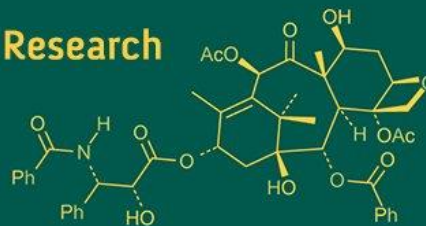


## International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693  
ISSN Online: 2617-4707  
NAAS Rating (2025): 5.29  
IJABR 2025; 9(7): 1692-1696  
[www.biochemjournal.com](http://www.biochemjournal.com)  
Received: 22-05-2025  
Accepted: 25-06-2025

**Vijaya H Bhajipale**  
PG Scholar, Department of  
Genetics and Plant Breeding,  
College of Agriculture, Nagpur,  
Maharashtra, India

**Dr. SA Patil**  
Assistant Professor,  
Agricultural Botany Section,  
College of Agriculture, Nagpur,  
Maharashtra, India

**Dr. MP Meshram**  
Senior Rice Breeder,  
Agricultural Research Station,  
Sakoli, District Bhandara,  
Maharashtra, India

**Dr. PV Shende**  
Professor, Agricultural Botany  
Section, College of Agriculture,  
Nagpur, Maharashtra, India

**Dr. Vandana S Madke**  
Assistant Professor,  
Agricultural Botany Section,  
College of Agriculture, Nagpur,  
Maharashtra, India

**Corresponding Author:**  
**Vijaya H Bhajipale**  
PG Scholar, Department of  
Genetics and Plant Breeding,  
College of Agriculture, Nagpur,  
Maharashtra, India

## Genetic divergence analysis in advanced breeding lines of rice (*Oryza sativa* L.)

**Vijaya H Bhajipale, SA Patil, MP Meshram, PV Shende, Vandana S Madke**

DOI: <https://www.doi.org/10.33545/26174693.2025.v9.i7u.5020>

### Abstract

A total of 120 advanced rice breeding lines along with five checks were evaluated for genetic divergence using Mahalanobis  $D^2$  statistics across nine agronomic traits. The research was carried out in Kharif 2024 using Augmented block design. The research was performed at Agriculture Research Station, Sakoli, Dist. Bhandara. Analysis using Wilk's criterion revealed significant variation among genotypes. Tocher's method grouped the lines into five clusters, with the highest inter-cluster distance observed between clusters II and V ( $D^2 = 84.05$ ), indicating maximum diversity. Superior lines such as SKL-18-22-230-77-187-120-60, SKL-18-20-283-108-184-160-105, and SKL-18-22-230-77-170-100-54 outperformed the check variety Sakoli-8 in grain yield. Lines like SKL-18-03-220-305-374-250-212 and SKL-18-03-200-305-236-235-134 were identified as promising advanced breeding programs.

**Keywords:** Rice, augmented block design, advanced breeding lines

### Introduction

Rice (*Oryza sativa* L.), a semi-aquatic grass of the family Gramineae, is one of the world's most important staple crops, cultivated in 116 countries by over 144 million farm families on around 162 million hectares, producing 480 million tonnes of milled rice. Of the 24 species in the genus *Oryza*, only *O. sativa* and *O. glaberrima* are cultivated. Rice is a diploid species ( $2n=24$ ) and typically grows 0.5 to 2 meters tall, though some varieties reach up to 6-9 meters. It provides 20% of global dietary energy, with 90% of milled rice used as human food. Nutritionally, rice contains about 87% carbohydrates and 7-8% protein, and is crucial for food security, especially in Asia. In India, rice is grown across nearly all states, with West Bengal and Uttar Pradesh leading in area and production. Punjab ranks highest in productivity (6.5 t/ha). India contributes 30% of global rice production and 55% of the country's total cereal output.

### Materials and Methods

The experimental material comprised of 120 advance breeding lines of  $F_7$  population along with five checks PDKV Sadhana, PDKV Kisan, SKL-8, PKV HMT, PDKV Tilak selected on the basis of yield performance of  $F_6$  used in the study, grown in Augmented block design with spacing of 20 cm  $\times$  15 cm. The research was performed at Agriculture Research Station, Sakoli, Dist. Bhandara. Total 10 plants were selected randomly from each  $F_7$  populations and checks in Kharif-2024-25. Observations were recorded on days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of tillers plant<sup>-1</sup>, number of spikelets panicle<sup>-1</sup>, number of panicles plant<sup>-1</sup>, 1000 grain weight (g) and grain yield plant<sup>-1</sup>(g).

### Results and Discussion

#### 1. Days to 50% flowering

The data on mean value for days to 50% flowering ranged from 59 to 118 days. Among the advance breeding lines studied, 16 were classified as early duration (less than 90 days), 93 were classified as medium duration (90 to 120 days) and 11 were classified as late duration (more than 110 days). The advanced breeding line SKL-18-12-185-166-218-178-105 (59) attained earliest flowering followed by SKL-18-05-65-10-48-48-30 (81). The early check PDKV-Sadhana flowered at 87 days while late check SKL-8 flowered at 110 days.

## 2. Days to Maturity

The data on mean value for days to maturity ranged from 89 days to 148 days. Among the advance breeding lines studied, 16 were classified in early group (less than 120 days), 93 were classified in medium group (120 to 140 days) and 11 advance breeding lines exhibited late maturity (more than 140 days). The advanced breeding line SKL-18-12-185-166-218-178-105 (89) attained early maturity followed by SKL-18-05-65-10-48-48-30 (111) over the early check PDKV-Sadhana (117 days).

## 3. Plant height (cm)

The data on mean value for plant height at maturity ranged from 100.6 cm to 132 cm. The advanced breeding line SKL-18-21-125-14-34-24-20 (132) was tallest followed by SKL-18-09-92-40-126-64-91 (130.1) while the advanced breeding line SKL-18-18-210-135-127-60-84 (100.6) cm was shortest followed by SKL-18-18-210-135-127-60-84 (100.8). The advanced breeding line SKL-18-21-125-14-34-24-20 (132) followed by SKL-18-09-92-40-126-64-91 (130.1) exhibited significant superiority over the best check PDKV-Tilak (117.2).

## 4. No. of Tillers plant<sup>-1</sup>

The data on mean value for number of tillers plant<sup>-1</sup> ranged from 5.4 to 11.8. The advanced breeding line SKL-18-22-230-77-187-120-60 (11.8) had maximum number of tillers plant<sup>-1</sup> followed by SKL-18-04-292-204-207-218-156 (11.6) while the advanced breeding line SKL-18-18-210-135-127-60-84 (5.4) had minimum number of tillers plant<sup>-1</sup> followed by SKL-18-18-70-50-34-28-35 (5.6).

## 5. No. of Panicles plant<sup>-1</sup>

The data on mean value for number of panicles plant<sup>-1</sup> ranged from 4.6 to 11.2. The advanced breeding line SKL-18-04-292-204-207-218-156 (11.2) and SKL-18-17-172-107-94-60-83 (11.2), had maximum number of panicles plant<sup>-1</sup> followed by SKL-18-07-106-184-103-94-27 (10.8) while the advanced breeding line SKL-18-18-210-135-127-60-84 (4.6) had minimum number of panicle plant<sup>-1</sup> followed by SKL-18-18-210-135-127-60-84 (4.8).

## 6. Panicle length (cm)

The data on mean value for panicle length ranged from 21 to 28.3 cm. The advanced breeding line SKL-18-20-200-30-88-80-50 (28.3) had highest panicle length followed by SKL-18-22-264-118-334-218-112 (28.2) while the advanced breeding line SKL-18-04-281-148-105-150-89 (21) had lowest panicle length followed by SKL-18-17-172-65-81-50-37 (21.2). The advanced breeding line SKL-18-20-200-30-88-80-50 (28.3) followed by SKL-18-22-264-118-334-218-112 (28.2) showed significant superiority over the best check PDKV-Sadhana (25.9).

## 7. No. of Spikelets Panicle<sup>-1</sup>

The data on mean value for no. of Spikelets Panicle<sup>-1</sup> ranged from 146.5 to 262.5 cm. The advanced breeding line SKL-18-18-70-42-18-24-18 (262.5) had highest no. of spikelets panicle<sup>-1</sup> followed by SKL-18-22-230-77-187-120-60 (252.3) while the advanced breeding line SKL-18-04-24-48-32-60-24 (146.5) had lowest number of Spikelets panicle<sup>-1</sup> followed by SKL-18-04-281-148-105-150-89 (160.4). The

advanced breeding line SKL-18-18-70-42-18-24-18 (262.5) followed by SKL-18-22-230-77-187-120-60 (252.3) showed significant superiority over the best check PDKV-Tilak (220.4).

## 8. 1000 grain weight (g)

The data on mean value for 1000 test weight ranged from 10.36 to 39.16 g. The advanced breeding line SKL-18-20-200-30-88-80-50 (39.16) had maximum 1000 seed weight followed by SKL-18-20-283-108-184-160-105 (28.56) while the advanced breeding line SKL-18-01-212-53-125-67-50 (10.36) had minimum 1000 seed weight followed by SKL-18-04-281-148-105-150-89 (10.8) g which is lower than the fine check variety PDKV-Tilak.

## 9. Grain yield plant<sup>-1</sup> (g)

The data on mean value for grain yield plant<sup>-1</sup> ranged from 5.51 to 67.46 g. The advanced breeding line SKL-18-22-230-77-187-120-60 (67.46) had maximum grain yield plant<sup>-1</sup> followed by SKL-18-20-283-108-184-160-105 (67.3) while the advanced breeding line SKL-18-18-210-135-127-60-84 (5.51) had minimum grain yield plant<sup>-1</sup> followed by SKL-18-04-281-148-105-150-89 (7.8). The advanced breeding line SKL-18-22-230-77-187-120-60 (67.46) followed by SKL-18-20-283-108-184-160-105 (67.3), SKL-18-22-230-77-170-100-54 (59.57), SKL-18-03-72-65-11-05-18 (56.9), SKL-18-20-200-30-88-80-50 (56.55) showed significant superiority over the best check Sakoli-8 (50.4).

From above observations, it is concluded that advanced breeding line SKL-18-12-185-166-218-178-105 shown early days to 50% flowering and days to maturity. Advanced breeding line SKL-18-01-212-53-125-67-50 exhibited minimum 1000 seed weight and the advanced breeding line SKL-18-22-230-77-187-120-60 had maximum grain yield plant<sup>-1</sup>. The advanced breeding line SKL-18-22-230-77-187-120-60 (11.8) had maximum number of tillers plant<sup>-1</sup>. The advanced breeding line SKL-18-18-70-42-18-24-18 (262.5) had highest no. of spikelets panicle<sup>-1</sup>. The advanced breeding line SKL-18-04-292-204-207-218-156 (11.2) had maximum number of panicles plant<sup>-1</sup>. The advanced breeding line SKL-18-20-200-30-88-80-50 (28.3) had highest panicle length.

## Wilk's criterion and D<sup>2</sup> statistics

The analysis of dispersion (Table 1) using Wilk's criterion showed highly significant differences among advanced breeding lines for nine traits. Due to the large number of D<sup>2</sup> values from 120 lines and five checks, individual values are not presented. Similar studies by Yadav *et al.* (2011)<sup>[9]</sup> and Ranjith *et al.* (2018)<sup>[6]</sup> also reported significant genetic divergence among rice genotypes.

Table 1: Analysis of dispersion

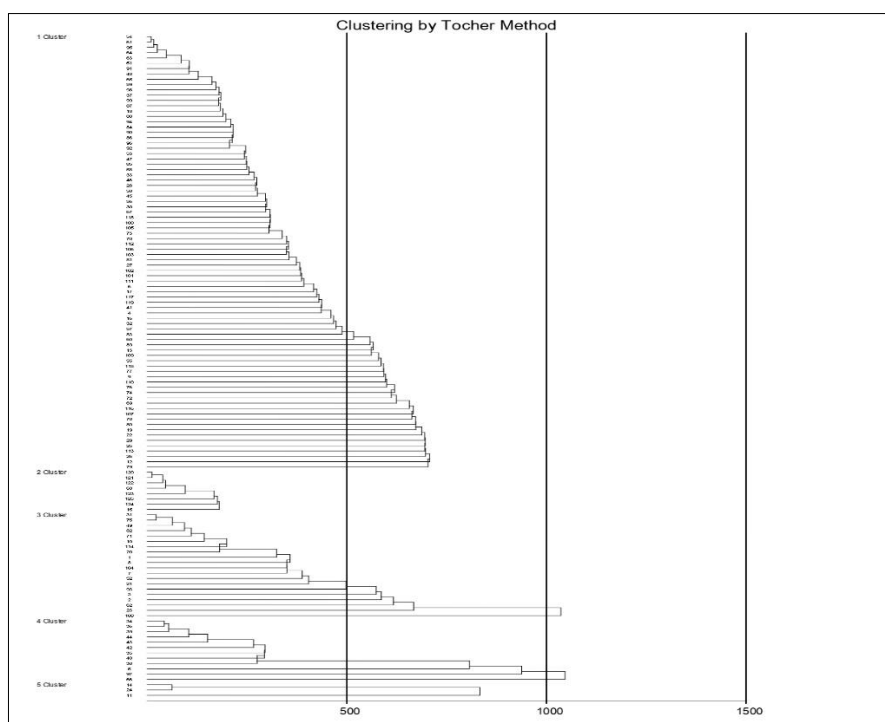
Source of variations	Df	Mean squares
Varieties	124	1.4260E12
Error	247	9.7906E-03

## Grouping of advanced breeding lines along with five checks into different clusters

The grouping of 120 advanced breeding lines along with five checks into different clusters were done by Tocher's method are presented in Table 2 and Fig. 1.

**Table 2:** Grouping of advanced breeding lines into different clusters

Cluster	Number of advanced breeding lines	Name of the advanced breeding lines
I	82	SKL-18-09-80-12-19-36-50, SKL-18-10-29-07-100-49-50, SKL-18-18-81-84-40-57, SKL-18-10-65-51-184-108-115, SKL-18-10-63-13-124-74-94, SKL-18-08-115-100-178-184-110, SKL-18-17-172-107-94-60-83, SKL-18-08-115-60-95-84-50, SKL-18-10-65-51-206-215-123, SKL-18-10-29-01-20-16-34, SKL-18-19-56-03-11-18-12, SKL-18-06-28-90-105-102-118, SKL-18-19-56-03-15-26-28, SKL-18-16-270-200-184-156-118, SKL-18-04-28-91-36-80-35, SKL-18-16-270-200-198-190-145, SKL-18-18-70-50-34-28-35, SKL-18-16-213-140-106-100-50, SKL-18-17-172-65-81-50-37, SKL-18-16-270-160-156-126-88, SKL-18-18-84-81-93-48-68, SKL-18-17-200-184-111-90-102, SKL-18-09-80-12-14-18-29, SKL-18-08-84-50-38-51-37, SKL-18-16-213-140-106-100-50, SKL-18-09-126-110-320-205-180, SKL-18-06-13-38-23-50-34, SKL-18-08-84-21-24-34-24, SKL-18-05-65-46-127-75-60, SKL-18-08-115-85-127-156-88, SKL-18-07-106-184-103-94-27, SKL-18-09-107-103-219-108-112, SKL-18-05-120-88-351-108-112, SKL-18-10-111-89-318-187-180, SKL-18-22-264-118-334-218-112, SKL-18-19-56-03-24-39-42, SKL-18-20-270-68-126-105-90, SKL-18-12-185-166-218-178-105, SKL-18-12-44-61-58-50-60, SKL-18-22-135-48-103-70-30, SKL-18-20-283-108-184-160-105, SKL-18-20-200-30-88-80-50, SKL-18-14-165-205-380-208-187, SKL-18-05-65-46-108-64-53, SKL-18-20-200-36-36-74-40, SKL-18-20-200-10-05-24-14, SKL-18-22-135-04-28-28-15, SKL-18-02-255-210-110-100-92, SKL-18-04-24-48-32-60-24, SKL-18-22-250-100-260-180-98, SKL-18-22-264-118-338-280-128, SKL-18-06-235-134-216-190-194, SKL-18-08-192-104-32-50-38, SKL-18-04-24-43-12-20-18, SKL-18-06-13-24-11-34-13, SKL-18-09-126-110-308-180-136, SKL-18-16-10-39-39-81-25, SKL-18-10-29-07-34-41-43, SKL-18-16-270-200-211-205-190, SKL-18-03-182-203-184-208-128, SKL-18-21-145-58-184-96-43, SKL-18-09-92-40-126-64-91, SKL-18-22-230-77-187-120-60, SKL-18-14-62-85-160-105-48, SKL-18-03-130-75-52-40-45, SKL-18-21-180-95-194-112-49, SKL-18-14-44-46-78-75-35, SKL-18-14-44-18-05-24-15, SKL-18-12-59-72-122-100-34, SKL-18-12-44-58-31-45-38, SKL-18-22-250-100-208-124-84, SKL-18-21-125-14-34-24-20, SKL-18-14-62-85-184-120-66, SKL-18-14-117-140-318-192-108, SKL-18-04-28-91-48-90-54, SKL-18-04-281-156-128-168-98, SKL-18-05-120-56-127-100-87, SKL-18-04-292-204-207-218-156, SKL-18-22-135-48-135-80-38, SKL-18-05-65-10-48-48-30, SKL-18-03-182-154-136-197-100, SKL-18-14-62-108-235-188-89
II	8	SKL-18-22-264-118-378-286-160, PDKV-Sadhana, PDKV-Kisan, SKL-18-12-44-48-12-20-30, SKL-8, PDKV-Tilak, PKV-HMT, SKL-18-03-220-305-374-250-212
III	20	SKL-18-05-120-103-368-120-140, SKL-18-14-44-18-34-65-26, SKL-18-08-115-60-102-102-67, SKL-18-16-10-39-28-34-10, SKL-18-12-44-61-102-78-70, SKL-18-03-130-75-81-50-50, SKL-18-22-230-77-170-100-54, SKL-18-04-260-130-92-145-74, SKL-18-01-74-27-30-18, SKL-18-03-130-75-52-25-30, SKL-18-20-270-68-104-100-83, SKL-18-03-72-65-11-05-18, SKL-18-08-115-100-202-190-135, SKL-18-04-281-148-105-150-89, SKL-18-18-70-42-18-24-18, SKL-18-02-184-58-12, SKL-18-01-212-53-125-67-50, SKL-18-10-29-07-108-63-88, SKL-18-04-292-186-138-184-118, SKL-18-21-125-48-134-38-37
IV	12	SKL-18-06-13-38-35-62-78, SKL-18-06-28-76-101-98-105, SKL-18-06-180-108-150-124-144, SKL-18-07-65-72-72-81-12, SKL-18-06-260-155-306-216-226, SKL-18-06-260-155-237-205-218, SKL-18-06-28-54-68-86-88, SKL-18-06-184-120-184-135-188, SKL-18-06-180-92-134-113-130, SKL-18-02-213-150-65-81-43, SKL-18-18-210-135-127-60-84, SKL-18-10-111-77-250-138-156
V	3	SKL-18-03-200-305-236-235-134, SKL-18-04-292-204-188-205-128, SKL-18-03-165-136-124-83-88

**Fig 1:** Dendrogram showing clustering of 120 advanced breeding lines along with five checks by Tocher's method

The entire advanced breeding lines (120) and checks (5) were grouped on the basis of  $D^2$  statistics into five clusters. The cluster I was largest comprising of 82 advanced breeding lines, followed by cluster III comprising of 20 advanced breeding lines, cluster IV comprising of 12 advanced breeding lines, cluster II comprising of 8 advanced breeding lines, cluster V comprising of 3 advanced breeding lines. All the checks i.e. PDKV-Sadhana, PDKV-Tilak, PKV-HMT, SKL-8 and PDKV-Kisan were grouped into cluster II. There were many advance breeding lines distributed in other cluster which were highly deviating from the check. From the data it can be seen that cluster I had maximum number of advance breeding lines. Those cluster which did not have the check varieties were genetically diverse from the checks and hence there is scope for selection of potential advanced breeding lines for yield and yield contributing characters.

#### Average intra and inter cluster distance

Average intra and inter cluster distance among nine characters were worked out by Tocher's method and presented in Table 3. Data showed that inter cluster distance in most of the cases were higher than the intra cluster distance. The intra cluster distance range from 12.64 to 29.23. Cluster V possessed highest intra cluster distance ( $D^2=29.23$ ) followed by cluster IV ( $D^2=24.87$ ), cluster III ( $D^2=23.08$ ), cluster I ( $D^2=22.45$ ) and cluster II ( $D^2=12.64$ ). The average inter cluster distance was maximum between cluster II and V ( $D^2=84.05$ ), followed by cluster IV and cluster V ( $D^2=76.13$ ), cluster I and cluster V ( $D^2=61.71$ ), cluster II and cluster III ( $D^2=56.84$ ), cluster III and cluster IV ( $D^2=50.90$ ) and cluster II and cluster IV ( $D^2=45.42$ ) suggesting more variability in genetic makeup of advanced breeding lines included in these clusters. From the data it can be observed that the average intra cluster distance was maximum in cluster V, cluster IV and cluster III and the average inter cluster distance was maximum between cluster II and cluster V, cluster VI and cluster V. Widely diverged clusters remain distinct in different environment. Khatun *et al.* (2015) [2] evaluated 43 genotypes in a randomized complete block design with three replications. Cluster analysis based on 22 traits grouped the 43 rice genotypes into five clusters. Cluster II was the largest and consisted of 20 genotypes mostly originating from the Philippines.

#### Cluster means

The cluster mean for all the nine characters are presented in Table 4 and discussed below. The comparison of cluster means for nine characters under study marked considerable genetic difference between groups. Highest cluster mean for days to 50% flowering was recorded by cluster IV (103.66) followed by cluster V (103.64) and cluster I (101.13) while cluster II (93.83) followed by cluster III (101.02) represented the lowest mean for days to 50% flowering. Highest cluster mean for days to maturity was recorded for

cluster V (133.78) followed by cluster IV (133.53) and cluster I (131.12) while cluster II (123.93) followed by cluster III (131.06) represented the lowest mean for days to maturity. Highest cluster mean for grain yield plant<sup>-1</sup> was recorded by cluster V (63.76) followed by cluster III (43.60) and cluster I (24.39) while cluster II (4.54) followed by cluster I (7.86) represented the lowest mean for grain yield plant<sup>-1</sup>. Highest cluster mean for number of panicle plant<sup>-1</sup> was recorded by cluster IV (10.76) followed by cluster V and Cluster III while cluster II followed by cluster I represented the lowest mean for number of panicle plant<sup>-1</sup>. Highest cluster mean for number of spikelets plant<sup>-1</sup> was recorded in cluster V (228.39) followed by cluster III (217.16) and cluster I (210.62) while cluster IV (180.27) followed by cluster II (201.00) represented the lowest mean for number of spikelets plant<sup>-1</sup>. Highest cluster mean for number of tillers plant<sup>-1</sup> was recorded cluster IV (11.05) followed by cluster V (9.93) and cluster III (8.99) while cluster II (5.36) followed by cluster I (8.41) represented the lowest mean for number of Tillers plant<sup>-1</sup>. Highest cluster mean for plant height was recorded in cluster I (114.33) followed by cluster III (114.02) and cluster II (112.17) while cluster V (108.64) followed by cluster IV (111.82) represented the lowest mean for plant height. Highest cluster mean for panicle length was estimated by cluster V (26.35) followed by cluster III (25.31) and cluster I (24.80) and minimum cluster mean was estimated for cluster IV (22.64) followed by cluster II (24.14). For 1000 test weight, highest cluster mean was estimated by cluster V (31.11) followed by cluster III (24.95) and cluster I (18.78) and minimum cluster mean was estimated for cluster IV (12.30) followed by cluster II (14.45). Over all study for cluster means considering all the characters indicated that cluster V possessed the highest cluster mean for days to maturity, grain yield plant<sup>-1</sup>, number of spikelets panicle<sup>-1</sup>, 1000 test weight, panicle length and Cluster IV showed the maximum mean for days to 50% flowering, number of panicle plant<sup>-1</sup>, number of tillers plant<sup>-1</sup>. Cluster II possessed lowest mean for most of the characters under study such as days to 50% flowering, days to maturity, grain yield plant<sup>-1</sup>, number of panicles plant<sup>-1</sup>, number of spikelets panicle<sup>-1</sup> and number of tillers plant<sup>-1</sup>. The variance for cluster means for all the characters indicated that the maximum variation was accounted for grain yield plant<sup>-1</sup> (472.63), number of spikelets panicle<sup>-1</sup> (330.87), 1000 test weight (59.6), days to flowering (16.24), days to maturity (16.24), number of panicles plant<sup>-1</sup> (5.19), plant height (5.15), number of tillers plant<sup>-1</sup> (4.57), and panicle length (1.4). It is suggested that the selection of advance breeding lines may be made on the basis of the characters exhibiting maximum variation and expected to be genetically diverse. Thus, from this study it can be reported that the advance breeding lines may be selected on the basis of these characters namely grain yield plant<sup>-1</sup> and number of spikelets panicle<sup>-1</sup>.

**Table 3:** Average intra and inter cluster distance  $D^2$  values in rice

Cluster	I	II	III	IV	V
I	22.45	34.12	35.86	34.35	61.71
II		12.64	56.84	45.42	84.05
III			23.08	50.90	37.39
IV				24.87	76.13
V					29.23

$\bar{D}=20.96$



**Table 4:** Cluster means for nine characters

Cluster	Days to 50% flowering	Days to maturity	Grain yield plant <sup>-1</sup> (g)	Number of panicle plant <sup>-1</sup>	No. of spikelets panicle <sup>-1</sup>	No. of tiller plant <sup>-1</sup>	Plant height (cm)	Panicle length (cm)	1000 grain weight (g)
1	101.13	131.12	24.39	7.86	210.62	8.41	114.33	24.80	18.78
2	93.83	123.93	10.03	4.54	201.00	5.36	112.17	24.14	14.45
3	101.02	131.06	43.60	8.62	217.16	8.99	114.02	25.31	24.95
4	103.66	133.53	17.60	10.76	180.27	11.05	111.82	22.64	12.30
5	103.64	133.78	63.76	9.02	228.39	9.93	108.64	26.35	31.11
SD	4.03	4.03	21.74	2.28	18.19	2.14	2.27	1.4	7.72
Variance	16.24	16.24	472.63	5.19	330.87	4.57	5.15	1.96	59.6

### Conclusion

Advance breeding lines SKL-18-03-220-305-374-250-212, SKL-18-03-200-305-236-235-134, SKL-18-02-213-150-65-81-43, SKL-18-20-200-30-88-80-50, SKL-18-22-230-77-170-100-54, SKL-18-03-72-65-11-05-18, are significantly superior over the checks for grain yield plant<sup>-1</sup>, number of spikelets panicle<sup>-1</sup>, number of tillers plant<sup>-1</sup>, number of panicles plant<sup>-1</sup>.

### Acknowledgement

I extend my heartfelt gratitude to all those who have been instrumental in the successful completion of this research endeavor. I would like to acknowledge the support of my research guide who shared their expertise and perspectives. My sincere thanks to Professor, agricultural botany section for providing the necessary resources and facilities.

### References

1. Anonymous. State Department of Agriculture, Maharashtra State. 2023-2024.
2. Khatun T, Mohamed MH, Yusop MR, Wong MY, Salleh FM, Ferdous J. Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. BioMed Res Int. 2015;2015:290861. 7 p.
3. Kumari L, Bastia DN, Pradhan B, Samal KC, Subramanyam SS. Multivariate analysis to study genetic diversity for yield improvement in advanced elite line of slender grain rice (*Oryza sativa* L.). Pharma Innov J. 2022;11(5):1785-1793.
4. Lakshmi M, Shanmuganathan M, Jeyaprakash P, Ramesh T. Genetic variability and diversity analysis in selected rice (*Oryza sativa* L.) varieties. Electron J Plant Breed. 2022;13(3):959-966.
5. Mahalanobis PC. On the generalized distance in statistics. Proc Natl Inst Sci India. 1936;2:49-55.
6. Ranjith P, Sahu S, Dash SK, Bastia DN, Pradha BD. Genetic diversity studies in rice (*Oryza sativa* L.). JPP. 2018;7(2):2529-2531.
7. Rao CR. Advanced statistical methods in biometrical research. New York: John Wiley and Sons Inc.; 1952. p. 236-272.
8. Singh RK, Choudhary BD. Biometrical methods in quantitative genetic analysis. New Delhi: Kalyani Publishers; 1977.
9. Yadav VK, Singh Y, Soni SK, Yadav AK. Genetic divergence analysis in salt tolerance rice (*Oryza sativa* L.) genotypes. Plant Arch. 2011;11(2):593-595.