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# Evaluation of genetic parameters for yield and its components in direct seeded rainfed rice (*Oryza sativa* L.)

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### Abstract
An experiment was carried out during *Kharif* season 2023 to estimate the genetic parameters of variation, correlation, direct and indirect effects of yield components on grain yield and genetic divergence in rice under rainfed condition. The experimental material consists fifty-seven rice genotypes including ten checks namely, Samleshwari, Bastar Dhan, Danteshwari, Sahbhagi Dhan-1, Narendra 97, Annada, Vandana, CR-Dhan-310, Protezin and Zinco Rice-MS were evaluated in a randomized block design (RBD) with two replications under direct seeded rainfed upland conditions. The analysis of variance of fifty-seven rice genotypes with nine quantitative characters was carried out and result indicated that there was significant differences present among the genotypes for all the quantitative traits studied. From the study of variability parameters, high to moderate estimates of GCV and PCV were observed for grain yield (q/ha) followed by filled grains per panicle, total number of grains per panicle, test weight (g) and plant height (cm) indicating the importance of selection for improving the grain yield in rice genotypes under rainfed upland condition. High heritability coupled with high genetic advance as percent of mean was observed for grain yield (q/ha), filled grains per panicle, total number of grains per panicle and test weight (g), suggesting that selection of these traits accumulate more additive genes leading to further improvement in their performance. The result of correlation revealed that grain yield (q/ha) had strong positive association with days to 50% flowering, days to maturity, panicle length (cm), filled grains per panicle, total number of grains per panicle, spikelet fertility (%) and test weight (g). The association studied indicated that grain yield of rice can be improved by selecting genotypes having higher performances for the above characters under rainfed upland condition. The path coefficient analysis between grain yield (q/ha) as dependent variable and its related traits indicated that traits *viz.* days to 50% flowering, days to maturity, panicle length (cm), filled grains per panicle and test weight(g) had high positive direct effect on grain yield (q/ha). On the basis of divergence analysis 57 genotypes were grouped into 11 clusters. The highest numbers of genotypes were present in cluster I which have 34 genotypes. The minimum inter cluster distance occurred between cluster VIII and cluster XI showing that the genotypes in these clusters were relatively less diverse. Maximum inter-cluster distance was observed between cluster VII and XI. The maximum inter cluster distance revealed that using parents from these clusters in a hybridization programme will result in a higher frequency of better segregants or desired pairings, which is important for the generation of valuable varieties. The contribution of traits to divergence was greatest for test weight(g), filled grain per panicle, grain yield (q/ha) and plant height(cm).Genotypes IR17A2769, R2739-86-1, R2744-119-1, R2744-19-1 and JDP-1212 were found to be the top 5 promising genotypes for yield and yield contributing traits under rainfed upland condition. Hence, these genotypes can be further promoted for advanced trails.

**Keywords:** Rice (*Oryza sativa* L.), genetic variability, heritability, correlation coefficient, path analysis and genetic diversity

### Introduction
Rice, the world's second most important staple food, nourishes two-thirds of India's population. Rice (*Oryza sativa* L.), with a chromosome number of 2n = 24, belongs to the genus *Oryza* in the family Poaceae. Rainfed agriculture, which is dependent on rainfall, accounts for 55% of net sown area (139.42 million ha) and 61% of India's farmer population. In Chhattisgarh, approximately 80% of the total rice area is rainfed. Rainfed agriculture is essential to the country's economy and food supply. India has the world's largest rainfed area but one of the lowest rainfed yields. Rainfed areas are recognized by water scarcity, fragile natural environments, and periods of drought. Rice is grown in a number of ecosystems defined in terms

of hydrology. Rice ecosystems are typically divided into four categories: irrigated, rainfed lowland, deep-water, and rainfed upland. Direct-seeded rainfed upland rice cultivation is a method of growing rice in un-bunded fields and seeded under dry condition, relying solely on rainfall for water supply in areas with limited or no irrigation. Rainfed upland rice cultivation suffers from low productivity, which is mainly caused by erratic rainfall, low soil fertility, and a lack of improved varieties. The low yield potential of traditional rice cultivars requires the development of higher-yielding cultivars for rainfed upland conditions. The development of high-yielding varieties necessitates an in-depth understanding of existing genetic variability as well as the magnitude and direction of genetic association among yield-attributing characters. The present investigation aimed to determine the extent of genetic variability, genetic parameters, correlation, and path coefficient with genetic divergence to enable researchers to select superior rice genotypes adapted to the rainfed upland ecosystem.

## Materials and Methods
The research was conducted in *Kharif*-2023 at the Barrister Thakur Chhedilal College of Agriculture and Research Station in Bilaspur, Indira Gandhi Krishi Vishwavidyalaya in Raipur, Chhattisgarh. The experimental materials comprised of fifty-seven rice genotypes including ten checks namely, Samleshwari, Bastar Dhan, Danteshwari, Sahbhagi Dhan-1, Narendra 97, Annada, Vandana, CR-Dhan-310, Protezin and Zinco Rice-MS. The experiment was laid out under rainfed upland condition in Randomized Block Design (RBD) with two replications. The characters studied were days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of filled grains per panicle, total number of grains per panicle, spikelet fertility (%), test weight (g) and grain yield (q/ha). Five competitive plants were chosen at random from each plot in each replication to record observations. Average of data from the sampled plant in term of different attributes were used for statistical analysis. The variability was estimated as per statistical procedure for analysis of variance suggested by Singh and Chaudhary (1985) [27]. PCV and GCV were computed according to the formula given by Falconer (1964) [7]. Heritability ($h^2$) in the broad sense was calculated according to the formula given by Allard (1960) [1]. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952) [5]. Genetic advance as percentage of mean was calculated and the range of genetic advance as per cent of mean was classified by using the formulae given by Johnson *et al*. (1955) [10]. Correlation coefficient analysis was estimated by formula given by Miller *et al*. (1958) [15]. Path coefficient analysis was suggested by Wright (1921) and expanded by Dewey and Lu (1959) [6]. The genetic diversity was calculated by D² analysis given by P.C. Mahalanobis in (1928) [14].

## Results and Discussion
### Analysis of variance
The analysis of variance (ANOVA) of fifty-seven rice genotypes with nine quantitative characters was carried out and result indicated that there was significant differences present among the genotypes for all the quantitative traits studied. The ANOVA was based on the mean values of nine quantitative traits across fifty-seven rice genotypes. The results on analysis of variance (ANOVA) for yield and yield component characters studied are presented in Table-1. The results indicated a significant level of variability present among the genotypes. This offers rice breeders the potential to enhance these traits through selection

and hybridization in order to improve the desired characteristics. Similar findings were also reported by Gupta *et al*. (2022) [8], Katkani *et al*. (2019) [12], Pandey *et al*. (2018) [18], Xaxa *et al*. (2018) [30], Sharma *et al*. (2017) [24] and Patel *et al*. (2014).

### Genetic parameter of variation
The extent of genotypic and phenotypic coefficient of variation, heritability and genetic advance as percentage of mean were recorded for all studied characters are presented in table-2. High to moderate estimates of GCV and PCV were observed for grain yield followed by filled grains per panicle, total number of grains per panicle, test weight (g) and plant height (cm) (only PCV). The high magnitude of genotypic coefficient of variation revealed the presence of high amount of genetic variability for the characters studied in the population and thus offers scope for genetic improvement through selection for these traits. Heritability estimates alone cannot be used to anticipate selection response, it is necessary to measure genetic advance in addition to heritability to determine the effectiveness of selection. High heritability coupled with high genetic advance as percent of mean was observed for grain yield (q/ha), filled grains per panicle, total number of grains per panicle and test weight (g), suggesting that selection of these traits accumulate more additive genes leading to further improvement in their performance. Similar results were also observed by Gupta *et al*. (2022) [8], Katkani *et al*. (2019) [12], Xaxa *et al*. (2018) [30] and Patel *et al*. (2014) [20].

### Correlation coefficient analysis
The correlation coefficient was partitioned into phenotypic and genotypic correlation coefficient. The magnitude of genotypic correlation was higher than phenotypic correlation. The phenotypic and genotypic correlation coefficient of studied characters are presented in table-3. Correlation coefficient depicted the nature of association among the characters. The study of correlation coefficient helps the breeder to formulate the selection criteria with desired combination of characters. The correlation study revealed that grain yield (q/ha) had strong positive association with days to 50% flowering ($r_g = 0.267** \, r_p = 0.267**$), days to maturity ($r_g = 0.523** \, r_p = 0.488**$), panicle length ($r_g = 0.447** \, r_p = 0.345**$), filled grains per panicle ($r_g = 0.629** \, r_p = 0.606**$), total number of grains per panicle ($r_g = 0.632** \, r_p = 0.623**$), spikelet fertility ($r_g = 0.414** \, r_p = 0.321**$) and test weight ($r_g = 0.265** \, r_p = 0.255**$) at both genotypic and phenotypic level. The association studied indicated that grain yield of rice can be improved by selecting genotypes having higher performances for the above characters under rainfed condition. Similar results were obtained by Zeleke and Worede (2021) [31] for panicle length , number of filled grains per panicle and number of total grains per panicle; Kathani *et al*. (2019) for panicle length, test weight and number of grains per panicle; Kampe *et al*. (2018) [11]; Bitew *et al*. (2018) [4] for days to 50% flowering, days to maturity and test weight; Khare *et al*. (2014) [13] for days to 50% flowering, panicle length, total grains per panicle and spikelet fertility; Singh *et al*. (2014) [25] for days to 50% flowering, total grains per panicle and spikelet fertility.

### Path coefficient analysis
The direct and indirect effect of all traits are presented in table-4 and table-5. The path coefficient analysis of the fifty-seven rice genotypes for nine characters revealed that highest positive direct effect on grain yield per ha at genotypic level was exhibited by filled grains per panicle (0.8037) followed by

panicle length (0.2479), test weight (0.0702), days to 50% flowering (0.0535) and days to maturity (0.0330). At phenotypic level highest positive direct effect was exhibited by total number of grains per panicle (0.2884) followed by filled grains per panicle (0.1955), panicle length (0.1318), days to 50% flowering (0.1151), test weight (0.0938), days to maturity (0.0675) and spikelet fertility (0.0442). The highest direct but negative effect at genotypic level was exhibited by total number of grains per panicle (-0.2071), plant height (-0.1456) and spikelet fertility (-0.1325). At phenotypic level highest negative direct effect was exhibited by plant height (-0.1198). Similar results were observed by Sudeepthi *et al.* (2020) [28] for test weight; Bhandari *et al.* (2019) [3] for panicle length, test weight, plant height and spikelet fertility (%); Katkani *et al.* (2019) [12] for days to 50% flowering, panicle length, test weight and total number of grains per panicle; Patel *et al.* (2017) [19] for days to maturity and total number of grains per panicle; Nayak *et al.* (2016) [17] for panicle length, plant height and days to 50% flowering; Patil *et al.* (2016) [21] for days to 50% flowering, test weight, filled grains per panicle; Seyoum *et al.* (2012) [23] for total number of grains per panicle, days to 50% flowering, panicle length, spikelet fertility and test weight.

**Table 1:** Values of mean sum of squares of analysis of variance for grain yield and its components character in rice genotypes

| S. No. | Traits | Mean sum of square (MSS) | | |
|---|---|---|---|---|
| | | Replication | Genotype | Error |
| | **Degree of freedom (DF)** | **1** | **56** | **56** |
| 1 | Days to 50% flowering | 3.509 | 83.727** | 3.437 |
| 2 | Days to maturity | 16.219 | 47.972** | 6.059 |
| 3 | Plant height (cm) | 0.507 | 177.643** | 12.04 |
| 4 | Panicle length (cm) | 0.509 | 7.283** | 1.496 |
| 5 | Filled grains per panicle | 13.569 | 573.729** | 20.138 |
| 6 | Total number of grains per panicle | 4.169 | 549.277** | 11.289 |
| 7 | Spikelet fertility (%) | 6.838 | 75.486** | 16.447 |
| 8 | Test weight (g) | 0.907 | 13.036** | 0.201 |
| 9 | Grain yield (q/ha) | 9.933 | 110.576** | 2.585 |

*Significant at 5% probability level, ** Significant at 1% probability level

**Table 2:** Genetic parameters of variation for grain yield and its component in rice genotypes

| S. No. | Traits | Mean | Range | | Variance | | Coefficient of variation (%) | | h² (bs) (%) | G.A. | GAM (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | Low | High | PV | GV | PCV | GCV | | | |
| 1 | Days to 50% flowering | 89.895 | 73 | 99 | 43.58 | 40.14 | 7.344 | 7.048 | 92.113 | 12.527 | 13.935 |
| 2 | Days to maturity | 121.298 | 110 | 133 | 27.98 | 24.03 | 4.361 | 4.041 | 85.879 | 9.358 | 7.715 |
| 3 | Plant height (cm) | 92.207 | 59.9 | 125.1 | 94.84 | 82.80 | 10.562 | 9.869 | 87.305 | 17.515 | 18.995 |
| 4 | Panicle length (cm) | 22.026 | 17.1 | 28.9 | 4.38 | 2.89 | 9.512 | 7.723 | 65.917 | 2.845 | 12.916 |
| 5 | Filled grains per panicle | 83.708 | 48.5 | 133.1 | 296.93 | 276.79 | 20.586 | 19.875 | 93.218 | 33.09 | 39.53 |
| 6 | Total number of grains per panicle | 109.372 | 71.5 | 154.0 | 280.28 | 268.99 | 15.307 | 14.996 | 95.972 | 33.099 | 30.263 |
| 7 | Spikelet fertility (%) | 76.127 | 61.6 | 88.0 | 45.96 | 29.51 | 8.906 | 7.137 | 64.22 | 8.969 | 11.782 |
| 8 | Test weight (g) | 21.861 | 16.3 | 28.7 | 6.61 | 6.41 | 11.768 | 11.588 | 96.965 | 5.139 | 23.507 |
| 9 | Grain yield (q/ha) | 21.625 | 8.6 | 39.6 | 56.58 | 53.99 | 34.783 | 33.979 | 95.432 | 14.787 | 68.38 |

**Note**: GCV=Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, h² (bs)= Heritability broad sense, GA= Genetic advance

**Table 3:** Genotypic and phenotypic correlation matrix. (Above diagonal Phenotypic and below diagonal Genotypic)

| | DFF | DM | PH | PL | FGPP | TNGPP | SF% | TW | GY |
|---|---|---|---|---|---|---|---|---|---|
| DFF | 1 | 0.288** | 0.059 | 0.309** | 0.186* | 0.240* | -0.028 | -0.060 | 0.267** |
| DM | 0.325** | 1 | -0.123 | 0.388** | 0.575** | 0.634** | 0.233* | 0.172 | 0.488** |
| PH | 0.087 | -0.152 | 1 | 0.329** | 0.120 | 0.087 | 0.125 | 0.078 | -0.016 |
| PL | 0.419** | 0.441** | 0.309** | 1 | 0.329** | 0.368** | 0.121 | 0.154 | 0.345** |
| FGPP | 0.210* | 0.632** | 0.137 | 0.374** | 1 | 0.917** | 0.728** | 0.266** | 0.606** |
| TNGPP | 0.241** | 0.715** | 0.101 | 0.412** | 0.951** | 1 | 0.400** | 0.315** | 0.623** |
| SF% | 0.020 | 0.253** | 0.162 | 0.178 | 0.776** | 0.551** | 1 | 0.063 | 0.321** |
| TW | -0.063 | 0.211* | 0.107 | 0.220* | 0.292** | 0.333** | 0.099 | 1 | 0.255** |
| GY | 0.267** | 0.523** | 0.006 | 0.447** | 0.629** | 0.632** | 0.414** | 0.265** | 1 |

**Note:**\*Significant at 5% probability level, ** Significant at 1% probability level, DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), PL= Panicle length (cm), FGPP = Filled grains per panicle, TNGPP = Total number of grains per panicle, SF% = Spikelet fertility (%), TW = Test weight (g), GY = Grain yield (q/ha)

**Table 4:** Genotypic path coefficient analysis showing direct effect (bold and diagonal values) and indirect effect (non-bold and off diagonal values)

| | DFF | DM | PH | PL | FGPP | TNGPP | SF% | TW | GY |
|---|---|---|---|---|---|---|---|---|---|
| DFF | 0.0535 | 0.0107 | -0.0127 | 0.1037 | 0.1687 | -0.0498 | -0.0027 | -0.0044 | 0.267** |
| DM | 0.0174 | 0.0330 | 0.0221 | 0.1093 | 0.5083 | -0.1481 | -0.0335 | 0.0148 | 0.523** |
| PH | 0.0047 | -0.0050 | -0.1456 | 0.0767 | 0.1099 | -0.0210 | -0.0215 | 0.0075 | 0.006 |
| PL | 0.0224 | 0.0146 | -0.0451 | 0.2479 | 0.3010 | -0.0854 | -0.0235 | 0.0155 | 0.447** |
| FGPP | 0.0112 | 0.0209 | -0.0199 | 0.0928 | 0.8037 | -0.1970 | -0.1028 | 0.0205 | 0.629** |
| TNGPP | 0.0129 | 0.0236 | -0.0148 | 0.1023 | 0.7646 | -0.2071 | -0.0730 | 0.0234 | 0.632** |
| SF% | 0.0011 | 0.0083 | -0.0237 | 0.0440 | 0.6235 | -0.1140 | -0.1325 | 0.0069 | 0.414** |
| TW | -0.0034 | 0.0070 | -0.0156 | 0.0546 | 0.2345 | -0.0689 | -0.0131 | 0.0702 | 0.265** |

**Residual effect: 0.5196**

**Note:** *Significant at 5% probability level, ** Significant at 1% probability level, DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), PL= Panicle length (cm), FGPP = Filled grains per panicle, TNGPP = Total number of grains per panicle, SF% = Spikelet fertility (%), TW = Test weight (g), GY = Grain yield (q/ha)

**Table 5:** Phenotypic path coefficient analysis showing direct effect (bold and diagonal values) and indirect effect (non-bold and off diagonal values)

|  | DFF | DM | PH | PL | FGPP | TNGPP | SF% | TW | GY |
|---|---|---|---|---|---|---|---|---|---|
| DFF | 0.1151 | 0.0195 | -0.0071 | 0.0407 | 0.0364 | 0.0691 | -0.0012 | -0.0056 | 0.267** |
| DM | 0.0332 | 0.0675 | 0.0147 | 0.0511 | 0.1123 | 0.1828 | 0.0103 | 0.0162 | 0.488** |
| PH | 0.0068 | -0.0083 | -0.1198 | 0.0434 | 0.0235 | 0.0251 | 0.0055 | 0.0073 | -0.016 |
| PL | 0.0355 | 0.0262 | -0.0394 | 0.1318 | 0.0644 | 0.1063 | 0.0054 | 0.0145 | 0.345** |
| FGPP | 0.0214 | 0.0388 | -0.0144 | 0.0434 | 0.1955 | 0.2644 | 0.0322 | 0.0249 | 0.606** |
| TNGPP | 0.0276 | 0.0428 | -0.0104 | 0.0486 | 0.1792 | 0.2884 | 0.0177 | 0.0295 | 0.623** |
| SF% | -0.0032 | 0.0157 | -0.0150 | 0.0160 | 0.1423 | 0.1155 | 0.0442 | 0.0059 | 0.321** |
| TW | -0.0069 | 0.0116 | -0.0093 | 0.0204 | 0.0519 | 0.0908 | 0.0028 | 0.0938 | 0.255** |

**Residual effect: 0.5526**

**Note:** *Significant at 5% probability level, ** Significant at 1% probability level, DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), PL= Panicle length (cm), FGPP = Filled grains per panicle, TNGPP = Total number of grains per panicle, SF% = Spikelet fertility (%), TW = Test weight (g), GY = Grain yield (q/ha)

**Table 6:** Rice genotypes were grouped into 11 cluster

| Cluster | Total no of genotypes | Genotypes |
|---|---|---|
| Cluster I | 34 | R1670-3269-2-3926, Samleshwari(check) , R2748-1-1, Narendra 97(check),IR18A1073, R2340-284-1-151-1, R2297-4-1-2-1, Sahbhagi Dhan-1(check), R2774-C 3-1-1, IR17A3050,R2759-20-1, Bastar Dhan (check) , R2322-180-1-169-1, R2775-C6-2-3, R2297-6-1-3-1, R2307-46-1-24-1, JDP 2018, R 2341-337-3-180-1, R 1877-41-1-13-1,R-RHZ-RKC-212, Danteshwari (check), R 2341-28123321, IR17A3105,R 2300-377-2-261-1, IR18A1072, IR18A1068, R2735-56-1,R-RHZ-MI-95, CR-Dhan-310(check), R2321-154-1-94-1, R2744-119-1,R2756-27-1, JDP-1212, JDP-5925 |
| Cluster II | 8 | IR17A2891, Protezin(check), IR18A1423, R 2341-339-2-182-1, IR18A1061, R2744-19-1, R2739-86-1, R2744-118-1 |
| Cluster III | 3 | R-RHZ-CC-162, R-RHZ-CC-164, R 2485-PHD-SPS-15-1 |
| Cluster IV | 4 | R2739-120-1, R2743-78-1, R2739-43-1, R2739-115-1 |
| Cluster V | 2 | IR18A1076, IR18A1042 |
| Cluster VI | 1 | IR17A2769 |
| Cluster VII | 1 | Annada (check) |
| Cluster VIII | 1 | Vandana (check) |
| Cluster IX | 1 | R-RHZ-RKC-211 |
| Cluster X | 1 | R-RGY-IS-110 |
| Cluster XI | 1 | Zinco Rice-MS (check) |

**Table 7:** Intra and inter-cluster distance in 57 rice genotypes under 11 clusters

|  | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII | Cluster VIII | Cluster IX | Cluster X | Cluster XI |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Cluster I | 151.30 | 292.38 | 349.27 | 242.04 | 509.07 | 501.77 | 657.91 | 390.27 | 484.2 | 258.82 | 434.49 |
| Cluster II |  | 138.42 | 753.79 | 404.14 | 318.74 | 354.55 | 234.93 | 799.31 | 727.28 | 270.02 | 943.04 |
| Cluster III |  |  | 134.88 | 376.59 | 879.9 | 919.85 | 1337.06 | 278.62 | 400.15 | 699.91 | 258.41 |
| Cluster IV |  |  |  | 114.18 | 395.05 | 643.36 | 810.88 | 363.11 | 575.44 | 234.27 | 677.47 |
| Cluster V |  |  |  |  | 136.72 | 636.63 | 506.85 | 741.98 | 576.01 | 394.73 | 1194.49 |
| Cluster VI |  |  |  |  |  | 0.00 | 596.21 | 1355.71 | 987.45 | 308.46 | 1260.41 |
| Cluster VII |  |  |  |  |  |  | 0.00 | 1357.22 | 1205.07 | 586.15 | 1598.65 |
| Cluster VIII |  |  |  |  |  |  |  | 0.00 | 291.54 | 712.88 | 221.21 |
| Cluster IX |  |  |  |  |  |  |  |  | 0.00 | 690.71 | 353.35 |
| Cluster X |  |  |  |  |  |  |  |  |  | 0.00 | 871.11 |
| Cluster XI |  |  |  |  |  |  |  |  |  |  | 0.00 |

**Note:** Non bold values-shows inter cluster distance, Bold values-shows intra cluster distance

**Table 8:** Contribution of quantitative traits toward genetic divergence in percentages

| S. No. | Traits | Contribution % | Times ranked 1st |
|---|---|---|---|
| 1 | Days to 50% flowering | 8.40 | 135 |
| 2 | Days to maturity | 5.50 | 88 |
| 3 | Plant height (cm) | 8.70 | 139 |
| 4 | Panicle length (cm) | 1.00 | 16 |
| 5 | Filled grains per panicle | 25.20 | 403 |
| 6 | Total number of grains per panicle | 6.50 | 104 |
| 7 | Spikelet fertility (%) | 3.00 | 48 |
| 8 | Test weight (g) | 29.00 | 463 |
| 9 | Grain yield (q/ha) | 12.50 | 200 |

**Genetic divergence**
Based on the degree of divergence 57 genotypes were grouped into 11 clusters on the basis of cluster analysis are presented in Table-6. cluster I was the largest cluster (34 genotypes) followed by cluster II (8 genotypes), cluster IV (4 genotype), cluster III (3 genotype), cluster V (2 genotype), cluster VI, VII ,VIII, IX, X, XI had only 1 genotype. The intra and inter cluster distance are presented in table-7. cluster I had the maximum intra-cluster distance, followed by cluster II, cluster V, cluster III, cluster IV indicating that the genotypes contained in these clusters were more diversified, hence might be utilized in the crop improvement programmes. Whereas, clusters VI, VII, VIII, IX,

X and XI exhibited the minimum intra-cluster distances. Cluster VII and XI had maximum inter cluster distances and minimum inter cluster distance was present between cluster VIII and cluster XI. The maximum inter cluster distance revealed that using parents from these clusters in a hybridization programme will result in a higher frequency of better segregants or desired pairings, which is important for the generation of valuable genetic stocks or varieties. The contribution of traits to divergence (Table-8) was greatest for test weight, filled grain per panicle, grain yield (q/ha) and plant height. Similar results were also found by Archana *et al*. (2018) [2], Sandhya *et al*. (2014) [22] for test weight and days to 50% flowering; Muthuramu *et al*. (2018) [16] for filled grains per panicle and grain yield; Singh *et al*. (2011) [26], Hedge and Patil (2000) [9] for test weight.

**Conclusion**
Analysis of variance revealed presence of significant variability for all the characters. Thus, there is an ample scope for selection and exploitation of different quantitative traits in crop improvement programme. The high to moderate GCV and PCV for grain yield, filled grains per panicle, total number of grains per panicle, test weight (g) and plant height (cm) demonstrated that there was enough variation among the genotypes. The high heritability with high genetic advance as percent of mean was observed for grain yield (q/ha), filled grains per panicle, total number of grains per panicle and test weight (g). This showed the existence of additive gene action. From the correlation and path coefficient analysis it is investigated that days to 50% flowering, days to maturity, panicle length (cm), filled grains per panicle and test weight (g) were most important traits which should be given proper emphasis during selection programmes for the improvement of grain yield in rice genotypes under rainfed upland condition. Selection of parent genotypes for hybridization from cluster VII and cluster XI would produce maximum heterosis and transgressive segregants. The contribution of traits to divergence was greatest for test weight (g), filled grain per panicle, grain yield (q/ha) and plant height(cm).In conclusion, the current study has revealed useful information on various yield traits for improving rice genotypes. Genotypes IR17A2769, R2739-86-1, R2744-119-1, R2744-19-1 and JDP-1212 were found to be the top 5 promising genotypes under rainfed upland condition for yield and yield contributing traits. Hence, these genotypes can be used in subsequent selection processes.

**References**
1. Allard RW. Principles of Plant Breeding. New York: John Wiley and Sons Inc, 1960, p. 145-7.
2. Archana RS, Rani MS, Vardhan KV, Fareeda G. Genetic diversity studies among rice (*Oryza sativa* L.) genotypes for grain yield, yield components and nutritional traits in rice. Int J Chem Stud. 2018;6(6):134-7.
3. Bhandari K, Sharma S, Poudel A, Upadhyay K. Genetic variability, correlation and path analysis of rice genotypes in rainfed condition at Lamjung, Nepal. Russ J Agric Socio-Eco Sci. 2019;8(92):274-80.
4. Bitew JM, Mekbib F, Assefa A. Correlation coefficient and path analysis among yield and yield related traits in upland rice (*Oryza sativa* L. and *Oryza glaberrima* Steud) genotypes in Northwestern Ethiopia. Int J Plant Breed Crop Sci. 2018;5(3):429-36.
5. Burton GW. Quantitative inheritance in grasses. Proceedings Sixth International Grassland Congress.
1952;1:227-283.
6. Dewey OR, Lu KH. A correlation and path coefficient analysis of crested wheat grass seed production. J Agron. 1959;57:515-518.
7. Falconer DS. An Introduction to Quantitative Genetics. Edinburgh, London: Oliver and Boyd, 1964, p. 312-24.
8. Gupta H, Purushottam Yadav G, Yadav SK, Singh S, Kumar S. Genetic variability, heritability and genetic advance for yield and its related traits in rainfed upland rice (*Oryza sativa* L.) genotypes. The Pharma Innovation J. 2022;11(2):2520-2524.
9. Hedge SG, Patil CS. Genetic divergence in rainfed rice. Karnataka J Agric Sci. 2000;13(3):533-539.
10. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agron J. 1955;47:314-318.
11. Kampe AK, Tassew AA, Gezmu AT. Estimation of phenotypic and genotypic correlation and path coefficients in rainfed upland rice (*Oryza sativa* L.) genotypes at Guraferda, Southwest Ethiopia. J Rice Res. 2018;6(3):1-5.
12. Katkani D, Payasi SK, Patel V, Tiwari S. Genetic variability, correlation and path analysis for quantitative traits in rainfed upland rice (*Oryza sativa* L.). Int J Chem Stud. 2019;7(6):2354-2358.
13. Khare R, Singh AK, Eram S, Singh PK. Genetic variability, association and diversity analysis in upland rice (*Oryza sativa* L.). SAARC J Agric. 2014;12(2):40-51.
14. Mahalanobis PC. On the need for standardization in measurement on living. Biometrika, 1928, p. 1-31.
15. Miller PA, Williams C, Robinson HF, Comstock RE. Estimates of genotypic and environmental variance and covariance and their implication in selection. Agron J. 1958;50:126-31.
16. Muthuramu S, Ragavan T. Genetic diversity analysis for yield traits in rainfed rice (*Oryza sativa* L.) under water stress condition. J Rice Res. 2018;11(2):6-9.
17. Nayak R, Singh VK, Singh AK, Singh PK. Genetic variability, character association and path analysis of rice genotypes. Ann Plant Soil Res. 2016;18(2):161-164.
18. Pandey S, Dayal D, Shashidhar H. Assessment of genetic variability, heritability and genetic advance for yield contributing and quality traits in rice (*Oryza sativa* L.) genotypes. J Pharma Phytochem. 2018;7(4):333-337.
19. Patel JR, Patel DK, Prajapati KN, Soni NV, Patel A. Correlation and path coefficient analysis in rainfed upland rice (*Oryza sativa* L.). Environ Ecol. 2017;35(2):789-794.
20. Patel JR, Saiyad MR, Prajapati KN, Patel RA, Bhavani RT. Genetic variability and character association studies in rainfed upland rice (*Oryza sativa* L.). Ele J Plant Biol. 2014;5(3):531-537.
21. Patil KH, Rani CL, Stephen R, Kumary L, Mar V, Jayalekshmy VG. Path analysis in rainfed upland rice (*Oryza sativa* L.) under natural stress. Int J Sci Res. 2016;5(5):237-239.
22. Sandhya GR, Lavanya G, Babu S, Kumar R, Kumar S, Rai B, Devi B. Study of genetic variability and D2 analysis in elite rice genotypes. Int J Food Agric Vet Sci. 2014;4(2):12-16.
23. Seyoum M, Alamerew S, Bantte K. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice. J Plant Sci. 2012;7(1):13-22.
24. Sharma MK, Parasar N, Bairagi P, Bora R, Baruah S. Genetic variability and diversity in rice (*Oryza sativa* L.)

under rainfed upland situation of Assam. Cont Res India. 2017;7(3):214-218.

25. Singh AK, Nandan R, Singh PK. Genetic variability and association analysis in rice germplasm under rainfed conditions. Crop Res. 2014;47(1-3):7-11.

26. Singh AK, Singh PK, Rao M. Diversity analysis in rice under rainfed condition. Ann Plant Soil Res. 2011;13(1):58-61.

27. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetics analysis. 3rd Ed. New Delhi: Kalyani Publishers, 1985.

28. Sudeepthi K, Srinivas T, Kumar BR, Jyothula DPB, Umar SN. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). Ele J Plant Breed. 2020;11(01):144-148.

29. Wright S. Correlation and causation. J Agric Res. 1921;20:257-287.

30. Xaxa E, Surin S, Ekka S. Genetic variability studies of important yield attributing traits in rainfed upland rice (*Oryza sativa* L.). J Pharma Phyto. 2018;7(1):2498-2500.

31. Zeleke B, Worede F. Correlation and path analysis for yield and related traits in upland rice (*Oryza sativa* L.) varieties. Black Sea J Agric. 2021;4(1):18-24.