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# Studies on genetic variability in rice (*Oryza sativa* L.) for control and complete flash flood Environments

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## Abstract

28 rice genotype of different origin were evaluated simultaneously under normal and artificially submerged conditions in Randomised Block Design with three replications to assess their genetic variability. Morphological data on yield and other important traits was collected and analysed for the control and submergence trial, respectively. The combined analysis of variance revealed statistically significant differences (p<0.01) for all the traits in both the conditions except number of unfilled grains/panicle which was found to be significant at p<0.05 indicating the presence of genetic variability among the genotypes. Grain yield was found to be ranging from 3116 kg$^{-1}$ (RYC-250) to 6033 kg$^{-1}$ (Rajendra Mahsuri$^{-1}$) under normal and 413 kg$^{-1}$ (Sabour Deep) to 4244 kg$^{-1}$ (RYC-743) under submergence. A higher value of phenotypic and genotypic coefficient of variations (GCV and PCV) was recorded for panicle weight under both the conditions. The highest heritability (broad sense) was recorded for days to 50 % flowering (98.68%) under control condition while for panicle weight (98.01) under submergence. High heritability coupled with high GCV and high genetic advance as percentage of mean were exhibited for panicle weight under both, control and submergence while for plant height at maturity and grain yield respectively under control and submergence.

**Keywords:** rice, genetic variability, heritability, genetic advance, submergence

## Introduction

Rice (*Oryza sativa* L.) belongs to the genus *Oryza* under tribe Oryzeae in the family Gramineae or Poaceae. The genus *Oryza* includes more than 25 wild species either perennial or annual. These species are either diploid or tetraploid. The *indica* and japonica are subspecies of *Oryza sativa*, grown and consumed largely in the world (Khush 1994) [6]. Being the most impotant food crop in the developing world, rice occupies 11% of the world's arable land with a total production of around 600 million tons. It is staple food crop for more than 60% of the world population and supplies 21% of the total calorie per person per day. In other words, for more than half of the humanity "rice is life". Most of these people live in Asia and Africa, the most populous continents of the world. In Asia, over 90% of the world's rice crop is produced and consumed (Mackill *et al*., 2012) [8]. In India also rice is the most important crop. India occupies the largest area under rice and is the second largest producer of rice after china. It is grown on about 43 million hectares with a production of around 105 million tons (http://eands.dacnet.nic.in/ Advance Estimate/ 3rdAdv150216 Eng.pdf) in the country. In rice growing areas of the country, Eastern region comprising of Bihar, Chhattisgarh, Jharkhand, Madhya Pradesh, Orissa, Eastern Uttar Pradesh and West Bengal has the highest intensity of rice cultivation.

Rice is grown under so diverse soil and climatic conditions that it is difficult to say there is hardly any type of soil in which it cannot be grown. Due to so wide adaptability, same time it faces lots of problems related to biotic and abiotic stresses. Among abiotic stresses, submergence is the third most important threat to the rice production. More than 16% of rice grown in lowlands is adversely affected by floods every year worldwide (Singh *et al*. 2011) [12]. These are either flash floods with complete submergence for a few days to two weeks, stagnant flooding of 20-50 cm water depth for longer time and deep flooding with water depth of more than 50 cm to few meters for long duration. Many times combination of these three conditions also occur (Khush, 1994; Sarkar *et al*., 2006) [6]. Due to the effect of climate change scenario, the incidences of uneven and erratic distribution of rainfall are coming in to the picture frequently making the situation of submergence and drought alarming. In the phase of development, many of important germplasms have been lost due to negligence and ignorance of the farmer and scientific community.

Genetic variability is the tendency of individual genetic characteristics in a population to vary

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from one another. It is the potential of a genotype to change or deviate when exposed to environmental or genetic factors. In other words, it is the magnitude of the differences among the individuals due to the differences in their genetic composition and the environment in which they were raised. Presence of genetic variability is essential for rice improvement which is a challenge to the rice breeders for yield improvement to meet the quantitative and qualitative demand of rice. Since, very less effort has been made earlier on these aspects simultaneously for control and submergence conditions, the present study was carried out to assess the extent of genetic variability, heritability and genetic advance among twenty eight rice genotypes for yield and related traits.

## Materials and methods
### Experimental site and location
The study was carried out at the Research Farm of Bihar Agricultural University (BAU) Sabour, Bhagalpur, Bihar, which is in Zone IIIA of Bihar state and geographically situated between 25°' 15'40'' N latitude to 87o2'42'' E longitude at 46 m above mean sea level. For submergence experiment, the selected field was surrounded all four sides by bunds of approx 1.5 m height to maintain required water depth. Both of the field i.e. for submergence and control experiments, were nearby bore well for continuous supply of irrigation water as per the requirement of the experiments. Work related to biochemical studies and molecular diversity was done in the lab of Molecular Biology and Genetic Engineering (MBGE) and PG lab of the Department of Plant Breeding and Genetics, BAC Sabour.

### Genotypes
Total 28 rice genotypes including three locally adapted extant varieties, three new varieties released/ identified by BAU Sabour, three released varieties for deep water situation, one line identified for deep water ecology, 14 genotypes of IRRI (International Rice Research Institute) origin survived from the flood at research farm of BAC Sabour during Kharif 2013, one genotypes being used as check in AICRIP trials for SDW (Shallow Deep Water) situation, and two checks namely Swarna Sub-1 and Swarna were used. Swarna Sub-1 is the most popular variety developed by IRRI for areas affected with the flash floods (Table-1).

**Table 1:** Detail of the genotypes used for the study

| S. No. | Entry Name | Origin | Ecology | Maturity |
|---|---|---|---|---|
| 1 | Rajendra Mahsuri-1 | BAU, Sabour | Lowland | Late |
| 2 | Rajendra Sweta | BAU, Sabour | Medium land | Medium |
| 3 | Sita | BAU, Sabour | Medium land | Medium |
| 4 | Rajendra Suwasini | BAU, Sabour | Medium land | Medium-early |
| 5 | Sabour Surbhit | BAU, Sabour | Medium land | Medium-early |
| 6 | Sabour Shree (RAU-724) | BAU, Sabour | Lowland | Late |
| 7 | Sabour Deep (RAU-3055) | BAU, Sabour | Upland | Medium-early |
| 8 | Satyam | BAU, Sabour | Lowland | Late |
| 9 | Sudha | BAU, Sabour | Lowland | Late |
| 10 | Vaidhi | BAU, Sabour | Lowland | Late |
| 11 | RAU-3001 | BAU, Sabour | Lowland | Late |
| 12 | RYC-743 | IRRI, Phillipines | Lowland | Late |
| 13 | RYC-250 | IRRI, Phillipines | Lowland | Late |
| 14 | IR 88904-7-1-1-3 | IRRI, Phillipines | Lowland | Late |
| 15 | IR 88906-27-1-1-1 | IRRI, Phillipines | Lowland | Late |
| 16 | IR 88793-2-2-2-1 | IRRI, Phillipines | Lowland | Late |
| 17 | IR 84895-B-127-CRA-5-1-1 | IRRI, Phillipines | Lowland | Late |
| 18 | IR 88964-24-2-1-4 | IRRI, Phillipines | Lowland | Late |
| 19 | IR 96321-315-402-B-1 | IRRI, Phillipines | Lowland | Late |
| 20 | IR 96321-1686-199-B-3 | IRRI, Phillipines | Lowland | Late |
| 21 | IR 96321-678-271-B-1-1 | IRRI, Phillipines | Lowland | Late |
| 22 | IR 96321 -1686-140-B-2 | IRRI, Phillipines | Lowland | Late |
| 23 | IR 96321-213-120-B-1-2 | IRRI, Phillipines | Lowland | Late |
| 24 | IR 96321-235-32-B-1-2 | IRRI, Phillipines | Lowland | Late |
| 25 | IR 96321 -213-120-B-1-1 | IRRI, Phillipines | Lowland | Late |
| 26 | Purnendu | IIRR, Hyderabad | Lowland | Late |
| 27 | Swarna Sub-1 (+Check) | IRRI, Phillipines | Lowland | Late |
| 28 | Swarna (- Check) | BAU, Sabour | Lowland | Late |

### Field experiments
Field experiments having the same set of 28 genotypes were conducted in two situations/ conditions simultaneously i.e. in normal transplanted condition (called as 'control condition') and submergence. The layout was done in the puddle field after field preparation for both control and submergence condition.

### Treatment for submergence
One of the experiments was submerged after 30 days of transplanting i.e. on 24th of August, 2015. A water flow using bore-well was maintained to completely submerge the plants in a shortest time which was maintained throughout the period of submergence. The field was de-submerged on 12th September, 2015 after 18 days of submergence. De-submergence was started at 1.00 PM in the afternoon and was ended in the late afternoon at around 5.00 PM. Outlets were opened one by one to slowly drain the field for avoiding the lodging of the seedlings due to fast drain out.

### Morphological Data recording
Observations of 21 important agronomical traits were recorded in control experiment whereas in submergence, observations for 11 such traits were recorded. In submergence trial, percent survival was also recorded after 21 of de-submergence. Detail of the observations taken is given in

Table-2.
In control experiment, plant population was observed before harvesting and same plant population was worked out for every plot. Grain yield was taken on net plot area to avoid border effect and to minimize the error. For this, two border rows were harvested and knocked out surrounding each of the plots in all the three replications. After threshing, threshes were sun dried for more than 20 days. Before taking weight of the plot yield, moisture percentage in the grain was recorded with the digital moisture meter. Yield was calculated then at a fix of 13% moisture for all the plots in three replications. Therefore, measures were taken to minimize possible errors in the experiment aiming to get more reliable results.

**Table 2:** List of economical traits recorded for control and submergence experiments

| S. No. | Observation | Control trial | Submergence trial |
|---|---|---|---|
| | **A. Pre harvest data** | | |
| 1. | Plant height (cm) at 30, 45 and 60 DAT | √ | - |
| 2. | Plant height (cm) at maturity | √ | √ |
| 3. | No. of tillers/ hill at 30, 45 and 60 DAT | √ | - |
| 4. | No. of tillers/ hill at maturity | √ | √ |
| 5. | Flag leaf: Length and width (cm) | √ | √ |
| 6. | Days to 50% flowering | √ | √ |
| 7. | Tillers/ m$^2$ | √ | - |
| 9. | Survival Index: 1-9 scale | - | √ |
| | **B. Post-harvest data** | | |
| 10. | Panicle length (cm) | √ | √ |
| 11. | No. of filled grain/ panicle (average of five panicle) | √ | √ |
| 12. | No. of unfilled grain/ panicle (average of five panicle) | √ | √ |
| 13. | Panicle weight (g) (average of 10 panicle) | √ | √ |
| 14. | 1000-grain weight (g) | √ | √ |
| 15. | Grain L/B ratio | √ | - |
| 16. | Grain yield (kg/ha) | √ | √ |

**Statistical analysis**
Morphological data recorded for both the trials were subjected to the statistical analysis separately.

**Analysis of Variance**
The analysis of variance was studied to test the differences among genotypes by F-test. Analysis of variance (ANOVA) was carried out according to the procedure of Randomized Complete Block Design (RCBD) for each character as per methodology advocated by Panse and Sukhatme (1967) [10]. ANOVA helps in partitioning the total variance into three component viz., replication, treatment and error.
Analysis of variance was done under the fixed effective model given below:
$Yij = μ + g_i + r_j + e_{ij}$
Where, μ = Overall mean
$Yij$ = phenotypic observation in the $i^{th}$ treatment and $j^{th}$ replication
$gi$ = effect of $i^{th}$ treatment
$rj$ = effect of $j^{th}$ replication
$eij$ = Random error associated with $i^{th}$ treatment and $j^{th}$ replication.
Here, i = 1, 2, 3 - - - - - - - - - - - - 16; j = 1, 2, 3
Null hypothesis, H0; g1 = g2 - - - - - 16
The sum of squares was arranged in following manner to test the significance between treatments.

**Variance:** It is the average of the square deviation from the mean. It is an effective measure of variability, which permits partition of variance into various components, like phenotypic, genotypic and environmental variances obtained from the ANOVA table with the help of following formula:

$$\text{Environmental Variance } (\sigma_e^2) = M_E$$

$$\text{Genotypic Variance } (\sigma_g^2) = \frac{M_T - M_E}{r}$$

$$\text{Phenotypic Variance}(\sigma_p^2) = \sigma_g^2 + \sigma_e^2$$

Where, r = number of replications
$M_T$ = mean sum square of treatment or genotype
$M_E$ = mean sum square of error

**Coefficient of Variation (CV)**
It is the ratio of standard deviation of a sample to its mean and expressed in percentage.

$$CV\ (\%) = \frac{\text{Standard Deviation}}{\text{Mean}} \times 100$$

Phenotypic and Genotypic coefficients of variation were calculated by the method suggested by Burton and Devane (1953).

**Phenotypic coefficient of variation (PCV)**

$$PCV = \frac{\text{Phenotypic standard deviation}}{\text{General mean}} \times 100$$

$$PCV = \frac{\sqrt{\sigma_p^2}}{\overline{X}},$$

Where, $\sigma^2_p$ = Phenotypic variance
$\overline{X}$ = General mean

**Genotypic coefficient of variation**

$$GCV = \frac{\text{Genotypic standard deviation}}{\text{General mean}} \times 100$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\overline{X}}$$

Where, $\sigma^2_g$ = Genotypic variance
$\overline{X}$ = General mean

PCV and GCV were classified as low, moderate or high by Sivasubramanian and Menon (1973) [19] as given below:

0 – 10 %     :    Low
10 – 20 %    :    Moderate
20 % and above :    High

## Results and discussions
### Analysis of Variance (ANOVA)
In control condition, the mean sum of square due to genotypes was found significant for all the traits under study at 1% level of significance except Number of unfilled grain/panicle which was found to be non-significant. In case of submergence, the mean sum of square due to genotype was found to be significant for all the parameter at 1% level of significance while unfilled grain/panicle was significant at 5% level of significance (Table-3). This indicated that considerable amount of variability were present in the genotypes included in the study under control as well as under submergence condition. Hence, roughly it can be said that the genotypes used under study can be used for various breeding purposes including submergence tolerance. Similar findings for various characters were also reported by Vange (2008) [20], Seyoum *et al.*, (2012) [16], Rai *et al.,* (2014) [12] and Senapati and Kumar (2015) [15].

**Table 3:** ANOVA for different economic traits for control and submergence experiment.

| S. No. | Character | Replications (df=02) | | Treatments (df=27) | | Error (df=54) | |
|---|---|---|---|---|---|---|---|
| | | Cont. | Sub. | Cont. | Sub. | Cont. | Sub. |
| 1 | Plant Height at 30 DAT (cm) | 14.681 | - | 346.849** | - | 11.385 | - |
| 2 | Plant Height at 45 DAT (cm) | 61.149 | - | 771.478** | - | 34.857 | - |
| 3 | Plant Height at 60 DAT (cm) | 136.848 | - | 1385.195** | - | 23.396 | - |
| 4 | Plant Height at Maturity (cm) | 195.368 | 24.68 | 2809.50** | 403.079** | 53.46 | 25.444 |
| 5 | No. of Tillers/Hill at 30 DAT | 0.428 | - | 11.156** | - | 0.763 | - |
| 6 | No. of Tillers/Hill at 45 DAT | 16.39 | - | 6.642** | - | 1.975 | - |
| 7 | No. of Tillers/Hill at 60 DAT | 30.958 | - | 7.161** | - | 1.738 | - |
| 8 | No. of Tillers/ Hill At Maturity | 7.586 | 12.872 | 5.128** | 8.12** | 1.06 | 2.309 |
| 9 | Flag Leaf Length (cm) | 52.271 | 1.358 | 42.711** | 23.271** | 7.879 | 3.964 |
| 10 | Flag Leaf Width (cm) | 0.21 | 0.086 | 0.107** | 0.109** | 0.024 | 0.015 |
| 11 | Days To 50% Flowering | 4.298 | 0.23 | 282.091** | 13.737** | 1.137 | 0.753 |
| 12 | Tillers /m$^2$ | 6364.54 | | 3184.252** | | 1025.968 | |
| 13 | Panicle Length (cm) | 8.586 | 0.118 | 9.854** | 7.572** | 1.028 | 1.979 |
| 14 | No. of Filled Grain/ Panicle | 239.602 | 87.589 | 2193.423** | 1551.523** | 664.817 | 46.101 |
| 15 | No. of Unfilled Grains/ Panicle | 78.8 | 12.191 | 6.923 | 6.823* | 7.871 | 3.918 |
| 16 | Panicle Weight (g) (Avg. of Ten Panicles) | 0.06 | 0.4 | 1.995** | 11.450** | 0.071 | 0.064 |
| 17 | 1000 Grain Weight (g) | 6.01 | 18.894 | 38.163** | 48.454** | 2.095 | 0.673 |
| 18 | Grain L/B Ratio | 0.045 | | 0.661** | | 0.044 | |
| 19 | Grain Yield (kg/ha) | 230739 | 18577 | 2030502.922** | 3211018.159** | 125321.59 | 91633.52 |
| 20 | Survival Index | - | 1.857 | - | 22.255** | - | 1.61 |

## Variance
Estimates of phenotypic variance ($\sigma_p^2$) and genotypic variance ($\sigma_g^2$) computed for data from for different characters are presented in Table- 4 and Table-5 for control and submergence, respectively. In control condition, the highest value of $\sigma_g^2$ was observed for grain yield (635060.4) followed by Plant height at maturity (916.3437), and tillers/m$^2$ (644.04), whereas the lowest value was observed for flag leaf width (0.026). The highest $\sigma_p^2$ was also observed for grain yield (760382) followed by tillers/m$^2$ (1896.16), number of filled grains/panicle (1174.35), and plant height (976.81) while the lowest value was observed for flag leaf width (0.055). In submergence condition the highest value of $\sigma_g^2$ was observed for grain yield (1039795) followed by filled grain/panicle (501.80) and Plant height at maturity (125.87), whereas the lowest value was observed for flag leaf width (0.030). The highest $\sigma_p^2$ was observed for grain yield (1131428) followed by filled grain/panicle (547.90) and plant height (151.32) while the lowest value was observed for flag leaf width (0.048).

For Days to 50% flowering, Plant height at maturity (cm), panicle weight (g), grain yield and 1000-grain weight, there was a little difference between genotypic and phenotypic variance, in both control and submergence. Environmental variance was also negligible indicating very less influence of environmental factors on these traits. Same trend was found for panicle length and L/B ratio in control and for flag leaf length and filled grain/ panicle in submergence. For other traits, proportion of environmental variance was found high which revealed higher environmental influences on these traits. Similar finding was reported by Chaubey and Singh (1994) [3]. Minimum difference between the respective estimates of $\sigma_p^2$ and $\sigma_g^2$ along with higher value of $\sigma_g^2$ in comparison to environmental variance ($\sigma_e^2$) was observed for all the characters in both the conditions which suggested that the variability present among the genotypes for those characters were mainly due to genotype with minimum influence of environment and hence heritable. Khan *et al.* (2009) [5] also showed less difference between $\sigma_p^2$ and $\sigma_g^2$ for days to flowering, panicle length and grains/panicle in rice.

## Coefficient of variation
The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for different characters are presented in Table- 4 and Table-5, respectively for control and submergence. In general, under control condition, the estimates of PCV were higher than their corresponding GCV with good correspondence for all characters. PCV ranged from 8.23 % (panicle length) to 25.92% (panicle weight), while GCV varied from 6.124% (unfilled grain /panicle) followed by 6.80 (panicle length) to 24.60% (panicle weight). In Submergence, PCV ranged from 1.644 % (Days to 50 % flowering) to 77.89 (panicle weight), while GCV varied from 1.51% (Days to 50 % flowering) to 77.11% (panicle weight).

In the control condition, higher magnitude of PCV was recorded for panicle weight (25.92), Plant height at maturity (25.12), filled grain/panicle (22.32), tiller/m$^2$ (20.42) and grain yield (20.26) while moderate estimates were observed for rest of the characters except for days to 50% flowering (9.49) and panicle length (8.23) whose PCV was relatively low. Higher magnitude of GCV was recorded for panicle weight (24.60), plant height at maturity (24.42), grain yield (18.52) and tillers/hill at 30 DAT (17.94). GCV was found low for unfilled grain (6.12), panicle length (6.80), days to 50% flowering (9.43) and tillers/hill at 45 days (9.32) while moderate estimates for rest of the characters. Similar findings were reported by Singh et al., (2006) [17], Lal and Chavan (2011) [7] and Seyoum et al., (2012) [16]. In the submergence condition also, higher magnitude of PCV was recorded for panicle weight (77.89), grain yield (54.90), filled grain/panicle (24.22), and thousand grain weight (19.90) while moderate estimates were observed for rest of the characters except for days to 50% flowering (1.64) and panicle length (9.04) whose PCV was relatively low. Higher magnitude of GCV was recorded for panicle weight (77.11), grain yield (52.63), and filled grain/panicle (23.18) and thousand grain weight (19.09). GCV was found low for days to 50% flowering (1.51), panicle length (6.30) and unfilled grain (6.56) while moderate estimates for rest of characters.

Relatively lower difference between the magnitude of GCV and PCV was observed for days to 50% flowering, plant height, panicle length, panicle weight, 1000 grain weight, and kernel L/B ratio, grain yield in control condition (Table 4.5) indicating less environmental influence in the expression of these attributes. Vange (2008) [20] also found less difference between GCV and PCV for days to 50% flowering and panicle length. For rest of the characters like, tillers/ hill, flag leaf length, panicles/m$^2$, grains/panicle and grain yield, relatively higher difference was observed suggesting greater influence of the environment in the expression of these traits. In case of submergence, relatively lower difference between the magnitude of GCV and PCV was observed for days to 50% flowering, plant height, panicle length, panicle weight, filled grain/panicle, 1000 grain weight, and kernel L/B ratio, grain yield in submerged condition indicating less environmental influence in the expression of these attributes.

**Heritability and Genetic Advance**
From data presented in Table- 4, it is revealed that under control condition, the heritability (broad sense) for different quantitative characters ranged from unfilled grain/panicle (16.97) followed by 33.6% (tillers/hill at 60 DAT) to 98.68 % (days to 50% flowering). High heritability was observed for the traits like days to 50 % flowering (98.68%), plant height at 60 DAT (94.28), plant height at maturity (93.81), panicle weight (90.03), 1000 grain weight (85.16 %), grain yield (83.52), L/B ratio (82.23), panicle length (68.3 %), and flag leaf length (53 %), whereas moderate heritability was noted for rest of the characters. Panse and Sukhatme (1967) [10] reported that characters showing high heritability were governed predominantly by additive gene action and could be improved through individual plant selection. Such high heritability estimates were also reported earlier for days to flowering, plant height, grain yield, and panicle length by Akinwaler et al. (2011) [1]. High estimates of heritability for test weight and grain yield was registered by Patil et al. (2003) [1]. In submergence, the range of heritability (broad sense) estimated was from unfilled grain/panicle (19.82) to

98.01 % (panicle weight). High heritability was observed for the traits like, panicle weight (98.01), grain yield (91.9), filled grain/panicle (91.59), days to 50% flowering (85.18), plant height (83.19), flag leaf width (63.24), flag leaf length (61.88) whereas moderate heritability was noted for rest of the character like panicle length (48.53), and tillers/hill (39.3) except unfilled grain/panicle were low heritability (19.82) (Table- 5).

A perusal of genetic advance in control condition revealed that it was ranged from 0.22 (flag leaf width) to 1500.25 (grain yield) (Table 4). High genetic advance was observed for grain yield (1500.25), plant height at maturity (60.397), plant height at 60 DAT (42.55), filled grain/panicle (30.62), tiller/m$^2$ (30.42), and days to 50 % flowering (19.79) and rest of the character exhibited low genetic advance. High genetic advance as % of mean in control condition (Table- 4.4) was observed for plant height (48.73), panicle weight (48.08), plant height at 60 DAT (42.28), grain yield (34.87), 1000 grain weight (28.87), filled grains/panicle (19.99), flag leaf width (14.93), tillers/hill at 30 DAT days (33.45), tillers/m² (14.28), flag leaf length (15.90), L/B ratio (26.85) as per the classification suggested by Johnson et al., (1955) [4]. These results are in accordance with the results of Seyoum (2012) [16], Sarwar et al. (2015) [14]. In submergence condition (Table- 5) for the characters under study revealed that it was ranged from 0.286 (flag leaf width) to 2013.73 (grain yield). High genetic advance was observed for grain yield (2013.73), filled grain/panicle (44.16), plant height at maturity (21.07), and rest of the character exhibited low genetic advance. High genetic advance as % of mean in submergence (Table- 5) was observed for panicle weight (157), grain yield (103.93), filled grains/panicle (45.70), plant height at maturity (25.99), flag leaf width (20.355), tillers/hill at maturity (15.37), flag leaf length (16.91) rest of the character exhibited low magnitude of genetic advance as % of mean.

According to Johnson (1955) [4] high heritability should be accompanied by high genetic advance to arrive at desired improvement in a particular character, but it may not necessary to obtain such results always. In the present study high heritability along with high genetic advance as % of mean was exhibited for panicle weight, plant height, grain yield, test weight, L/B ratio, flag leaf length in control condition and for Panicle weight, plant height, flag leaf length, flag leaf width, filled grains/panicle, grain yield in submergence condition. The results for these characters indicated that heritability is most likely due to additive gene effects and selection may be effective. This type of characters could be improved by mass selection and other breeding methods based on progeny testing. Chaubey and Singh (1994) [3] reported greater magnitude of broad sense heritability coupled with high genetic advance in grain yield and provided the evidence that these plant parameters were under the control of additive genetic effects. High heritability coupled with high genetic advance for yield and yield contributing traits were also reported in past by Padmaja et al. (2008) [9] and Rai et al. (2014) [12].

High heritability associated with moderate genetic advance was observed for days to 50% flowering, panicle length, suggesting greater role of non-additive gene action in their inheritance for which heterosis breeding could be exploited. Tillers/hill, flag leaf width recorded moderate heritability with moderate genetic advance as percent of mean.

**Conclusion**
The present study was able to identify the magnitude of

genetic variability present in the 28 genotypes used under study for various economically important traits. Results may be quite useful in the selection of the genotypes, which may be used as parental material in future rice breeding programmes, based on the traits having high heritability coupled with high GCV and high genetic advance as percentage of mean i.e. exhibited for panicle weight under both, control and submergence while for plant height at maturity and grain yield respectively under control and submergence.

## Acknowledgements

**Table 4:** Genetic parameters of morphological traits in control condition.

| S. No. | Character | Range | | Mean | $\sigma^2_g$ | $\sigma^2_p$ | $\sigma^2_e$ | GCV | PCV | h² (Broad Sense) % | Genetic Advance | GA as % of Mean |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Lowest | Highest | | | | | | | | | |
| 1 | Days to 50 % flowering | 85 | 118 | 103 | 93.6111 | 94.8673 | 1.2562 | 9.4316 | 9.4947 | 98.68 | 19.7987 | 19.3001 |
| 2 | Plant height 30 DAT | 46 | 89 | 60 | 111.8211 | 123.2065 | 11.3854 | 17.5093 | 18.379 | 90.76 | 20.7527 | 34.3621 |
| 3 | Plant height 45 DAT | 61 | 127 | 87 | 245.5403 | 280.3971 | 34.8568 | 17.9424 | 19.1737 | 87.57 | 30.2067 | 34.5878 |
| 4 | Plant height 60 DAT | 75 | 153 | 101 | 452.5711 | 480.0533 | 27.4823 | 21.1431 | 21.7756 | 94.28 | 42.5509 | 42.2897 |
| 5 | Plant height at maturity | 101 | 217 | 124 | 916.3437 | 976.8189 | 60.4752 | 24.4237 | 25.2168 | 93.81 | 60.3975 | 48.7305 |
| 6 | Panicle length | 20 | 29 | 25 | 2.8445 | 4.165 | 1.3205 | 6.8072 | 8.2371 | 68.3 | 2.8712 | 11.5887 |
| 7 | panicle weight | 2 | 6 | 3 | 0.6415 | 0.7125 | 0.071 | 24.601 | 25.9274 | 90.03 | 1.5655 | 48.0853 |
| 8 | Tillers/hill at 30 DAT | 6 | 14 | 10 | 3.4645 | 4.2274 | 0.7629 | 17.9404 | 19.8176 | 81.95 | 3.4711 | 33.4566 |
| 9 | Tillers/hill at 45 DAT | 9 | 17 | 12 | 1.3558 | 3.9306 | 2.5748 | 9.3292 | 15.8847 | 34.49 | 1.4087 | 11.2868 |
| 10 | Tillers/hill at 60 DAT | 8 | 15 | 10 | 1.4389 | 4.2818 | 2.8429 | 11.4333 | 19.7229 | 33.6 | 1.4325 | 13.6534 |
| 11 | Tillers/hill at maturity | 7 | 12 | 10 | 1.2648 | 2.5985 | 1.3337 | 11.4771 | 16.4508 | 48.67 | 1.6163 | 16.4946 |
| 12 | Flag leaf length | 23 | 39 | 31 | 11.0016 | 20.7075 | 9.7059 | 10.5954 | 14.5363 | 53.13 | 4.9804 | 15.9093 |
| 13 | Flag leaf width | 1.37 | 2 | 1.53 | 0.026 | 0.0551 | 0.0291 | 10.5507 | 15.3523 | 47.23 | 0.2283 | 14.9368 |
| 14 | Tiller/ m² | 158 | 292 | 213 | 644.0454 | 1896.161 | 1252.116 | 11.9026 | 20.4231 | 33.97 | 30.4681 | 14.2899 |
| 15 | Filled Grains/panicle | 109 | 241 | 153 | 509.5354 | 1174.353 | 664.8172 | 14.7338 | 22.368 | 43.39 | 30.6297 | 19.9926 |
| 16 | Unfilled grain/panicle | 12 | 19 | 15 | 0.8769 | 5.1688 | 4.2919 | 6.1244 | 14.8688 | 16.97 | 0.7946 | 5.1965 |
| 17 | Grain yield | 3116 | 6033 | 4302 | 635060.4 | 760382 | 125321.6 | 18.5243 | 20.2698 | 83.52 | 1500.259 | 34.8738 |
| 18 | 1000 grain weight | 19 | 30 | 23 | 12.0226 | 14.1181 | 2.0954 | 15.1958 | 16.4669 | 85.16 | 6.5914 | 28.8871 |
| 19 | Kernel L/B ratio | 3 | 4 | 3 | 0.2051 | 0.2494 | 0.0443 | 14.374 | 15.8513 | 82.23 | 0.846 | 26.8509 |

**Table 5:** Genetic parameters of morphological traits of Submergence condition.

| S. No. | Character | Range | | Mean | $\sigma^2_g$ | $\sigma^2_p$ | $\sigma^2_e$ | GCV | PCV | h² (Broad Sense) % | Genetic Advance | GA as % of Mean |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Lowest | Highest | | | | | | | | | |
| 1 | Days to 50 % flowering | 133 | 141 | 137 | 4.33 | 5.0811 | 0.7531 | 1.5177 | 1.6445 | 85.18 | 3.9553 | 2.8856 |
| 2 | Plant height | 65 | 110 | 81 | 125.8782 | 151.3226 | 25.4444 | 13.8371 | 15.1712 | 83.19 | 21.0798 | 25.9977 |
| 3 | Panicle length | 18 | 25 | 22 | 1.8651 | 3.8435 | 1.9784 | 6.3026 | 9.0474 | 48.53 | 1.9598 | 9.0443 |
| 4 | panicle weight | 1 | 4 | 3 | 3.791 | 3.868 | 0.077 | 77.1181 | 77.8976 | 98.01 | 3.9708 | 157.2734 |
| 5 | Tillers/hill | 8 | 15 | 11 | 1.7867 | 4.5463 | 2.7596 | 11.9056 | 18.9912 | 39.3 | 1.7262 | 15.375 |
| 6 | Flag leaf length | 15 | 28 | 24 | 6.4352 | 10.3993 | 3.964 | 10.4363 | 13.2668 | 61.88 | 4.1108 | 16.912 |
| 7 | Flag leaf width | 0.96 | 1.84 | 1.41 | 0.0306 | 0.0483 | 0.0178 | 12.4252 | 15.6241 | 63.24 | 0.2864 | 20.3555 |
| 8 | Filled Grains/panicle | 52 | 143 | 97 | 501.8073 | 547.9086 | 46.1013 | 23.1838 | 24.2253 | 91.59 | 44.1621 | 45.7052 |
| 9 | Unfilled grain/panicle | 11 | 17 | 15 | 0.9685 | 4.8864 | 3.9179 | 6.5681 | 14.7531 | 19.82 | 0.9025 | 6.0236 |
| 10 | Grain yield | 414 | 4244 | 1937 | 1039795 | 1131428 | 91633.52 | 52.6305 | 54.9006 | 91.9 | 2013.7305 | 103.9358 |
| 11 | 1000 grain weight | 14 | 28 | 21 | 15.7244 | 17.0967 | 1.3723 | 19.0906 | 19.9062 | 91.97 | 7.834 | 37.7153 |

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