International Journal of Economic Plants

https://ojs.pphouse.org/index.php/IJEP

Crossref

IJEP November 2025, 12(6): 01-06

Article IJEP6576a

Full Research

Natural Resource Management

Doi: HTTPS://DOI.ORG/10.23910/2/2025.6576a

Assessment of Genetic Diversity for Yield and Grain Quality Traits among Heat Tolerant Germplasm Accessions of Rice (*Oryza sativa* L.)

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Article History

Received on 23rd July, 2025
Received in revised form on 03rd November, 2025
Accepted in final form on 15th November, 2025
Published on 28th November, 2025

Abstract

The present experiment was conducted during *summer,* 2013 (February–May) and *kharif,* 2013 (June–October) at research cum instructional farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) to evaluate yield attributing and grain quality traits among 33 heat tolerant rice germplasm lines including three standard checks (Mahamaya, Karma-Mahsuri and Indira Sona). Based on the result experimental material were grouped into 5 clusters each for both grain yield and grain quality traits. Cluster I (11) carried highest number of genotypes for grain yield. For grain quality traits cluster II (13) was notified to retain highest accession numbers. The highest inter-cluster distance was observed between cluster V and cluster III for yield traits (8.351) as well as grain quality traits (7.675) indicating the presence of wide genetic diversity among accessions to be used in hybridization programme for improving grain quality traits and maximize yield. The highest cluster mean value was observed for total spikelet plant^{-1} (256.7) and hulling % (81.54) might offer for direct selection of plants for higher yield and better grain quality traits. Cluster III and cluster IV group members were recognized as the most important individuals as they possessed highest cluster mean for several agronomic as well as grain quality traits such as productive tiller plant^{-1}, 100 seed wt., harvest index, spikelet fertility%, biological yield, kernel length, hulling%, milling%, head rice recovery (HRR) and amylose content. These individuals would be used in future breeding programme to transmit genes of quality seeds into off-springs.

Keywords: Germplasm, heat tolerant, cluster analysis, hybridization, harvest index

1. Introduction

The cultivated rice (*Oryza sativa* L. 2n=24) is the principal cereal and significant calorie source for one-half to two-third of the world's population (Sen et al., 2020). Globally, rice is harvested at 713.10 mt for 2024–25 in the cultivated area of 169.88 mha and productivity of 4740 kg ha^{-1} (Anonymous, 2025). Over the past decade (2014–2023), the average global surface temperature has risen by 1.20 °C, reaching an increase of 1.45 °C in 2023 (Yu et al., 2024), which was noted warming at 0.85 °C over the period (1880–2012) and projected to increase by the end of the 21st century (2081–2100) by 2.6 °C–4.8 °C (Anonymous, 2014); 3.3 °C to 5.7 °C (Lee and Romero, 2023). Summer rice is considered as the most critical season to cultivate because not only water scarcity but also heat stress becomes the most limiting factor due to spikelet sterility that leads to poor grain yield. It is estimated that every 1°C increase in global mean temperature will reduce yields of wheat by 6.0%, maize by 7.4%, soybean 3.1% and rice by 3.2%, 10%, 21% respectively by Zhao et al., (2017), Peng et al., (2004) and Liu et al., (2021). Global warming and climate change has become a serious limiting factor to the productivity and grain quality of field crops worldwide therefore urgent need of breeding heat-tolerant rice variety (Janni et al., 2020; Tang et al., 2023). The optimal temperature range for rice seedling growth is typically between 25–28 °C (Sarker et al., 2024). The most critical stage to high temperatures includes the flowering stage, reproductive and grain-filling stages (Jagadish et al., 2007; Fahad et al., 2017). High temperature stress affects the plants during life cycle in various ways such as heat stress (42–45 °C) during the seedling stage decreased root growth and eventually seedling death (Xu et al., 2021; He et al., 2023). When rice plant is exposed to high temperature (39–40 °C) endosperm get collapsed and seed viability get reduced significantly (Begcy et al., 2018), spikelet number was reduced (Soda et al., 2018), pollen viability and seed setting rate were lowered (Shrestha et al., 2022), during grain filling stage lowered grain weight (Wu et al., 2021). Quality parameters of rice that are main contributor are hulling %, milling %, HRR, amylose content and gel consistency. The elevated temperature significantly reduced grain length, milled rice rate and head rice rate by whereas, increased grain thickness, chalky area and chalkiness respectively (Liu et al., 2021). Physico-chemical properties of grains are not only determined by maturity time, but it's an inherent property of plant that is governed by genes hence, breeding programme is an effective and useful tool to enhance grain quality properties of crop plants (Naik et al., 2023). Broad genetic base in germplasm plays a vital role in favorable alleles integration (Thuy et al., 2023). Rice landraces have shown excellent adaptation to local conditions and genetic potential for rice improvement, particularly for stress tolerance and quality improvement. The presence of wide genetic variability in the population is a prerequisite for an efficient breeding programme for the development of stable varieties (Pravalika et al., 2024; Gupta, et al., 2022; Sreedhar, 2018). Cluster analysis, a multivariate technique that has been done in this study for selection of potential genotypes based on estimation of genetic diversity among rice genotypes (Nagamani et al., 2022; Naik et al., 2021; Pillai et al., 2020). The present experiment was conducted to evaluate yield attributing and grain quality traits among 33 heat tolerant rice germplasm lines including three standard checks to be used in future breeding programme to develop climate resilient cultivars.

2. Materials and Methods

The present experiment was conducted during *summer,* 2013 (February–May) and *kharif,* 2013 (June–October) at research cum instructional farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.). Raipur the capital of the Chhattisgarh state lied at 21°16'N latitude and 81°36'E longitude with an altitude of 289.60 m above mean sea level. The experimental material comprised of 33 indigenous rice germplasm accessions (source- IGKV, Raipur) including three standard checks namely Mahamaya, Karma-Mahsuri and Indira Sona. The experimental material was raised under randomized complete block design (RCBD) with two replications. Twenty-four days old seedlings were transplanted at 20×15 cm^2 row to plant spacing. Five representative plants of each accession from each replication were randomly selected to record observations for 35 quantitative (16) and grain quality (20) characters. The mean value of five representative sample were used for analysis of genetic divergence using D^2 statistics suggested by Mahalanobis (1936). The genotypes were grouped into different clusters by applying Euclidean distances and similarity index (Spark, 1973).

3. Results and Discussion

Cluster analysis for grain quality and quantitative characters was estimated separately. For quantitative characters all genotypes were grouped into 05 clusters (Table 1) and 05 clusters again for grain quality characters (Table 2) using non-hierarchical Euclidean cluster analysis. For yield attributing parameters, maximum number of genotypes was identified under cluster I (11) followed by cluster IV (9). The minimum number of genotypes were reported under cluster V (3). For grain quality parameters, maximum genotypes were observed in cluster II (13) followed by cluster IV (7) and the minimum genotypes felled under cluster I and V each contain 4 genotypes. Similar kind of results were also observed by the following researchers such as Sree et al., 2023, Bhusal et al., 2023; Rao et al., 2021; Akter et al., 2018; Khaire et al., 2022; Bhargavi et al., 2023. Grouping of genotypes revealed that within the cluster similar type plants than the genotypes in another cluster. The distribution of genotypes from different geographical origins into various clusters was at random indicating that there was no influence of ecological location on divergence. Similar findings of non-correspondence of geographic origin with genetic diversity were also reported by Banumathy et al. (2010) and Devi et al. (2020).

Table 1: Grouping of 33 heat tolerant rice accessions in different clusters for yield attributing traits

Cluster no.	No. of genotypes	Genotype name
I	11	IR 58025A×Danteshwary-Dagaddeshi, IR 58025A×Karmamahsuri, IR 58025A ×TOX981-11-2-3, IR 58025A ×Suraksha, IR 79156A ×Danteshwary-Dagaddeshi, IR 79156A ×Karmamahsuri, IR 79156A×Suraksha, CRMS 32A×Danteshwary-Dagaddeshi, CRMS 32A×Karmamahsuri, CRMS 32A×Suraksha, Indira Sona
II	06	IR 58025A, IR 79156A, CRMS 32A, Kanakgopala, IR 79156A×Kanakgopala, IR 79156A×Inger-2-114
III	04	Danteshwary-Dagaddeshi, Karmamahsuri, Suraksha, Mahamaya
IV	09	Bagdidhan, Inger-2-114, TOX981-11-2-3, IR58025A×Bagdidhan, IR58025A ×Inger-2-114, IR 79156A×Bagdidhan, IR 79156A×TOX981-11-2-3, CRMS 32A×Bagdidhan, CRMS 32A×TOX981-11-2-3
V	03	IR58025A×Kanakgopala, CRMS 32A×Kanakgopala, CRMS 32A×Inger-2-114

Intra and inter-cluster distances result for both grain yield and grain quality characters were depicted in table 3 and table 4. The highest intra-cluster distance was recorded for cluster III (3.291) followed by cluster IV (3.013) and the lowest intra-cluster distance was estimated in cluster I (2.057) for

Table 2: Grouping of 33 heat tolerant rice accessions in different clusters for grain quality traits

Cluster no.	No. of genotypes	Genotype name
I	04	Kanakgopala, IR58025A×Kanakgopala, IR 79156A×Bagdidhan, CRMS 32A×Kanakgopala
II	13	IR 58025A×Bagdidhan, IR 58025A×Danteshwary-Dagaddeshi, IR 58025A×Karmamahsuri, IR 58025A×TOX981-11-2-3, IR 58025A×Suraksha, IR 79156A×Kanakgopala, IR 79156A×Danteshwary-Dagaddeshi, IR 79156A×Inger-2-114, IR 79156A×Karmamahsuri, IR 79156A×TOX981-11-2-3, CRMS 32A×Danteshwary-Dagaddeshi, CRMS 32A×Karmamahsuri, CRMS 32A×TOX981-11-2-3
III	05	Bagdidhan, Danteshwary-Dagaddeshi, Inger-2-114, TOX981-11-2-3, CRMS 32A×Bagdidhan
IV	07	Karmamahsuri, Suraksha, IR 58025A×Inger-2-114, IR 79156A×Suraksha, CRMS 32A×Suraksha, Indira Sona, Maha-maya
V	04	IR 58025A, IR 79156A, CRMS 32A, CRMS 32A×Inger-2-114

Table 3: Estimation of intra and inter-cluster distance among 33 rice accessions (Quantitative traits)

Clusters	I	II	III	IV	V
I	2.057				
II	3.576	2.598			
III	3.543	4.659	3.291		
IV	3.444	4.915	4.523	3.013	
V	7.058	5.032	8.351	6.848	2.381

*Diagonal values=Intra-cluster distances

Table 4: Estimation of intra and inter-cluster distance among 33 rice accessions (Grain quality traits)

Clusters	I	II	III	IV	V
I	2.637				
II	4.977	2.959			
III	4.809	5.355	2.855		
IV	5.916	3.634	4.393	3.550	
V	5.821	4.242	7.675	6.235	2.638

*Diagonal values=Intra-cluster distances

yield attributing traits. For grain quality traits the highest intra-cluster distance was recorded for cluster IV (3.550) followed by cluster II (2.959) and the lowest intra-cluster distance was recorded in cluster I (2.637). The results revealed that accession under highest intra-cluster distance cluster were genetically diverse, whereas genetically similar plants felled under lowest intra-cluster distances. Hence, selection of genotypes within these clusters might be exercised for improvement through inter-varietal hybridization (Bhusal et al., 2023; Khaire et al., 2022; Rao et al., 2021).

The highest inter-cluster distance was recorded between cluster V and cluster III (8.351) followed by cluster V and cluster I (7.058) whereas, lowest inter-cluster distance was recorded between cluster IV and cluster I (3.444) for yield attributing traits. For grain quality traits the highest inter-cluster distance was recorded between cluster V and cluster III (7.675) followed by cluster V and IV (6.235) whereas, lowest inter-cluster distance was recorded between cluster IV and cluster II (3.634). The highest inter-cluster distance indicated the presence of wide genetic diversity in between groups might offer selection of pronounced individuals for hybridization and production of elite type hybrids/progenies. The least inter-cluster distance states that closed relationship between the genotypes and hence, might not be emphasized upon to be used in hybridization programme. Narrow genetic base did not give rise to produce vigorous progeny (Nagamani et al., 2022; Khaire et al., 2022; Rao et al., 2021; Akter et al., 2018).

The cluster mean value showed ample variation among genotypes of different clusters. Cluster mean analysis for yield traits (Table 5) and grain quality traits (Table 6) explained information such that highest cluster mean for grain yield plant^{-1} and panicle length were established by cluster I. Highest cluster mean for productive tiller plant^{-1}, 100 seed wt., and harvest index were noticed by cluster III whereas, cluster IV exhibited the highest cluster mean for days to 50% flowering, plant height, flag leaf length, flag leaf area, pollen fertility%, fertile spikelet plant^{-1}, spikelet fertility % and biological yield. Cluster V illustrated highest cluster mean for flag leaf width, sterile spikelet plant^{-1} and total spikelet's plant^{-1} for the yield attributing traits. Similar kind of results were supported by Sar and Kole (2023); Bhusal et al., 2023; Rao et al., 2021; Akter et al., 2018; Banumathy et al. (2010); Bose and Pradhan (2005).

For grain quality traits, cluster III was notified as a highest cluster mean for brown rice breadth, hulling %, milling %, elongation ratio, gel consistency, amylase content and HRR. Cluster IV showed highest cluster mean for paddy breadth, brown rice length, kernel length, kernel breadth, cooked rice length and cooked rice breadth. Cluster V exhibited highest cluster mean for paddy length, paddy L/B ratio, brown rice L/B ratio and kernel L/B ratio. Highest cluster mean for protein content and cooked rice L/B ratio was observed in cluster I (Nagamani et al., 2022; Rao et al., 2021; Akter et al., 2018).

Table 5: Cluster mean for different yield attributing traits among 33 rice accessions

Sl. No.	Characters	I	II	III	IV	V
1.	DFF	88.18	92.17	92.12	95.28	94.0
2	Plant height	108.75	95.42	109.14	129.63	99.82
3.	Flag leaf length	34.32	32.94	32.95	36.7	35.43
4.	Flag Leaf width	1.23	1.32	1.33	1.60	1.65
5.	Flag Leaf area	32.47	33.2	33.24	44.94	44.79
6.	Productive tiller plant^{-1}	11.68	10.67	16.75	9.44	8.33
7.	Panicle length	28.31	26.97	22.54	26.92	27.73
8.	Pollen fertility %	74.08	25.39	77.18	78.12	11.87
9.	Fertile spikelet plant^{-1}	113.02	80.25	87.12	131.63	44.43
10.	Sterile spikelet plant^{-1}	66.00	85.75	42.38	57.57	212.27
11.	Total spikelet plant^{-1}	179.02	166	129.5	189.2	256.7
12.	Spikelet fertility %	63.02	48.3	67.8	68.44	16.77
13.	100 seed wt.	2.55	2.16	3.06	2.60	1.88
14.	Biological yield plant^{-1}	57.63	41.92	56.19	73.57	57.37
15.	Harvest index	41.73	26.7	42.33	30.7	9.48
16.	Grain yield plant^{-1}	22.55	12.34	22.15	21.63	11.1

Table 6: Cluster mean for different grain quality traits in 33 rice accessions

Sl. No.	Characters	I	II	III	IV	V
1.	Paddy Length	8.41	9.95	8.7	9.87	10.16
2	Paddy Breadth	2.35	2.48	2.84	2.89	2.31
3.	Paddy L/B	3.61	4.03	3.09	3.44	4.40
4.	Brown R Length	6.41	7.49	6.5	7.50	7.29
5.	Brown R Breadth	2.07	2.12	2.44	2.41	1.83
6.	Brown R L/B ratio	3.11	3.55	2.68	3.12	4.00
7.	Kernel Length	5.59	6.82	6.08	6.96	6.68
8.	Kernel Breadth	1.98	2.02	2.21	2.24	1.75
9.	Kernel L/B Ratio	2.84	3.39	2.76	3.11	3.94
10.	Cooked R Length	8.12	9.3	8.76	9.54	8.55
11.	Cooked R Breadth	2.71	3.03	3.28	3.36	3.00
12.	Cooked R L/B	3.06	3.00	2.67	2.84	2.85
13.	Hulling %	81.38	81.50	81.54	79.9	80.72
14.	Milling%	74.15	75.26	77.98	73.05	76.8
15.	Elongation Ratio	1.30	1.24	1.35	1.27	1.15
16.	Gel consistency	5.93	6.77	6.78	6.11	2.97
17.	Amylose content	17.91	20.6	23.52	19.67	16.31
18.	Protein	10.22	7.47	8.8	8.81	9.79
19.	HRR	62.43	60.15	68.84	52.19	60.24

4. Conclusion

Identification of the best heat tolerant lines with higher grain yield and good grain quality for the breeding of climate resilient variety was the main goal of the study. Cluster V and cluster III were identified as the most genetically diverse group. Two germplasm lines, CRMS 32A×Inger-2-114 (cluster V) and Danteshwary-Dagaddeshi (cluster III) were identified as a common line for both grain yield as well as grain quality traits might give opportunity to cross and produce hybrids with quality seeds.

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