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Research Article

Genetic Diversity studies in Elite Rice Landraces of North Western Himalayas

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Abstract

Forty elite rice landraces were evaluated for their morphological diversity by raising in Randomized Complete Block Design with three replications during *kharif*, 2022. Data was recorded for yield and its contributing traits viz., days to 50% flowering, days to 75% maturity, plant height, panicle length, total tillers per plant, spikelet per panicle , grains per panicle , grain yield per plant and grain yield per plot. Among all the traits under study, 1000 grain weight was found to be maximum contributing trait towards divergence followed by grain yield per plant. All the 40 genotypes were divided into 7 distinct clusters in accordance on the basis of morphological data. Out of these, Cluster I consisted of the highest number of genotypes (29 genotypes) while with 5 genotypes, Cluster II has been found to have the largest intra-cluster distance. The highest inter-cluster distance was observed between Cluster VI and Cluster VII, suggesting the possibility of generating segregating populations, if parents are chosen for a hybridization programme from these clusters.

Keywords: landraces, diversity analysis, red rice, D^2-analysis

1. Introduction

India is the home to a diverse range of rice cultivars, landraces, and lesser-known kinds that have been cultivated for centuries by farmers and local entrepreneurs. Besides grain production, these cultivars were selected for aroma, grain length, cooking quality and resistance to various abiotic challenges. Since majority these cultivars are known by their local or common dialect names, there aren't many (if any) records of their genetic makeup and history. Some of these kinds are thought to have originated in another state or region and undergone a protracted domestication process hundreds of years ago (Prathepha, 2009). The morphological characterization of these landraces might therefore show their phylogeny, and this knowledge would be very helpful in using these germplasms to genetically enhance the existing rice cultivars.

The Himalayan red rice, also known as Red Pearls of the Himalayas, is one of a kind and has made a reputation for itself in the global market because to its long grains and aroma (Kaushik et al. 2014). In Himachal Pradesh, a significant number of landraces, such as *Jattoo, Matali, Laldhan, Deval, Chohartu*, and *Sukaradhan*, are cultivated in different pockets. These landraces vary in terms of morphological and quality attributes.

Since nearly half of the world's population depends on rice for their food, increasing rice productivity is one of the important issues. During its domestication and genetic development, in agriculture rice underwent extensive selection. Additionally, modern rice improvement programmes continuously rely on the selection of desirable traits under extremely controlled conditions to achieve an ideotype, which exacerbates the shrinkage of the cultivar gene pool. Exploitation of local landraces and germplasm which are reservoirs of diverse genes, can overcome this limitation. Landraces are traditionally cultivated, have been developed over generations with special features over wild relatives and serve as a treasure trove of useful genes. They have played a very important role in the local food security and sustainable development of agriculture (Shengxiang et al. 2002). Selecting appropriate and diverse parents is a crucial step in any crop improvement program aimed at obtaining desired recombinants. The genetic diversity present in the available genotypes plays a significant role in enhancing specific traits of interest. Estimating the genetic distance is essential to identify parents that are different enough in their genetic makeup for the desired traits. Therefore, the efforts were made to study the extent of variability with the help of D^2- analysis to group different genotypes and landraces into distinct clusters for further implications in breeding programme.

2. Materials and methods

The present study was carried out at CSKHPKV Rice and Wheat Research Centre, Malan during *kharif* 2022. The Experimental materials comprised of 40 elite rice genotypes (Table 1) which includes red rice, white rice and aromatic rice along with three released varieties (HPR-2880, Kasturi and HPR-2720) as checks. Each entry was raised in plot size of 4m × 0.4m with row to row and plant to plant spacing of 20 cm and 15 cm, respectively (having 2 rows/ genotype) in 3 replications. The recommended cultural practices were followed as mentioned in package of practices for *kharif* crops. Data was recorded on days to 50% flowering, days to 75% maturity, plant height, panicle length , total tillers/ plant , spikelets/ panicle , grains/ panicle , grain yield/ plant and grain yield per plot . Observations were recorded on five randomly selected plants in each replication for all the traits except for days to 50% flowering and days to 75% maturity for which data was recorded on the plot basis. Analysis of variance (ANOVA) was estimated as per Panse and Sukhatme (1989). In the current investigation, genetic divergence was estimated using the Mahalanobis D^2 generalised distance, as per Rao in 1952. Mahalanobis D^2-analysis is a potent method for evaluating the genetic diversity among various genotypes and choosing appropriate parents for hybridization. The original variable means were transformed into uncorrelated variables using the fundamental condensation approach using inversion matrices. D^2 values were evaluated for significance using chi-square at p degrees of freedom, where p is the number of characters taken into consideration. After arranging the D^2-values of all combinations of one genotype with the others in ascending order of magnitude, the genotypes were divided into a number of clusters using Tocher's method, which was first proposed by Rao (1952). The requirement for this strategy was that any two kinds belonging to the same cluster had an average lower D^2 value than those kinds belonging to two different clusters. After that, the inter- and intra-cluster distances were calculated, and their relationships were visually shown.

Table 1. List of germplasm lines of rice evaluated under present study

Sr. no.	Genotypes	Sr. no.	Genotypes
1	*Deval Kullu*	21	*Bongal Dhan*
2	*Jhini*	22	*Totu*
3	*Sattu Dhan*	23	*Saila Dhan*
4	*Karad 21-4*	24	*Roda Dhan*
5	*Karad*	25	*Parmal Byada - 2*
6	*Karad 21-2*	26	*Kalhaina*
7	*Nirmand Choharu*	27	*Byada -3*
8	*Chattar -2 Parmal*	28	*Parmal Byada -1*
9	*Chattar Parmal -1*	29	*Byada – 4*
10	*Lakhamandal*	30	*Chohartu*
11	*Jattu*	31	*Gharsai*
12	*Gocha Dhan*	32	*Local Lal Dhan*
13	*Acchoo*	33	*Byada Basmati*
14	*Matali*	34	*Red Rice Boh*
15	*Chaina*	35	*Local Jhemka*

16	*Phulpatas*	36	*Lalnakanda*
17	*Deval*	37	*Ramjuwain*
18	*Bhagolta Local*	**38**	**HPR-2720**
19	*Purple*	**39**	**Kasturi**
20	*Sukara*	**40**	**HPR- 2880**

3. Results and discussion

Analysis of variance for all the ten quantitative characters in forty rice genotypes has been presented in Table 2. All the genotypes taken under study were highly significant for the quantitative characters viz., days to 50% flowering, days to 75% maturity, plant height, panicle length, total tillers/ plant, spikelets/ panicle, grains/ panicle, 1000-grain weight, grain yield/ plant and grain yield/ plot. Rachappanavar (2017) and Alagappan and Bhardwaj (2022) reported similar findings in relation to several parameters, namely the duration of 50% flowering, the duration of 75% maturity, plant height, total tillers/ plant, spikelets/panicle, grains/ panicle, 1000-grain weight, grain yield/ plant and grain yield/ plot.

Table 2. Analysis of variance of rice genotypes for yield and related traits

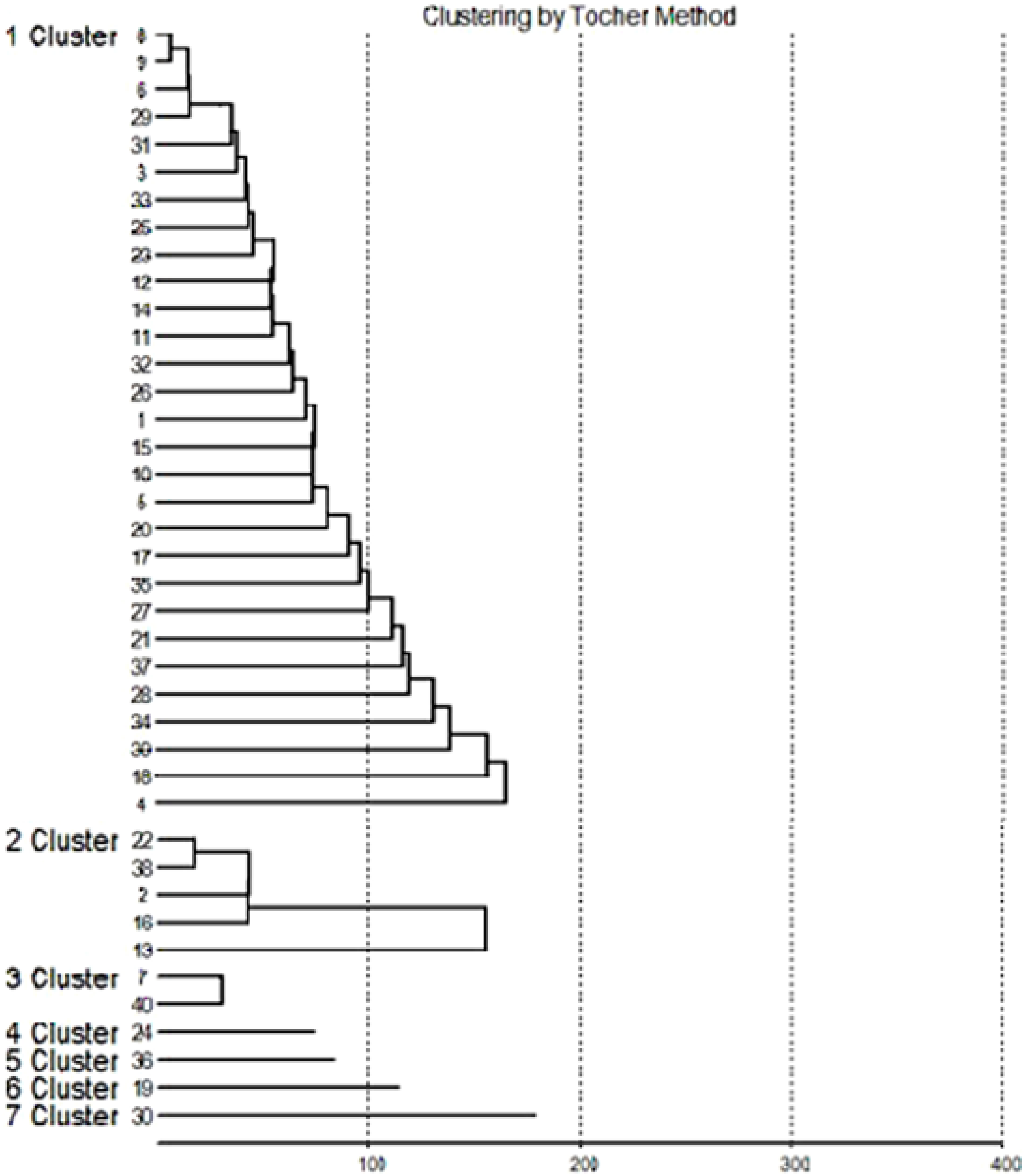
	Mean sum of square		
Source of variation	**Replication**	**Treatment**	**Error**
Degrees of freedom	2	39	78
Days to 50 % flowering	109.55	30.32*	2.92
Days to 75 % maturity	123.46	41.10*	4.14
Plant height	830.62	93.91*	43.16
Panicle length	20.49	33.88*	2.79
Total tillers/plant	3.15	9.15*	0.704
Spikelet/ panicle	4626.88	129.40*	539.11
Grains/ panicles	3833.59	118.05*	292.47
1000- grain weight	20.06	2.00*	0.14
Grain yield/ plant	30.49	0.31*	1.00
Grain yield/ plot	23950.23	2035.29*	1624.28

Date presented in table 3 represents the grouping of genotypes on the basis of Mahalanobis D^2-analysis. Maximum numbers of genotypes are placed in cluster I (29 genotypes) followed by cluster II (5genotypes), then cluster III (2 genotypes), while cluster IV, cluster V, cluster VI and cluster VII consists of 1 genotype each (Fig 1). Clustering of 29 traditional varieties adapted to agroclimatic condition of Himachal Pradesh into one group indicated strong affinity in genotypes of same geographical distributions. The pattern of distribution of genotypes which got distributed into several clusters suggests that the kind of genetic diversity found among the genotypes belonging to same geographic origin might be due to differences in adaptation, selection criteria, selection pressure and environmental conditions. Present findings are in confirmation with Devi et al. (2015), Kumar (2015), Rachappanavar (2017) and Akhtar et al. (2022). Similar reports were obtained by Gnaneswari et al. (2023) and Meena et al. (2023).

Table 3. Grouping of rice genotypes into different clusters on the basis of Mahalanobis D^2-analysis

Clusters	**Total number of genotypes**	**Genotypes**
Cluster I	29	*Chattar -2 Parmal, Chattar Parmal -1, Karad 21-2, Byada – 4, Parmal Byada – 2, Gharsai, Sukara, Byada Basmati, Sattu Dhan, Saila Dhan, Karad 214, Lakhamandal, Gocha Dhan, Kalhaina, Local Jhemka, Bhagolta Local, Jattu, Matali, Byada -3, Bongal Dhan, Karad, Chaina, Deval, Local Lal Dhan, Parmal Byada -1, Deval Kullu, Ramjuwain, Kasturi, Red Rice Boh*
Cluster II	5	*Totu,* HPR-2720*, Jhini, Phulpatas, Acchoo*
Cluster III	2	*Nirmand Choharu*, HPR- 2880
Cluster IV	1	*Roda Dhan*

Cluster V	1	*Lalnakanda*
Cluster VI	1	*Purple*
Cluster VII	1	*Chohartu*



The average intra and inter-cluster distances are presented in Table 4. The highest intra-cluster distance is observed for cluster II (10.48). High intra-cluster distances revealed that genotypes within the same cluster were quite diverse; hence the selection of parents within the cluster would be effective. The minimum intra-cluster distance is observed for cluster III (5.59). The highest inter-cluster distance is observed between cluster VI and VII (28.65). Genotypes belonging to these clusters are diverse from each other whereas, cluster V and VII (13.35) indicates that the genotypes belonging to these clusters were comparatively less diverse. Hybridization between the most diversed genotypes (with a greater inter cluster distance) may result in ideal segregants with an accumulation of beneficial genes in the segregating generation, facilitating in hybridization (Netam et al. 2021).

Table 4. Average intra and inter-cluster distance

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	**10.20**	20.41	13.68	13.91	15.33	16.17	19.44
Cluster II		**10.48**	16.30	28.01	27.78	23.41	28.25
Cluster III			**5.59**	16.74	18.78	23.49	17.99
Cluster IV				**0.00**	10.23	21.79	15.28
Cluster V					**0.00**	21.51	13.35
Cluster VI						**0.00**	28.65
Cluster VII							0.00

Bold values are intra cluster distance

Table 5 depicts clusters mean values for yield and related traits. The perusal of the data revealed that the cluster VII showed maximum cluster mean value for grain yield/ plot and grain yield/ plant. Cluster VI was observed with maximum cluster mean values for spikelet/ panicles, grains/ panicle and plant height. Cluster I showing maximum value for total tillers/ plant. Cluster IV had maximum mean value for 1000- grain weight, early flowering and maturity. On the basis of cluster mean value, cluster IV, VI and VII included genotype which was superior for most of the traits.

Table 5. Cluster means of six clusters for different traits of rice genotypes.

Clusters/ Characters	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**MEAN**	**MIN**	**MAX**
DFF	90.55	90.27	80.83	80.67	86.67	99.00	82.67	87.24	80.67	99.00
DSM	117.86	117.33	107.50	106.00	114.00	127.00	121.67	115.91	106.00	127.00
PH	118.12	133.78	118.90	115.40	169.88	103.33	153.52	130.42	103.33	169.88
PL	25.50	26.01	22.83	23.07	27.67	23.20	23.93	24.60	22.83	27.67
TPP	9.08	7.09	9.53	6.20	6.07	5.53	4.13	6.80	4.13	9.53
SPP	144.45	189.29	179.59	109.80	172.35	206.42	124.10	160.91	109.80	206.42
GPP	118.33	162.52	146.33	79.50	142.46	180.63	99.42	132.74	79.50	180.63
1000-gw	24.23	17.80	22.31	27.44	26.66	23.73	25.67	23.98	17.80	27.44
GYP PL	13.85	13.01	18.08	14.37	15.38	5.90	20.17	14.39	5.90	20.17
GYP PLOT	398.86	379.79	496.57	422.10	443.49	185.07	584.46	418.58	185.07	584.46

Note-days to 50% flowering (DFF), days to 75% maturity (DSM), plant height (PH), panicle length (PL), total tillers/ plant (TTPL), spikelet/ panicle (SPP), grains/ panicle (GPP), grain yield/ plant (GYPP) and grain yield per plot (GYPPlot)

Table 6. Relative contribution of individual trait towards divergence among rice genotypes

Trait	**Rank**	**Contribution (%)**
Days to 50% flowering	132	16.92
Days to 75% maturity	9	1.15
Plant height (cm)	39	5.00
Panicle length (cm)	13	1.67
Total tillers/ plant	54	6.92
Spikelets/ panicle	3	0.38
Grains/ panicle	6	0.76
1000-grain weight (g)	326	41.79
Grain yield/ plant (g)	187	23.97
Grain yield/ plot (g)	11	1.41

The relative percent contribution of the individual trait to the genetic divergence among genotypes is presented in Table 6. The highest contribution towards the genetic divergence was exhibited by 1000 grain weight followed by grain yield/ plant, days to 50% flowering while, spikelet/ panicle, grains/ panicle, days to 75% maturity, grain yield/ plot have least contribution towards divergence. Similar results of high contribution of maturity period, 1000 grain weight and grain yield were reported by Tarunam et al. (2023).

Author Contributions

AT, NK and NB prepared the manuscript and preparing the final version of the manuscript and correspond to the journal.

Ethical Approval

This article does not contain any studies involving human or animal participants performed by any of the authors.

Conflicts of Interest:

The authors declare no conflict of interest.

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