RESEARCH ARTICLE

GENETIC DIVERGENCE FOR YIELD AND ITS COMPONENTS IN MYANMAR LOCAL RICE (*Oryza sativa* L.) GERMPLASM

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Manuscript Info	Abstract
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The experiment was conducted at the Department of Plant Breeding, Physiology and Ecology field, Yezin Agricultural University in Myanmar, 2017 (dry season) to determine the genetic diversity among forty-two local rice genotypes by using cluster and principle components analysis. The field was laid out in a randomized complete block design with three replications. Genotypes showed highly significant difference for all the traits studied, which suggests that the genotypes constitute a pool of germplasm with adequate genetic variability. Five major groups were observed among 42 local rice genotypes based on multivariate analysis. The genotypes within the Cluster V has highest mean value for yield plant^{-1}, spikelet panicle^{-1}, filled grain percent, harvest index, panicle/straw weight ratio, panicle weight, effective tiller^{-1}, and lowest value of straw weight. Therefore, these genotypes should be selected for potential genotypes used in future breeding programs. The maximum inter cluster distances were observed between cluster II and V followed by cluster I and II. Therefore, crosses involving between cluster V and cluster II might exhibit high heterosis for yield and crosses between cluster I and II might exhibit higher heterosis for earliness and dwarf stature. The first three principal components explained 81.627% of the total variations, thus suggesting that traits such as yield per plant, harvest index, panicle/straw weight ratio, panicle weight, filled grain percent, effective tillers hill^{-1} and spikelet panicle^{-1} were the principal discriminatory characteristics. Therefore, the high level of genetic variation and the traits contributing for the variation was identified. Hence these genotypes can be utilized for trait improvement in breeding programs for the traits contributing for major variation.

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Introduction:-
Rice (*Oryza sativa* L.) is one of the most important cereal crops worldwide. Myanmar is one of the centers of origin of cultivated rice (Chang, 1976; Matsuo and Hoshikawa, 1993). As a potential for export, rice is grown extensively around the country of Myanmar. Myanmar is the world's sixth-largest rice-producing country (Wunna *et al.*, 2016). (Yamanaka *et al.*, 2011) also found that many ethnic groups still maintained their preferred landraces which is

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locally adapted, as a good example of on-farm conservation of genetic diversity in Myanmar. Tun *et al.* (2006) indicated that the high genetic diversity could be seen in the materials grown on farms in Myanmar.

The germplasm materials are fully characterized and evaluated for their potential use in breeding programs, effective utilization of germplasms can be enhanced. Evaluation of these germplasms is important to assess their potential as donor parents for the breeding of new varieties with resistant to various abiotic and biotic stresses. The success of any plant breeding programmes largely depends on the existence of diversity among the genotypes (Allard, 1960). Success in recombination breeding depends on the suitable exploitation of genotypes as parents for obtaining high heterotic crosses and transgressive segregants. The crosses between parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981).

Hybridization programme involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene groups of diverse nature (Ranjith *et al.*, 2018). Inclusion of more diverse parents (within a limit) is believed to increase the chances for obtaining stronger heterosis and gives broad spectrum of variability in segregating generations (Joshi and Dhawan, 1966; Anand and Murty, 1968). In addition, crossing in moderately diverse parents also showed maximum heterosis (Chauhan and Singh, 1982).

The divergence can be studied based on multivariate analysis and grouped into various cluster as given by (Spark, 1973). The necessity of principal component analysis (PCA) for measuring the degree of divergence has been established by several investigators in rice and other crops (De *et al.*, 1988; Selvakumar *et al.*, 1989; Pathan *et al.*, 1993). These are considered as the most effective method for qualifying the degree of genetic diversity among the genotypes included in the study. The quantification of divergence among the biological population and assessing the relative contribution of different components to the total divergence at intra and inter-cluster levels have now become possible. Hence, the present investigation was carried out to determine the genetic diversity among forty-two local rice genotypes by using cluster and principle components analysis.

Materials and Methods:-
Forty-two collected rice germplasm was grown in randomized complete block design with three replications at Department of Plant Breeding, Physiology and Ecology field, Yezin Agricultural University, Myanmar in 2017 dry season (Table 1). The spacing was 20 cm × 20 cm with one seedling per hill was planted. Observations were recorded on five randomly chosen plants of each genotype per replication for agronomical traits. Recommended cultural practices were follows whenever needed to obtain optimum performance. The data on days to flowering (days), plant height (cm), effective tillers hill[-1] (no.), panicle weight (g), straw weight (g), panicle/straw weight ratio, panicle length (cm), filled grain percent, spikelet panicle[-1] (no.), 1000 grain weight (g), harvest index, yield plant[-1] (g) were collected according to the Standard Evaluation System for Rice (SES 2013). Analysis of variance (ANOVA) was carried out on the data to assess the genotypic effects for randomized complete blocks design in STAR 2.0.1 (STAR, 2014). Cluster analysis was done by using XLSTAT. The genotypes were grouped into different clusters by using Gower clustering method. Intra and inter-cluster distances and mean performance of the clusters for the characters were also computed.

Table 1. List of local rice genotypes used for the study

No.	Germplasm	Source
1	BaKauk	DaWai, YAU collection
2	BayKyaung	DAR, Seed Bank
3	GaukRa	DAR, Seed Bank
4	KalarGyi	Mon, YAU collection
5	KalarLay	DAR, Seed Bank
6	KuTaungMyoTun	DAR, Seed Bank
7	KhaingShweWar	Myeik, YAU collection
8	KhaoHline	DAR, Seed Bank
9	KhaoLai	DAR, Seed Bank
10	KhaoLamil	DAR, Seed Bank
11	KhaoLan	DAR, Seed Bank
12	KhaoLin	DAR, Seed Bank
13	KhaoLiPaw	DAR, Seed Bank

14	KhaoMaPhut	DAR, Seed Bank
15	KhaoNyoHon	DAR, Seed Bank
16	KhaoPhaLin	DAR, Seed Bank
17	KhaoPiPaung	DAR, Seed Bank
18	KhaoTan	DAR, Seed Bank
19	KhaowaA	DAR, Seed Bank
20	KunLone	DAR, Seed Bank
21	KyweChaeManaing	DAR, Seed Bank
22	LawThawGyi	DAR, Seed Bank
23	LetYoneGyi	DAR, Seed Bank
24	LetYwesin	DAR, Seed Bank
25	LopaZa	DAR, Seed Bank
26	MaeKhalar-5	DAR, Seed Bank
27	MaungPhaLo	DAR, Seed Bank
28	MuyinSaba	DAR, Seed Bank
29	PaDinThuMa	DAR, Seed Bank
30	PhoKawGyi	DAR, Seed Bank
31	PyawtTun	YAU collection
32	SeinGyi	DAR, Seed Bank
33	ShweHinThar	DAR, Seed Bank
34	ShweYinAye	Shan, YAU collection
35	TaTaungPo	DAR, Seed Bank
36	TaungAtBeSaba	DAR, Seed Bank
37	TaungHtakePan	Bago, YAU collection
38	TaungYarSaba	DAR, Seed Bank
39	TinTayar	YAU collection
40	WetSiPhyu	DAR, Seed Bank
41	YarPyae	YAU collection
42	YawShweWar	DaWai, YAU collection

Results and Discussion:-
Analysis of Variance (ANOVA) for agronomic traits of 42 local rice genotypes
The mean squares values due to genotypes were highly significant differences for days to flowering, plant height, effective tillers hill[-1], panicle weight, straw weight, panicle/straw weight ratio, panicle length, filled grain percent, spikelet panicle[-1], 1000 grain weight, harvest index and yield plant[-1] (Table 2). This result indicated that there was the high genetic variability within the genotypes and it would be beneficial for improvement of the crop.

Table 2. Analysis of variance on agronomic traits of 42 local rice genotypes

Source of variation	Replication	Genotypes	Error	CV
Days to flowering	13.883	496.163**	4.309	2.04
Plant height	4.661	1180.33**	9.377	2.40
Effective tillers hill[-1]	0.372	36.129**	1.901	10.55
Panicle weight	0.814	401.813**	8.455	11.16
Straw weight	74.563	6729.992**	88.087	9.48
Panicle/Straw weight ratio	0.003	0.246**	0.003	14.31
Panicle length	3.369	22.613**	2.437	6.76
Filled grain percent	158.030	1222.443**	44.659	11.10
Spikelets panicle[-1]	474.289	2472.382**	173.79	15.35
1000 grain weight	1.211	43.433**	0.452	2.74
Harvest Index	0.0001	0.061**	0.0006	9.77
Yield plant[-1]	20.047	415.924**	8.321	15.72

   * and ** significant at 0.05 and 0.01 level respectively.

Cluster Analysis

Based on the degree of genetic divergence 42 local rice genotypes (Figure 1 & Table 4) were group into five major groups based on multivariate analysis. Cluster V contained the maximum number of genotypes (12). Clusters I, II and IV consisted of eight genotypes. Cluster III consisted of only six genotypes. It could be suggested that hybridization among the genotypes within cluster will not be effective because their genetic content is almost similar. In addition, the genotypes among different clusters could be hybridized to crease a wider genetic variability for yield and other superior traits.
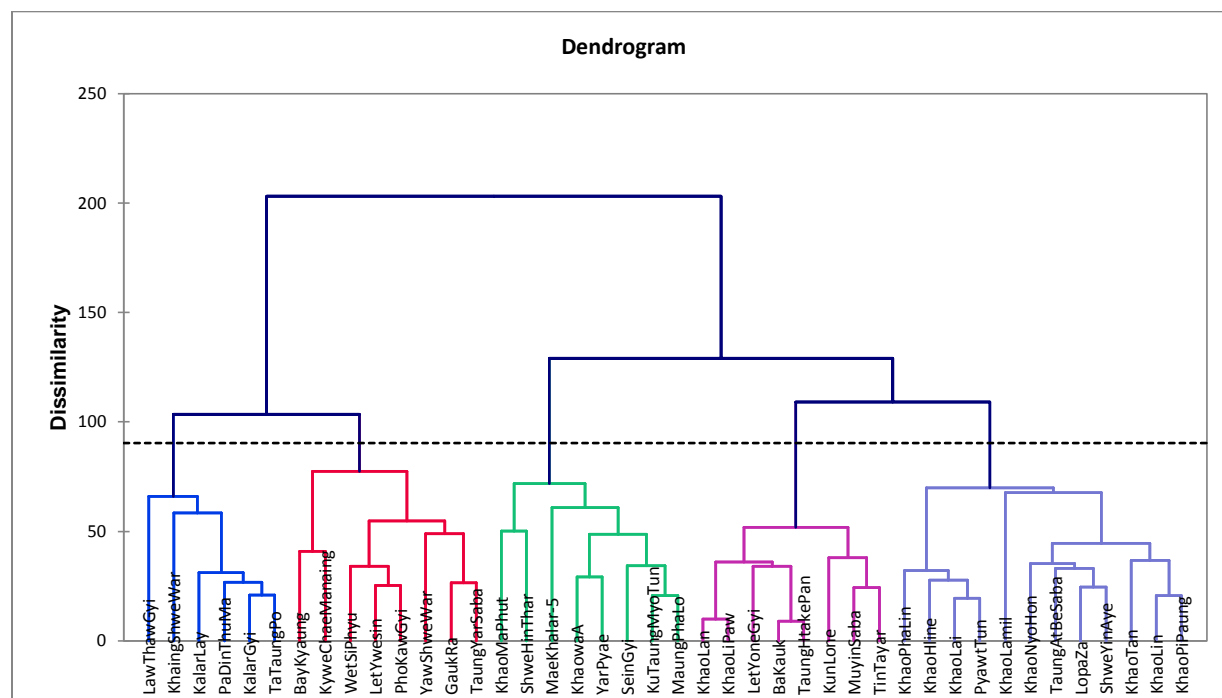

Figure 1. Dendrogram generated by cluster analysis of agronomic characters using complete linkage based on Gower similarity coefficient estimated from 12 agronomic traits analyzed in 42 genotypes

Table 4. Distribution of 42 rice genotypes into different clusters based on 12 agronomic characters

Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
BaKauk	BayKyaung	KalarGyi	KuTaungMyoTun	KhaoHline
KhaoLan	GaukRa	KalarLay	KhaoMaPhut	KhaoLai
KhaoLiPaw	KyweChaeManaing	KhaingShweWar	KhaowaA	KhaoLamil
KunLone	LetYwesin	LawThawGyi	MaeKhalar-5	KhaoLin
LetYoneGyi	PhoKawGyi	PaDinThuMa	MaungPhaLo	KhaoNyoHon
MuyinSaba	TaungYarSaba	TaTaungPo	SeinGyi	KhaoPhaLin
TaungHtakePan	WetSiPhyu		ShweHinThar	KhaoPiPaung
TinTayar	YawShweWar		YarPyae	KhaoTan
				LopaZa
				PyawtTun
				ShweYinAye
				TaungAtBeSaba

The cluster mean values showed a wide range of variations for all the characters (Table 5). Cluster V exhibited highest mean value for yield plant^{-1}, spikelet panicle^{-1}, filled grain percent, harvest index, panicle/straw weight ratio, panicle weight, effective tiller^{-1}, and lowest value of straw weight. Cluster IV contained genotypes with highest mean value for panicle length and 1000 grain weight. Cluster I recorded lowest value for days to flowering and plant height. These clusters are suggested to provide a broad spectrum of variability and the genotypes present in them may be used as parents for future hybridization programme to develop desirable types and creation of further variability for these characters (Mishra and Pravin, 2004).

Table 5. Cluster mean of 12 characters for genetic divergence in 42 rice genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Days to flowering	**87.500**	106.104	113.611	103.583	101.222
Plant Height (cm)	**115.900**	126.844	133.617	154.441	115.124
Effective tillers hill[-1]	13.819	9.500	11.213	13.443	**15.662**
Panicle Weight	23.248	13.165	15.545	31.557	**38.118**
Straw Weight	61.796	169.265	136.247	106.356	**53.401**
Panicle/Straw weight ratio	0.400	0.079	0.116	0.306	**0.742**
Harvest Index	0.279	0.072	0.103	0.230	**0.419**
Panicle Length	20.355	23.945	23.518	**24.706**	23.064
Filled grain percent (%)	67.533	42.949	36.233	62.713	**77.091**
Spikelet panicle[-1]	75.357	45.878	78.824	98.454	**114.750**
1000 grains weight	23.422	25.029	23.903	**27.913**	23.064
Yield plant[-1]	16.498	4.618	7.794	22.884	**30.991**

Average intra and inter-cluster distances have been shown in Table 6. The highest intra-cluster distance was observed in cluster IV (30.860) followed by cluster II (30.826) and cluster V (29.832) indicating wide genetic diversity among the genotypes belonging to these clusters. Therefore, genotypes from these clusters should be given attention for selection of parents for hybridization programme because most of the elite breeding cultivars were included in this cluster. The minimum intra-cluster distance was observed in clusters I and III. Crossing the genotypes of the same cluster showing low values for intra-cluster distance may be low to get good segregants. Therefore, the crosses should be made between the genotypes of clusters separated by large inter-cluster distances (Chandra *et al.*, 2007; Sandhyakishore *et al.*, 2007).

Highest inter-cluster distance was observed between clusters II and V (144.416) suggesting high divergence of genotypes included in these two clusters. Therefore, genotypes belonging to these clusters may be used in hybridization programme for the improvement of rice. Second largest inter-cluster distance was found between cluster I and II. The least inter-cluster distance was observed between clusters II and III (48.405) followed by clusters III and IV (54.362) indicating close relationship between the genotypes of these clusters and hence, may not be emphasized upon to be used in hybridization programme. According to Rahman *et al.* (1997), crossing between highly divergent genotypes would produce a broad spectrum of variability enabling further selection and improvement. Thus, selection of genotypes from these clusters for a crossing programme will produce desirable transgressive segregants. The greater the distance between two clusters the wider the genetic diversity between their genotypes. Therefore, the genotypes from the clusters having maximum inter-cluster distance can be selected to yield superior segregants (Mishra *et al.*, 2003; Chaturvedi and Maurya, 2005). In this study, genotypes from cluster I, II and V can be selected for crossing programme to get desirable transgressive segregants.

Table 6. Intra (diagonal) and inter cluster average distance in rice genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**25.821**	117.328	87.650	66.599	48.421
Cluster II		**30.826**	48.405	92.611	144.416
Cluster III			**26.298**	54.962	106.713
Cluster IV				**30.860**	70.484
Cluster V					**29.832**

Principal Component Analysis

Principal component analysis was done to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson, 1972; Morrison, 1978). It can be also used to determine and identify the selection criteria and also to rank genotypes on the basis of PC scores. The result of PCA explained the genetic diversity among the rice accessions. According to Brejda *et al.*, (2000), the PCA with eigen values >1 and which explained at least 5% of the variation in the data were considered. The PC with higher eigen values and variables, which had high factor loading were considered as best attributes in principal components.

In this study eigen value of >1 found in 3 components and showed cumulative variation of 81.627% to the total variation. Its indicated that the identified characters within these components exhibited immerse influence on the phenotype. The first principle component accounted for 55.596% of the total variation in the rice genotypes (Table

7). Harvest index (0.965) contributed highest to the variation followed by yield per plant (0.939), panicle/straw weight ratio (0.937), panicle weight (0.917), filled grain percent (0.844), effective tillers hill[-1] (0.819), spikelet panicle [-1] (0.782). All other characters contributed negatively to the first component. Second principle component contributed 15.387% of the total variation. Characters that contributed to the component include all characters except filled grain percent that are negatively contributed. The third principle component accounted for 10.644% of the total variation and 1000 grains weight, plant height, harvest index, filled grain percent, panicle/straw weight ratio contributed positively.

Therefore, PCA revealed principle discriminatory characteristics such as yield plant[-1], harvest index, panicle/straw weight ratio, panicle weight, filled grain percent, effective tillers hill[-1] and spikelet panicle[-1], in diverse PCs which are responsible for the observed genotypic variation within a group of genotypes. Important characters coming together in different PCs have tendency to remain together, which may be kept into consideration during utilization of these characters in breeding programme to bring about rapid improvement for yield and other associated traits. Such result indicated that these seven characters contributed maximum towards divergence. It is interesting that the greater divergence in the materials under study was due to these seven characters, which will offer a good scope for improvement of yield through rational selection of parents.

Table 7. Eigen value, contribution of variability and factor loading for the principal component axis in rice genotypes

	F1	F2	F3	F4	F5
Eigenvalue	6.671	1.846	1.277	0.625	0.548
Variability (%)	55.596	15.387	10.644	5.210	4.570
Cumulative %	55.596	70.982	81.627	86.836	91.407
	Factor loadings value				
Days to flowering	-0.295	0.507	-0.646	-0.426	-0.134
Plant Height (cm)	-0.430	0.731	0.233	-0.163	0.305
Effective tillers hill[-1]	0.819	0.036	-0.203	0.142	0.279
Panicle Weight	0.917	0.329	-0.100	0.023	0.109
Straw Weight	-0.856	0.113	-0.299	0.078	0.227
Panicle/Straw weight ratio	0.937	0.008	0.055	-0.041	-0.230
Harvest Index	0.965	0.044	0.111	-0.030	-0.165
Panicle Length	-0.255	0.746	-0.018	0.577	-0.161
Filled grain percent (%)	0.844	-0.083	0.109	-0.038	0.359
Spikelet panicle[-1]	0.782	0.390	-0.118	-0.071	-0.197
1000 grains weight	-0.275	0.385	0.789	-0.218	-0.065
Yield plant[-1]	0.939	0.256	-0.038	-0.026	0.133

Conclusions:-

The agronomic performance of the rice genotypes showed the highly significant differences among the genotypes in respect to all the traits. This indicates that the genotypes constitute a pool of germplasm with adequate genetic variability. Five major groups were observed among 42 local rice genotypes based on multivariate analysis. Cluster V was the largest containing 12 genotypes followed by cluster I, II and IV with 8 genotypes each. The genotypes within the Cluster V has highest mean value for yield plant[-1], spikelet panicle[-1], filled grain percent, harvest index, panicle/straw weight ratio, panicle weight, effective tiller[-1], and lowest value of straw weight. Therefore, these genotypes should be selected for potential genotypes used in future breeding programs.

The maximum distances were observed between cluster II and V. Thereby, considering yield plant[-1], spikelet panicle[-1], filled grain percent, harvest index, panicle/straw weight ratio, panicle weight, effective tiller[-1], crosses involving cluster V and cluster II might exhibit high heterosis for yield. Again, considering growth duration, and plant height, crosses between cluster I and II might exhibit higher heterosis for earliness and dwarf stature. Therefore, the genotypes under cluster I and cluster II, cluster II and cluster V might be selected for future breeding program.

The results of PCA revealed that the three principal components explained 81.627% of the total variations, thus suggesting that traits such as yield per plant, harvest index, panicle/straw weight ratio, panicle weight, filled grain

percent, effective tillers hill^{-1} and spikelet panicle^{-1} were the principal discriminatory characteristics. Therefore, the important characters coming collectively in various PCs and contributing towards explaining the variability and have the tendency to remain together this may be kept into consideration during utilization of these traits in breeding program.

Acknowledgement:-

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