GENETICDIVERGENCEANALYSISFOR QUANTITATIVE TRAITS IN RICE(*Oryza sativa* L.) GERMPLASMUNDER IRRIGATEDCONDITIONS

Abstract

The present study was with aim to know genetic divergence analysis for quantitative traits among the rice genotypes for agronomical and yield traits. The present study comprising 36 genotypes of rice with 13 quantitative characters. The results indicated that the genotype Nagarjuna shows greater yield among the genotypes, The genetic parameters shows High GCV and PCV in Grain yield per plant and according to D^2 *analysisthe thirty six genotypes were grouped into six clusters based on the Tocher's method of cluster formation. In Cluster I is the largest cluster consisting of 29 genotypes while Cluster II has 3 genotypes Cluster III, IV, V & VI was the smallest with only a single genotype. The maximum intra cluster distance was found in cluster II (39.19), followed by Cluster I (30.15), maximum inter cluster distance shown in between Cluster VI and Cluster II (178.97) followed by Cluster VI and Cluster V (151.75). Based on Cluster Means Cluster III (39.67) shows greater among six clusters for grain yield per plant as contribute highest among all the quantitative characters. Hence these traits could be focused for selection while improving seed yield and seed quality. On the basis of their greater inter cluster distance, high value of cluster means and performance of the individual germplasms for the character, the germplasm could be used in improving seed yield and seed quality programme for improvement of different plant characters of the rice.*

Keywords: Rice,GeneticVariability,Heritability, Genetic Advance and Diversity.

Introduction

Rice belongs to the botanical genus Oryza and the grass family Poaceae. There are two main species of cultivated rice: Oryza sativa (Asian rice) and Oryza glaberrima (African rice) has chromosome number 2n=24. It is the staple food crop for nearly four billion people around the world, providing 27% of calories in low- and medium-income countries. Almost 95% of the rice production happens in Asian countries and nearly half of the global population consumes it.

Rice is a cereal crop important for food security, is a staple in the diets of many billions ofpeople worldwide. More over one-third of the world's population relies on it as their main source of food. The world's demand for food production, particularly rice, is expected to rise in the ensuing decades as a result of the population growth. The majority of people on the planet eat rice as their primary staple meal, and it accounts for 19% of worldwide per capita energy consumption**.** Compared to other crop species, rice germplasm possesses a vast reservoir rich in genetic variation but only a very small part has been incorporated into breeding programmes, resulting in high genetic similarity in commercial rice cultivars.

The selection of parents is very important for hybridization for better crop improvement. The parents involved in the development in varieties should be divergent. The germplasm provides immense scope for wide variability. Breeding programme depends on the nature and magnitude of genetic diversity present among the genotypes.

Rice yield is a quantitatively complex property. Selecting parents solely on yield is frequently deceptive. As a result, understanding the link between yield and its contributing features is critical for plant breeders to develop an effective selection strategy in order to produce an economically viable variety. A plant breeder relies heavily on information concerning phenotypic and genotypic interactions of many economic variables while selecting and breeding different genotypes to increase yield potential. Such analysis studies also include the selection of the genetically divergent parents to obtain desirable combinations. Information about the degree and nature of genetic divergence would aid plant breeders in selecting the appropriate parent for future hybridization. Genetic divergence is an effective tool for parent selection for hybridization programmes.**(Koli *et al.*, 2022)**

Objectives

1. To evaluate rice genotype for yield and yield attributing traits
2. To identify the divergent parents for future Hybridization program
3. To study about diversity for morphological characters genetic

Materials and Methods

The experiment was conducted with 36 rice genotypes in crop research farm, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj – 211007.The experimental site is situated at 98m above sea level at 25.57^0 N latitude and 81.56^0 N longitude. Thisareas climate changes drastically like the temperature may drop as 1^0 C at the winter and reaches nearly 50^0 C during summer.The 36 rice genotypes are taken from Indian Institute of Rice Research (IIRR), Hyderabad. These genotypes are used to perform the experiment, conducted in Randomised Block Design with three replications with performed spacing row to row is 20cm and plant to plant is 15cm. In each replication five randomly competitive plants were selected are examined were recorded following 13 quantitative characters*viz.*Days to 50% flowering, Days to maturity, Flag leaf length, Flag leaf width, Plant height, Number of total tillers, Panicle length, Number of Grains per panicle, Number of productive tillers, Test weight, Biomass, Harvest Index and Grain yield per plant. Analysis of variance was carried out for all the traits and the data were subjected multivariate analysis following Mahalanobis's D^2statistics (Mahalanobis, 1936) to measure the genetic divergence followed by the clustering of genotypes based on 13 characters following Tocher's method. (Kumar *et al.*, 2014).

Experimental material

The 36 rice genotypes used in this research are mentioned in table 1.

Table 1. Experimental material used in the research

S.NO	NAMEOFGENOTYPES	S.NO	NAMEOFGENOTYPES
1	SAMPADA	19	DHAN-58
2	NAGARJUNA	20	NIDHI
3	SURAKSHA	21	LAGEDHAN
4	DHAN-57	22	KAUKA SEL
5	MANDHYA VIJAYA	23	NLR-145
6	JARAVA	24	NLR-40054
7	BINA-17	25	NLR-30491
8	DHAN-46	26	NLR-33641
9	DHAN-53	27	NLR-4001
10	DHAN-62	28	NLR-33359
11	BINA DHAN-10	29	JGL-3828
12	DRRH-3	30	JGL-1118
13	DHAN-54	31	JGL-3855
14	DHAN-52	32	WGL-18833
15	PHALGUNA	33	WGL-401
16	GAUTAM	34	WGL-4727
17	KRISHNA HAMSA	35	WGL-962
18	DHAN-69	36	NDR-359 (CHECK)

RESULTS AND DISCUSSION

- **Analysis of Variance**

  Analysis of variance for different characters are presented in table 2. The mean sum of squares shows significant differences of all the characters to all the genotypes. The variability indicates among the genotypesthis helps for selection of desirable. The performance of genotypes displays statistically different and these differences with help in selection and for better crop improvement. The mean sum of squares of analysis of varianceshows significant at 1% level of significance for all 13quantitative traits indicating the presence of genetic differences in the experimental material suggesting the importance of the genetic variability to identify the desirable genetic make-up provide better scope for selection and better crop improvement.

- **Genetic Parameters**

  The genetic parameters such as Phenotypic coefficient of variance (PCV), Genotypic coefficient of variance (GCV), Heritability (h^2) in broad sense, genetic advance (GA), Genetic advance as percent of mean (GA%) for thirteen characters are explained as follows.

- **Phenotypic and Genotypic coefficient of variance**

  Based on the PCV and GCV estimates,PCV is showing greater than GCV in all the characters indicating that there is variability presence due to environment**(Reddy *et al.*2023).**In PCV Grain yield per plant (29.23) is showing greater among the characters followed by number of spikelets per panicle (27.10), Biological yield per plant (20.94). In GCV Grain yield per plant (31.34) is showing greater among the characters followed by Number of spikelets per panicle (28.66), Biological yield per plant (23.74).

- **Heritability (broad sense)**

  Heritability is showing high range of estimates in all the characters indicating that there is less influence of environment in the variability among the genotypes. Number of spikelets per panicle (89.40) exhibiting greater in the heritability followed by Number of tillers per plant (88.06), Grain yield per plant (87.02).

- **Genetic advancement and its percent of mean.**

  Genetic advancement exhibits greater in Number of spikelets per panicle (86.43%) followed by Plant height (27.96%), Days to 50% flowering (25.81%) while Flag leaf width (0.28), Number of panicles per plant (2.70%), Panicle length (2.90%) shows least among the characters. In Genetic advancement as percent of mean shows Grain yield per plant (56.18%) exhibit greater and followed by Number of spikelets per panicle (52.79%), Biological yield (38.03%) while the Panicle length (11.84%), Days to maturity (14.00%) was exhibit least.

  All the characters showed high in heritability coupled with genetic advance as percent of mean indicating the characters are predominantly regulated by additive gene action. As a result, the more additive genes are accumulated for the crop improvement, based on the phenotypic expression selection would be more desirable that leads to better crop improvement.

Table 2. Analysis of variance of 13 traits in 36 promising rice genotypes for agronomic traits evaluated under field condition in *Kharif*, 2022.

Sl.No.	Source	Mean Sum of Squares (MSS)		
		Replication	Treatment	Error
	Degrees of freedom	2	35	70
1	Days to 50% flowering	16.4540	598.822**	36.378
2	Days to maturity	11.5930	379.374**	47.916
3	Plant height (cm)	51.3070	822.022**	82.939
4	Flag leaf length (cm)	4.8970	79.485**	7.732
5	Flag leaf width (cm)	0.0160	0.084**	0.008
6	Panicle length (cm)	1.7920	15.282**	3.665
7	Number of tillers per plant	1.0710	8.748**	0.378
8	Number of panicles per plant	1.6940	7.108**	0.576
9	Number of Spikelets per panicle	465.9140	6140.816**	233.282
10	Test weight (g)	3.1260	43.582**	4.06
11	Biological yield per plant (g)	75.0920	284.547**	24.772
12	Harvest Index (%)	15.4110	230.184**	25.276
13	Grain yield per plant (g)	14.0320	112.167**	5.311

Table 3. Genetic parameters of yield and yield components 36 promising rice genotypes for agronomic traits evaluated under field condition in *Kharif*, 2022

Sl.No.	Characters	GCV	PCV	h2 (Broad Sense)	Genetic Advancement 5%	Gen.Adv as % of Mean 5%
1	Days to 50% flowering	14.147	15.459	83.75	25.813	26.67
2	Days to maturity	8.141	9.747	69.75	18.084	14.006
3	Plant height (cm)	12.269	14.184	74.814	27.967	21.86
4	Flag leaf length (cm)	13.191	15.174	75.57	8.758	23.622
5	Flag leaf width (cm)	13.018	14.932	76.011	0.286	23.38
6	Panicle length (cm)	8.024	11.194	51.378	2.906	11.848
7	Number of tillers per plant	18.729	19.958	88.064	3.229	36.206
8	Number of panicles per plant	17.302	19.457	79.078	2.703	31.696
9	Number of Spikelets per panicle	27.104	28.664	89.408	86.437	52.794
10	Test weight (g)	16.213	18.543	76.442	6.537	29.2
11	Biological yield per plant (g)	20.94	23.747	77.756	16.903	38.038
12	Harvest Index (%)	17.803	20.839	72.99	14.545	31.333
13	Grain yield per plant (g)	29.237	31.341	87.025	11.469	56.185

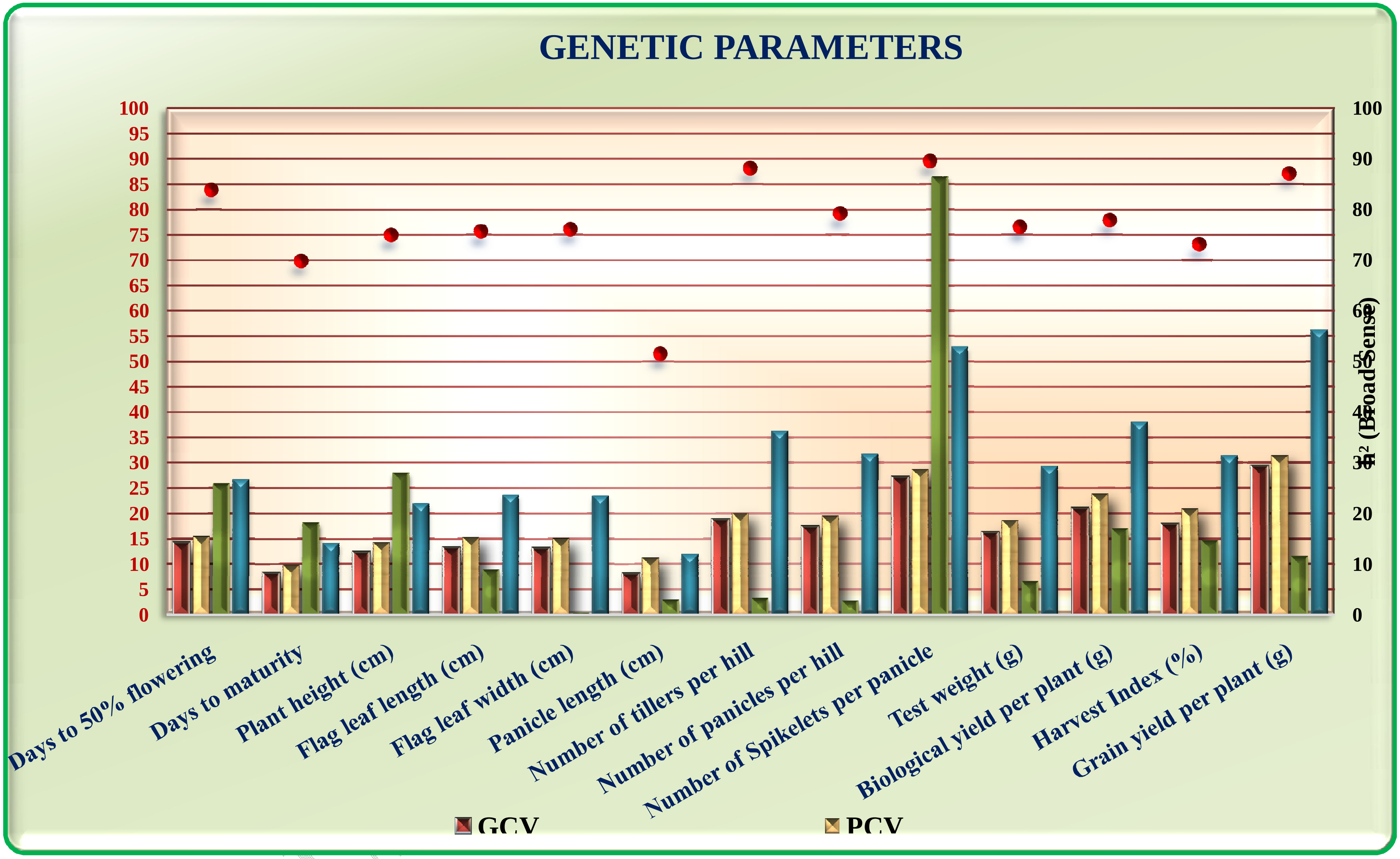

Fig 1. Bar diagram depicting GCV, PCV, Heritability and Genetic advance for 13 quantitative characters of ri

Table 4. Grouping of 36 rice genotypes into different clusters

Cluster Group	**No. of Genotypes**	**List of Genotypes**
1 Cluster	29	DHAN - 54, DHAN - 52, DHAN - 46, DHAN - 69, DHAN - 57, SURAKSHA, GAUTAM, SAMPADA, BINA - 17, NLR - 4001, DRRH - 3, NLR -145, JGL - 3828, DHAN - 62, PHALGUNA, KRISHNA HAMSA, BINA DHAN - 10, JARAVA, WGL - 1 8833, DHAN - 53, DHAN - 58, NIDHI, WGL - 401, NLR - 30491, NLR - 40054, WGL - 962, MANDHYA VIJAYA, JGL- 3855 & NLR - 33359
2 Cluster	3	LAGEDHAN, KAUKASEL & NLR - 33641
3 Cluster	1	NAGARJUNA
4 Cluster	1	JGL - 1118
5 Cluster	1	WGL- 4727
6 Cluster	1	NDR-359 (Check)

Table 5. Inter and Intra cluster distances of 36 genotypes of rice

Cluster Distances						
	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**
Cluster 1	30.15	78.87	66.78	51.88	50.41	109.73
Cluster 2		39.19	105.53	70.18	141.15	178.97
Cluster 3			0.00	60.19	94.24	138.27
Cluster 4				0.00	73.53	141.27
Cluster 5					0.00	151.75
Cluster 6						0.00

Table 6. Cluster mean of 13 biometrical traits of 36 rice genotypes

	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**
Days to 50% flowering	93.68	123.89	106.00	108.00	77.00	105.00
Days to maturity	126.99	142.22	139.00	143.00	126.00	131.00
Plant height (cm)	124.22	158.09	151.40	116.33	136.14	125.00
Flag leaf length (cm)	37.10	35.99	30.07	39.50	45.43	35.81
Flag leaf width (cm)	1.18	1.29	1.16	1.44	1.45	1.83
Panicle length (cm)	24.34	23.09	23.68	24.33	31.74	27.97
Number of tillers plant	8.79	7.40	11.53	8.40	8.33	15.60
Number of panicles plant	8.41	7.36	11.53	7.80	7.67	14.00
Number of Spikelet panicle	156.00	206.87	127.00	254.27	157.47	210.60
Test weight	22.78	17.39	22.00	18.66	29.34	23.11
Biological yield per plant (g)	41.50	56.07	69.27	56.40	50.80	51.50
Harvest Index (%)	47.00	31.34	56.75	57.43	55.99	44.01
Grain yield per plant (g)	19.31	17.38	39.67	32.40	28.07	22.67

SL.NO.	**Source**	**Contribution %**	**Times ranked 1st**

1	**Days to 50% flowering**	9.52	60
2	**Days to maturity**	9.00	57
3	**Plant height (cm)**	4.52	29
4	**Flag leaf length (cm)**	5.64	36
5	**Flag leaf width (cm)**	2.54	16
6	**Panicle length (cm)**	3.21	20
7	**Number of tillers per hill**	10.41	66
8	**Number of panicles per hill**	6.32	40
9	**Number of Spikelets per panicle**	5.65	36
10	**Test weight (g)**	8.89	56
11	**Biological yield per plant (g)**	6.65	42
12	**Harvest Index (%)**	12.00	76
13	**Grain yield per plant (g)**	15.65	99

Table 7. Percent contribution of 13 biometrical traits of 36 rice genotypes towards genetic divergence

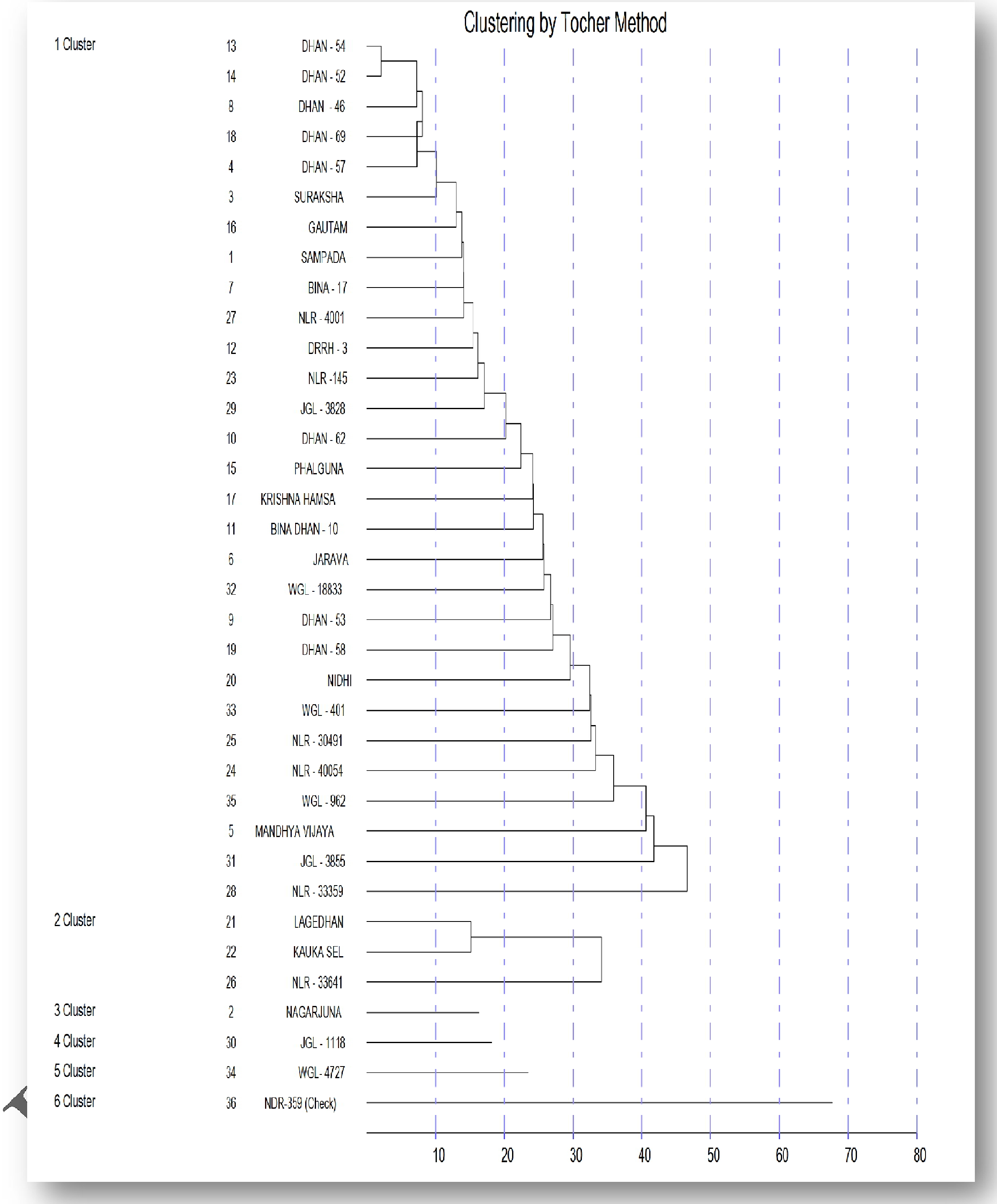

Fig 2. Dendrogram showing distribution of 36 rice genotypes into different clusters.

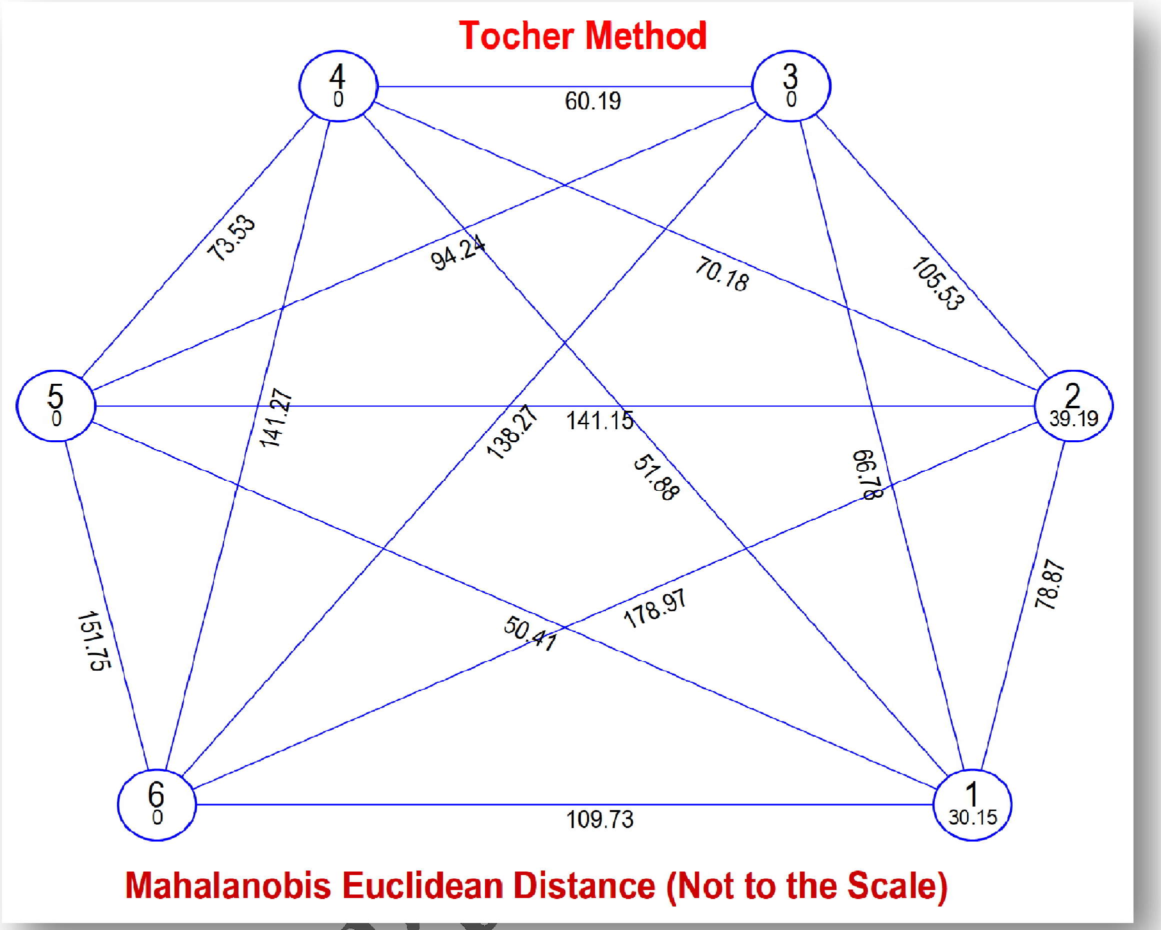

Fig 3. Inter and Intra cluster distance of 36 genotypes of rice.

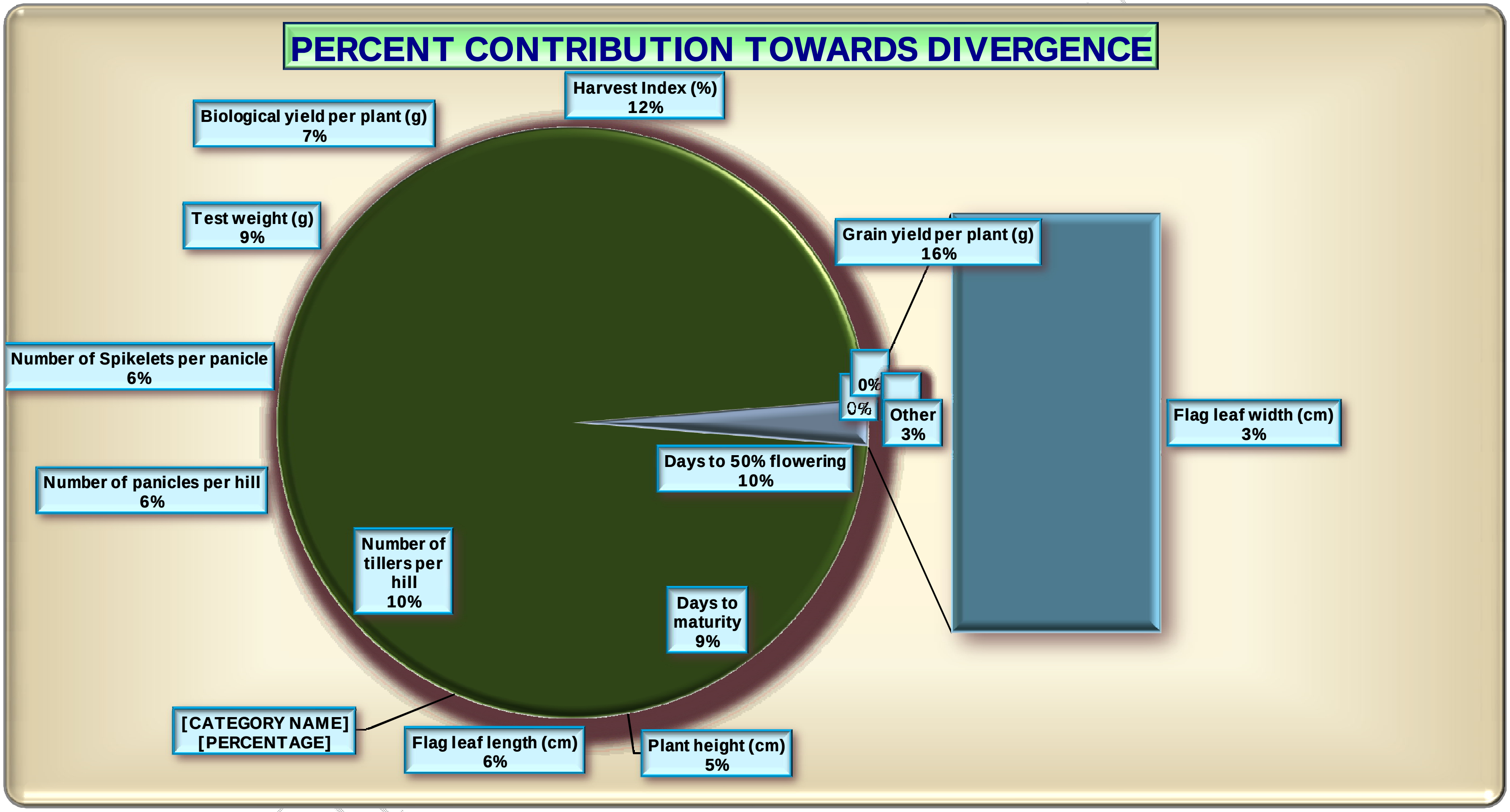

Fig 4. Pie chart showing percentage contribution of 13 biometrical traits of 36 rice genotypes towards genetic divergence

- **Cluster analysis**

Cluster analysis is performed among the 36 rice genotypes, result displaced that all genotypes are divided into 6 clusters. Cluster I (29) has greater number of genotypes followed by cluster II (3) and remaining Clusters III, IV, V and VI contains single genotype in each cluster shown in the table 4. Based on the cluster distances Cluster II (39.19) has greater in Intra cluster distances and Cluster I (30.15) shown and remaining displays zero. According to Inter cluster distancesCluster VI and Cluster II (178.97) has greater among the clusters followed by Cluster VI and Cluster V (151.75), shown in Table 5.

Based on the distances of clusters, best lines should be selected as parents for future hybridization and this helps in better in crop improvement.

- **Cluster Means**

Among the six clusters the means grouped on the basis of 36 rice genotypes of every character, Cluster III (39.67) has greatest among the clusters in Grain yield per plant followed by Cluster IV (32.40), Cluster V(28.07), Cluster VI (22.67), Cluster I (19.31), Cluster II (17.38), shown in Table 6.

- **Percentage Contribution of different Characters**

Based on the percentage contribution Grain yield per plant (15.65%) exhibits greater among the characters followed by Harvest Index (12%), Number of tillers per hill (10.41%).

Considerable variability existed in the genotypes for all the characters studied. Thesewere the genotypeswithhighmeanvaluesin desirable directioni.e., Fromthe presentinvestigation it is concluded that among 36 genotypes of rice, WGL-401 showed earlyflowering (75 days), NLR-33359 had characters like early maturity (109 days), High Grain Yield per Plant is seen in Nagarjuna (39.6 g), Kaukasel showed high plant height (177.6 cm) and high Biomass is seen in Nagarjuna (69.2 g), WGL-4727 (31.74 cm) showed high Panicle Length. Highest GCV and PCV were depicted for Grain Yield per Plant, Number of Spikelets per Panicle, Biological Yield per hill and Number of tillers per hill. The highest Heritability was observed for Number of Spikelets per panicle followed byNumber of tillers per hill, Grain yield per plant (g), Days to 50% flowering, Number of panicles per hill, biological yield per plant (g). the Genetic Advance in percent of mean is high for Grain yield per plant, Number of Spikelets per panicle, biological yield per plant, Number of tillers per hill, Number of panicles per hill. Based on D^2 values 36 genotypes grouped into 6clusters. Among 6 clusters, cluster I had a greater number of genotypes (29) followed by cluster II (3), III, IV, V, andVI(1)genotype each. cluster VI and cluster II (178.97) followed by cluster VI and cluster V (151.75), were most diverse from each other and the genotypes present in these clusters provide a broad spectrum of variability in segregation and may be used as parents in the future hybridization programme to develop desirable genotypes for grain yield improvement in rice genotypes. ThetraitGrainyieldperhillhad maximum contribution towards to genetic divergence followed by Harvest Index, Number of tillers per hill, Days to 50% flowering, Days to maturity, Test Weight. Therefore, all these charactersshould begivendueconsideration during selectionforcrop improvement.

References

Anwar, Mohammad Abdul & Sudarshan Reddy, Maddula& Lal, Gaibriyal& Lavanya, G.. (2022). Genetic Analysis for Grain Yield and Its Attributing Characters in Rice (Oryza sativa L.) under Irrigated Conditions of Prayagraj, Uttar Pradesh. International Journal of Plant & Soil Science. 98-107. 10.9734/ijpss/2022/v34i2131288.

Burton, G.W. (1952). Quantitative Inheritance of Grasses.Proc.*6th Int. Grass land congress*, 1:277-283.

Burton,G.W.andDevane.(1953).EstimationofHeritabilityinTall Fescue*Festulaarundnacea*from replicated clonal material. *Agronomy Journal*,45: 478-481.

Fisher, R.A. (1918). The correlation between relative on the supposition of Mendelian Inheritance Trance Royale Soc. Edinburg,52: 399-403.

Fisher, R.A., Yates, F. (1967). Statistical tables for biological, Agricultural and Medical Research, Congress Group Limited, London.

Johnson, H.W., Robison, H.F and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soyabean. *Agronomy Journal*, 47: 314-318.

Koli, Ganesh & Upadhyay, Sameer & Gupta, Sneha & Kumawat, Gayatri & Sinha, India & Rathi, Sanket & Singh, Pawan Kumar & Sinha, Bliss. (2022). Study of genetic divergence for yield and yield attributing traits of wild germplasm in rice.

Kumar, B., Kour, A. & Laxami, J. (2017). Genetic Diversity for Agro-morphological Traits in Rice Germplasm, *Electronic Journal of Plant Breeding*, 8(4): 1216-1222.

Lush, J.L. (1949). Heritability of quantitative traits in farm animals, Proceeding of 8thInternational Congress genetic Heridas (Sippl.), 336-357.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proceedings of National Institute of Sciences*, India, 12: 49-55.

M. A. Latif, M. M. Rahman, M. S. Kabir, M. A. Ali, M. T. Islam and M. Y. Rafii.Genetic diversity analyzed by quantitative traits among rice (Oryza sativa L.) genotypes resistant to blast disease. *African Journal of Microbiology Research* Vol. 5(25), pp. 4383-4391, 9 November, 2011

Panse, V.G and Sukhatne, P.V. (1961). Statistical methods for agricultural workers. *2nd Edn*ICARNewDelhiP:361.

P. K. Bhati, S. K. Singh, S. Y. Dhurai and Amita Sharma. Genetic divergence for quantitative traits in rice germplasm.*Electronic Journal of Plant Breeding*, 6(2): 528-534 (June 2015) ISSN 0975-928X

Priyanka, k., Jaiswal, H.K., Waza, S.A. and Sravan, T. (2015). Genetic divergence inIndigenous aromatic rice (*Oryzasativa*L.). *Electronic Journal of Plant Breeding.*6(4):1096-1102

Reddy, Paleru & Lal, Gabrial & Narendra Reddy, Y Venkata. (2023). Assessment of Genetic variability, Cause and Effect Inter-relationship among Yield Component Characters in Maize (*Zea mays* L.). *International Journal ofPlant & Soil Science*. 35. 1611-1620. 10.9734/IJPSS/2023/v35i183433.

Rai, S.K., Chandra, R., Suresh B.G., Rai, P.K., Kumar, R., Sandhya, (2014). Genetic Diversity Analysis of Rice Germplasm Lines for Yield Attributing Traits. *International Journal of Life Sciences Research*, 2(4): 225-228.

Sujitha, R., Arumugam Pillai M., Kannan R. and Shoba D. (2020). Genetic diversity and association studies in Rice (Oryza sativa L.). *Journal of Pharmacognosy and Phytochemistry*,9(6): 487-492.

Suresh, K., Kiran, K.K., Krishnappa, M. R and Shivakumar, N. (2014). Genetic Diversity Analysis for Grain Yield and Its Attributes among Diverse Genotypes of Rice (*Oryza sativa* L.). *Trends in Biosciences*,7(11): 994-997.

Shrivastav, Shiv & Verma, Om Prakash & Lal, Kanhaiya & Singh, Vishal & Srivastava, Kuldeep. (2022). Genetic Divergence Analysis in Rice (*Oryza sativa* L.) Germplasmsunder Sodic Soil. *Indian Journal of Agricultural Research.* 10.18805/IJARE.A-5976.

Tang, Ruyu, Cui, Di, Zhou Jian, Li, Wenqiu, Ma, Xiaoding, Han, Bing, Guo, Xiaohong,Zhao, Zhengwu, Han, Longzhi. (2021). Comparative analysis of genetic diversity ofrice (*Oryza sativa* L.) varieties cultivated in different periods in China. Genetic Resources and Crop Evolution. 68. 10.1007/s10722-020-01073-5.