**	0.31*	-0.31*	0.22
PH					-0.24	0.27*	0.15	0.15	0.07	-0.08
PPP							-0.35*	0.56**	-0.28*	0.23
PL								0.51**	0.50**	0.27
TGPP									0.94**	0.37**
FGPP										-0.04
TSW										0.43**
EYPP										0.23

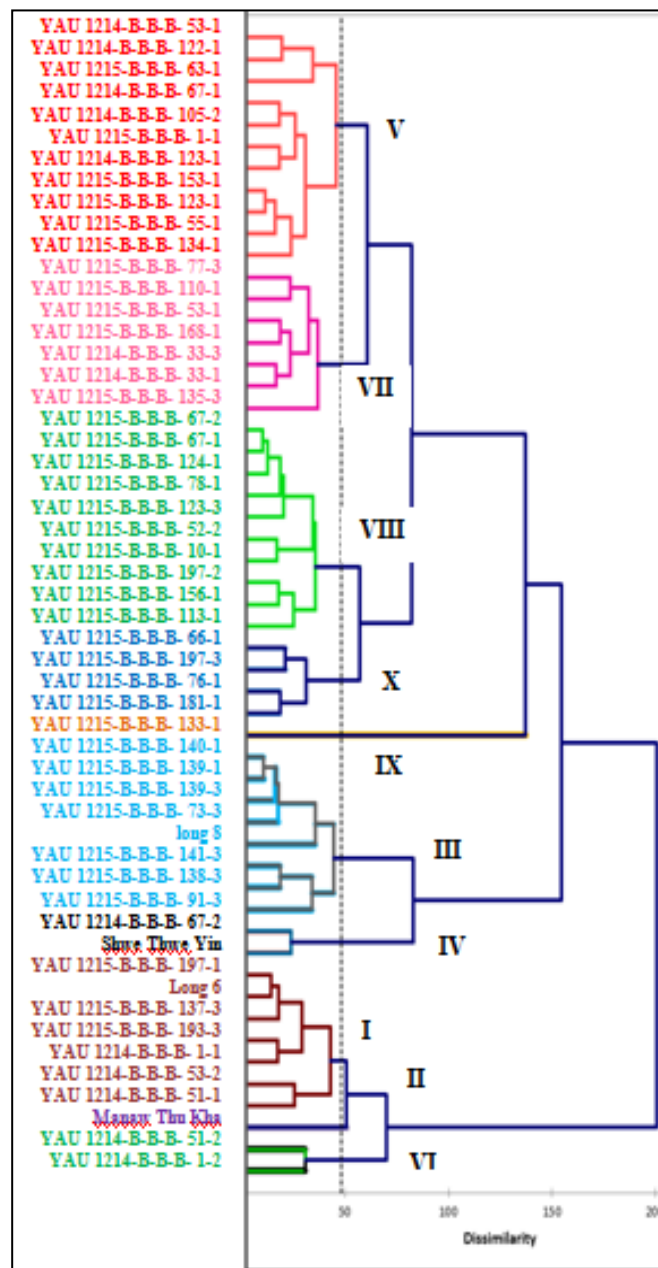
" \*\*\* " Significant at 1% probability level

" \* " Significant at 5% probability level

DFFF=Days to first flowering, DFFPF=Days to 50% flowering, HPF=Days to 100% flowering, DTM=Days to maturity, PH=Plant height, PPP=No. of panicles plant<sup>-1</sup>, PL=Panicle length, TGPP=No. of total grains panicle<sup>-1</sup>, FGPP=No. of filled grains panicle<sup>-1</sup>, TSW=1000 seed weight, EYPP=Effective yield plant<sup>-1</sup> Yield is a complex quantitative trait, greatly influenced by environmental fluctuations. Selection based on yield performance alone may give a biased result and leads to ambiguity. A study of nature and degree of association of component characters with yield assumes greater importance for fixing up characters and selection would be more effective. Effective yield plant<sup>-1</sup> showed significantly positive correlation with, panicle length (0.38\*), number of total grains panicle<sup>-1</sup> (0.37\*\*) and number of filled grains panicle<sup>-1</sup> (0.43\*\*). These results were in accordance with findings of Priya (2017), and Ashok (2015) for, grains per panicle, and panicle length. Number of productive tillers per plant had positive and significant association with grain yield per plant while negative and non-significant association with 1000 grain weight. The results were in unison with Reddy et al. (1997). It indicated that grain yield can be increased whenever there is an increase in characters that showed positive and significant association with grain yield. Hence, these characters can be considered as criteria for selection for higher yield as these were mutually and directly associated with yield.

### 3.6. Cluster analysis based on dissimilarity characters

In cluster analysis, the fifty-three rice genotypes were grouped based on quantitative and qualitative traits as shown in Figure 1.



**Figure 1.** Dendrogram based on quantitative and qualitative characters of fifty-three rice genotypes

There were ten clusters based on dissimilarity of coefficients of fifty-three genotypes. Critical assessment of clusters exposed that clusters were heterogeneous within and between each other based on major character relations. The only one genotype consisting each of cluster II and IX is due to their specific characters. The two genotypes contain in cluster IV and VI. The four genotypes include in only cluster X. The seven genotypes contain in cluster I and VII, eight genotypes in cluster III, and ten genotypes in cluster VIII. Cluster V, the biggest group among clusters, includes the eleven genotypes.

### 4. Conclusion

Among the YAU promising lines derived from bulk population method of selection, YAU 1215-B-B-B-138-3 (112 days), YAU 1215-B-B-B-123-3 (112.5 days) and YAU 1215-B-B-B-91-3 (113.5 days) were identified as the early maturity promising lines although these were older than

Shwe Thwe Yin (107 days). The best mean performances for effective yield plant<sup>-1</sup> were shown in YAU 1214-B-B-B-51-2 (66.16 g) followed by YAU 1215-B-B-B-156-1 (62.3 g) but the life-span of these lines were medium (128-129 days). The germplasm could be tested as replicated trails to confirm the results. Plant height, total grains plant<sup>-1</sup>, no. of filled grains panicle<sup>-1</sup> and 1000 seed weight showed high heritability and high genetic advance. Therefore, progeny selection will be effective to improve these characters. Days to first flowering, days to 50% flowering, days to 100% flowering and days to maturity showed high heritability with low genetic advance. These characters can be exploited through heterotic breeding. According to correlation analysis, panicle length, number of total grains panicle<sup>-1</sup> and number of filled grains panicle<sup>-1</sup> were found to be the main yield contributing traits in rice seed production. In cluster analysis, Rice F7 RILs were grouped as ten clusters according to different genetic background. The diverse groups could be candidates for potential breeding sources for production of climate-friendly cultivars grown on limited resources. Recombinant inbred lines in cluster VI had medium number of panicle plant<sup>-1</sup>, longest panicle length, largest number of total grains plant<sup>-1</sup>, medium 1000 seed weight and highest seed yield were identified as highly valuable sources to be incorporated in rice breeding programs. These lines can also be used for selection of high yielding cultivars with desirable traits.

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### Author Profile



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