Journal of Agriculture and Natural Resources (2023) 6(1):60-73
ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

Research Article

Agro-morphological characterization and diversity assessment of advanced breeding lines of spring rice in the plains of eastern Nepal

Babita Bhusal*, Bandana Bhattarai, Ramita Badu, Ajay Kumar Yadav, Shiv Shankar Loniya, Manoj Sapkota, Anisha Gyawali, Sandip Timilsina and Dipendra Kumar Ayer

Gauradaha Agriculture Campus, Institute of Agriculture and Animal Science, Jhapa, Nepal

*Correspondence: babitabhusal2023@gmail.com
*ORCID: https://orcid.org/0009-0001-3094-3427

Received: June 15, 2023; Revised: September 25, 2023
Accepted: November 7, 2023; Published: November 25, 2023

ABSTRACT

Agro-morphological characterization and genetic diversity analysis is pivotal to identify elite genes for further improvement of germplasms. In Spring 2022, 52 spring (Chaite) rice accessions were evaluated for 12 agro-morphological traits in alpha lattice design with two replications under irrigated condition at agronomic farm of Gauradaha Agriculture Campus, Jhapa, Nepal. Results showed the existence of considerable amount of diversity in rice accessions. The first three principal components (PC1, PC2 and PC3) with eigen value greater than one were identified with a total cumulative variation of 95.04% showing that the accessions could be grouped at least into three main varied classes. The accessions were grouped into 5 clusters. The accessions falling in cluster II had the maximum grain yield. The accessions namely Hardinath-1 (4.87 t/ha), IR17A3019 (4.37 t/ha), IR17A2949 (4.12 t/ha) were found to have high yielding accessions. High genetic variability among the rice accessions was found for the traits viz., grain yield, thousand grain weight, length breadth ratio, days to flowering, days to maturity, panicle length, effective tiller per hill and have pertinency in future spring rice breeding programs for the selecting potential parent lines based on those traits.

Keywords: Agro-morphological trait, Principal Component, Cluster Analysis, Spring rice

Correct citation: Bhusal, B., Bhattarai, B., Badu, R., Yadav, A. K., Loniya, S.S., Sapkota, M.,Gyawali, A., Timilsina, S., & Ayer, D.K. (2023). Agro-morphological characterization and diversity assessment of advanced breeding lines of spring rice in the plains of eastern Nepal. *Journal of Agriculture and Natural Resources, 6*(1), 60-73.
DOI: https://doi.org/10.3126/janr.v6i1.71880

INTRODUCTION

Rice, (*Oryza sativa* L.) belonging to the Poaceae family is renowned as one of the most staple food crops globally. It holds significant agricultural importance and is cultivated in diverse agroclimatic conditions, contributing to the sustenance of a large portion of the world's population. It is believed to have originated and cultivated in tropical and subtropical Asia, with the one of oldest record dating to 5000 years BC (better to cite very renowned rice scientist) (Watanable *et al.*, 1997 and Kandel & Shrestha, 2018). The wide distribution of rice across continents and sub-continents is a testament to its diverse genetic makeup (Naaz *et al.*, 2022). By 2050, the global population is projected to reach 9.8 billion, ensuring food security along with maintaining environmental sustainability has become a paramount challenge.

Journal of Agriculture and Natural Resources (2023) 6(1):60-73
ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

Moreover, based on current consumption patterns, rice production needs to increase by 35-40% by 2025 to meet demand (Shah *et al.*, 2020). To satisfy the demands of an expanding population, any breeding program must successfully capitalize on the heterogeneity across germplasms. So, genetic diversity must be conserved, assessed, and used for sustainable agricultural production.

Nepal is a center of rice diversity with 2,500 landraces, including 50 aromatic types, 93 improved varieties, 34 registered varieties, over 1,000 introduced genotypes, and 4 wild species (Joshi, 2017). Characterizing germplasm agro-morphologically is crucial for providing essential information to support plant breeding programs (Lin, 1991). Genetic variation is vital for plant breeders as it provides a rich reservoir of genes to select from, enabling the enhancement of traits and the advancement of crop varieties with exceptional productivity, premium quality, and robust resilience. (Aswini *et al.*, 2023). Understanding the nature and extent of genetic divergence assists plant breeders in selecting appropriate parents for breeding programs (Guru *et al.*, 2017). Comprehensive analysis and profiling of rice germplasm are vital for harnessing desired traits and safeguarding unique rice varieties in the current age (Sao *et al.*, 2019). Plant breeders often measure numerous traits for germplasm evaluation, but consolidating this data and drawing accurate conclusions can sometimes be challenging (Mohanlal *et al.*, 2023). Multivariate statistical tools are widely employed to summarize and describe the inherent variations among landraces (Dhakal *et al.*, 2020). Principal component analysis (PCA) is a non-parametric multivariate method used to examine datasets containing multiple interrelated quantitative variables (Tiwari *et al.*, 2022) and reveals the patterns and eliminates the redundancy in given data sets (Maji & Shaibu, 2012). Cluster analysis is another useful statistical tool for assessing the genetic diversity of germplasm with respect to the studied attributes collectively (better to cite the author who initially studied/used this analysis) (Hair *et al.*, 1998 and Shrestha *et al.*, 2021). A large inter-cluster distance reflects substantial diversity between the groups, whereas a small distance indicates a closer genetic relationship (Devi *et al.*, 2019).The present study aimed to assess the diversity and agro-morphological characterization of 12 quantitative traits using multivariate analysis techniques among accessions of spring rice.

MATERIALS AND METHODS

Experimental site

The research was carried out at the field of Institute of Agriculture and Animal Science, Gauradaha Agriculture Campus during the spring season of 2022 in Gauradah-2, Jhapa under irrigated condition. The experiment site was situated in a tropical climatic zone and laid within the fertile Terai plains of Nepal. Geographically, it lies at altitude 79M asl, Latitude: 26° 33' 42" N, Longitude: 87° 43' 02" E and covers an area of 1,606 km^2. In majority sandy loam soil dominates in the research area. The pH of the research area was found to be moderately acidic i.e., 5.6.

Journal of Agriculture and Natural Resources (2023) 6(1):60-73
ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

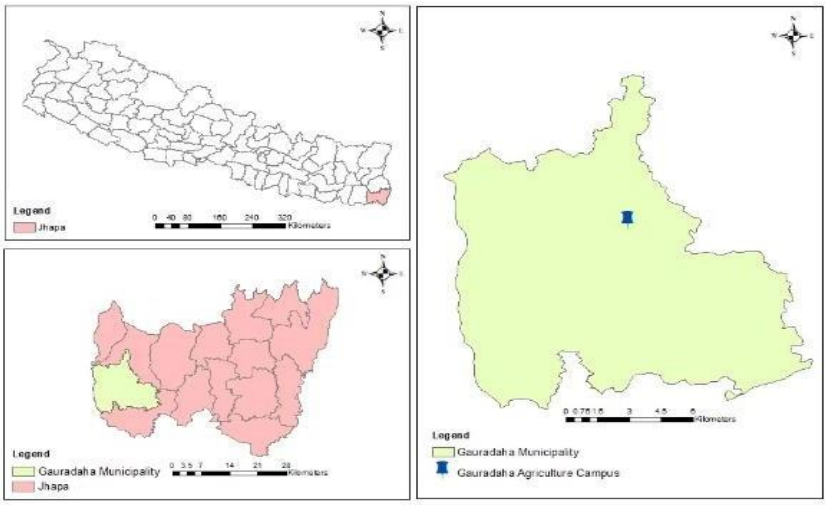

Figure 1: Site location of the research study

Plant materials

A total of 52 accession of spring rice were collected using various sources i.e., 24 from National Rice Research Program, Baniniya, Hardinath, 5 from National Genetic Resource Centre, Khumaltar, 20 from Anmol Seed, Surunga research station and 3 from same locality. A list of accessions are mentioned in Annex 1.

Experimental design and field layout

The research plot was laid out in alpha lattice design with two replications having 52 rice accessions as treatment in each block. Each replication possessed 4 blocks, and each block had 13 plots having treatments. Each plot was of the size of 3 m x 1.5 m. Inter block spacing was maintained at 0.5 meters and the distance between replications was 1 meter. Transplanting was done by maintaining spacing of 15 cm x 15 cm both for Row to Row and Plant to Plant. Two seedlings were planted per hill maintaining the total population within each plot of 200. A recommended dose of 120:40:40 kg/ha NPK was used in the form of Urea, Diammonium Phosphate (DAP), and Muriate of Potash (MOP). Full dose of phosphorous and potassium was applied and only half dose of nitrogen was applied at the basal dose. However, remaining nitrogen i.e., ¼ th was applied during tillering and the remaining ¼ th was applied during flowering. Other remaining agronomic practices was in accordance to (Krishi Diary, 2079).

Data collection and analysis

Data were collected for total 12 quantitative characters viz., plant height, flag leaf area (mm^2), tiller per hill, effective tiller per hill, days to flowering, days to maturity, panicle length(cm), grain sterility, length breadth ratio, total grain weight, grain yield (g), thousand grain weight (g) from five random plants from each plot and were cleaned by using Excel 2013. Multivariate Analysis (Principal Component Analysis and Cluster Analysis) was done by using Statistical Analysis System (SAS on Demand for Academics 9.4). Hierarchical clustering was performed to understand the patterns of variation among genotypes using Ward's method.

Journal of Agriculture and Natural Resources (2023) 6(1):60-73
ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

RESULTS AND DISCUSSION

Mean performance of agro-morphological traits

The mean performance of agro-morphological traits was given in Table 1.

Table 1: The mean performance (minimum, maximum, mean, standard deviation (SD) and coefficient of variance (CV)) for 12 quantitative traits

Variable	Mean	SD	CV (%)	Maximum Value	Accession	Minimum Value	Accession
GY (kg/ha)	2110.6	1302.96	61.73	4866.75	Hardinath-1	110.61	R341-153-SST
PH (cm)	102.72	11.63	11.3	122.2	IR18A1789	75.96	IR18A1069
FLA ($mm^{2)}$	27.29	5.84	21.4	45.925	IR13N152	14.4	P#14-27-SP#36
TPH	9.25	1.94	20.97	13.5	PR101	6	IR17A3036
ETPH	6.097	2.42	39.69	9.5	IR17A2796	1	IR17A3036
DF (days)	61.22	9.48	15.49	88	R341-153-SST	39	P#14-27-SP#36
DM (days)	93.67	10.90	11.64	117.01	R341-153-SST	74	IR17A1845
PL (cm)	24.36	2.31	9.48	27.56	IR17A3075	18.84	PR101
GS	33.67	17.62	52.33	70.92	R341-153-SST	8.38	Hardinath-1
GT (g)	1.54	0.71	46.10	2.84	IR17A3036	0.495	Sukkha-7
LBR	3.75	0.62	16.53	4.975	Sukkha-5	2.62	IR18A1789
TGW (g)	22.72	2.44	10.73	27.78	IR17A2854	18.55	P11-P2-3-1

DF-Days to Flowering, DM-Days to Maturity, ETPH-Effective Tiller Per Hill, FLA-Flag Leaf Area, GS-Sterile Grains, GT- Grain Per Effective Tiller, GY-Grain Yield, LBR- Length Breadth Ratio, PH- Plant Height, PL-Panicle Length, TGW-Thousand Grain Weight, TPH- Tiller Per Hill

Among all the accessions Hardinath-1(4866.75 kg/ha) produced the highest grain yield and the lowest grain yield was given by R341-153-SST (110.61 kg/ha). It also showed the highest coefficient of variation of 61.73% indicating the greatest variability of grain yield across the accessions than other traits. The result for this trait is parallel with the previous findings of (Gyawali *et al.*, 2018 and Shrestha *et al.*, 2021). Mean for plant height of thirty-six rice accessions was 102.72 cm with a maximum value of 122.2 cm in genotype IR18A1789. IR18A1069 was dwarf genotype with plant height of 75.96 cm. The highest flag leaf area was noted in genotype IR13N152 (45.92 mm^2) and minimum was observed on P#14-27-SP#36(14.4 mm^2). The numbers of tiller per plant were varied from PR101(13.5) to IR17A3036(6). Similarly, the highest effective tiller per hill was recorded in IR17A2796 (9.5) whereas IR17A3036 had the lowest one. The overall mean of flowering for the studied genotype was 61 days. The genotype R341-153-SST had taken maximum days (88 days) for 50% flowering meanwhile P#14-27-SP#36 had earliest 50% of flowering (39 days). The same genotype i.e. R341-153-SST showed the longest days of maturity(117days) while IR17A1845 had the shortest stature. The panicle length had the lowest coefficient of variation i.e. 9.48%. The genotype IR17A3075 (27.56cm) recorded the highest panicle length whereas PR101 has the shortest panicle length of (18.84 cm). Khan *et al.*, 2023, reported that panicle length, an important trait that directly affect the grain yield, varied with the planting techniques. Accession with lowest yield i.e. R341-153-SST had the greatest grain sterility (70.92) and the accession with highest yield recorded the lowest grain sterility (8.38) within the studied accessions. Thousand grain weight was found maximum in IR17A2854 (27.78 g) and the least was in P11-P2-3-1(18.55g). Dhungana *et al.* (2020) studied twenty rice genotypes and observed a significant difference for the weight of thousand grains. The

Journal of Agriculture and Natural Resources (2023) 6(1):60-73
ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

significant mean and genotypic difference among the studied genotypes across all twelve traits disclosed noticeable genetic variability and this finding was supported by Sharifi (2019), Ogunbayo *et al.*(2014), and Ilieva *et al.*(2017).

Principal component analysis

Principal Component Analysis (Tables 2 and 3) was used to assess the relative contributions of each 12 quantitative traits to total variability, providing a framework for trait selection. In the given study, the first three principal components exhibited eigenvalue greater than 1 and contributed 95.05% of the total variability. As the principal components with eigenvalues less than one are unlikely to hold practical significance so, PC1, PC2 and PC3 were only considered for the analysis which was supported by (Tejaswini *et al.*, 2018, Bassuony *et al.*, 2022 and Yadav *et al.*, 2013). Tables 2 and 3 reveal that the first component PC1 contributed maximum variability (48.09%) where the traits GY, PH, FLA, DF, DM, PL, GS and GT were loaded positively meanwhile, ETPH, TPH, LBR and TGW were negatively loaded. Likewise, PC2 accounted for 31.96% of the total variability. The major traits with positive loading in this principal component included TPH, ETPH, DF, DM, PL, GS and LBR while the rest GY PH, FLA GT and TGW were loaded negatively. Thus, this component differentiated those genotypes with higher tiller per hill, effective tiller per hill, and length breadth ratio. The third component PC3 delineated 14.99% contribution of total variance. Characters viz; DM, GS and GT contributed negatively and the remaining nine characters contributed positively. The positive and negative loading of each principal component elucidated the existence of correlation between the trait and the component. In comparison to remaining PCs the first component summarizes most of the variability inherent in the original data.

The given biplot illustrated the distribution of rice accessions based on PC1 and PC2 and showed the phenotypic variation among the studied genotypes.

Table 2: Principal component analysis (PCA) for studied rice accessions which illustrated the contribution of first four major components

Variables	PC1	PC2	PC3	PC4
Eigen value	5.77	3.83	1.80	0.29
Proportion	0.4809	0.3196	0.1499	0.0238
Cumulative variance	0.4809	0.8006	0.9505	0.9743

Furthermore, the analysis indicates that R341-153-SST, IR18A1789, and IR17A3036 displayed significant divergence in the studied traits, whereas most of the accessions were closely clustered and overlapped with one another and was supported by Sao *et al.* (2019). The initial components for traits accumulate a relatively high percentage of total variation generally above 80% which satisfactorily explains the variability among individual and effective for selection of elite parents (Cruz and Carneiro 2003). The variability among the accessions might be either due to genetic variation among the accessions, environment influences, or both.

Khan *et al.*, 2023 noted that biplot analysis shows the interaction between genotype and trait, acute angles (less than 90°) suggesting strong positive relations and obtuse angles (higher than 90°) indicating negative relations among the trait studied. The traits manifesting both positive and negative impacts on the principal components (PCs) serve as primary drivers of diversity and significantly contribute to distinguishing rice genotypes with each other. The

Journal of Agriculture and Natural Resources (2023) 6(1):60-73
ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

Table 3: Contribution of each trait for first three principal components with eigen value greater than one

Contribution of each traits	PC1	PC2	PC3
GY	0.36695	-0.2366	0.36695
PH	0.7536	-0.18998	0.5136
FLA	0.36212	-0.11357	0.87886
TPH	-0.3847	0.81068	0.31185
ETPH	-0.28844	0.9512	0.04636
DF	0.91315	0.27144	0.26454
DM	0.88358	0.354	-0.24414
PL	0.88522	0.24817	0.3458
GS	0.91265	0.0847	-0.30925
GT	0.26636	-0.95725	-0.01956
LBR	-0.27622	0.95388	0.03436
TGW	-0.81109	-0.27034	0.37754

Where, FLA-Flag Leaf Area, DM-Days to Maturity, DF-Days to Flowering, GS- Grain Sterility, PL-Panicle Length, PH- Plant Height, GT- Grain Per Effective Tiller, GY-Grain Yield, TGW-Thousand Grain Weight ETPH-Effective Tiller Per Hill, LBR- Length Breadth Ratio, TPH- Tiller Per Hill.

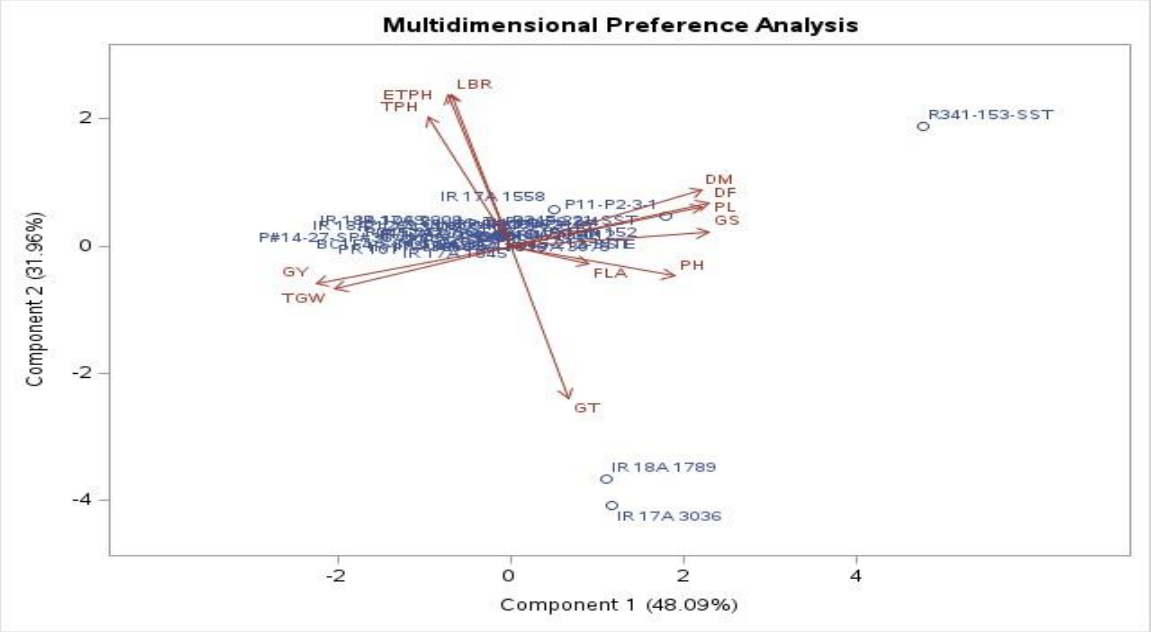

Figure 2: Principal Component Analysis (PCA) of studied rice accessions showing genotypic relationship in a graphical representation biplot on the basis of twelve quantitative characters

comprehensive examination of genotypes (Figure 2) revealed variation and notable differences, making them invaluable assets for rice germplasm improvement and was supported by (Sharifi and Ebadi, 2018). The given biplot analysis showed that the traits such as ETPH, TPH, and GT are positively corelated and the traits GY, TGW were negatively corelated with GS. Accessions IR18A1789 and IR17A3036 were best for grains with effective tiller. The analytical framework aids in detecting less significant traits and emphasizes those suitable for selection of key traits (Yan and Kang, 2003). The given study

Journal of Agriculture and Natural Resources (2023) 6(1):60-73
ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

demonstrated the examined genotypes were salient for different traits that will assist the breeders to develop elite varieties of rice in upcoming days. Genotypes IR17A137, R341-153-SST and IR13N152 were superior for flag leaf area. Hardinath-1, IR17A2949 and IR17A3019 have good potential for selection as these genotypes had lowest grain sterility among the studied genotypes. IR18A1269 and P#14-27-SP#36, and PR101 were genotypes with lowest height and can be used to develop dwarf varieties. IR17A2854, Sukkha-6, Sukkha-5, IR17A3137 and R345-213-INTE were best for developing long grain rice. Identifying and leveraging genotypes with key target traits as parent plants is essential for rice breeders to develop populations that lead to the creation of new, improved cultivars (Samonte *et al.*, 2013).

Cluster analysis

To visualize the pattern of clustering among 36 accessions, the mean performance of the clusters was calculated and presented on (Table 4) and (Figure 3). Similar research was performed on rice by (Rahman *et al*., 2011) for 21 rice genotypes based on 14 physiological traits.

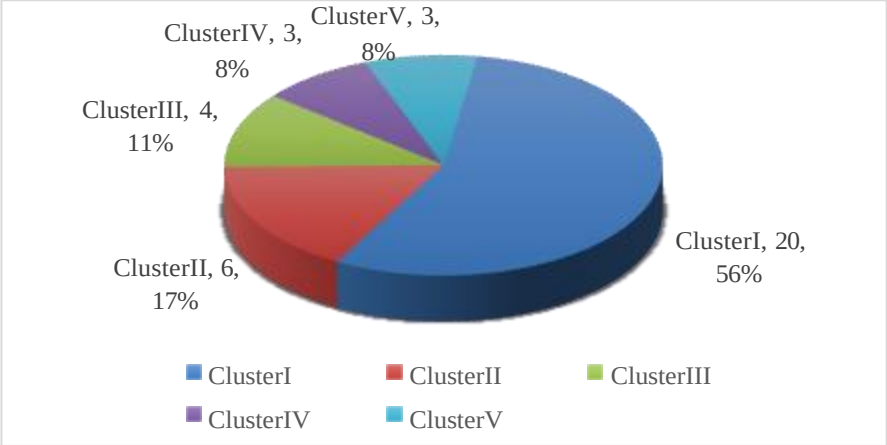

Figure 3: Frequency distribution and percentage value of five clusters for studied germplasm of rice.

The given table illustrated that there is significant variation of mean values between the traits, indicating the presence of variation among the rice accessions. Cluster I, II, III and IV consist of 20 (56%), 6 (17%), 4 (11%), 3 (8%) and 3 (8%) rice accessions respectively as shown in (Figure 3). Cluster –I had accessions having the highest value of LBR and TGW. Accession within the cluster-II had higher TPH, ETPH GY, intermediate GT and LBR in comparison with other clusters and minimum GS. Thus, Cluster II's genotypes has got good potential for breeding program to enhance the feature like number of effective tiller and grain yield. Also, these genotypes can be used to develop dwarf varieties. Cluster III has the highest value of FLA, GT and PH and higher value of TPH, intermediate value of DF and lowest value of ETPH and LBR. Similarly, cluster IV consists of higher value of ETPH, intermediate value of LBR and lower GT. Accession with early flowering and early maturity having lowest PL lies within this cluster. The accessions which took maximum days of flowering and maturity with highest panicle length and lowest grain yield were clubbed into Cluster V.

The dendrogram presented in (Figure 4) was obtained by using quantitative traits. Based on R-squared value of 0.5, total accessions were grouped in 5 clusters, explaining 50% of the

Journal of Agriculture and Natural Resources (2023) 6(1):60-73
ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

total variation present among the accessions. The distribution of the genotype within the 5 clusters was shown in (Table 6). The highest yielding genotype lied within the cluster II which includes majorly lines recommended by the research station. Genotypes such as Hardinath-1 with production (4866.75 kg/ha) followed by IR17A3019 (4364.32 kg/ha) and IR17A2949 (4122.55 kg/ha) were top three genotype as compared to the check genotype i.e. Chaite-5. Accessions within the same cluster demonstrate a strong genetic similarity among the genotypes, setting them apart from those in other clusters based on distinct traits which was supported by Khare *et al.* (2014).

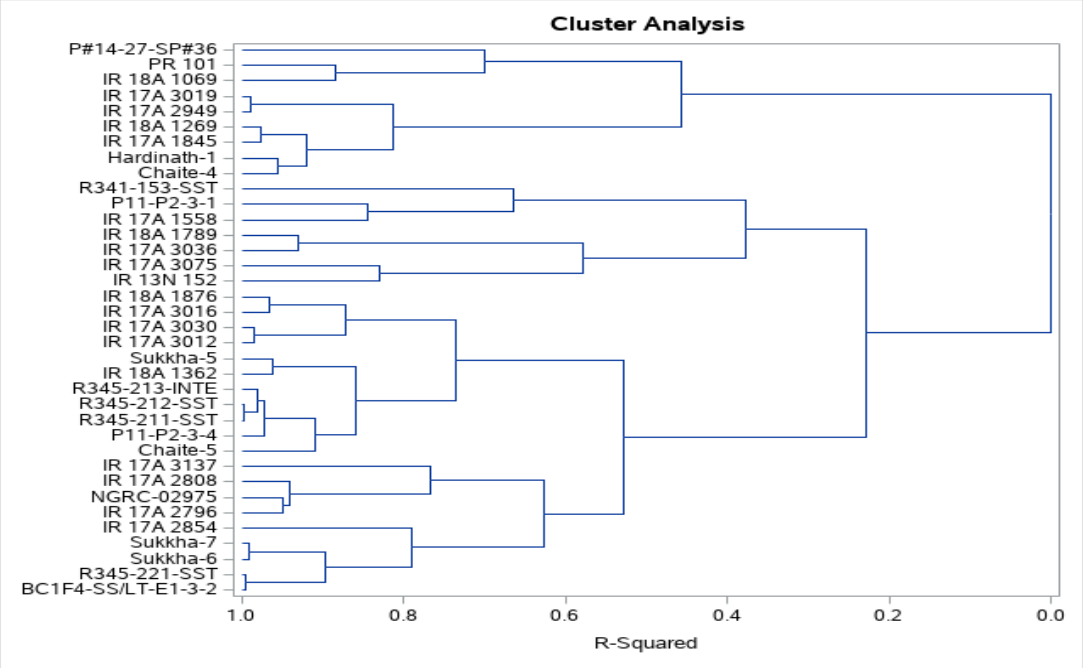

Figure 4: Dendrogram showing relationship among studied accessions in five clusters using Ward methods.

Table 4: Means of each quantitative trait under five clusters.

Cluster	I	II	III	IV	V
GY	2235.983	3818.128	847.99	1497.327	155.8167
PH	106.3805	92.315	113.5	77.07667	110.34
FLA	27.407	25.22333	35.2	19.66167	27.71
TPH	9.025	8.25	9.625	12.33333	9.166667
ETPH	7	7.416667	1.875	6.5	2.666667
DF	64.25	52.66667	63.25	42.33333	74.33333
DM	94.30375	84.33117	95.99675	82.50033	116.1667
PL	24.82	22.53	25.93	20.33	26.79
GS	31.79624	13.29487	50.32855	33.28337	65.02667
GT	1.39564	2.0002	2.59655	1.3066	0.45
LBR	4.0644	3.17325	3.117375	3.3772	4.06
TGW	23.537	22.01167	21.83125	22.85333	19.76

Where, FLA-Flag Leaf Area, DM-Days to Maturity, DF-Days to Flowering, GS- Sterile Grains, PL-Panicle Length, PH- Plant Height, GT- Grain Per Effective Tiller, GY-Grain Yield, TGW-Thousand Grain Weight ETPH-Effective Tiller Per Hill, LBR- Length Breadth Ratio, TPH- Tiller Per Hill

Journal of Agriculture and Natural Resources (2023) 6(1):60-73
ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

Table 5: Average intra and inter cluster distance between five clusters in examined genotypes of rice.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	.	5.328	6.763	4.600	5.729
Cluster II		.	6.249	4.428	4.637
Cluster III			.	4.372	8.530
Cluster IV					5.717
Cluster V					

Distance between the cluster centroid ranged from 4.38 to 8.53. The intra-cluster distance between cluster I and II was 5.33, cluster I and III was 6.76, cluster III, IV was 4.60 and cluster IV and V was 5.73. The inter cluster distance (Table 6) was maximum in between cluster II and cluster III and minimum in between cluster III and IV (4.38). Furthermore, the study revealed that the genotype had heterogeneity within the cluster and can be effective breeding materials for achieving optimal genetic progress in hybridization programs which was supported by (Mandavi *et al.*, 2023), (Yadav *et al.*, 2011) and (Shrestha *et al.*, 2021).

Table 6: Distribution of genotype and clustering pattern based on 12 quantitative traits within five clusters

Cluster	Number of accessions	Name of accessions
I	20	R345-211-SST, R345-212-SST, BC1F4-SS/LT-E1-3-2, R345-221-SST, Sukkha-6, Sukkha-7, IR17A3012, IR17A3030, R345-213-INTE, P11-P2-3-4, IR17A 3016, IR18A1876, IR18A1362, Sukkha-5, IR17A2796, NGRC-02975, IR17A2808, Chaite-5, IR17A 2854, IR17A 3137
II	6	IR17A2949, IR17A3019, IR17A1845, IR18A1269, Chaite-4, Hardinath-1
III	4	IR17A3036, IR18A1789, IR13N152, IR17A3075
IV	3	IR18A1069, PR101, P#14-27-SP#36
V	3	P11-P2-3-1, R341-153-SST, P11-P2-3-1, R341-153-SST

CONCLUSION

From the overall findings of the study concluded that there exists a significant variation among the accession for yield and yield related traits, highlighting a potential for the future breeding programs. The genotypes with high mean value and larger intra cluster distance can be useful assets for selecting pioneer parent lines for hybridization in rice. Cluster II was clubbed with superior genotypes with highest yield, effective tillers and dwarf in nature followed by cluster I, III, IV and V for traits like thousand grain weight, grain per effective tiller days to maturity, flag leaf area and panicle length respectively. Hardinath-1, IR17A2796, IR17A3036 and IR17A2854 were promising genotypes based on preliminary evaluation of important traits viz., yield, effective tiller per hill, grain per effective tiller and thousand grain weight respectively. In essence, the explored accessions have huge scope for improving productivity of rice in Nepal via strategic breeding intervention.

ACKNOWLEDGEMENT

Authors' sincere gratitude goes to NRRP, Hardinath, NGRC Khumaltar, Farmers and Anmol Seed Company for providing the valuable accessions for this research.

ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

Authors' Contributions

B. Bhusal, B. Bhattarai, R. Badu, A.K. Yadav, S. S. Loniya, M. Sapkota, A. Gyawali, S. Timilsina and D. K. Ayer conceptualized and executed the experiment, collected and analyzed data, wrote this paper.

Conflict of interest

The author declares no conflicts of interest regarding publication of this manuscript.

REFERENCES

AITC. (2021). Agriculture and Livestock Diary 2079. Agriculture Information and Training Centre Hariharbhawan, Lalitpur.

Aswini, M. S., Lenka, B., Shaniware, Y. A., Pandey, P., Dash, A. P., & Haokip, S. W. (2023). The Role of Genetics and Plant Breeding for Crop Improvement: Current Progress and Future Prospects. *International Journal of Plant & Soil Science, 35*(20), 190-202.

Bassuony, N. N., Zsembeli, J., Nofal, R. S., Essa, W. M., & Fazaa, M. (2022). Genetic variability of some physiological traits, yield components and grain quality characters in rice entries. *Agriculture (Pol'nohospodárstvo), 68*(4), 143-154.

Cruz CD and Carneiro PCS (2003). Biometric models applied to genetic improvement. Vol.2. University Press. Vicosa. 585p.

Devi M., Jyothulal D.P.B., Krishnaveni1 B. and. Rao V.S. 2019. Genetic Divergence Studies in Rice (Oryza sativa L.) Hyrids for Yield, Yield Component Traits and Quality Parameters. *Int. J. Curr. Microb. Appl. Sci., 8*(6),1577-1583.

Dhakal, A., Pokhrel, A., Sharma, S., & Poudel, A. (2020). Multivariate analysis of phenotypic diversity of rice (Oryza sativa L.) landraces from Lamjung and Tanahun Districts, Nepal. *International journal of agronomy, 2020*(1), 8867961.

Dhungana, A., Puri, C., Shah, K., Yogi, S., Dhakal, D. P., Acharya, B., & Shrestha, J. (2020). Screening rice genotypes for brown spot disease resistance. *Tunisian Journal of Plant Protection, 15*(2), 29-39.

Guru, T., Padma, V., Reddy, D. V. V., Rao, P. R., Rao, D. S., Ramesh, T., & Radhakrishna, K. V. (2017). Genetic diversity analysis for yield attributing traits in rice genotypes. *Research on Crops, 18*(2), 311-315.

Gyawali, S., Poudel, A., & Poudel, S. (2018). Genetic variability and association analysis in different rice genotypes in mid hill of western Nepal. *Acta Scientific Agriculture, 2*(9), 69-76.

Hair, J. F., Anderson, R. E., Tatham, R. L., & Black, W. C. (1998). Multivariate data analysis. englewood cliff. *New jersey, USA, 5*(3), 207-2019.

Ilieva, V., Ruzdik, N. M., Karov, I., Mihajlov, L., Ilievski, M., & Kovacevik, B. (2017). Genetic variability for yield and some yield-related traits in rice (Oryza sativa L.). *Journal of Agriculture and Plant Sciences, 15*(1/2), 75-80.

Joshi, B. K. (2017). Local germplasm of rice in Nepal: Diversity, characters and uses. Rice Science and Technology in Nepal [Internet]. Khumaltar, Nepal: Crop Development Directorate (CDD), and Agronomy Society of Nepal (ASoN), 158-78.

Kandel, B. P., & Shrestha, J. (2018). Characterization of rice (Oryza sativa L.) germplasm in Nepal: A mini review. *Farming and Management, 3*(2), 153-159.

Khan, M. A. R., Mahmud, A., Islam, M. N., Ghosh, U. K., & Hossain, M. S. (2023). Genetic variability and agronomic performances of rice genotypes in different growing seasons in Bangladesh. *Journal of Agriculture and Food Research, 14*, 100750.

ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

Khare, R., Singh, A. K., Eram, S., & Singh, P. K. (2014). Genetic variability, association and diversity analysis in upland rice (Oryza sativa L). *SAARC J. Agri., 12*(2), 40-51

Lin, M. S. (1991). Genetic base of japonica rice varieties released in Taiwan. Euphytica, 56(1),

Maji, A. T., & Shaibu, A. A. (2012). Application of principal component analysis for rice germplasm characterization and evaluation. *Journal of Plant Breeding and Crop Science, 4*(6), 87-93.

Mandavi, J. S., Lokesh, P., Nair, S. K., Sao, A., Verulkar, S. B., & Saxena, R. R. (2023). Cluster analysis of 55 Rice (Oryza sativa L.) germplasm. *International Journal of Statistics and Applied Mathematics, SP-8(*6), 71-74

Mohanlal, V. A., Saravanan, K., & Sabesan, T. (2023). Application of principal component analysis (PCA) for blackgram [Vigna mungo (L.) Hepper] germplasm evaluation under normal and water stressed conditions. *Legume Research, 46*(9), 1134-1140.

Naaz, S., Pandey, V., & Yadav, H. K. (2022). Evaluation of genetic diversity in rice (Oryza sativa L. ssp. Indica) accessions using SSR marker. *Vegetos, 35*(4), 961-968.https://doi.org/10.1007/s42535-022-00378-3

Ogunbayo, S. A., Si&e, M., Ojo, D. K., Sanni, K. A., Akinwale, M. G., Toulou, B., ... & Gregorio, G. B. (2014). Genetic variation and heritability of yield and related traits in promising rice genotypes (Oryza sativa L.). *Journal of Plant Breeding and Crop Science, 6*(11), 153-159.

Rahman, M. M., Hussain, A., Syed, M. A., Ansari, A., & Mahmud, M. A. A. (2011). Comparison among clustering in multivariate analysis of rice using morphological traits, physiological traits and simple sequence repeat markers. American-Eurasian *Journal of Agriculture and Environmental Science, 11*(6), 876-882.

Roy, S. K., Ali, M. Y., Jahan, M. S., Saha, U. K., Ahmad-Hamdani, M. S., Hasan, M. M., & Alam, M. A. (2014). Evaluation of growth and yield attributing characteristics of indigenous Boro rice varieties. *Life Science Journal, 11*(4), 122-126.

SAMONTE, S. O. P., Tabien, R. E., & Wilson, L. T. (2013). Parental selection in rice cultivar improvement. *Rice science, 20*(1), 45-51.

Sao, R., Saxena, R. R., & Sahu, P. K. (2019). Assessment of genetic variation and diversity in rice germplasm based on principal component analysis. *Journal of Plant Development Sciences, 11*(12), 725-730.

Shah, B.H., F.S. Hamid, S. Islam, N. Ahmed, F. Ahmad, N. Khan, and Q. Zaman. 2020. Evaluation of elite rice (Oryza sativa L.) lines for yield and yield components. *Pakistan Journal of Agricultural Research, 33*(1), 135-139. DOI | http://dx.doi.org/10.17582/journal.pjar/2020/33.1.135.139

Sharifi, P. (2019). Genetic variation for grain yield, yield components and qualitative traits in rice (Oryza sativa L.) mutants. *Genetika, 51*(3), 829-843.

Sharifi, P., & Ebadi, A. A. (2018). Relationships of rice yield and quality based on genotype by trait (GT) biplot. *Anais da Academia Brasileira de Ciências, 90*(01), 343-356.

Shrestha, J., Subedi, S., Kushwaha, U. K. S., & Maharjan, B. (2021). Evaluation of growth and yield traits in rice genotypes using multivariate analysis. *Heliyon, 7*(9).

Shrestha, J., Subedi, S., Subedi, N. R., Subedi, S., Kushwaha, U. K. S., Maharjan, B., & Subedi, M. (2021). Assessment of variability, heritability and correlation in rice (Oryza sativa L.) genotypes. *Natural Resources and Sustainable Development, 11*(2), 181-192

Tejaswini, K. L. Y., Manukonda, S., Kumar, B. R., Rao, P. R., & Raju, S. K. (2018). Application of principal component analysis for rice f5 families characterization and evaluation. *Emergent Life Sciences Research, 4*, 72-84.

ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

Tiwari, S., Singh, Y., Upadhyay, P. K., & Koutu, G. K. (2022). Principal component analysis and genetic divergence studies for yield and quality-related attributes of rice restorer lines. *Indian Journal of Genetics and Plant breeding*, *82*(01), 94-98.

Watanabe, Y., Matsuo, T., Futsuhara, Y., Kikuchi, F., & Yamaguchi, H. (1997). Genomic constitution of genus Oryza. *Tokyo: food and agriculture policy research center*.

Yan, W., & Kang, M. S. (2002). GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC press.

Journal of Agriculture and Natural Resources (2023) 6(1):60-73
ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

Annex 1: List of accessions of rice collected along with place of collection.

S. N	Name of Accession	Places of collection
1	GM/SS PLOT-55	Anmol Seed, Surunga
2	GM/SS PLOT-83	Anmol Seed, Surunga
3	R341-153-SST	Anmol Seed, Surunga
4	R345-211-SST	Anmol Seed, Surunga
5	R345-213-INTE	Anmol Seed, Surunga
6	P11-P2-3-4	Anmol Seed, Surunga
7	R343-188-SST	Anmol Seed, Surunga
8	R345-212-SST	Anmol Seed, Surunga
9	R345-221-SST	Anmol Seed, Surunga
10	BC1F4-SS/LT-E1-3-2	Anmol Seed, Surunga
11	P#14-27-SP#36	Anmol Seed, Surunga
12	P11-P2-3-1	Anmol Seed, Surunga
13	R341-150-SST	Anmol Seed, Surunga
14	R342-165-SST	Anmol Seed, Surunga
15	R342-168-SST	Anmol Seed, Surunga
16	R344-193-SST	Anmol Seed, Surunga
17	R344-196-SST	Anmol Seed, Surunga
18	R344-202-SST	Anmol Seed, Surunga
19	PR101	Anmol Seed, Surunga
20	Chaite-4	Locality, Gauradaha
21	IR17A3036	National Rice Research Program, Baniniya
22	IR18A1789	National Rice Research Program, Baniniya
23	IR18A1269	National Rice Research Program, Baniniya
24	IR17A1845	National Rice Research Program, Baniniya
25	IR17A3019	National Rice Research Program, Baniniya
26	IR17A3075	National Rice Research Program, Baniniya
27	IR17A3030	National Rice Research Program, Baniniya
28	IR18A1876	National Rice Research Program, Baniniya
29	IR17A1558	National Rice Research Program, Baniniya
30	IR18A1069	National Rice Research Program, Baniniya
31	IR18A1042	National Rice Research Program, Baniniya
32	IR17A2854	National Rice Research Program Baniniya
33	IR13N152	National Rice Research Program Baniniya
34	IR18A1362	National Rice Research Program Baniniya
35	IR17A2808	National Rice Research Program, Baniniya
36	IR17A2796	National Rice Research Program, Baniniya
37	IR17A3016	National Rice Research Program, Baniniya
38	IR17A3012	National Rice Research Program, Baniniya
39	IR17A3137	National Rice Research Program, Baniniya
40	IR17A2947	National Rice Research Program, Baniniya
31	IR18A1042	National Rice Research Program, Baniniya
32	IR17A2854	National Rice Research Program, Baniniya
33	IR13N152	National Rice Research Program, Baniniya
34	IR18A1362	National Rice Research Program, Baniniya
35	IR17A2808	National Rice Research Program, Baniniya
36	IR17A2796	National Rice Research Program, Baniniya
37	IR17A3016	National Rice Research Program, Baniniya
38	IR17A3012	National Rice Research Program, Baniniya
39	IR17A3137	National Rice Research Program, Baniniya
40	IR17A2947	National Rice Research Program, Baniniya
41	IR16A3838	National Rice Research Program, Baniniya
42	IR17A2949	National Rice Research Program, Baniniya
43	Hardinath-1	National Rice Research Program, Baniniya
44	Chaite-5	National Rice Research Program, Baniniya
45	NGRC-02975	National Genetic Resource Centre, NGRC, Khumaltar
46	NGRC-02976 (Sukkha-5)	National Genetic Resource Centre, NGRC,

Journal of Agriculture and Natural Resources (2023) 6(1):60-73
ISSN: 2661-6270 (Print), ISSN: 2661-6289 (Online)
DOI: https://doi.org/10.3126/janr.v6i1.71880

S. N	Name of Accession	Places of collection
		Khumaltar
47	NGRC-02977 (Sukkha-6)	National Genetic Resource Centre, NGRC, Khumaltar
48	NGRC-09061 (Sukkha-7)	National Genetic Resource Centre, NGRC, Khumaltar
49	NGRC-09058 (Sukkha-3)	National Genetic Resource Centre,NGRC, Khumaltar
50	Ranjit	Locality, Gauradaha
51	Sunaulo suganda	Anmol Seed, Surunga
52	Loktantra	Anmol Seed, Surunga