Genetic Divergence and Genetic Variability Assessment of Rice (*Oryza sativa* L.) Genotypes for Yield and its Contributing Traits

Abstract:

For over half the world's population, rice is the primary food. An increasing population requires higher yield levels, which must be achieved. In order to construct breeding strategies and improve production, variability must be created. Fourteen distinct parameters were used to examine genetic variability in ~~40 ~~fortyenhanced rice genotypes.Genotypes exhibited moderate values of GCV and PCV for effective tillers per plant, panicle length, grains per panicle, 1000 grain weight, grain yield per plant, straw yield per plant and L/B ratio and high values for protein content indicating the greater scope of improving these characters by applying judicious selection. High heritability coupled with high genetic advance as per cent mean showed by straw yield per plant, grain yield per plant, grains per panicle, 1000 grain weight and effective tillers per plant indicated higher additive gene action in these traits thus improvement by direct phenotypic selection over the genotypes would be worth it. D^2 statistics was estimated on forty genotypes which revealed generalized distance (D) from 17.54 to 55.25 between five clusters, indicating the presence of vast diversity. Considerable higher intra and inter cluster values revealed a very interesting trend of genetic diversity. The maximum inter cluster distance was found between clusters II and III followed by clusters III and V. Based on cluster analysis inter crossing among the genotypes in distant clusters would produce highly heterotic progenies. Maximum contribution towards the divergence was exhibited by protein content followed by days to 50 per cent flowering and 1000 grain weight.

Comment [NMH1]: L=?, B=?

Key words: Variability, Heritability, Diversity, Rice, Grain yield

Introduction:

For about half of the world's population, rice is the main staple food. Even while high yielding varieties have enabled to improve yield levels significantly in recent years, much needs to be produced to feed the world's expanding population.Varietal adaptation and resilience to biotic and abiotic stresses depend on genetic variation. When there is a high level of genetic variability~~ety~~ among the individuals in the populations, then only selection is effective. The greater diversity in the material, have high~~more the~~ genetic potential and there are better chances of producing desired genotypes. Therefore, variability in the population must be taken into account by plant breeders before initiating an appropriate breeding programme. Breeding tools that measure variation include genetic advancement, heritability and coefficient of variation.Many researchers have emphasized the significance of determining the level of genetic divergence in rice and using that information to choose suitable parents or donors, either to take advantage of hybrid vigour or to produce attractive recombinants (Anand and Murty, 1968). Mahalanobis's D^2 statistics have shown to be a successful technique of measuring genetic divergence within a particular population. Before the hybridization programme is started, D^2 statistics can be utilised to choose the parent combinations without doing crosses (Bhatt, 1970). The stability of D^2 statistics across many environments determines their usefulness. Combination breeding can induce diverse genotypes or collections from various eco-geographical zones may generate them.

Comment [NMH2]: Objectives of the study?

Materials and Methods:

The investigation was carried out with 40 rice~~diverse~~ genotypes during *kharif*, 2021 at Main Rice Research Centre, Navsari Agricultural University, Navsari, Gujarat. The source of seeds is the Main Rice Research Centre,Navsari Agricultural University, Navsari. The genotypes used in the investigation are presented in Table 1. The experimental material was divided into three replications and in which each plot consisted of 12 rows of 3.0 meter length. Each row comprised of 20 plants of single genotype with 20 cm and 15 cm row to row and plant to plant spacing, respectively. The observations were recorded on five randomly selected plants from each genotype in each replication excluding border rows to minimize border effects. The following fourteen characters were studied during the experiment *viz.*, days to 50 per cent flowering, plant height (cm), effective tillers per plant, panicle length (cm), grains per panicle, 1000 grain weight (g), grain yield per plant (g), straw yield per plant (g), hulling percentage (%), milling percentage (%), head rice recovery (%), L/B ratio, amylose content (%) and protein content (%).The amylose content was estimated from each sample as per the simplified colorimetric procedure of Juliano (1971). The nitrogen content was estimated from each sample by Micro-kjeldahl's procedure (Jackson, 1967) and the protein percentage was calculated using the factor 6.25 as multiplier. Variability parameters were estimated according to Dewey and Lu (1959). Theheritabilityinbroadsensewasestimatedaccordingtomethodgivenby allard(1960). Genetic diversity between genotypes wasestimated by using analysis givenby Mahalanobis (1936). For analysis of genetic divergence, the D^2values, grouping and clustering of genotypes were done with the help of INDOSTAT software. Calculation of variance, heritability, genetic advance were done in R-STUDIO and OPSTAT.

Comment [NMH3]: How to divide the rice genotypes to 3 rep.?
It should be "grown with three replication"

Results and Discussion:

Genetic variability:

The analysis of variance was performed to test the differences among genotypes for all the fourteen characters and presented here in Table 2.The mean sum of squares resulting from genotypes were found to be highly significant for all quantitative and qualitative characteristics, according to the results. This show that there is ample scope to generate early, high yielding and lodging resistance materials by applying a judicious selection pressure for specific traits. Similar results for most of characters were also recorded by Meena *et al*. (2015), Ekka *et al*. (2015), Manjunatha *et al*. (2017), Bandi *et al.* (2018), Longjam*et al.* (2019) and Sharma and Jaiswal (2020). The mean values of different genotypes for all the fourteen characters studied, depicting high phenotypic variation, are depicted graphically in Figure 1 (a), 1 (b), 1 (c) and 1 (d).

Comment [NMH4]: Did not find the lodging tolerant traits in data collection.

In present study, on overall basis large phenotypic differences were observed between the minimum and maximum values for all the fourteen traits under study. The wide range of variation obtained may be due to inclusion of divergent genotypes in the present study. The moderate to high as well as closer values of genotypic and phenotypic variance were observed for effective tillers per plant, panicle length, grains per panicle, 1000 grain weight, L/B ratio, grain yield per plant and straw yield per plant indicating higher contribution of genetic components to the total variation. Therefore, these traits could be considered and easily exploited through selection. Bastia *et al.* (2008), Ekka *et al.* (2015) and Patel *et al.* (2018) obtained same kind of results.The ~~higher and~~closer values of phenotypic coefficient of variation (PCV) than the respective genotypic coefficient of variation (GCV) for all the fourteen traits under study indicated ~~the inherent connection between genotypes and phenotypic~~that less environmental influence on the expression of the traits under study.Higher heritability coupled with high genetic advance as per cent mean is observed for protein content, straw yield per plant, grain yield per plant, grains per panicle, 1000 grain weight and effective tillers per plant. This confirmed higher additive gene action and thus improvement could be brought about by direct phenotypic selection over the genotypes. These findings were similar to results by Ekka *et al.* (2015), Gunasekaran *et al.* (2017) and Sharma and Jaiswal (2020).

Comment [NMH5]: Why? Genotype = additive + dominant

Genetic Diversity:

The 40 rice genotypes of rice were grouped into five distinct clusters using Tocher's cluster method.(Table 3).Dendogram is represented in Figure 2. Cluster-I, containing thirty two genotypes, emerged with highest number of genotypes, while clusters-III, IV and V with one genotype contained lowest number of entries. Cluster-II was represented by five genotypes. The discrimination of lines into so many discrete clusters suggested presence of high degree of genetic diversity among the genotypes evaluated.

The intra and inter cluster distances between all possible pairs of five clusters were computed and presented in Table 4 and Figure 3. The analysis revealed that the inter cluster distance (D) ranged from 20.06 to 55.25. The inter cluster distance between cluster-I and cluster-II was found 37.18, while between cluster-I and cluster-III was found 28.81. The inter cluster distance between cluster-I and cluster-IV was 28.30 reported, while it was 36.72 between cluster-I and cluster-V. The inter cluster distance between cluster-II and cluster-III (D = 55.25), cluster-II and cluster-IV (D = 43.20), cluster-II and cluster-V (D = 45.33) was observed. The inter cluster distance between cluster-III with cluster-IV and cluster-V found, 35.00 and 47.94, respectively. The inter cluster distance (D = 20.06) was observed between clusters-IV and V. The maximum inter cluster distance (D = 55.25) was observed between clusters-III and II followed by those between clusters-III and V (D = 47.94) and between clusters-II and V (45.33). The minimum inter cluster distance (D = 20.06) was depicted between cluster-IV and cluster-V.

Comment [NMH6]: What could be done for this result? Discussion?

Analysis of all fourteen characters for genetic divergence indicated that the trait protein content (58.97 %) had maximum contribution towards divergence followed by days to 50 per cent flowering (12.69 %), while the minimum contribution towards divergence was imparted by effective tillers per plant (0.26 %) and straw yield per plant (0.51 %). Plant height, panicle length and milling percentage had nil contribution towards genetic divergence. The results indicated that the traits *viz*., protein content, days to 50 per cent flowering, 1000 grain weight, grains per panicle and amylose content had major contribution towards genetic divergence in the present material (Table 5 and Figure 4).The results were in parity with the findings of Devi *et al*. (2015).Cluster-III had shown highest mean values for effective tillers per plant (10.68), grains per panicle (235.82), milling percentage (73.59) and L/B ratio (2.89). Cluster-I had shown highest values for 1000 grain weight (25.95), grain yield per plant (27.78), straw yield per plant (35.13) and amylose content (23.01). Cluster-V shown lowest mean values for panicle length (14.23), grains per panicle (154.32), grain yield (21.60), hulling percentage (63.22) and L/B ratio (2.16). While cluster-III had shown lowest mean values for days to 50 per cent flowering (76.67), 1000 grain weight (20.02), straw yield per plant (26.06), milling percentage (51.22), protein content (3.11). Similar results reported by Devi *et al.* (2018)and Bekis *et al.* (2021)(Table 6).

Comment [NMH7]: What could be done for this result? Discussion?

Conclusion:

From the analysis of variance (ANOVA), significant variations were observed for all the traits among the genotypes. Significant variation among genotypes showed existence of wide genetic diversity that would provide better scope of selection. The PCV was greater than the GCV for all the characters studied, which indicated that there was less environmental influence on the expression of the characters. High heritability coupled with high genetic advance as per cent mean showed by straw yield per plant, grain yield per plant, grains per panicle, 1000 grain weight and effective tillers per plant indicated higher additive gene action in these traits. Future breeding program can be focused on these traits that would be a milestone for the improvement of rice. Forty genotypes were grouped into five clusters.The maximum inter cluster distance was found between cluster-II and cluster-III followed by cluster-V and cluster-III. The diverse parents must be selected for hybridization purpose from these clusters to have higher heterotic effects.

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Table 1: Name of the rice genotypes used in the present study

Sr. No.	Name of genotypes	Sr. No.	Name of genotypes	Sr. No.	Name of genotypes	Sr. No.	Name of genotypes
1	NVSR-898	11	NVSR-890	21	NVSR-909	31	NVSR-924
2	NVSR-910	12	NVSR-894	22	NVSR-911	32	NVSR-929
3	NVSR-912	13	NVSR-897	23	NVSR-913	33	NVSR-932
4	NVSR-931	14	NVSR-900	24	NVSR-914	34	NVSR-3426
5	NVSR-834	15	NVSR-902	25	NVSR-915	35	NVSR-3437
6	NVSR-835	16	NVSR-903	26	NVSR-916	36	NVSR-3449
7	NVSR-857	17	NVSR-904	27	NVSR-918	37	Gurjari
8	NVSR-859	18	NVSR-906	28	NVSR-919	38	GNR-3
9	NVSR-874	19	NVSR-907	29	NVSR-920	39	GR-17
10	NVSR-889	20	NVSR-908	30	NVSR-922	40	GR-15

Table 2: Analysis of variance (mean sum of square) of experimental design for yield and yield contributing characters in rice

Source	d.f.	Days to 50 per cent flowering	Plant height (cm)	Effective tillers per plant	Panicle length (cm)	Grains per panicle	1000 grain weight (g)	Grain yield per plant (g)
Replication	2	6.81^{**}	123.36	2.60^{*}	34.55^{**}	228.61^{*}	1.17^{*}	46.83^{**}
Genotypes	39	117.77^{**}	219.38^{*}	7.28^{**}	23.38^{**}	2645.03^{**}	37.75^{**}	96.22^{**}
Error	78	0.84	129.88	0.82	3.29	54.73	0.60	9.39

Source	d.f.	Straw yield per plant (g)	Hulling (%)	Milling (%)	Head rice recovery (%)	L/B ratio	Amylose content (%)	Protein content (%)
Replication	2	7.30	2.17	2.59	2.20	0.003	1.52*	0.007
Genotypes	39	146.13**	41.91**	39.83**	30.29**	0.24**	12.86**	8.06**
Error	78	8.91	3.02	3.27	1.75	0.01	0.39	0.02

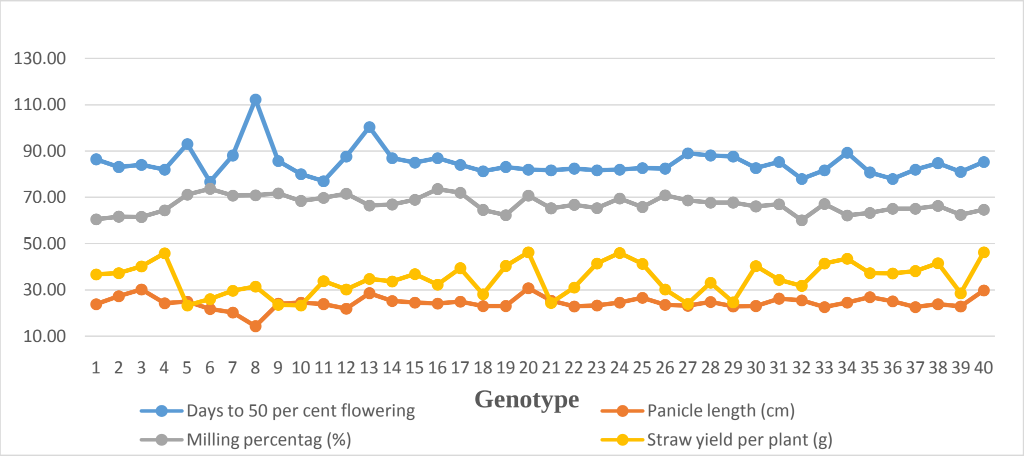


Figure 1 (a): Comparative mean performance of forty genotypes for days to 50 per cent flowering, panicle length (cm), milling percentage (%) and Straw yield per plant (g).

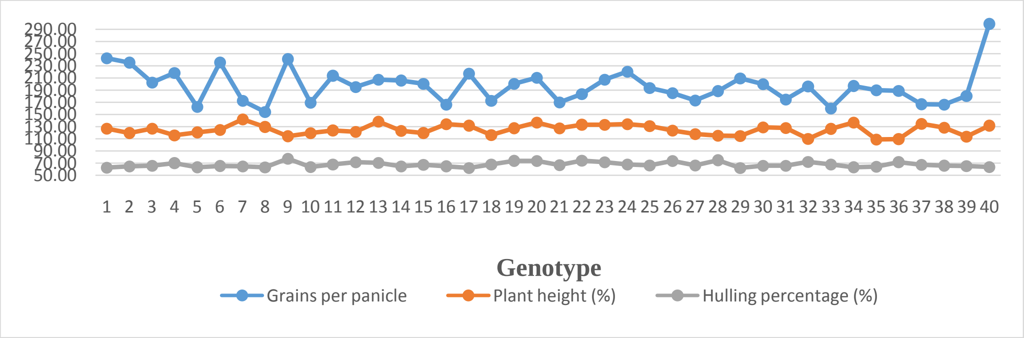


Figure 1 (b): Comparative mean performance of forty genotypes for grains per panicle (g), plant height (cm) and hulling percentage (%).

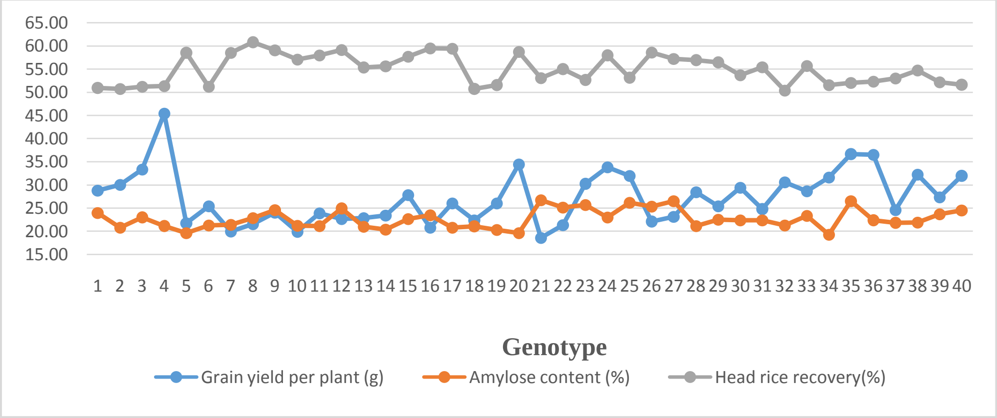


Figure 1 (c): Comparative mean performance of forty genotypes for grain yield per plant (g), amylose content (%) and head rice recovery (%)

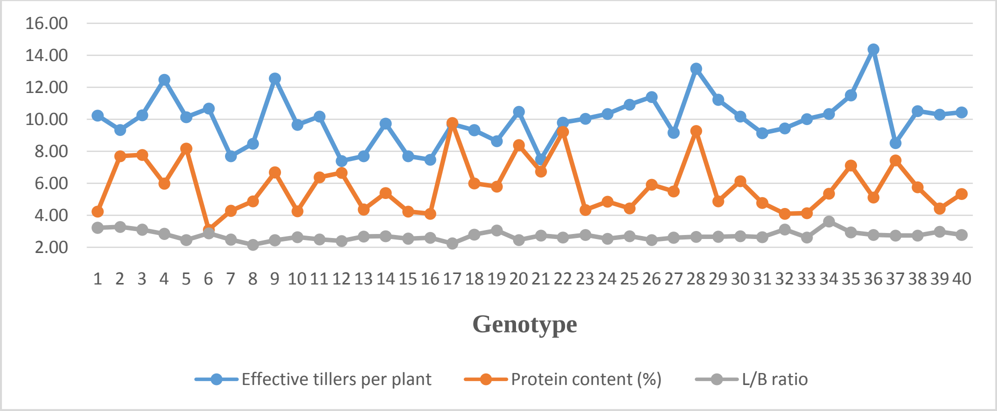


Figure 1 (d): Comparative mean performance of forty genotypes for effective tillers per plant, protein content (%) and L/B ratio.

Table 3: The distribution of forty genotypes of rice into five different clusters based on Mahalanobis's D^2 statistics

Clusters	**No. of genotypes**	**Genotypes**
I	**32**	NVSR-913, NVSR-915, NVSR-902, NVSR-924, NVSR-914, NVSR-932, NVSR-3449, NVSR-929, NVSR-889, NVSR-903, NVSR-857, NVSR-900, NVSR-922, NVSR-907, NVSR-931, GNR-3, NVSR-918, NVSR-920, NVSR-906, NVSR-3426, NVSR-898, GR-

		17, NVSR-916, NVSR-3437, NVSR-890, NVSR-874, GR-15, NVSR-909, Gurjari, NVSR-894, NVSR-910, NVSR-912
II	**5**	NVSR-911, NVSR-919, NVSR-834, NVSR-904, NVSR-908,
III	**1**	NVSR-835
IV	**1**	NVSR-897
V	**1**	NVSR-859

Table 4: Estimation of average intra and inter cluster distances for fourteen characters in forty rice genotypes

Clusters	**I**	**II**	**III**	**IV**	**V**
I	**20.74**	37.18	28.81	28.30	36.72
II		**17.54**	55.25	43.20	45.33
III			**0.00**	35.00	47.94
IV				**0.00**	20.06
V					**0.00**

Bold figures indicate the intra cluster distances

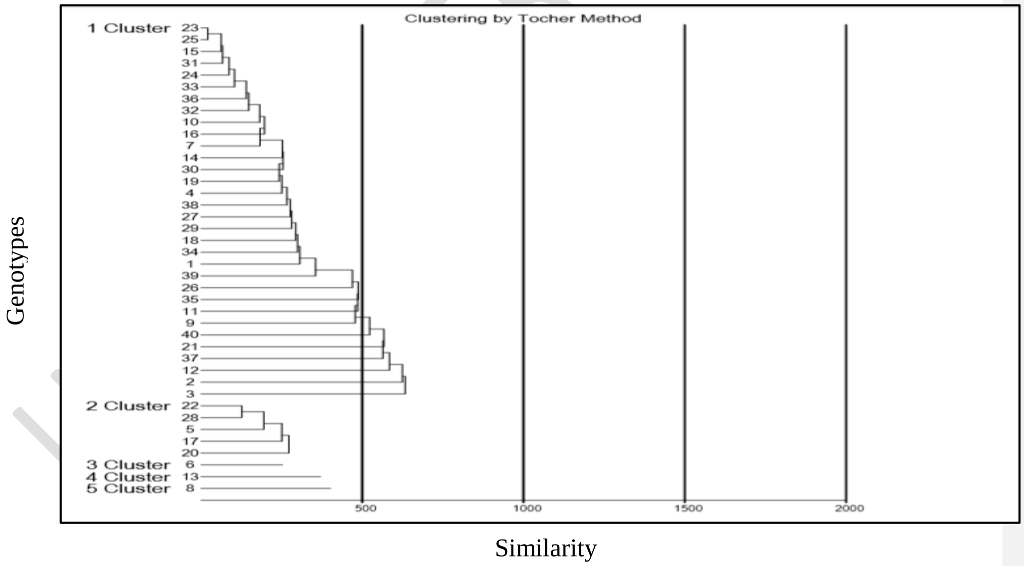
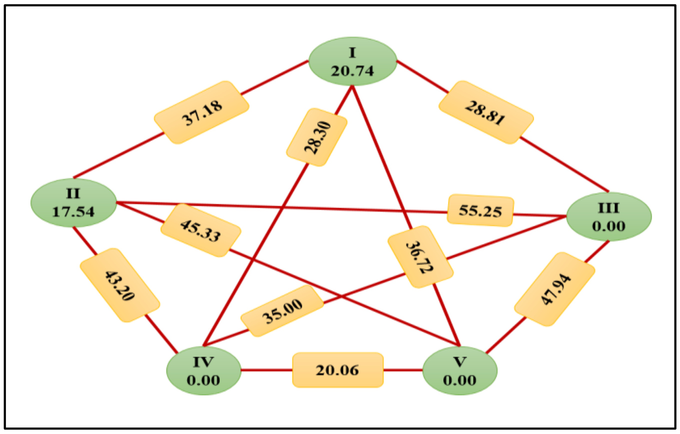


Figure 2: Dendrogram of forty rice genotypes for fourteen characters



Characters	**Times Ranked 1st**	**Per cent Contribution**
Days to 50 per cent flowering	99	12.69 %
Plant height (cm)	0	0.00 %
Effective tillers per plant	2	0.26 %

Figure 3: Cluster diagram based on D^2 statistics

Panicle length (cm)	0	0.00 %
Grains per panicle	50	6.41 %
1000 grain weight (g)	92	11.79 %
Grain yield per plant (g)	7	0.90 %
Straw yield per plant (g)	4	0.51 %
Hulling percentage	7	0.90 %
Milling percentage	0	0.00 %
Head rice recovery	4	0.51 %
L/B ratio	15	1.92 %
Amylose content (%)	40	5.13 %
Protein content (%)	460	58.97 %

Table 5: Contribution of fourteen characters under study to total divergence

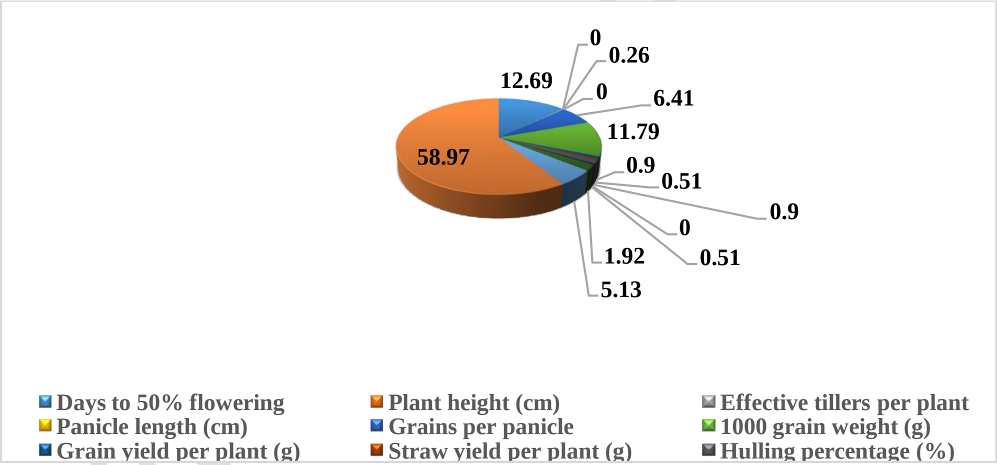


Figure4 : Contribution of fourteen characters under study towards total genetic divergence

Table 6: Cluster means for fourteen characters in forty rice genotypes

Clusters	Days to 50 per cent flowering	Plant height (cm)	effective tillers per plant	Panicle length (cm)	Grains per panicle	1000 grain weight (g)	Grain yield per plant (g)
I	83.52	**123.94**[#]	9.94	24.49	197.63	**25.95**	**27.78**
II	85.87	127.27	10.66	26.83	192.39	25.55	26.45
III	**76.67**	124.74	**10.68**	21.77	**235.82**	**20.02**	25.43
IV	100.33	**138.18**	**7.70**	**28.50**	207.25	22.81	22.89
V	**112.33**	129.13	8.49	**14.23**	**154.32**	24.46	**21.60**

Clusters	Straw yield per plant (g)	Hulling (%)	Milling (%)	Head rice recovery (%)	L/B ratio	Amylose content (%)	Protein content (%)
I	**35.13**	67.06	**66.21**	54.48	2.77	**23.01**	5.50
II	34.61	69.43	69.70	57.72	2.49	21.29	**8.97**
III	**26.06**	64.99	**73.59**	**51.22**	**2.89**	21.31	**3.11**
IV	34.74	**70.71**	66.50	55.34	2.69	**21.04**	4.35
V	31.73	**63.22**	70.88	**60.79**	**2.16**	22.92	4.89

Bold figures are indicated maximum and minimum mean values for each character.