



ISSN (E): 2277- 7695

ISSN (P): 2349-8242

NAAS Rating: 5.23

TPI 2022; 11(2): 472-474

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Received: 02-11-2021

Accepted: 13-01-2022

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## Study of genetic divergence for yield and yield attributing traits of wild germplasm in rice

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### Abstract

An experiment was conducted with forty wild rice germplasm lines (*Oryza nivara* and *Oryza rufipogon*) at Banaras Hindu University, Varanasi during *kharif* season 2018 and evaluated for twelve quantitative characters using D<sup>2</sup> analysis in order to study the diversity pattern among the wild genotypes. The genotypes were grouped into 7 clusters. Maximum number of genotypes (32) were grouped under cluster I followed by cluster IV with 3 genotypes, while clusters II, III, V, VI and VIII, had only one genotype each. The maximum inter-cluster distance was observed between II and VII (588.21) followed by clusters I and VII (305.92). Hence, the genotypes in cluster II *viz.*, WRG(NKS)-426 had wider diversity with WRG(NKS)-440 in cluster VII and the genotypes in cluster I *viz.*, WRG(NKS)-401, WRG(NKS)-402, WRG(NKS)-403, WRG(NKS)-404, WRG(NKS)-405, WRG(NKS)-406, WRG(NKS)-407, WRG(NKS)-408, WRG(NKS)-409, WRG(NKS)-410, WRG(NKS)-411, WRG(NKS)-412, WRG(NKS)-413, WRG(NKS)-414, WRG(NKS)-415, WRG(NKS)-416, WRG(NKS)-417, WRG(NKS)-418, WRG(NKS)-419, WRG(NKS)-422, WRG(NKS)-423, WRG(NKS)-425, WRG(NKS)-427, WRG(NKS)-428, WRG(NKS)-430, WRG(NKS)-431, WRG(NKS)-432, WRG(NKS)-433, WRG(NKS)-435, WRG(NKS)-436, WRG(NKS)-437 and WRG(NKS)-438 had wider diversity with WRG(NKS)-440 in cluster VII, and these lines may be utilized in further breeding programme for the exploitation of hybrid vigour. The intra-cluster distance was maximum in cluster I (44.67) followed by cluster IV (40.31) indicating hybridization involving genotypes within the same clusters may result in good cross combinations. The trait, total grain yield per plant contributed maximum (32.18%) towards total genetic divergence followed by filled grain per panicle (15.00%) and test weight of grain (14.36%). Therefore, these characters may be given importance during hybridization programmes.

**Keywords:** Genetic diversity, wild rice germplasm, quantitative traits, D<sup>2</sup> analysis, divergence.

### Introduction

Rice is the staple food for 2.7 billion people and it covering 9% of the earth's arable land. 21% of global human per capita energy provided by rice and 15% of per capital protein (IRRI, Rice Almanac, 4th Edition). Rice is the staple food crop of India, providing 43% of caloric requirement for more than 70% Indian population. In order to meet the food requirement of growing population of world and India development of high yielding rice varieties is essential. The selection of parents for hybridization is very important for success of any breeding programme. The parents involved in the development in varieties should be divergent. The germplasm provides immense scope for wide variability. Crop improvement programme depends on nature and magnitude of genetic diversity present among the genotypes. Rice yield is a complex quantitative character. Selection of parents based only on yield is often misleading. Hence, it is very important to know about relationship between yield and its contributing characters is needed for an efficient selection strategy for the plant breeders to evolve an economic variety. The information about phenotypic and genotypic interactions of various economic traits is of immense importance to a plant breeder for the selection and breeding of different genotypes for increasing yield potential.

Genetic divergence is an efficient tool for selection of parent for hybridization programme. Such study also include selection of the genetically divergent parents to obtain desirable combinations. Information about degree of genetic divergence and nature would help the plant breeder's in choosing the right parent for the breeding programme (Vivekananda and Subramanian, 1993). The degree of divergence in germplasm is provided by D<sup>2</sup> analysis which was developed by Mahalanobis (1936) [6]. This analysis gives information about inter and intra cluster distance that provide information of diversity at cluster level and crossing between germplasm of diverse cluster may give heterotic progeny.

## Materials and Methods

The present experiment on genetic variability and diversity analysis for yield and yield attributing traits of wild germplasm in rice was carried out during the *Kharif* 2018. This field experiments were conducted at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (UP). This research work consisted of forty different rice genotypes. The experiment was carried out in randomized block design (RBD) with three replications. The nursery was sown on 25<sup>th</sup> June, 2018 and twenty one days old seedlings were transplanted in the main field. Normal spacing of (15 × 20) cm with recommended cultural practices were followed for raising a good and healthy crop. The experimental material used in present study comprised of forty late maturing wild rice germplasm lines (*Oryza nivara* and *Oryza rufipogon*) viz. WRG(NKS)-401, WRG(NKS)-402, WRG(NKS)-403, WRG(NKS)-404, WRG(NKS)-405, WRG(NKS)-406, WRG(NKS)-407, WRG(NKS)-408, WRG(NKS)-409, WRG(NKS)-410, WRG(NKS)-411, WRG(NKS)-412, WRG(NKS)-413, WRG(NKS)-414, WRG(NKS)-415, WRG(NKS)-416, WRG(NKS)-417, WRG(NKS)-418, WRG(NKS)-419, WRG(NKS)-420, WRG(NKS)-421, WRG(NKS)-422, WRG(NKS)-423, WRG(NKS)-424, WRG(NKS)-425, WRG(NKS)-426, WRG(NKS)-427, WRG(NKS)-428, WRG(NKS)-429, WRG(NKS)-430, WRG(NKS)-431, WRG(NKS)-432, WRG(NKS)-433, WRG(NKS)-434, WRG(NKS)-435, WRG(NKS)-436, WRG(NKS)-437, WRG(NKS)-438, WRG(NKS)-439, WRG(NKS)-440. These lines were received from Dr. N. K. Singh, National Research Center on Plant Biotechnology, New Delhi. Lines were evaluated for 12 quantitative characters viz. days of 50% flowering, days of maturity, effective tillers, plant height, panicle length, per panicle weight, filled grain, unfilled grain, grain Number per panicle, spikelet fertility, test weight, total grain yield. Five plants were randomly selected from each entry in each replication and their mean were used for the statistical analyses. Genetic divergence amongst different genotypes is assessed based on the estimated *inter-se* genetic distances amongst the genotypes. D<sup>2</sup> statistics of Mahalanobis (1928) is one of the most effective tools to measure the genetic distance between genotypes as measured by allelic frequencies at a sample of loci. Genetic similarity is defined as the converse of the genetic divergence i.e. the extent of gene similarity among the genotypes. After arranging the D<sup>2</sup> values of all combinations of one genotype with the others in ascending order of magnitudes, the genotypes were grouped into a number of clusters by Tocher's method described by Rao (1952).

## Results and Discussion

The results of analysis of variance showed that there is

significance differences for all the twelve quantitative characters under study. On the bases of D<sup>2</sup> value forty wild germplasms under study were grouped into seven clusters (Table 1). Clustering pattern indicated that thirty two out of forty germplasms belong to the same cluster i.e. cluster I. On the other hand, three belong to cluster IV while cluster II, III, V, VI, and VII, contain only 1 germplasm. (Hegde *et al.* 2000)<sup>[5]</sup>.

Intra and inter-cluster distances among the genotype i.e. D<sup>2</sup> values have been presented in the Table 2. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. The highest intra-cluster distance was observed in the cluster I (44.67) which comprised of thirty two germplasms followed by cluster IV (40.31). Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would be made use of in improvement through intervarietal hybridization. Remaining Clusters II, III, V, VI and VII showing 0.00 intra cluster distance. The highest inter-cluster distance (588.21) was found between cluster II and VII followed by cluster I and VII (354.02) and cluster V and VII (332.73). The smallest inter-cluster distance (72.91) was observed between III and VI followed by cluster III and VI (72.98) and cluster V and VI (81.27) (Garg *et al.* 2011)<sup>[3]</sup>.

Mean values for different quantitative traits for different clusters have been presented in Table 3. The extreme mean values of the traits under study were observed to fall in different clusters. The highest mean values for filled grains per panicle (103.20), total grain number per panicle (124.73), effective tiller (17.86) and spikelet fertility (81.33) were observed in cluster IV. Highest mean values for days of 50% flowering (118.67) and days of maturity (148.67) were observed in cluster II. Highest mean value for unfilled grain (36.88), plant height (147.84), and panicle length (27.93) were exhibited in cluster III. Cluster VII exhibited highest mean values for total grain yield (53.41), panicle weight (3.45), and test weight (24.62). Thus, the germplasms in cluster II, III, IV, and VII seems to be quiet promising for many of the traits under study. (Bhadru *et al.* 2012)<sup>[1]</sup> and (Kar *et al.* 2013)<sup>[4]</sup>.

All the characters contributed to genetic divergence except days of maturity and spikelet fertility (Table 4). The percentage of contribution towards genetic divergence by all the characters is presented in table 4.9 and figure 4.7. The character grain yield per plant contributed maximum to genetic divergence (32.18%) followed by filled grain number per plant (15.00%), test weight (14.36%). Contribution of other characters were plant height (12.69%), unfilled grain (11.54%), effective tiller (7.18%), panicle weight (3.85%), days of 50% flowering (2.82%), panicle length (00.26%) and grain number per panicle (00.13%). (Chandramohan *et al.* 2016)<sup>[2]</sup>.

**Table 1:** Grouping of 40 rice germplasm into seven clusters (by Tocher method)

Cluster	Germplasm	Number
I	WRG(NKS)-427, WRG(NKS)-431, WRG(NKS)-415, WRG(NKS)-423, WRG(NKS)-410, WRG(NKS)-414, WRG(NKS)-425, WRG(NKS)-408, WRG(NKS)-407, WRG(NKS)-404, WRG(NKS)-419, WRG(NKS)-403, WRG(NKS)-411, WRG(NKS)-405, WRG(NKS)-435, WRG(NKS)-428, WRG(NKS)-433, WRG(NKS)-417, WRG(NKS)-412, WRG(NKS)-437, WRG(NKS)-401, WRG(NKS)-430, WRG(NKS)-432, WRG(NKS)-436, WRG(NKS)-418, WRG(NKS)-406, WRG(NKS)-422, WRG(NKS)-413, WRG(NKS)-438, WRG(NKS)-402, WRG(NKS)-416	32
II	WRG(NKS)-426	1
III	WRG(NKS)-429	1
IV	WRG(NKS)-420, WRG(NKS)-421, WRG(NKS)-434	3
V	WRG(NKS)-39	1

VI	WRG(NKS)-424	1
VII	WRG(NKS)-440	1

Where, (DF)= Days of 50% flowering, (DM)= Days of maturity, (ET)= Effective tillers, (PH)= Plant height, (PL)= Panicle length, (PPW)= per panicle weight, (FG)= Filled grain, (NFG)= Unfilled grain, (GNPP)= Grain Number per panicle, (SF%)= Spikelet fertility, (TW)= Test weight, (TGY)= Total grain yield

**Table 2:** Average Intra and inter-cluster D<sup>2</sup> value among 7 Clusters (by Tocher method)

Cluster	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	44.67	86.41	98.30	153.56	73.83	101.23	354.02
Cluster 2		0.00	214.15	305.92	86.81	184.40	588.21
Cluster 3			0.00	72.91	72.98	101.57	215.30
Cluster 4				40.31	132.21	116.14	104.04
Cluster 5					0.00	81.27	332.73
Cluster 6						0.00	173.73
Cluster 7							0.00

Where, (DF)= Days of 50% flowering, (DM)= Days of maturity, (ET)= Effective tillers, (PH)= Plant height, (PL)= Panicle length, (PPW)= per panicle weight, (FG)= Filled grain, (NFG)= Unfilled grain, (GNPP)= Grain Number per panicle, (SF%)= Spikelet fertility, (TW)= Test weight, (TGY)= Total grain yield

**Table 3:** Mean values of different characters of 40 rice germplasms grouped in seven clusters

S.NO.	DF	UFG	FG	GNPP	TGY	PPW	PH	TWT	ET	PL	DM	SF
Cluster 1	96.29	17.42	44.15	61.56	14.02	1.08	120.83	21.30	15.58	22.79	128.65	70.62
Cluster 2	118.67	22.62	14.61	37.23	6.16	0.46	142.81	14.46	15.98	25.57	148.67	42.01
Cluster 3	89.33	36.88	76.91	113.79	21.51	1.82	147.84	24.56	13.35	27.93	119.33	69.16
Cluster 4	102.11	21.53	103.20	124.73	30.71	2.80	145.87	24.00	17.86	25.30	131.56	81.33
Cluster 5	99.00	28.81	60.17	88.98	16.34	1.15	135.02	12.43	12.80	24.42	129.00	69.32
Cluster 6	89.67	22.31	39.60	61.91	34.31	0.99	88.54	16.22	11.60	16.77	127.33	66.57
Cluster 7	88.33	20.51	99.72	120.23	53.41	3.45	129.95	24.62	16.77	26.92	124.33	81.09

Where, (DF)= Days of 50% flowering, (DM)= Days of maturity, (ET)= Effective tillers, (PH)= Plant height, (PL)= Panicle length, (PPW)= per panicle weight, (FG)= Filled grain, (NFG)= Unfilled grain, (GNPP)= Grain Number per panicle, (SF%)= Spikelet fertility, (TW)= Test weight, (TGY)= Total grain yield

**Table 4:** Percent contribution of each character towards total genetic divergence in 40 Germplasms

Source	Times Ranked 1st	Contribution%
DF	22	2.82%
UFG	90	11.54%
FG	117	15.00%
GNPP	1	00.13%
TGY	251	32.18%
PPW	30	3.85%
PH	99	12.69%
TWT	112	14.36%
ET	56	7.18%
PL	2	00.26%
DM		00.00%
SF		00.00%

Where, (DF)= Days of 50% flowering, (DM)= Days of maturity, (ET)= Effective tillers, (PH)= Plant height, (PL)= Panicle length, (PPW)= per panicle weight, (FG)= Filled grain, (NFG)= Unfilled grain, (GNPP)= Grain Number per panicle, (SF%)= Spikelet fertility, (TW)= Test weight, (TGY)= Total grain yield

## Conclusion

Genetic diversity analysis was carried out through D<sup>2</sup> analysis in order to assess the genetic divergence among genotype under study. Based on D<sup>2</sup> analysis forty rice genotypes were grouped in seven clusters. The maximum numbers of genotypes (32) belong to cluster I and due to maximum numbers of member genotypes this cluster showing highest intra cluster distance followed by cluster IV which is second largest cluster with 3 genotypes while cluster II, III, V, VI and VII showed zero intra cluster distance because of single member in these clusters. The highest inter cluster distance observed between cluster II and Cluster VII, indicates high

genetic divergence found between these two clusters and more suitability for breeding programme than other clusters. The highest contribution towards the total genetic divergence observed in total grain yield per plant followed by filled grain.

## References

- Bhadru D, Rao VT, Mohan YC, Bharathi D. Genetic variability and diversity studies in yield and its component traits in rice (*Oryza sativa* L.). SABRAO Journal of Breeding & Genetics. 2012, 44(1).
- Chandramohan Y, Srinivas B, Thippeswamy S, Padmaja D. Diversity and variability analysis for yield parameters in rice (*Oryza sativa* L.) genotypes. Indian Journal of Agricultural Research, 2016, 50(6).
- Garg P, Pandey DP, Kaushik RP. Genetic divergence for yield and quality traits in rice (*Oryza sativa* L.). Journal of Rice Research. 2011;4(1):1-5.
- Kar AK, Das SR, Bastia D. Genetic divergence in selected indigenous aromatic rice of Odisha. ORYZA-An International Journal on Rice. 2013;50(2):185-188.
- Hegde SG, Patil CS. Genetic divergence in rainfed rice. Karnataka Journal of Agricultural Sciences. 2000;13(3):549-553.
- Mahalanobis PC. On the generalized distance in statistics. National Institute of Science of India, 1936.