Assessment of variability and Genetic Diversity for Elite Rice (*Oryza sativa* L.) Genotypes of Telangana and Andhra Pradesh

Comment [CC1]: Name of country???

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ABSTRACT

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The current investigation was undertaken with eighteen elite rice genotypes to study the genetic diversity, variability, heritability and genetic advance for yield and yield attributing traits. The ANOVA revealed the significant variability among the genotypes for the traits studied. 1000 seed weight is having highest phenotypic coefficient variation and genotypic coefficient variation (24.882 & 24.835) followed by grain yield per plant (20.315 & 19.523 respectively). Heritability estimates of yield attributing traits ranged from 58.3% (Panicle length) to 99.6% (1000 seed weight). High heritability along with higher genetic advance observed for 1000 seed weight, numbers of productive tillers, plant height and grain yield per plant indicating that selection for these traits would be effective. The diversityanalysis revealed that genotypes were grouped into four clusters, cluster I was the largest comprising 14 genotypes and cluster II with two genotypes followed by Cluster III and IV with one variety each indicating a high degree of divergence among the genotypes.

KEY WORDS: Cluster analysis, Genetic diversity, GCV, Heritability, D^2 statistics.

INTRODUCTION

Comment [CC4]: Back ground of research???

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Rice (oryza sativa L.) is one of the most important leading cereal grain produced, consumed and traded in the world after wheat. It is the staple food crop for more than half of world human populations. India has shown a tremendous increase in its rice production over the past few decades and this trend has continued in recent years. In India, it is grown on around 45.5 m.ha area withestimated production of 124.0 MT during 2022-23 crop seasons (Anonymous, USDA, 2022-23)[1]. Yield enhancement is the vital breeding objective in any rice breeding programmes and knowledge on the nature and magnitude of genetic variation governing the inheritance of quantitative characters like yield and its components is essential for effective genetic improvement. A critical analysis of the genetic variability parameters, namely, genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability and genetic advance for different traits of economic importance is a major pre-requisite for any plant breeder to work with crop improvement programmes.

Comment [CC7]: As a staple food of some Asian countries but yield is low as compare to world why ????

The genetic diversity available in the crop determines the success of any crop improvement programme. Genetic diversity determines the inherent potential of a cross for heterosis and the frequency of the desirable recombinants in the advanced generation. So, genetic distance plays a vital role, as optimum parental diversity is required to obtain superior genotypes in segregating population (Ranjith et al., 2018) [2]. Genetic diversity is very effective to predict potential genetic gain.Hybridization programme involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature, promising hybrid derivatives resulted probably due to complementary interaction of divergent genes in parents.The assessment of divergence in the genotypes is indispensable to know the spectrum of diversity. Improvement in grain yield is normally accomplished through the involvement of genetically diverse parents in breeding programmes. Mahalanobis's D^2 statistics (1936) [3] have been used in several crops, forgrouping genotypes into different clusters based on the magnitude of diversity. It is a multivariate statistical tool used to estimate the diversity and cluster the genotypes based on genetic divergence (Murthy et al., 1965) [4].Further, it also considers the contribution of each trait towards total diversity. Hence, provides the idea about the total genetic divergence among the genotypes with the estimates of inter-cluster and intra-cluster distance (Rathan et al., 2020) [5].This will assist in identifying diverse parents for hybridization programmes by estimating divergence at intervarietal, species and subspecies levels in classifying problems in crop plants (Murthy and Arunachalam 1966, Siddiq et al., 1971 and Rahman, 1997) [6,7,8]. Hence in the current study, 18 elite rice genotypes are evaluated to assess the nature and magnitude of genetic diversity for further utilization in breeding programmes.

Comment [CC8]: Aims & objective of research

MATERIALS AND METHODS

Plant material

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The present study, comprised of eighteen elite rice genotypes includes medium slender and long slender genotypes, which were grown commercially in Telangana and Andra Pradesh India, have high market demand and are in the regular seed chain. Details of the genotypes along with the name of the research centers where the selected genotypes were developed are furnished in Table 1.

Table 1: List of rice genotypes and research centers where they developed and released

Genotypes	Name of the research center
JGL 1798, JGL 3855, JGL 11470, JGL 18047, JGL 11118, JGL 17004 and JGL 24423	Regional Agricultural Research Station, Polasa, Jagtial
KNM 118	Agricultural Research Station, Kunaram, Karimnagar District
RNR 15048, Tellahamsa, RNR 2458 and RNR 2465	Rice Research Unit, Rajendranagar, Hyderabad
WGL 44, Ramappa and WGL 32100	Regional Agricultural Research Station, Warangal
BPT 5204 and MTU 1010	Acharya N. G. Ranga Agriculture University, Bapatla and Maruteru
KPS 2874	Agricultural Research Station, Kamapasagar, Nalgonda District

Field experiments

The Nucleus seeds of selected genotypes obtained from the respective research stations were raised at Seed Research and Technology Center (SRTC), Professor Jayashankar Telangana State Agricultural University, Hyderabad, India (17.3226° N, 78.4172° E and 559 meter above MSL) during kharif, 2018-19.Thirty days old seedlings of each variety were transplanted in 4 rows of 4 meters length with a spacing of 30 cm between rows and 20 cm between plants in a randomized complete block design (RCBD) with three replications. All the necessary precautions and management practices were adopted to maintain a uniform plant population. The observation was recorded for yield and yield attributing traits, namely, days to 50 per cent flowering, productive tillers per plant, 1000 grain weight, plant height, grains per panicle, panicle length, days to maturity and seed yield per plant. The observations on plant height, panicle length, productive tillers per plant and number of filled grains per panicle were recorded from ten randomly selected plants for each entry in each replication. However, days to 50 per cent flowering, days to maturity and grain/seed yield were recorded on plot basis. In contrast, observations for 1000-grain weight were obtained from a random grain sample drawn from each plot in each entry and replication.

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Data Analysis

The data obtained was subjected to standard statistical procedures. Analysis of variance (ANOVA) is used to test the whether significant difference among the treatments or not, by following the procedure of randomized complete block design (RCBD) analysis (Panse and Sukhatme, 1967) [9]. Genotypic and phenotypic co-efficients of variation were computed following the methodology outlined by Burton (1952) [10], while the estimates of heritability and genetic advance were obtained as per the procedures outlined by Burton and Devane (1953) [11] and Johnson et al. (1955) [12] respectively.The D^2 statistics was used to assess the genetic diversity among the 18 elite rice genotypes for eight yield attributing traits, and the procedure was given by C R Rao (1952) [13]. The genotypes were grouped into several different clusters by Tocher's method described by Rao (1952) based on the genetic divergence.

RESULTS AND DISCUSSION

For the crop to be properly described, assessed, and enhanced, genetic variation within the crop is a crucial component. The genotypic variability of any crop is directly correlated with its improvement.Eighteen elite rice genotypes were assessed in light of the potential threat of genetic erosion and the unrestrained introduction of new variations. All rice genotypes shown substantial magnitudes of variance for all the investigated variables are expressed in Table 2.

Table 2. Mean performance for yield and yield attributing traits of elite rice genotypes

Sl. no	Genotypes name	Days to 50% flowering	Days to maturity	Plant height(cm)	Productive tillers	Panicle length(cm)	Grains/ panicle	1000 grain weight (g)	Seed yield/plant (g)
1	**BPT 5204**	112	142	83.6	10.2	20.1	214	13.2	31.3
2	**JGL 11118**	88	118	95.7	10.4	21.6	233	15.2	36.1
3	**JGL 11470**	104	134	82.7	9.7	20.5	279	14.3	35.5
4	**JGL 17004**	72	103	83.7	9.5	20.5	166	13.5	32.6
5	**JGL 1798**	90	120	94.3	8.8	20.1	185	13.7	27.6
6	**JGL 18047**	85	120	88.2	10.3	20.7	191	23.1	49.4
7	**JGL 24423**	89	121	95.5	9.9	22.0	236	23.5	49.1
8	**JGL 3855**	99	129	90.0	10.9	20.6	201	13.7	46.4
9	**KNM 118**	91	121	99.2	11.0	21.0	182	21.5	48.1
10	**KPS 2874**	101	131	91.4	10.1	19.9	256	13.5	53.5
11	**MTU 1010**	92	121	86.9	9.6	19.5	183	23.9	36.5

12	**Ramappa**	95	123	98.0	9.9	20.8	231	14.9	44.3
13	**RNR 15048**	93	123	94.5	10.5	21.8	256	12.5	35.1
14	**RNR 2458**	93	129	90.5	10.1	20.3	227	14.7	43.2
15	**RNR 2465**	100	130	89.3	10.2	21.8	207	14.5	47.1
16	**Tellahamsa**	90	121	90.1	8.0	20.8	174	21.5	37.6
17	**WGL 32100**	101	132	97.4	9.4	20.7	176	13.3	33.0
18	**WGL 44**	105	132	89.1	9.9	21.9	198	12.5	29.5
Mean		**94**	**125**	**91.1**	**9.9**	**20.8**	**211**	**16.3**	**39.8**
Range		72-112	103-142	82.7-99.2	8.0-11.0	19.5- 22.0	166-279	12.5-23.9	27.6-53.5
S.E.		0.773	0.9	0.47	0.266	0.29	10.1	0.44	1.29
C.V.		1.4	1.2	0.9	4.6	2.4	8.3	4.7	5.6
C.D. 5%		2.22	2.62	1.36	0.76	0.84	29.31	1.28	3.71
C.D. 1%		2.98	3.51	1.83	1.02	1.13	39.35	1.73	4.98

Morphological variability

The mean values of eight morphological features examined for eighteen elite genotypes were shown in Table 1. The rice genotype JGL 11470 (82.7 cm) was found to be the shortest, and KNM 118 to be the tallest (99.1 cm). Abbasi et al. (1995)[14] suggested that reducing plant height could increase the plants' resilience to lodging and lessen the significant yield losses inflicted on by this attribute. Genotype Tellahamsa showed less productive tillers per plant (8), whereas KNM 118 has showed highest (11). Rice grain yield and biomass output are closely related to the number of productive tillers (Tanaka et al., 1966) [15] . It is demonstrating its value in programmes to boost yield. Thegreater number of grains per panicle (279) were observed in JGL 18047; on the other hand, genotype JGL 17004 produced lowest number of grains per panicle. The grain yield per plant varies from 27.6 g (JGL 1798) to 53.5g (KPS 2874) with average of 39.8g. The highest 23.9g of 1000 seed weight were recorded in the MTU 1010 and lowest observed for (12.5g) genotype WGL44.

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The days to maturity to vary from 103 days to 142 days among the studied genotypes. The rice genotype JGL17004 recorded early flowering (72days) and maturity (103 days), whereas genotype BPT5204 locally called samba mashuri showed late flowering (105 days) and maturity(142days), having very long vegetative phase.In the current study, the panicle length was found to vary from 19.5 cm (MTU 1010) to 22.0 cm (JGL 18047), with a mean value of 20.70 cm across the genotypes panel. Singh et al, (2018) [16] suggested, when choosing parents for a rice crop development programme, one factor to take into consideration is the association between various attributes and the manifestation of genetic variance.

Genetic variability, Heritability and genetic advance

ANOVA showed the significant difference for the yield and yield attributing traits among the genotypes (Table 3). A Wide range of variability was observed for days to 50 percent flowering (72-112days), days to maturity (103-142 days), plant height (82.7-99.2cm), number of productive tillers per plant (8.0-11.0), panicle length (19.5- 22.0cm), grain per panicle (166-279), 1000 seed weight (12.5-23.9gm), grain yield per plant (27.6-53.5gm). The greater magnitude of genetic variability in the population provides good opportunities for the selection of traits to obtain the elite genotypes (Lalitha et al., 2019) [17].

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Table 3. Analysis of variance (ANOVA) for yield and its attributing traits in rice

Mean sum of square		**Source of variation**		
		Replications	**Treatments**	**Error**
	D.F	**2**	**17**	**34**
Days to 50 percent flowering		5.65	245.14**	1.79
Days to maturity		3.53	215.95**	2.49
Plant height (cm)		0.31	76.64**	0.68
Number of productive		0.15	1.52**	0.21

tillers per plant				
Panicle length (cm)		0.69	1.62**	0.26
Grain per panicle		579.5	3168.35**	312.06
1000 seed weight (g)		0.48	52.80**	0.60
Grain yield per plant (g)		0.69	186.30**	5.00

*& **significance at 5 & 1per cent probability levels, respectively

The magnitude of the difference between GCV and PCV indicates the extent of environmental influence on a particular trait (Asante et al., (2019) [18]. In the current study, PCV was little greater in magnitude than the corresponding GCV for all the traits studied (Table 4), which showed little influence of environment on the expression of these traits. Similar results are delineated by Rashid et al., (2017) [19] and Gyawali et al., (2018) [20], Lalitha et al., (2019) [16]. PCV ranges from 3.686 to 24.882 and GCV ranges from 2.814 to 24.835. The 1000 seed weight is having highest PCV and GCV (24.882 & 24.835) followed by grain yield per plant (20.315 & 19.523 respectively) indicates that selection for these traits would be effective. The magnitude of difference between PCV and GCV is nearly negligible for the 1000 seed weight and plant height indicating the limited role of the environment in the expression of these traits. The panicle length (2.814) and days to maturity (4.034) have low GCV, which indicates the little scope for improvement of these traits. Similar results were reported by Lalitha et al., (2019) [16], Kumar et al. (2018) [21] and Srujana et al. (2017) [22]. However, days to 50% flowering, plant height, number of productive tillers and grains per panicle showed moderate levels of GCV which argues the considerable scope for genetic improvement of these traits. This result is in line with the reports of Tiwari et al. (2019) [23].

Table 4. Estimation of Variability, Heritability, and Genetic advance as percent mean of mean for yield attributing traits in rice genotypes

Characters	**Range**		**Mean**	**PCV**	**GCV**	**ECV**	H^2_{bs} **(%)**	**GA**
	Mini.	**Maxi.**						
Days to 50 percent flowering	72	112	94	6.551	6.281	1.862	91.9	15.89
Days to maturity	103	142	125	4.470	4.034	1.926	81.4	9.611
Plant height (cm)	82.7	99.2	91.1	9.449	9.342	1.418	97.7	24.384

Number of productive tillers per plant	8.0	11.0	9.9	9.830	8.952	4.060	82.9	21.523
Panicle length (cm)	19.5	22.0	20.8	3.686	2.814	2.381	58.3	5.671
Grain per panicle	166	279	211	15.619	12.554	9.292	64.4	26.639
1000 seed weight (g)	12.5	23.9	16.3	24.882	24.835	1.517	99.6	65.444
Grain yield per plant (g)	27.6	53.5	39.8	20.315	19.523	5.619	92.4	49.530

PCV-Phenotypic coefficient variation, **GCV**- Genotypic coefficient variation, **ECV** - environment coefficient variation, **H^2_{bs} (%) -** Heritability in broad sense**, GA**-Genetic advance as % of Mean (%)

The variability should be heritable for selection to be efficient (Lalitha et al., (2019) [16]. The heritability estimates of yield attributing traits ranged from 58.3% (Panicle length) to 99.6% (1000 seed weight) (Table 4). 1000 seed weight, plant height, grain yield per plant and days to 50% flowering showed high (>90%) heritability compared to other traits. Hossain et al., (2015) [24] also reported similar results for days to 50% flowering and panicle length, Mohsin et al., (2009) [25] for yield traits of wheat.High heritability indicates the predominance of the genetic component in the expression of phenotype and hence the selection is effective for high heritable traits.

The genetic advance as per-cent of mean indicates the genetic gain through selection, which is the prime indication of the effectiveness and success of any selection programme. In the current study, the genetic advance as percent of mean ranged from 5.67% to 65.44%. Genetic advance is higher (>20%) for 1000 seed weight (65.44%), grain yield per plant (49.53%), grains per panicle (26.63%), plant height (24.38%) and number of productive tillers per plant (21.52%), which shows the presence of additive gene action for this traits.Therefore, selection is effective for the improvement of these traits. The heritability accompanying genetic advance will give a reliable picture of the quantum of genetic enhancement made through phenotypic selection. Higher heritability along with higher genetic advance observed for 1000 seed weight, number of productive tillers, plant height and grain yield per plant renders the selection more effective. Also, it showed the presence of greater additive gene action in the inheritance of these traits. A similar result was reported by Nandan et al., (2010) [26] for panicle weight and single plant yield.

Genetic diversity

The rice genotypes were grouped into four clusters (Fig.1) based on D^2 values such that the genotypes belonging to the same cluster had a smaller divergence than those belonging to different clusters. The distribution of genotypes into four clusters is shown in Table 5. Out of four clusters, cluster I was the largest comprising 14 genotypes and cluster II with two genotypes (BPT 5204, JGL 11470) followed by Cluster III (MTU 1010) and IV (JGL 17004) with one genotype each indicating a high degree of divergence among the genotypes. Similar results of grouping the genotypes into four clusters was reported by Biswash et al., (2016) [27] while studying 15 modern aman genotypes of rice based on the D^2 values (O. sativa L.) and Soe, (2015) [28] and Rathan et al., (2020) [5] reported that the rice genotypes were clustered into seven and five clusters respectively.The average intra and inter cluster D^2 values can be computed from the cluster diagram where the statistical distances among the 18 genotypes were exhibited (Table 6).

Table 5. The grouping of 18 rice genotypes into different clusters by D^2 analysis

Clusters	No. of Entries	Genotypes
I	14	JGL 11118, JGL 1798, JGL 18047, JGL 24423, JGL 3855, KNM 118, KPS 2874, Ramappa, RNR 15048, RNR 2458, RNR 2465, Tellahamsa, WGL 32100, WGL 44
II	2	BPT 5204, JGL 11470
III	1	MTU 1010
IV	1	JGL 17004

Table 6. Average Inter and intra cluster distances of 18 rice genotypes obtained by D^2 analysis using eight yield and yield contributing traits

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	**72.53**	177.10	125.02	184.86
Cluster II		**26.04**	151.56	284.47
Cluster III			**0.0**	149.24
Cluster IV				**0.0**

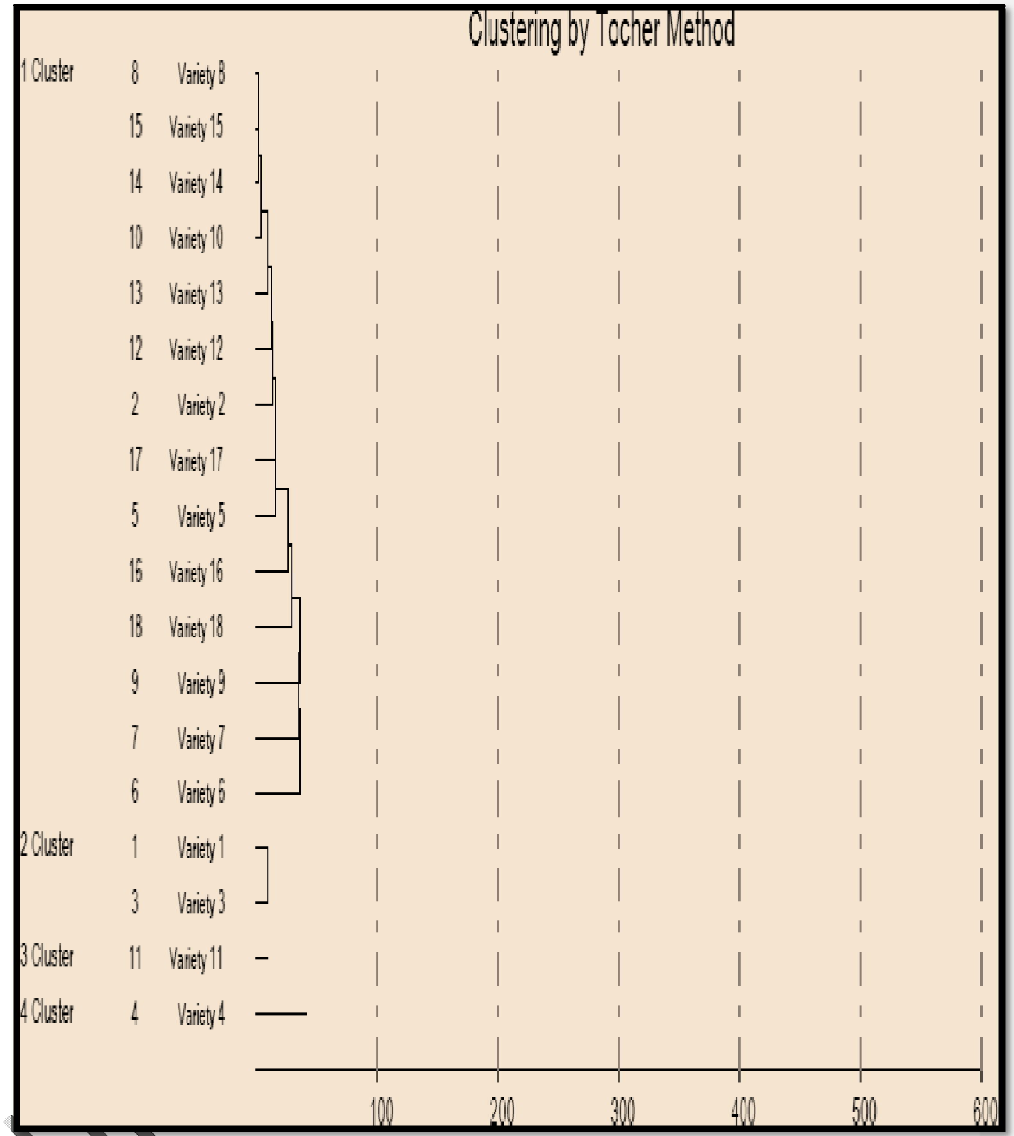

Fig. 1 Cluster Diagram of 18 elite rice genotypes by Tocher method

1- JGL1798, 2- JGL3855, 3- JGL11470, 4- JGL18047, 5- JGL11118, 6- JGL17004, 7- JGL24423, 8- KNM118, 9 - RNR15048, 10- Tellahamsa, 11- RNR2458, 12- RNR2465, 13- WGL44, 14-Ramapa, 15- WGL32100, 16- BPT5204, 17- MTU1010, 18- KPS2874.

The maximum intra cluster distance was observed in cluster I (72.53) with 14 genotypes, followed by cluster II (26.04) with two genotypes, indicating the existence of some genetic divergence among the accessions within clusters. Intra cluster distance for clusters III and IV was zero, since it contains only one genotype each. Rathan et al., (2020) reported similar results among the 24 genotypes of rice studied. From the inter cluster D^2 values of the four clusters, it can be seen that the highest divergence was noticed between clusters II and IV (284.47) followed by clusters I and IV (184.86), clusters II and I (177.1), clusters II and III (151.56) and clusters III and IV (149.24), while the lowest was noticed between clusters I and III (125.02). It is assumed that the maximum amount of heterosis would be manifested in cross combinations of the parents belonging to divergent cluster like clusters II (BPT5204, JGL11470), clusters III (MTU1010) and clusters IV (JGL17004). Similar results were observed by Rajesh et al. (2010) [29] in 29 land- races of rice using Mahalanobis's D^2 statistics for eight quantitative characters. The maximum inter cluster distance was recorded between cluster II (BPT5204, JGL11470) and cluster IV (JGL17004), these genotypes may serve as potential donors for future hybridization programmes. The objective is set for high heterosis not only for yield but also for other characters. The greater the distance between two clusters, the wider the genetic diversity between the accessions. The cluster mean revealed the existence of a considerable difference in the mean values for yield attributing traits (Table 7). The distribution of highest and lowest mean values for different characters in distinct clusters indicated the traits contributing to the total divergence. The percent contributions of each trait towards genetic divergence were presented in Figure 2. The results showed that the contribution of plant height was highest towards genetic divergence (32.68%), followed by 1000 seed weight (31.37%), Days to 50 percent flowering (20.92%), Grain yield per plant (12.42%) The plant height, 1000 seed weight, days to 50% flowering and grain yield per plant contributed 97.39 % towards total divergence. Therefore, these characters should be given importance during parental selection in each clusters for hybridization. Similar results were reported by Prasad et al. (2013) [30] and Rathan et al., (2020) [5]in 37 and 24 accessions of rice (O. sativa L.) respectively.

Table 7. Mean values of eight yield attributing characters of 18 rice genotypes grouped in four clusters

Clusters	DFF	DM	PH	PL	PTP	GPP	TSW	GYP
Cluster I	94.83	125.10	93.08	21.03	9.97	211	16.30	41.48
Cluster II	108.00	137.83	83.13	20.32	10	246.33	13.80	33.46
Cluster III	92.33	121.33	86.86	19.58	9.60	183.33	23.93	36.50
Cluster IV	72.40	102.83	83.67	20.47	9.50	166.00	13.50	32.63

DFF- Days to 50% flowering, **DM**- Days to maturity, **PH**- Plant height, **PL**- Panicle length, **PTP**- Productive tillers per plant, **GPP**- Grains per panicle, **TSW**- Thousand seed weight, **GYP**- Grain yield per plant.

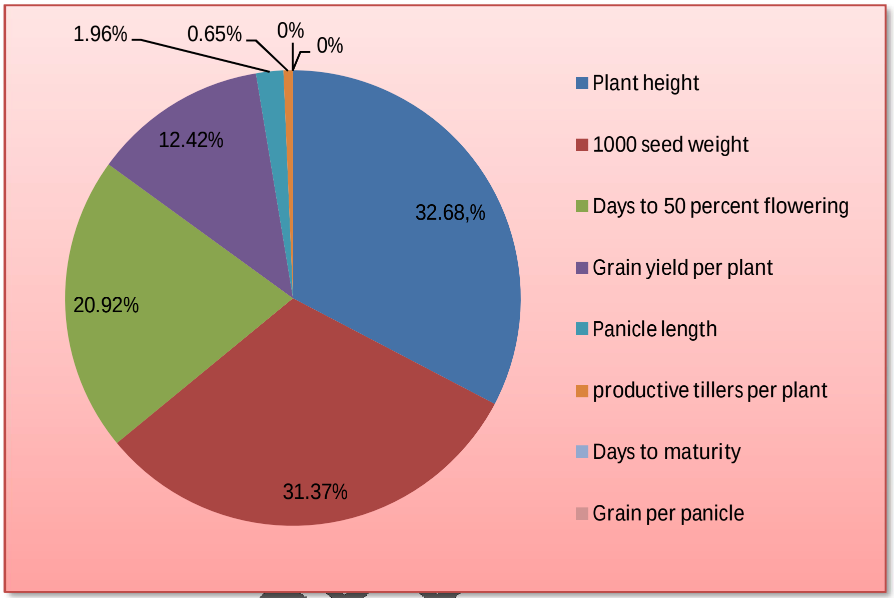

Figure 2. The relative contribution of different characters to genetic diversity

Conclusion

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The ANOVA indicated the significant differences among the rice genotypes for the traits studied. The 1000 seed weight, grain yield per plant, grain yield per panicle, numbers of productive tillers and plant height have high PCV and GCV along with greater heritability and genetic advance. So, these traits can show greater effectiveness during selection. Further, the high variability existed between the genotypes in different clusters for yield and yield attributes. Among all the characters, 1000 seed weight, plant height, days to 50% flowering and grain yield per plant contributed maximum in the towards genetic divergence. The maximum inter-cluster distance was noticed between cluster II and IV, cluster I and IV, cluster II and I, cluster II and III. So, the crosses involving elite genotypes BPT5204, JGL11470, MTU1010, and JGL17004 would certainly be rewarding to isolate desirable recombinants during the hybridization programme.

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