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RESEARCH ARTICLE

GENETIC VARIATION AND PATH ANALYSIS ON AGRONOMIC TRAITS OF RECOMBINANT INBRED LINES IN RICE (*Oryza sativa* L.).

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Abstract

Genetic variability, heritability of traits, their association and direct and indirect effects on yield are essential for crop improvement. Therefore, forty nine recombinant inbred lines (RILs) were studied to evaluate these parameters, and to select the potential RILs with good agronomic characters among the tested lines. Significant genotypic variation was found in days to first flowering, days to 50% flowering, plant height, panicle length and total grains plant⁻¹. Selection can be done among the RILs for these traits. These characters also showed a small difference between phenotypic coefficient of variation and genotypic coefficient of variation, and had high heritability indicating that the characters were less influenced by environment. Effective yield plant⁻¹ showed significant positive correlation with effective tillers plant⁻¹, number of total grain plant⁻¹ and 1000 grain weight. This showed that direct selection on effective tillers plant⁻¹, number of total grain plant⁻¹, and 1000 grain weight would result yield improvement. The highest and positive direct effect on effective yield plant⁻¹ was found in total grain plant⁻¹ followed by effective tillers plant⁻¹ and 1000 grain weight. Therefore, these three characters should be given priority for yield improvement. According to the heterosis, three RILs such as YAU 1215-B-B-B-168-1, YAU 1215-B-B-B-193-3 and YAU 1215-B-B-B-78-1 should be selected as promising lines.

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Introduction:-

Plant breeders have to develop high yielding cultivars with desirable agronomic traits to meet the required demand for increased population and attend rice self-sufficiency. The development of new genotypes requires some knowledge about the genetic variability presents in the germplasm of the crop to build efficient breeding

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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).

Most important criteria in any crop improvement programme is the selection of genotypes with all possible desirable yield contributing traits (Vanaja and Babu, 2006). In selection methods, bulk method is one of the most popular methods in rice breeding program. Bulk population method of breeding in self-pollinated crop is also known as mass method or population method of breeding. It refers to a species is grown in bulk plot (from F₁ to F₅) with or without selection, a part of the bulk seed is used to grow the next generation and individual plant selection is practiced in F₆ or later generation. In this method duration of bulking may vary from 6-7 to 30 generations.

Bulk method is simple and cheap and involves less work than pedigree selection in the earlier generations. It is necessary to plant large populations to ensure that the best segregates are selected when selection starts. Segregating generations are subjected to another single plant selection step. Fewer records are kept during earlier generations than with pedigree selection. This type of selection is especially carried out with crops which are usually planted at high planting densities, e.g. small grain crops. Bulk population method eliminates undesirable types and increases the frequency of desirable types by artificial selection.

Recombinant inbred lines are one of the useful methods to create the genetic variability. Recombinant inbred lines that during several generations from selfing of progeny from crosses between two divergent parents, due to different recombination of parental genes, are considered as desirable genetic resources for the production of new varieties (Esch *et al.*, 2007). However, multiple or poly genes control traits are difficult to select. Grain yield is a complex trait and is highly influenced by many genetic factors and environmental fluctuations (Prasad *et al.*, 2001). In a plant breeding programme, direct selection for yield could be misleading. Therefore, plant breeders require knowing the relationship between yield and its component characters.

Path coefficient analysis has been widely used in crop breeding to determine the nature of relationships between grain yield and its contributing components, (Kumar *et al.*, 2014). This analysis has been used to define the best criteria for selection in biological and agronomic studies (Mishra and Drolson, 1973; Williams *et al.*, 1990). Path coefficient analysis separates the direct effects from the indirect effects through other related characters by partitioning the correlation coefficient (Dixit and Dubey, 1984).

Therefore, to fulfill these requirements, this study was carried out with the following objectives: (1) to evaluate the genotypic variability and heritability of rice recombinant inbred lines based on agro-morphological traits and (2) to find out the direct and indirect effects of yield component characters to yield, and (3) to select the potential recombinant inbred lines with good agronomic characters among the tested lines.

Materials and Methods:-

Experimental site:-

The experiment was conducted in the research field of Department of Plant Breeding, Physiology and Ecology, Yezin Agricultural University, Yezin, Nay Pyi Taw, Myanmar from 2016 (monsoon season).

Experimental materials:-

The experimental materials consisted of 36 recombinant inbred lines derived from a cross of Long 8 which is a tall, medium maturing and high yielding variety with Shwe Thwe Yin which is a semi-dwarf, early maturing and high yielding rice variety, and 13 recombinant inbred lines derived from a cross of Long 6 which is a tall, medium maturing and high yielding variety with Shwe Thwe Yin. The RILs population which comprised of 49 individuals was developed using bulk population method. The 49 individuals, their parents and one check variety (Manaw Thu Kha) were used in this study (Table 6).

The rice genotypes were raised in a randomized complete block (RCB) design with three replications. Each plot consisted of ten rows, each row 2.3m long adopting a spacing of 25.4 cm × 25.4 cm. The fully five-leaf aged seedlings were transplanted from nursery to the plots with a single seedling per hill.

Data collection:-

The data were collected in each of the genotypes for each replication. The nine agronomic characters, days to first flowering, days to 50% flowering, plant height, effective tillers plant⁻¹, panicle length, total grain plant⁻¹, filled grain %, 1000 grain weight, and effective yield plant⁻¹, were recorded by the Standard Evaluation System for Rice (IRRI, 2002) in this study.

Statistical analysis:-

The data were statistically analyzed according to STAR 2014 for simple analysis of variance, correlation and path analysis.

Estimation of genetic parameters:-

The phenotypic and genotypic coefficients of variation were computed by the formula suggested by (Singh and Chaudhary, 1985).

$$\text{Genotypic coefficient of variation (GCV \%)} = \frac{\sqrt{\sigma_G^2}}{\bar{x}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV \%)} = \frac{\sqrt{\sigma_P^2}}{\bar{x}} \times 100$$

where,

$$\sigma_P^2 = \text{Phenotypic variance}$$

$$\sigma_G^2 = \text{Genotypic variance}$$

$$\bar{x} = \text{Grand mean}$$

Estimation of heritability:-

Heritability in broad sense (H_{bs}) was computed by the formula suggested by (Singh and Chaudhary, 1985).

$$\text{Heritability (H}_{bs}) = \frac{\sigma_G^2}{\sigma_P^2}$$

Estimation of heterosis:-

Heterosis was computed by the formula suggested by (Shull, 1914).

$$\text{Standard Heterosis (\%)} = \frac{\text{F1-check variety}}{\text{check variety}} \times 100$$

Results and Discussion:-**Analysis of variances for yield and yield component characters of recombinant inbred lines:-**

The mean squares obtained from the analysis of variance (ANOVA) for yield and yield components of recombinant inbred lines (RILs) are presented along with coefficient of variation (CV%) in Table (1). According to the table shown below, days to first flowering, days to 50% flowering, plant height, panicle length and total grain plant⁻¹ are highly significant. Filled grain %, 1000 grain weight and yield are non-significant. Effective tiller is only significant among them. Therefore, there was much genetic variation among genotypes in days to first flowering, days to 50% flowering, plant height, panicle length, effective tillers plant⁻¹ and total grain plant⁻¹.

Genotypic and phenotypic coefficients of variation and heritability for quantitative traits:-

Different parameters such as the phenotypic variance, genotypic variance, phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV), and heritability estimates for all the characters are presented in Table 2. The genotypic variance was high in days to first flowering, days to 50% flowering, total grain plant⁻¹ and plant height. This indicated that selection can be done in among the RILs for those traits.

The phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all characters. This indicated that the environment had an important role in the expression of these characters. There was a small difference between PCV and GCV estimates for days to first flowering, days to 50% flowering, plant height, panicle length and total grain plant⁻¹ 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. Plant height, effective tillers plant⁻¹, panicle length, total grain plant⁻¹ and 1000 grain weight showed high PCV and GCV estimates. This value is enough scope for selection based on these characters, and the diverse genotypes can be provided materials for a sound breeding program. The broad sense heritability estimates obtained were high for all the characters studied except effective tillers plant⁻¹ and 1000 grain weight which recorded medium heritability. Therefore, it indicated that a predominance of additive gene effect and low environmental variation.

Correlation coefficient between yield and yield component characters:-

Correlation coefficient between yield and yield component characters in rice genotypes were shown in Table 3. 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. Total grain plant⁻¹ was positively and significant correlation with days to first flowering (0.322*), days to 50% flowering (0.387**) and panicle length (0.465**) this showed that the longer days to flowering, the higher number of grain per panicle can get. While negative and significant association with effective tillers plant⁻¹ (-0.356*) was found and this indicated that the lower the effective tillers plant⁻¹, the higher total grain plant⁻¹ will be found.

Days to 50% flowering was positively and significant correlation with days to first flowering (0.733**). The 1000 grain weight, effective tillers plant⁻¹ and plant height were non-significant correlation with all characters. Filled grain % was negatively and significant correlation with total grain plant⁻¹ (-0.474**).

Effective yield plant⁻¹ showed significantly positive correlation with effective tillers plant⁻¹ (0.436**), total grains plant⁻¹ (0.413**) and 1000 grain weight (0.403**). This showed that indirect selection on effective tiller, total grains plant⁻¹, 1000 grain weight will improve grain yield. (Chandra *et al.*, 2009) studied on correlation show that effective tillers plant⁻¹ and 1000 grain weight showed positive and significant association with effective yield plant⁻¹ and also among themselves indicating that simultaneous selection for these characters would result in improvement of yield.

Path analysis in recombinant inbred lines:-

Path analysis revealed that days to first flowering, days to 50% flowering, effective tillers plant⁻¹, panicle length, total grain plant⁻¹, filled grain % and 1000 grain weight had positive direct effect on yield (Table 4 and 5). It means when there is an increase in the performance of these characters; effective yield plant⁻¹ can also increase. However, plant height showed negative effect on yield. Total grain had high positive correlation with yield (1.0359) compared to the other characters. Its direct effect on yield was also positive (2.7731) and higher than its correlation coefficient. The direct effect of the effective tillers plant⁻¹, total grain plant⁻¹ and 1000 grain weight were higher than the indirect effects of the characters so that direct selection can be done for that particular character which had highest direct effect on yield. Hence, utmost importance should be given to this character during selection for single plant yield improvement. Selection of plants on the basis of this trait would certainly lead to improvement in grain yield. Effective tillers plant⁻¹ (1.5868) has positive and direct effect on effective yield plant⁻¹. It means that increase in effective tillers plant⁻¹, effective yield plant⁻¹ can be high and therefore direct selection through this trait will be effective for yield improvement. Filled grain (%) had high positive direct effect on yield (0.3557). This direct influence of this character was a signal of its important role in defining yield. However, these characters had negative association and significant with yield (-4.387). This finding are in agreement with (Gopikannan and Ganesh, 2013), they found that effective tillers plant⁻¹ and filled grain % had high and positive direct effect on grain yield plant⁻¹.

The 1000 grain weight had negative correlation with yield (-0.0247) and positive direct effect on yield (1.0662). The indirect effect of this character via plant height, effective tillers plant⁻¹ and total grain plant⁻¹ were negative. This suggested that the direct selection for 1000 grain weight would likely be effective in increasing yield. Plant height had high negative correlation with yield (-0.0366) and negative direct effect on yield (-0.1305). This means that increasing the plant height will not affect the improvement of effective yield plant⁻¹. Therefore, direct selection on the basic of plant height would not be more effective in improving yield.

The present study observed that days to 50% flowering had high positive correlation with yield (1.1992) and exhibited positive direct effect on yield (0.0604). Panicle length had positive direct effect on yield (0.0803) and highly positive correlated with yield (1.0759). Panicle length had positive indirect effect via on total grain plant⁻¹ and 1000 grain weight toward yield. Therefore, correlation explained the true relationship between the traits and a direct selection of this character would be effective for yield improvement. The residual effect was 0.344 and this indicated

that the contribution of component characters on grain yield was 65.6%, by the seven characters studied in path analysis, the rest 34.4 % was the contribution of other factors, characters not studied.

Estimation of heterosis:-

Standard heterosis was calculated by using Manaw Thu Kha as check variety. In heterosis of effective tillers plant⁻¹, 39 inbred lines were observed positive heterosis and 10 inbred lines were negative heterosis (Figure 1). Among these lines, 22 inbred lines were higher than the check variety. Therefore, YAU 1215-B-B-B-113-1, YAU 1215-B-B-B-168-1 and YAU1215-B-B-B-78-1 were shown highest heterosis for effective tillers plant⁻¹.

In total grain plant⁻¹, 47 inbred lines showed positive heterosis and 2 inbred lines were negative heterosis (Figure 2). The 40 inbred lines showed higher heterosis than the check variety. Among these 40 inbred lines YAU 1214-B-B-B-1-2, YAU 1214-B-B-B-51-1 and YAU 1214-B-B-B-51-2 have highest heterosis for total grain than the other RILs. As a result, all the inbred lines show better performance than the local check variety for effective yield plant⁻¹ except the 4 lines, YAU 1215-B-B-B-55-1, YAU 1215-B-B-B-91-3, YAU 1214-B-B-B- 122-1 and YAU1214-B-B-B- 67-2 (Figure 3). While there were 4 inbred lines with low value of standard heterosis, there were also 4 recombinant inbred lines whose standard heterosis percentage is highest. High standard heterosis percentage means that these RILs have better performance and better vigour than the check variety. These 4 RILs are YAU 1215-B-B-B-168-1 (90%) the one that has the highest standard heterosis %, YAU 1214-B-B-B- 53-1, YAU 1215-B-B-B-78-1 (70%), YAU 1214-B-B-B-51-2, YAU 1215-B-B-B-193-3. These RILs with highest vigour can be selected to be used in further breeding program.

Conclusion:-

As in the present study, days to first flowering, days to 50% flowering, effective tillers plant⁻¹, panicle length and total grain plant⁻¹ were significant and these characters have high genetic variation. Therefore, these traits can be used for selection of yield improvement. The PCV was greater than GCV for all characters. Days to first flowering, days to 50% flowering, plant height, panicle length and total grain plant⁻¹ have a small difference between PCV and GCV indicating that the characters were less influenced by the environment. High heritability such as days to first flowering, days to 50% flowering, plant height, panicle length and total grain plant⁻¹ suggest high components of heritable portion of variation that can be exploited by breeders in the selection of superior genotype on the basis of phenotypic performance. Medium heritability observed in effective tillers plant⁻¹ indicates greater role of environment on the expression of this trait. Therefore direct selection for these traits will be ineffective.

Among the agronomic traits, effective tillers plant⁻¹, total grain plant⁻¹ and 1000 grain weight are significantly and positively correlated with effective yield plant⁻¹. The higher in effective tillers plant⁻¹, total grain plant⁻¹, 1000 grain weight and effective yield plant⁻¹ can also be increased. Therefore, progeny selection among these traits can also be effective for yield improvement. From the view of path analysis, The 1000grain weight and effective tillers plant⁻¹ are high positive direct effect on yield; this positive direct effect show that indirect selection on these traits leads to yield improvement.

For effective tiller per plant⁻¹, YAU1215-B-B-B-113-1, YAU1215-B-B-B-168-1 and YAU1215-B-B-B-78-1 showed the higher standard heterosis among the RILs. YAU1214-B-B-B-1-2, YAU1214-B-B-B-51-1 and YAU1214-B-B-B-51-2 have the higher heterosis for total grain plant⁻¹. The four highest RILs for heterosis of effective yield plant⁻¹ were found in YAU1215-B-B-B-55-1, YAU1215-B-B-B-91-3, YAU1214-B-B-B- 122-1 and YAU1214-B-B-B- 67-2. These lines should be selected as promising lines due to higher heterosis than Manaw Thu Kha check variety.

Table 1:- Mean square for agronomic characters of rice recombinant inbred lines derived from bulk:-

Source	d.f.	FFW	HFS	PH	EffTill	PL	TG	FGP	TSW	YLD
Replications	1	2.000 ^{ns}	34.327 ^{ns}	115.650 ^{ns}	17.153 ^{ns}	6.055 ^{ns}	248.295 ^{ns}	24.282 ^{ns}	30.800 ^{ns}	47.018 ^{ns}
Treatments	48	57.495 ^{**}	58.434 ^{**}	454.421 ^{**}	9.417 [*]	18.564 ^{**}	1987.217 ^{**}	62.192 ^{ns}	18.008 ^{ns}	126.310 ^{ns}
Error	48	9.646	14.077	101.246	5.461	6.073	376.150	56.691	11.731	112.203
CV		3.291	3.618	9.251	17.094	10.099	12.784	9.303	12.375	23.498

"**" and "ns" Significant at 1% probability level and Non-significant

FFW= days to first flowering, FPF= days to 50% flowering, PH= plant height, EffTill= effective tiller plant⁻¹, PL= panicle length, TG= total grain plant⁻¹, FGP= filled grain%, TGW= 1000 grain weight, YLD= effective yield plant⁻¹

Table 2:- Genetic viability for yield and yield related characters of recombinant rice inbred lines

	Days to first flowering	Days to 50% flowering	Plant height	Effective tiller plant ⁻¹	Panicle length	Total grain plant ⁻¹
σ^2_G	23.925	22.179	176.587	1.978	6.246	805.534
σ^2_P	28.748	29.217	227.210	4.708	9.282	993.609
PCV %	5.682	5.213	13.858	15.872	12.485	20.778
GCV %	5.183	4.542	12.217	10.286	10.242	18.708
H	0.832	0.759	0.777	0.420	0.673	0.811

Table 3:- Phenotypic correlation coefficients of yield and yield related characters of rice recombinant inbred lines

	HFS	PH	EffTill	PL	TG	FGP	TSW	YLD
FFW	0.733 ^{**}	-0.030	-0.129	0.190	0.322 [*]	-0.173	-0.018	0.100
HFS		-0.103	-0.043	0.144	0.387 ^{**}	-0.269	0.043	0.222
PH			-0.171	0.122	-0.053	0.103	0.185	-0.067
EffTill				-0.256	-0.356 [*]	0.096	-0.210	0.436 ^{**}
PL					0.465 ^{**}	-0.228	0.206	0.239
TG						-0.474 [*]	0.023	0.413 ^{**}
FGP							-0.004	0.052
TSW								0.403 ^{**}

"**" and "*" Significant at 1% and 5% probability level respectively

FFW= days to first flowering, FPF= days to 50% flowering, PH= plant height, EffTill= effective tillers plant⁻¹, PL= panicle length, TG= total grain plant⁻¹, FGP= filled grain%, TGW= 1000 grain weight, YLD= effective yield plant⁻¹

Table 4:- Direct and indirect effect of yield components and their correlation with yield of recombinant rice inbred lines

Traits	Effect of Association	Estimate
Days to First Flowering	Direct Effect	0.0181
	Indirect Effect Via 50% Flowering	0.0504
	Indirect Effect Via Plant Height	0.0012
	Indirect Effect Via Effective Tillers	-0.2156
	Indirect Effect Via Panicle Length	0.023
	Indirect Effect Via Total Grains	1.2774
	Indirect Effect Via Fill Grain Percent	-0.3505
	Indirect Effect Via 1000 Grain Weight	0.1933
	Total Effect	0.9973
Days to 50% flowering	Indirect Effect Via First Flowering	0.0152
	Direct Effect	0.0604
	Indirect Effect Via Plant Height	0.0163
	Indirect Effect Via Effective Tillers	0.0335

	Indirect Effect Via Panicle Length	0.0157
	Indirect Effect Via Total Grains	1.3764
	Indirect Effect Via Fill Grain Percent	-0.6065
	Indirect Effect Via 1000 Grain Weight	0.2883
	Total Effect	1.1992
Plant Height	Indirect Effect Via First flowering	-0.0002
	Indirect Effect Via 50% Flowering	-0.0076
	Direct Effect	-0.1305
	Indirect Effect Via Effective Tillers	-0.5249
	Indirect Effect Via Panicle Length	0.0068
	Indirect Effect Via Total Grains	0.0384
	Indirect Effect Via Fill Grain Percent	-0.0442
	Indirect Effect Via 1000 Grain Weight	0.6255
	Total Effect	-0.0366
Effective Tillers	Indirect Effect Via First Flowering	-0.0025
	Indirect Effect Via 50% Flowering	0.0013
	Indirect Effect Via Plant Height	0.0432
	Direct Effect	1.5868
	Indirect Effect Via Panicle Length	-0.018
	Indirect Effect Via Total Grains	-1.665
	Indirect Effect Via Fill Grain Percent	0.1104
	Indirect Effect Via 1000 Grain Weight	-0.4253
	Total Effect	-0.3692

Table 5:- Direct and indirect effect of yield components and their correlation with yield of recombinant rice inbred lines

Traits	Effect of Association	Estimate
Panicle Length	Indirect Effect Via First Flowering	0.0052
	Indirect Effect Via 50% Flowering	0.0118
	Indirect Effect Via Plant Height	-0.0111
	Indirect Effect Via Effective Tillers	-0.3558
	Direct Effect	0.0803
	Indirect Effect Via Total Grains	1.1718
	Indirect Effect Via Fill Grain Percent	-0.4496
	Indirect Effect Via 1000 Grain Weight	0.6232
	Total Effect	1.0759
Total Grains	Indirect Effect Via First Flowering	0.0084
	Indirect Effect Via 50% Flowering	0.03
	Indirect Effect Via Plant Height	-0.0018
	Indirect Effect Via Effective Tillers	-0.9528
	Indirect Effect Via Panicle Length	0.0339
	Direct Effect	2.7731
	Indirect Effect Via Fill Grain Percent	-0.6639
	Indirect Effect Via 1000 Grains Weight	-0.191
Total Effect	1.0359	
Filled Grain %	Indirect Effect Via First Flowering	-0.0179
	Indirect Effect Via 50% Flowering	-0.103
	Indirect Effect Via Plant Height	0.0162
	Indirect Effect Via Effective Tillers	0.4925
	Indirect Effect Via Panicle Length	-0.1015
	Indirect Effect Via Total Grains	-5.1755
	Direct Effect	0.3557
	Indirect Effect Via 1000 Grain Weight	0.1465
Total Effect	-4.387	

1000 Grain Weight	Indirect Effect Via First Flowering	0.0033
	Indirect Effect Via 50% Flowering	0.0163
	Indirect Effect Via Plant Height	-0.0766
	Indirect Effect Via Effective Tillers	-0.633
	Indirect Effect Via Panicle Length	0.047
	Indirect Effect Via Total Grains	-0.4968
	Indirect Effect Via Fill Grain Percent	0.0489
	Direct Effect	1.0662
	Total Effect	-0.0247
	Residual Effect	0.3442

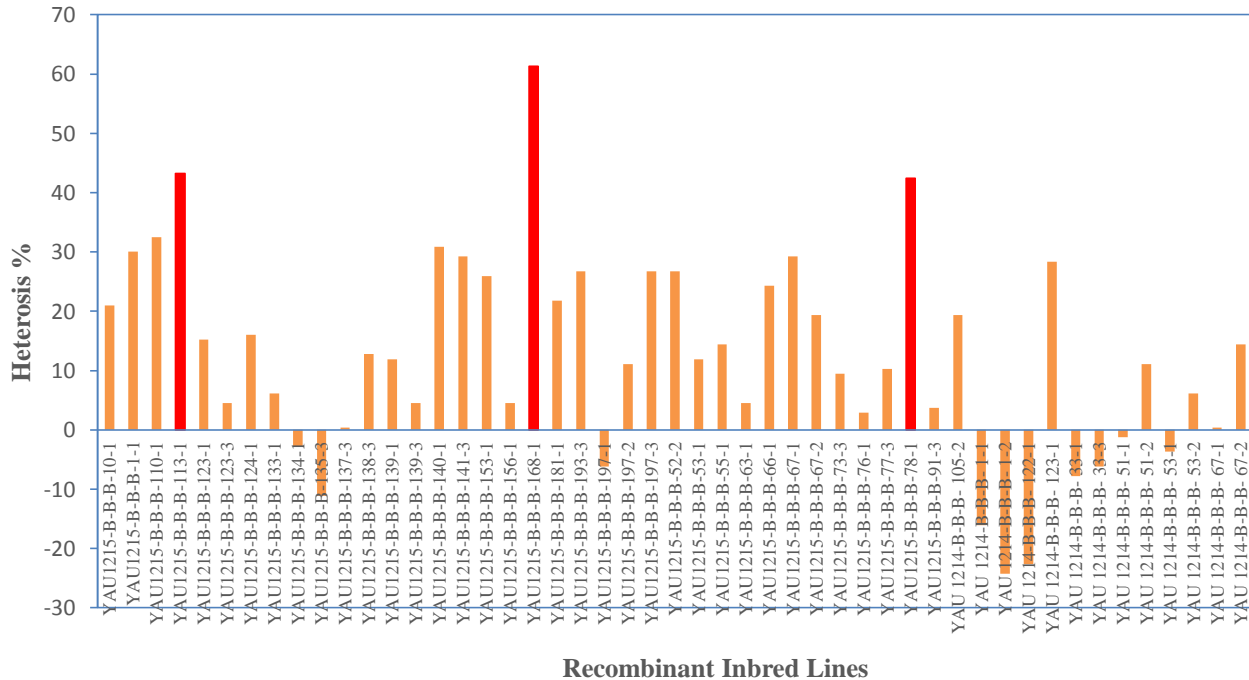


Figure 1:- Heterosis of effective tillers plant⁻¹ in recombinant inbred lines compared with check variety (Manaw Thu Kha)

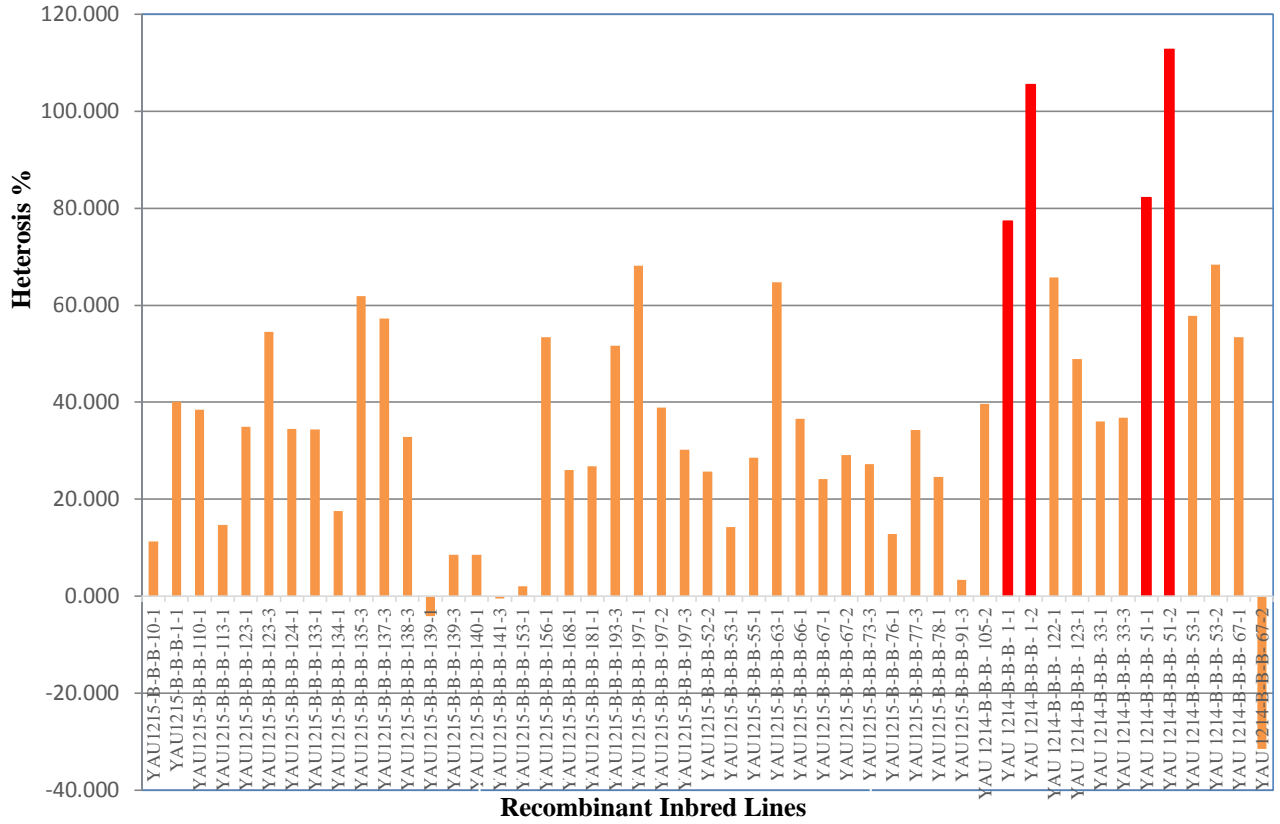


Figure 2:- Heterosis of total grain plant⁻¹ in recombinant inbred lines compared with check variety (Manaw Thu Kha)

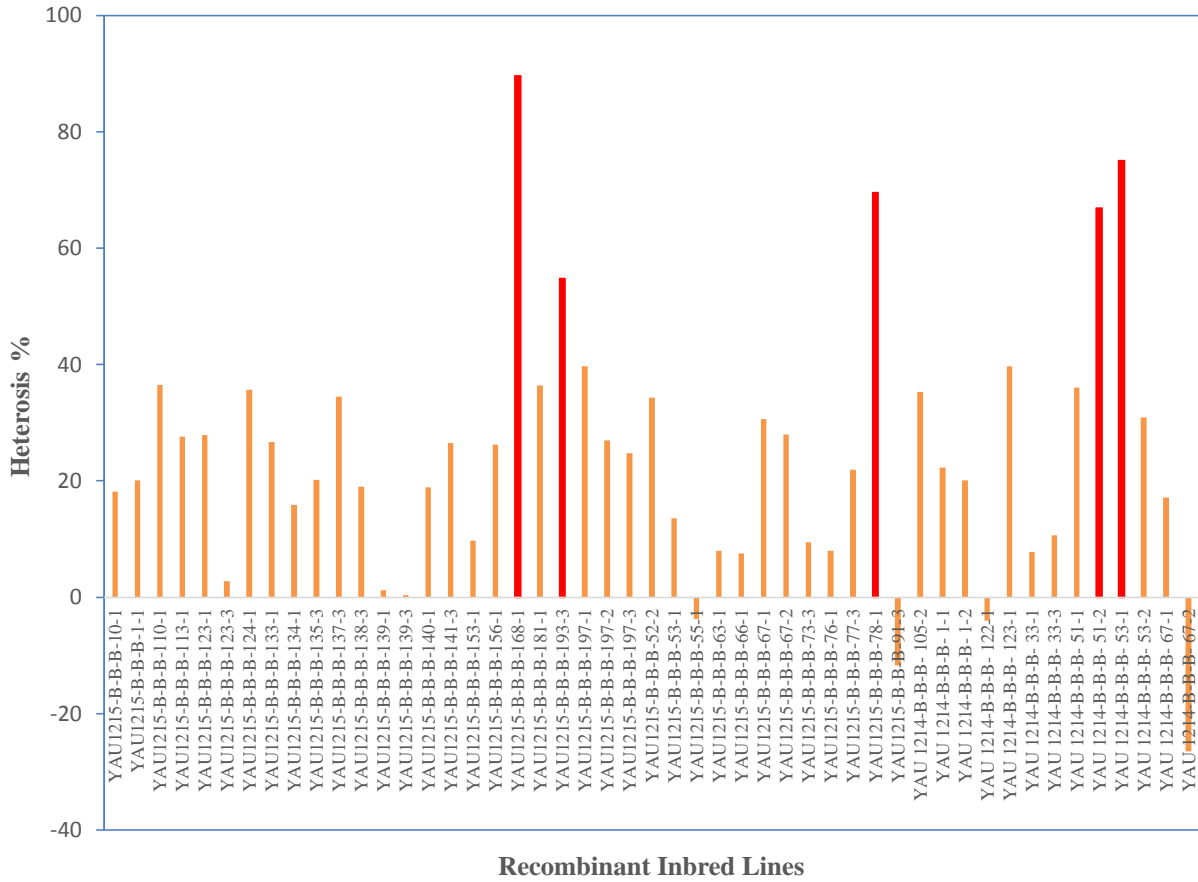


Figure 3:- Heterosis of effective yield plant⁻¹ in recombinant inbred lines compared with check variety (Manaw Thu Kha)

Table 6:- List of fifty-three rice genotypes and their original sources

No.	Genotypes	Source	Remarks
1	Long 6	DAR	R line
2	Manaw Thu Kha	DAR	High yielding variety
3	Long 8	DAR	R line
4	Shwe Thwe Yin	DAR	Early maturity variety
5	YAU 1214-B-B-B- 105-2	YAU	Breeding lines
6	YAU 1214-B-B-B- 1-1	YAU	Breeding lines
7	YAU 1214-B-B-B- 1-2	YAU	Breeding lines
8	YAU 1214-B-B-B- 122-1	YAU	Breeding lines
9	YAU 1214-B-B-B- 123-1	YAU	Breeding lines
10	YAU 1214-B-B-B- 33-1	YAU	Breeding lines
11	YAU 1214-B-B-B- 33-3	YAU	Breeding lines
12	YAU 1214-B-B-B- 51-1	YAU	Breeding lines
13	YAU 1214-B-B-B- 51-2	YAU	Breeding lines
14	YAU 1214-B-B-B- 53-1	YAU	Breeding lines
15	YAU 1214-B-B-B- 53-2	YAU	Breeding lines
16	YAU 1214-B-B-B- 67-1	YAU	Breeding lines
17	YAU 1214-B-B-B- 67-2	YAU	Breeding lines
18	YAU 1215-B-B-B- 10-1	YAU	Breeding lines
19	YAU 1215-B-B-B- 1-1	YAU	Breeding lines
20	YAU 1215-B-B-B- 110-1	YAU	Breeding lines

21	YAU 1215-B-B-B- 113-1	YAU	Breeding lines
22	YAU 1215-B-B-B- 123-1	YAU	Breeding lines
23	YAU 1215-B-B-B- 123-3	YAU	Breeding lines
24	YAU 1215-B-B-B- 124-1	YAU	Breeding lines
25	YAU 1215-B-B-B- 133-1	YAU	Breeding lines
26	YAU 1215-B-B-B- 134-1	YAU	Breeding lines
27	YAU 1215-B-B-B- 135-3	YAU	Breeding lines
28	YAU 1215-B-B-B- 137-3	YAU	Breeding lines
29	YAU 1215-B-B-B- 138-3	YAU	Breeding lines
30	YAU 1215-B-B-B- 139-1	YAU	Breeding lines
31	YAU 1215-B-B-B- 139-3	YAU	Breeding lines
32	YAU 1215-B-B-B- 140-1	YAU	Breeding lines
33	YAU 1215-B-B-B- 141-3	YAU	Breeding lines
34	YAU 1215-B-B-B- 153-1	YAU	Breeding lines
35	YAU 1215-B-B-B- 156-1	YAU	Breeding lines
36	YAU 1215-B-B-B- 168-1	YAU	Breeding lines
37	YAU 1215-B-B-B- 181-1	YAU	Breeding lines
38	YAU 1215-B-B-B- 193-3	YAU	Breeding lines
39	YAU 1215-B-B-B- 197-1	YAU	Breeding lines
40	YAU 1215-B-B-B- 197-2	YAU	Breeding lines
40	YAU 1215-B-B-B- 197-2	YAU	Breeding lines
41	YAU 1215-B-B-B- 197-3	YAU	Breeding lines
42	YAU 1215-B-B-B- 52-2	YAU	Breeding lines
43	YAU 1215-B-B-B- 53-1	YAU	Breeding lines
44	YAU 1215-B-B-B- 55-1	YAU	Breeding lines
45	YAU 1215-B-B-B- 63-1	YAU	Breeding lines
46	YAU 1215-B-B-B- 66-1	YAU	Breeding lines
47	YAU 1215-B-B-B- 67-1	YAU	Breeding lines
48	YAU 1215-B-B-B- 67-2	YAU	Breeding lines
49	YAU 1215-B-B-B- 73-3	YAU	Breeding lines
50	YAU 1215-B-B-B- 76-1	YAU	Breeding lines
51	YAU 1215-B-B-B- 77-3	YAU	Breeding lines
52	YAU 1215-B-B-B- 78-1	YAU	Breeding lines
53	YAU 1215-B-B-B- 91-3	YAU	Breeding lines

DAR=Department of Agricultural Research, Yezin, Myanmar

YAU= Yezin Agricultural University, Yezin, Myanmar

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