

## Genetic Divergence Analysis for Himalayan Rice Genotypes

Vinaykumar Rachappanavar<sup>1\*</sup>, JK Sharma<sup>1</sup>, Vipin Kumar<sup>2</sup>, Geeta G<sup>1</sup>.

<sup>1</sup>\*Department of Seed Science and Technology, Palampur HP-176062

<sup>2</sup>Ph. D Scholar, Dept of forest products, Dr YSP UHF, Nauni. HP-173230

Corresponding author: agrivinay123@gmail.com

### ABSTRACT

*In this present study, thirty rice genotypes consisting of Himalayan landraces were used for genetic diversity analysis. Germplasm were morphologically studied at Rice &Wheat Research Center, CSKHPKV, Malan (N 32 ° 07', E 76 ° 23'), and Himachal Pradesh during Kharif-2016 season. Selected genotypes were grouped into six clusters based on both quantitative and quality characters. Among six clusters, cluster-I has the highest genotypes (14) followed by cluster-III (6) and cluster-V (4) and single genotype (Sailadhan) in cluster VI. The data indicated that the cluster mean for grain yield per plot was highest in Cluster III (0.59 kg) and the lowest in Cluster VI (0.13 kg). the contribution of seed yield per plot was maximum towards genetic divergence (49.20%) by ranking 240 times, followed by grain length (14.94%) by 65 times, The intra cluster distance was maximum in cluster V (3283.06) and minimum in cluster VI (0), whereas, highest inter cluster distance (21168.41) was recorded between VI and IV and lowest (1955.07) was observed between cluster II and I. The genotypes from these clusters with desired parameter may be used as potential contributor for future hybridization program to develop new varieties.*

**Key words:** inter and intra cluster, improved lines, landraces, *Oryza sativa*.

Received 22.05.2019

Revised 23.06.2019

Accepted 12.07.2019

### CITATION OF THIS ARTICLE

V Rachappanavar, JK Sharma, V Kumar, Geeta G. Genetic Divergence Analysis for Himalayan Rice Genotypes. Int. Arch. App. Sci. Technol; Vol 10 [3] September 2019 : 108-112

### INTRODUCTION

Rice (*Oryza sativa* L.) is an annual grass and one of the most important crop cultivated throughout world belong to graminiae family. It is a main source of 35-60% dietary calories consumed by more than 3 billion people and probably the most versatile crop [5]. Agro-morphological classification of germplasms is fundamental information for plant breeding programs [7]. India has a rich diverse genetic wealth of rice and it has been estimated about nearly 50,000 types of rice varieties are still being cultivated in the country [15]. Replacing well adopted landraces by high yielding varieties with the spread of modern agriculture, has posed a great threat to the old landraces which may have immense potential for different important characters [10, 14, 16]. Chakravorty *et al.* [2] studied 51 rice landraces for 18 agro-morphological traits in West Bengal. Based upon assessment of genetic diversity is very useful in rice breeding from the standpoint of selection, conservation of different land races variety of rice and proper application [8]. For variety development, Evaluation and documentation of existing land races of rice is required for future use. To meet the continuously growing needs of varietal development, the assemblage, evaluation, preservation and characterization of the entire existing germplasm are essential to more rewarding breeding efforts. In order to avoid any further gene erosion, collection and conservation of such important genetic resources of rice is essential. Characterization of variety is beneficial to identify and avoid duplication. Characterization should eventually

lead to a system of recording and storing useful data that can be readily retrieved and made accessible to others and help in planning breeding programmes [4].

## MATERIAL AND METHODS

The present investigation entitled “Genetic Divergence Analysis for Himalayan Rice Genotypes” was conducted in the Dept. of Seed Science and Technology CSKHPKV, Palampur during *kharif* season 2016-17. Thirty germplasm of paddy collected from different parts of Himachal Pradesh were utilised for this study, which include 10 released cultivating varieties, 9 improved lines and 11 landraces were grown in a Randomized Block Design (RBD) with three replications with a block size of 2 x 1.25 m<sup>2</sup> with spacing 30 x 15 cm, respectively. The recommended cultural practices were followed as mentioned in package of practices for *kharif* crops. Observations were recorded on 10 randomly selected plants in each entry and in each replication for plant height (cm), panicle length (cm), effective tillers per plant (no), leaf length (cm), leaf width (cm), leaf area index (cm<sup>2</sup>), days to panicle initiation (days), days to pollen shed (days), Days to panicle completion (days), Seeds per panicle (no), 100 seed wt (gm), Grain width (mm), Grain length (mm), Seed yield per plot (kg). The data were subjected statistical analysis using Mahalanobis D<sup>2</sup> method (1936) and clustering of genotypes was done according to Ward [18].

## RESULT AND DISCUSSION

On the basis of D<sup>2</sup> values, 30 genotypes were grouped into VI clusters (Table 1; Fig 1) indicating the presence of considerable genetic diversity among all the genotypes. Cluster I was the maximum (14) genotypes namely HPR-1068, HPR-1156, HPR-2687, HPR-2697, HPR-2612, HPR-2766, HPR-2143, HPR-2748, Kasturi, Kalijhini-1, Kalijhini-2, HPR-2656, Chinudhan and jhinidhan. Cluster II contains three genotypes namely Saaldhan, Ramjawandhan and Chohartu; cluster III contains six genotypes namely HPR-2720, HPR-2699, HPR-2707, HPR-2711, HPR-2880 and HPR-2682. Cluster IV contains two genotypes namely RP-2421 and VL-221. Cluster V contains four genotypes namely Sukara, Karad, Kaludhan and HPR\_2748 and cluster VI containing a single genotype Sailadhan. Similar attempts for clustering have also been earlier reported by various workers [1, 2, 6, 11, and 13].

There Cluster means of the characters studied according to D<sup>2</sup> values (Table 2). The cluster mean for plant height highest in cluster VI (141.62) and the lowest in cluster IV (94.93). Panicle length was highest in cluster I (25.11 cm) and lowest in cluster IV (20.92 cm). Cluster III recorded the highest tillers per plant (7.38) and the lowest was recorded in cluster IV (4.45). Cluster III recorded the highest leaf length (37.35 cm) and the lowest in cluster IV (25.24 cm). Cluster III and Cluster V recorded the highest leaf width (13.82) and lowest in Cluster IV (10.95). Leaf area index was height in Cluster III (38.82 cm<sup>2</sup>) and the lowest was recorded in Cluster IV (20.48 cm<sup>2</sup>). Mean for days to panicle initiation is highest in Cluster VI (75.67) and the lowest in Cluster IV (40). Days to pollen shed s highest in cluster IV (75.33) and the lowest in Cluster VI (51.33). Days to panicle completion was highest in Cluster VI (88.67) and the lowest in Cluster IV (47.33). Seeds per panicle were highest in Cluster III (146.03) and the lowest in Cluster VI (48.29). 100 Seed weight was height in Cluster V (2.39 gm) and the lowest in Cluster IV (1.71gm). Grain width was highest in Cluster VI (3.85 mm) and the lowest in Cluster I (2.72). Grain length was highest in Cluster I (8.99 mm) and the lowest in Cluster VI (7.65 mm). Grain yield per plot was highest in Cluster III (0.59 kg) and the lowest in Cluster VI (0.13 kg). Those genotypes from these clusters having highest mean values may be directly used for adaptation or as parents in forthcoming hybridization programme.

There were intra and inter-cluster distances worked out in terms of average D<sup>2</sup> valves (Table 3). The intra cluster distance was maximum in cluster V (3283.06) and minimum in cluster VI (0), whereas, highest inter cluster distance (21168.41) was recorded between VI and IV and lowest (1955.07) was observed between cluster II and I (Table: 3; fig: 2).

Relative contribution of characters towards genetic divergence (Table; 4) showed that the contribution of seed yield per plot was highest towards genetic divergence (49.20%) by ranking 240 times first, followed by grain length (14.94%) by 65 times, days to panicle completion (13.10%) by 57 times, days to pollen shed (6.67%) by 29 times, seeds per panicle (5.75%) by 25 times, grain width (5.52%) by 24 times, plant height(2.53%) by 11 times, 100 seed weight (2.07%) by 9 times, leaf length (0.231%) by 1 times, panicle length,

effective tillers, leaf width, leaf area index, days to panicle initiation (0.01%) by 00 times to the genetic divergence in decreasing order. The results were in conformity with Pragnya *et al.* [12] for filled grain per panicle, Nayak *et al.* [9] for panicle length, Garg *et al.* [6] for days to maturity, grain yield per plant and for plant height [3].

**Table 1: Distribution of rice genotypes among different clusters on the basis of Mahalanobis D<sup>2</sup>- analysis**

Clusters	Number of genotypes	Genotypes
I	14	HPR-1068, HPR-1156, HPR-2687, HPR-2697, HPR-2612, HPR-2766, HPR-2143, HPR-2748, Kasturi, Kalijhini-1, Kalijhini-2, HPR-2656, Chinudhan and jhinidhan
II	3	Saaldhan, Ramjawandhan and Chohartu
III	6	HPR-2720, HPR-2699, HPR-2707, HPR-2711, HPR-2880 and HPR-2682
IV	2	RP-2421 and VL-221
V	4	Sukara, Karad, Kaludhan and HPR-2748
VI	1	Sailadhan

**Table 2: Cluster means of four clusters for different traits of rice genotypes**

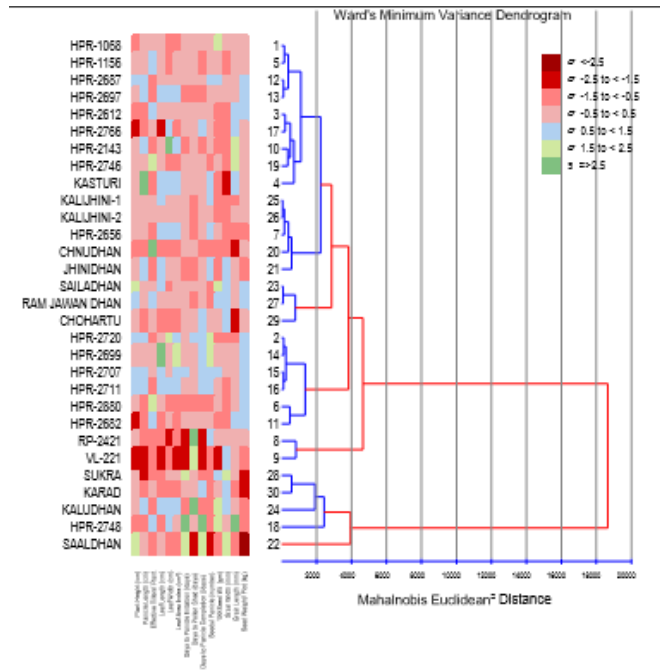
	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster	VI Cluster
Plant height (cm)	109.28	124.56	114.20	94.93	111.75	141.62
Panicle length (cm)	25.11	23.87	24.72	20.92	21.66	23.94
Effective tillers/ plant	7.13	7.20	7.38	4.45	6.67	5.13
Leaf length (cm)	35.01	34.93	37.35	25.24	31.15	32.08
Leaf width (cm)	13.34	12.24	13.82	10.95	13.82	12.07
Leaf area index (cm <sup>2</sup> )	35.02	32.04	38.82	20.48	32.68	29.00
Days to Panicle Initiation (days)	56.38	58.78	59.89	40.00	68.33	75.67
Days to pollen shed (days)	59.88	60.11	61.72	75.33	66.58	51.33
Days to panicle completion ((days)	64.93	69.33	69.61	47.33	70.17	88.67
Seeds/ Panicle (number)	109.78	80.69	146.03	118.47	67.10	48.29
100 Seed wt. (gm)	1.95	2.31	1.97	1.71	2.39	1.74
Grain width (mm)	2.72	3.69	2.89	3.19	3.47	3.85
Grain length (mm)	8.99	8.48	8.66	8.51	8.92	7.65
Seed yield/ plot (kg)	0.46	0.51	0.59	0.44	0.31	0.13

**Table 3: Average inter and intra cluster distance (D<sup>2</sup>)**

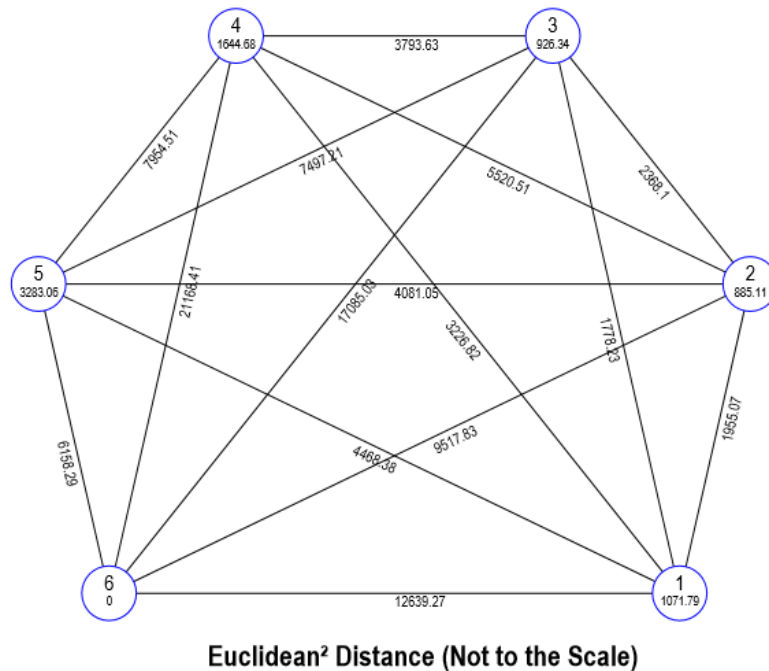
Euclidean <sup>2</sup> : Cluster Distances: Ward						
	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster	VI Cluster
<b>I Cluster</b>	1071.79					
<b>II Cluster</b>	1955.07	885.11				
<b>III Cluster</b>	1778.23	2368.10	926.34			
<b>IV Cluster</b>	3226.82	5520.51	3793.63	1644.68		
<b>V Cluster</b>	4468.38	4081.05	7497.21	7954.51	3283.06	
<b>VI Cluster</b>	12639.27	9517.83	17085.03	21168.41	6158.29	0.00

**Table 4: Relative contribution of characters towards genetic divergence**

Source	Contribution %	Times Ranked 1 <sup>st</sup>
1. Plant height (cm)	2.53	11
2 .Panicle length (cm)	0.01	0
3 .Effective tillers/ Plant	0.01	0
4 .Leaf length (cm)	0.23	1
5 .Leaf width (cm)	0.01	0
6 .Leaf area index (cm <sup>2</sup> )	0.01	0
7 .Days to panicle initiation	0.01	0
8 .Days to pollen shed (days)	6.67	29
9 .Days to panicle completion	13.10	57
10 .Seeds/ Panicle (number)	5.75	25
11 .100 Seed wt. (gm)	2.07	9
12 .Grain width (mm)	5.52	24
13 .Grain length (mm)	14.94	65
14 .Seed weight/ Plot (kg)	49.20	214



**Fig 1: Clustering pattern of thirty rice genotypes by Mahalanobis’s D<sup>2</sup> method (not in scale)**



**Fig 2: Cluster diagram showing Euclidean distance (not to scale) in paddy germplasm.**

**CONCLUSION**

In this study cluster III (HPR-2720, HPR-2699, HPR-2707, HPR-2711, HPR-2880 and HPR-2682) showed the highest cluster mean values in D<sup>2</sup> analysis for maximum number of traits, suggesting that these traits could be used in varietal identification programme.

**ACKNOWLEDGEMENT**

Author is grateful to Dr. J. K. Sharma, Professor and Head, Department of Seed Science and Technology, CSK HPKV, Palampur for valuable guidance.

## REFERENCES

1. Chakma, S.P, Huq, H, Mahmud, F. and Husna, A. (2012). Genetic diversity analysis in rice (*Oryza sativa* L.). *Bangladesh Journal of Plant Breeding of Genetics*, 25: 31-39.
2. Chakravorty, A, Ghosh, P.D. and Sahu, P.K. (2013). Multivariate analysis of phenotypic diversity of landraces of rice of West Bengal. *American Journal of Experimental Agriculture*, 3:110-23.
3. Chandra, R, Pradhan, S.K, Singh, S, Bose, L.K. and Singh, O.N. (2007). Multivariate analysis in upland genotypes. *World Journal of Agricultural Sciences*, 3:295-300.
4. Dabas, S.D, Suthar, B.N. and Kavani, S.F. (1997). Seasonal variations in seminal characteristics of Patanwadi ram. *Indian Journal of Animal Reproduction*, 18:70-72.
5. Fageria, N.K. (2003). Plant tissue test for determination of optimum concentration and uptake of nitrogen at different growth stages in lowland rice. *Communications in Soil Science and Plant Analysis*, 34: 259-270.
6. Garg, P, Pandey, D.P. and Singh, D. (2011). Genetic variability for yield and quality traits in rice (*Oryza sativa* L.). *Research on Crops*, 12: 182-184.
7. Lin, M.S. (1991). Genetic base of japonica rice varieties released in Taiwan. *Euphytica*, 56: 43-46.
8. Mohammadi-Nejad, A, Arzani, A.M, Rezai, R.K, and Singh, G.B. (2008). Assessment of rice genotypes for salt tolerance using microsatellite markers associated with the salt tolerant QTL. *African Journal Biotechnology*, 7:730-736.
9. Nayak, D, Bose, L.K, Singh, U.D, Singh, S. and Nayak, P. (2008). Measurement of genetic diversity of virulence in populations of *Xanthomonas oryzae* pv. *Oryzae* in India. *Communications in biometry and crop science*, 3:16-28.
10. Patra, B.C. (2000). Collection and characterization of rice genetic resources from Keonjhar district of Orissa. *Oryza*, 34: 324-326.
11. Pragnya, K, Radha Krishna, K.V, SubbaRao, L.V. and Suneetha, K. (2018). Studies on genetic divergence analysis in soft Rice (*Oryza sativa* L.) Genotypes. *International Journal of Pure and applied bioscience*, 1: 68-97.
12. Pragnya, K, Radha Krishna, K.V. and SubbaRao, L.V. (2018). Variability parameters in soft rice (*Oryza sativa* L.) genotypes. *International Journal Current Microbiology and Applied Science*, 7: 2029-2042.
13. Rathod, A.J, Mistry, P.M, Pampaniya, A.G, Patel, H.R. and Chetariya, C.P. (2017). D<sup>2</sup> Statistics for grain yield and quality traits in rice (*Oryza sativa* L.). *International Journal of Pure Applied Bioscience*, 5: 54-58.
14. Richharia, R.H. (1979). An aspect of genetic diversity in rice. *Oryza*, 16:1-31.
15. Roy, J.K, De, R.N, Ghorai ,D.P. and Panda, A. (1985). Collection and evaluation of genetic resources of rice in India. *Phytological breeding*, 1: 1-9.
16. Sharma, D.K, Sahu, G.R. and Shrivastava, M.N. (1987). Present status of rice germplasm in Madhya Pradesh (India). *Oryza*, 24: 127-131.
17. Vangaru, S. and Bijoy, K.S. (2017). Study of genetic diversity in some newly developed rice genotypes. *International Journal of Current Microbiology and Applied Science*, 6: 2693-2698.
18. Ward, J.H. (1963). Hierarchical grouping to optimize an objective function. *Journal of American Statistics Association*, 58: 236-244.