Received: 27 Jul 2023 | Revised: 02 Aug 2023 | Accepted: 28 Aug 2023

Electronic Journal of Plant Breeding

Research Article

# Estimation of narrow sense heritability in early segregating generations of rice introgressed with *Sub1* QTL

**S. Viswabharathy[1], T. Kalaimagal[1*], S. Manonmani[1], P. Jeyakumar [2] and M. Raveendran[3]**

[1]Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore-641 003
[2]Directorate of Planning and Monitoring, Tamil Nadu Agricultural University, Coimbatore-641 003
[3]Directorate of Research, Tamil Nadu Agricultural University, Coimbatore-641 003
***E-Mail:** kalaimagal.t@gmail.com

**Abstract**
Rice, often termed the golden cereal, sustains billions globally but faces submergence as a significant constraint in semi deep and deep-water ecosystems in India. The primary aim of this study was to evaluate the genetic potential of yield and yield-contributing traits in the cross ASD 16 x BIL of CO 51 Sub1 (12 x 9-7-6-12-3-45) across the $F_2$ and $F_3$ generations. The research revealed a wide range of variation for all traits in both generations. Specifically, positively skewed and platykurtic curves were observed for the number of productive tillers per plant and the number of chaffy grains per panicle, indicating the influence of a large number of genes with dominance-based gene interaction on these traits. The study also found highly significant correlation and regression coefficients for all recorded traits. Interestingly, while broad sense heritability showed high values for certain traits, narrow sense heritability percentages were only moderate for the same traits. Thus, focusing on selecting individuals based on narrow sense heritability would be more effective in improving those traits, as it targets the genetic variation that can be passed on to future generations.

**Keywords:** Submergence, heritability, parent offspring regression, Skewness, kurtosis, intergenerational correlation, Rice

## INTRODUCTION

Rice, is a critically important crop on a global scale, ranking just behind wheat in overall production (Ali *et al*., 2023). Major global rice production, amounting to 89.9%, takes place in Asia, with China as the leading producer, followed by India, Bangladesh, Indonesia, and Vietnam (FAO, 2021). Out of the 42 biotic and abiotic stresses that impact rice production, submergence is regarded as the third most significant constraint to achieve higher productivity in eastern India (Setter *et al*., 1997). Excessive flooding not only poses risks to human life but also plays a crucial role in aggravating poverty among marginalized communities. Designing crops that can tolerate submergence stress is crucial to address this issue. Marker-assisted selection (MAS) has been successfully used for introgression of flood tolerance genes (*Sub1*) in several mega varieties of rice. The availability of elite lines containing heritable target genes and the assessment of introgressed gene stability under various conditions have enabled a more effective approach to submergence tolerance breeding in rice, requiring early-generation selection for high yield along with the target quantitative trait loci (QTL). Yield depends on many components, mostly under polygenic control, so changes in yield involve related component changes (Grafius, 1959;Solanke *et al*., 2023). The ultimate aim of every plant breeding program is to produce improved genotypes that outperform the existing ones in one or more traits, leading to higher economic yields. The success and effectiveness of a breeding program depend on the genetic information that regulates the inheritance of the traits being studied

(Riyanto *et al*., 2023). Heritability, a concept introduced by Sewall Wright and Ronald Fisher nearly a century ago, plays a crucial role in the response to selection in evolutionary biology and agriculture, as well as in predicting disease risk in medicine; however, it can vary within a population due to changes in measurement methods, environmental conditions, migration, selection pressures, and inbreeding effects (Nyquist and Baker, 1991;Visscher *et al*., 2008). Heritability estimates provide valuable guidance to plant breeders, allowing them to understand the extent to which variation in traits is influenced by genetics or specifically by additive genetic effects. Broad sense heritability reflects the proportion of variation that can be inherited, while the Narrow sense heritability, represents the portion of genetic variation that can be fixed in pure lines. The most prevalent biometrical genetics approach for calculating heritability is PO regression. In the current study, parent-offspring regression analysis was utilized to assess the association and heritability of variables influencing yield in the early segregating population of rice introgressed with *Sub1* QTL.

## MATERIALS AND METHODS

The current study aimed to assess the genetic potential for yield and yield contributing traits of the cross ASD 16 x BIL of CO 51 Sub1 (12 x 9-7-6-12-3-45) in the $F_2$ and $F_3$ generations during the *Kuruvai* season (Jun.-Sept. 2022) and from December 2022 to the middle of May 2023 at Paddy Breeding Station, AC&RI, Coimbatore, Tamil Nadu, India. Cultural practices and plant protection techniques were implemented as needed. ASD 16, a well-known rice cultivar in Tamil Nadu and other southern regions of India, served as the female parent and possesses short bold grains, moderate tillering capacity, and resistance to blast disease but is susceptible to submergence. The donor parent for the introgression of *Sub1* QTL was the Backcross Inbred Line of CO 51 Sub1 (12 x 9-7-6-12-3-45) (Viswabharathy *et al*., 2023). Progenies from $F_2$ underwent foreground selection for *Sub1* QTL, and 31 positive plants for *Sub1* QTL along with good yield performance were selected for further analysis in the $F_3$ generation. Twelve biometrical traits *viz.,* Days to fifty per cent flowering (days); Plant height (cm); Number of productive tillers per panicle; Panicle length (cm); Flag leaf length (cm); Number of filled grains per panicle; Number of chaffy grains per panicle; Spikelet fertility (%); Single plant yield (g); Hundred seed weight (g); Grain length (mm) and Grain width (mm) were recorded on five plants, and their average values were used for subsequent analysis, including PCV, GCV, broad sense heritability, Genetic advance percent of mean, skewness, kurtosis, intergenerational correlation, and parent-progeny regression, employing Microsoft Excel and R software for data processing and graphing.

Narrow sense heritability (Smith and Kinman, 1965)

$$h^2 = \frac{b_{yx}}{2r_{xy}} x\ 100$$

$b_{yx}$ $b_{yx}$: regression coefficient of $F_3$ progeny means on $F_2$ parental values for respective characters

$r_{xy}$ $r_{xy}$: Intergenerational correlation coefficient between the parent "x" and its offspring "y"

## RESULTS AND DISCUSSION

Wide variation in segregating generations enables the selection of superior rice genotypes with desirable traits such as earliness, reduced plant height to avoid lodging, high tillering capacity, and high single plant yield. A total of 31 plants, which exhibited positivity for the Sub1 QTL and displayed better agronomic performance compared to the parental lines, were selfed, and forwarded to the $F_3$ generation as 31 distinct families. For the parental lines and 31 progenies in $F_2$ and $F_3$ generations, the mean, range, and critical difference for the various characteristics were tabulated (**Table 1 and Table 2**). In both the $F_2$ and $F_3$ generations, a broad range of variation was observed. In the $F_2$ generation, the duration from sowing to fifty percent flowering ranged from 75 to 107 days, with an average of 92 days. Plant height varied from 83 to 110 cm, with a mean value of 101.14 cm, and the hundred-seed weight ranged from 0.787 to 2.272 g. In the $F_3$ generation, plant height ranged from 79 cm to 110 cm, while spikelet fertility percentage ranged from 63% to 99%, with an average of 87%. Furthermore, in the $F_3$ generation, the average plant height and the number of filled grains per panicle closely resembled those of the donor parent, and the average value of panicle length and flag leaf length was similar to the mean values of both parental lines.

The traits, namely number of productive tillers per plant, number of filled grains per panicle and number of chaffy grains per panicle, exhibited high phenotypic coefficient of variation (PCV) and high genotypic coefficient of variation (GCV) in both the generations (Table 3). Additionally, flag leaf length displayed high PCV and GCV in the $F_2$ generation alone. These results indicate significant phenotypic diversity and genetic variability in these traits, emphasizing their potential as target traits for selection and improvement in breeding programs. Similar observations were made by Renuprasath *et al*., (2023) concerning traits related to drought tolerance and their contribution to yield. Similarly, Manojkumar *et al*., (2022) and Swapnil *et al*., (2020) reported comparable findings for yield-contributing traits in intraspecific crosses in rice. In the $F_2$ generation alone, number of productive tillers per plant, flag leaf length, number of filled grains per panicle, spikelet fertility, and single plant yield exhibited high heritability and genetic advance. Given their strong heritability and genetic advances, these traits can be effectively prioritized in selection and breeding programs to enhance desirable characteristics in rice cultivars. The findings of Renuprasath *et al*., (2023), Manojkumar *et al*., (2022), Swapnil *et al*., (2020), Singh *et al*., (2020) and Lingaiah (2018) were consistent with each other.

**Table 1. Performance of yield and its associated traits in $F_2$ progenies**

| S. No. | Plant No. | FS | DFF | PH | NPT | PL | FLL | FG | CG | SF | SPY | GL | GW | HSW |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 5 | HETERO | 102 | 104 | 24 | 25.2 | 21.6 | 241 | 28 | 89.59 | 52.81 | 7.77 | 2.1 | 1.892 |
| 2 | 6 | HOMO | 77 | 94 | 15 | 22.3 | 30 | 104 | 38 | 73.24 | 22.98 | 7.8 | 2.5 | 1.836 |
| 3 | 9 | HOMO | 86 | 103 | 20 | 24 | 23.4 | 162 | 57 | 73.97 | 49.32 | 7.37 | 2.6 | 2.272 |
| 4 | 10 | HETERO | 102 | 102 | 20 | 25.5 | 26 | 207 | 13 | 94.09 | 48.83 | 6.93 | 2.13 | 1.928 |
| 5 | 12 | HETERO | 85 | 100 | 24 | 26.8 | 31 | 231 | 19 | 92.4 | 57.4 | 7.87 | 2.3 | 1.788 |
| 6 | 16 | HETERO | 107 | 103 | 22 | 21.5 | 22.5 | 193 | 8 | 96.02 | 53.52 | 7.4 | 2.27 | 1.824 |
| 7 | 21 | HOMO | 102 | 105 | 21 | 25.3 | 23.5 | 202 | 30 | 87.07 | 62.03 | 7.53 | 2.3 | 1.918 |
| 8 | 22 | HETERO | 75 | 92.3 | 13 | 22.3 | 23.6 | 158 | 69 | 69.6 | 25.47 | 7.77 | 2 | 1.646 |
| 9 | 27 | HOMO | 102 | 98 | 33 | 23 | 29 | 139 | 72 | 65.88 | 67.98 | 7.37 | 2.13 | 1.82 |
| 10 | 32 | HETERO | 106 | 100.3 | 16 | 23 | 22 | 190 | 24 | 96 | 59.83 | 8.03 | 2.27 | 2.16 |
| 11 | 46 | HOMO | 75 | 83 | 15 | 19 | 18 | 53 | 15 | 77.94 | 3.23 | 7.63 | 2.27 | 0.787 |
| 12 | 52 | HOMO | 80 | 100 | 13 | 23 | 24.5 | 196 | 40 | 83.05 | 42.73 | 7.9 | 2.27 | 2.102 |
| 13 | 67 | HOMO | 90 | 106 | 16 | 25 | 23 | 256 | 35 | 87.97 | 62.71 | 7.6 | 2.37 | 2.017 |
| 14 | 68 | HETERO | 81 | 102 | 20 | 22.9 | 25.1 | 202 | 28 | 87.83 | 55.78 | 6.83 | 2.33 | 2.049 |
| 15 | 69 | HOMO | 82 | 95 | 12 | 21.4 | 21.5 | 219 | 35 | 86.22 | 32.07 | 6.63 | 2.43 | 1.95 |
| 16 | 70 | HOMO | 102 | 103 | 16 | 27.1 | 29.6 | 318 | 10 | 96.95 | 48.11 | 7.63 | 2.43 | 1.854 |
| 17 | 74 | HOMO | 104 | 106 | 14 | 22.2 | 28 | 141 | 73 | 65.89 | 21.42 | 7.33 | 2.4 | 1.456 |
| 18 | 78 | HOMO | 103 | 103.4 | 17 | 25 | 23.8 | 232 | 36 | 86.57 | 38.85 | 7.7 | 2.4 | 1.912 |
| 19 | 84 | HETERO | 96 | 107 | 23 | 26 | 30 | 270 | 32 | 89.4 | 64.15 | 7.5 | 2.13 | 1.778 |
| 20 | 85 | HETERO | 93 | 99 | 18 | 26.5 | 33 | 155 | 22 | 87.57 | 55.49 | 7.4 | 2.27 | 2.008 |
| 21 | 86 | HETERO | 98 | 110 | 19 | 17.5 | 33 | 171 | 12 | 93.44 | 59.54 | 7.13 | 2.37 | 2.005 |
| 22 | 100 | HOMO | 99 | 102 | 24 | 24.5 | 22 | 304 | 14 | 95.6 | 47.14 | 7.4 | 2.07 | 1.638 |
| 23 | 117 | HETERO | 86 | 101 | 24 | 23.7 | 27.6 | 284 | 26 | 91.61 | 66.39 | 6.97 | 2.4 | 2.139 |
| 24 | 119 | HETERO | 86 | 104 | 18 | 24.5 | 26 | 267 | 52 | 83.7 | 55.86 | 7.23 | 2.27 | 1.902 |
| 25 | 122 | HOMO | 89 | 100 | 20 | 24.5 | 34 | 268 | 49 | 84.54 | 60.68 | 7.33 | 2.23 | 1.7637 |
| 26 | 143 | HETERO | 98 | 101 | 24 | 23.5 | 25 | 195 | 32 | 85.9 | 53.51 | 6.93 | 2.13 | 1.8457 |
| 27 | 147 | HETERO | 99 | 104 | 15 | 25 | 22.6 | 230 | 18 | 92.74 | 58.39 | 7.3 | 2.33 | 1.8371 |
| 28 | 148 | HETERO | 98 | 101.4 | 17 | 25.5 | 35 | 296 | 32 | 90.24 | 55.96 | 7.34 | 2.44 | 1.5856 |
| 29 | 150 | HETERO | 89 | 101 | 22 | 25.6 | 28 | 259 | 30 | 89.62 | 57.24 | 7.17 | 2.2 | 2.0248 |
| 30 | 153 | HETERO | 86 | 100 | 15 | 23.3 | 22 | 173 | 8 | 95.58 | 59.06 | 7.4 | 2.33 | 2.0824 |
| 31 | 162 | HETERO | 100 | 105 | 12 | 22.5 | 22.7 | 238 | 24 | 90.84 | 41.01 | 7.56 | 2.41 | 2.039 |
| Range | | | 75 - 107 | 83 - 110 | 12 – 33 | 17.5 - 27.1 | 18 - 35 | 53 - 318 | 8 - 73 | 65.88 - 96.95 | 3.23 - 67.98 | 6.63 - 8.03 | 2 - 2.6 | 0.787 - 2.272 |
| Mean | | | 92.84 | 101.14 | 18.77 | 23.78 | 26.03 | 211.42 | 31.65 | 86.49 | 49.66 | 7.41 | 2.29 | 1.87 |
| Standard Error | | | 1.75 | 0.90 | 0.84 | 0.38 | 0.77 | 10.83 | 3.24 | 1.57 | 2.69 | 0.06 | 0.02 | 0.05 |
| CD (P= 0.05) | | | 3.57 | 1.83 | 1.72 | 0.78 | 1.58 | 22.11 | 6.62 | 3.21 | 5.50 | 0.12 | 0.05 | 0.10 |
| CD (P =0.01) | | | 4.80 | 2.47 | 2.31 | 1.05 | 2.13 | 29.78 | 8.91 | 4.32 | 7.41 | 0.16 | 0.07 | 0.13 |
| **ASD 16** | | | 81 | 106.6 | 12.2 | 26.5 | 29.74 | 212.2 | 32.2 | 86.82 | 43.16 | 7.27 | 2.76 | 2.4614 |
| **12 x 9-7-6-12-3-45** | | | 98 | 100 | 30 | 22.2 | 24.2 | 122 | 20 | 92.42 | 44 | 7.5 | 2.23 | 1.742 |

DFF: Days to fifty percent flowering, PH: Plant height, NPT: Number of productive tillers per plant, PL: Panicle length, FLL: Flag leaf length, FG: Number of filled grains per plant, CG: Chaffy grains per panicle, SF: Spikelet fertility percentage, HGW: Hundred seed weight, SPY: Grain yield per plant, GL: Grain length, GW: Grain width.

Table 2. Performance of yield and its associated traits in $F_3$ progenies

| S. No. | Family No. | DFF | PH | NPT | PL | FLL | FLW | FG | CG | SF | SPY | GL | GW | HSW |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 5 | 97 | 99.8 | 23.3 | 24.2 | 22 | 1.1 | 236.3 | 27.6 | 90.6 | 54.4 | 7.8 | 2 | 1.9 |
| 2 | 6 | 75 | 96.6 | 14.4 | 22.8 | 29.6 | 1.2 | 99.7 | 36.3 | 76.4 | 23.5 | 7.8 | 2.5 | 1.9 |
| 3 | 9 | 83 | 105.2 | 20.2 | 25 | 22.6 | 1.3 | 161.8 | 57 | 73 | 49.7 | 7.4 | 2.6 | 2.2 |
| 4 | 10 | 105 | 97 | 20.5 | 25.1 | 26.1 | 1.3 | 203.7 | 13.3 | 91.2 | 47.6 | 7 | 2.1 | 2 |
| 5 | 12 | 89 | 95.5 | 23.4 | 26.1 | 31.6 | 1.2 | 222.2 | 19.4 | 90.3 | 58.3 | 7.8 | 2.2 | 1.9 |
| 6 | 16 | 104 | 99.6 | 21.5 | 20.7 | 22.3 | 1.2 | 194.4 | 7.8 | 93.7 | 55.9 | 7.2 | 2.4 | 1.8 |
| 7 | 21 | 99 | 108.6 | 20.5 | 26.4 | 23.6 | 1.2 | 192.9 | 30.3 | 90.3 | 60.5 | 7.7 | 2.4 | 1.9 |
| 8 | 22 | 75 | 89.6 | 12.4 | 22.9 | 24.1 | 1.2 | 155.9 | 70.2 | 70.6 | 24.9 | 7.4 | 2 | 1.6 |
| 9 | 27 | 105 | 100.6 | 31.5 | 22.3 | 29.9 | 1.4 | 135.8 | 69.5 | 64.9 | 66.3 | 7.1 | 2.2 | 1.8 |
| 10 | 32 | 102 | 98.6 | 15.4 | 21.9 | 21.6 | 1 | 188.3 | 24 | 100.6 | 61 | 7.8 | 2.2 | 2.2 |
| 11 | 46 | 75 | 79.2 | 14.9 | 18.8 | 18.2 | 0.9 | 55.2 | 15.7 | 81.5 | 33.3 | 7.6 | 2.3 | 0.8 |
| 12 | 52 | 76 | 97.7 | 13.3 | 21.9 | 23.7 | 1.1 | 190.9 | 38.8 | 82.2 | 43.8 | 7.6 | 2.3 | 2.2 |
| 13 | 67 | 90 | 104.2 | 16.5 | 24.3 | 23 | 1.2 | 258.6 | 33.6 | 89.1 | 61.9 | 7.4 | 2.4 | 1.9 |
| 14 | 68 | 80 | 105.1 | 20.2 | 22.6 | 25.6 | 1 | 208.1 | 26.7 | 88.1 | 54.2 | 7.1 | 2.4 | 2.1 |
| 15 | 69 | 84 | 99.4 | 12.6 | 20.7 | 21 | 1 | 223.8 | 33.7 | 85.7 | 33.5 | 6.7 | 2.5 | 2 |
| 16 | 70 | 98 | 102.3 | 16.1 | 28 | 30.1 | 1.3 | 308.5 | 9.9 | 98.6 | 49.2 | 7.7 | 2.5 | 1.9 |
| 17 | 74 | 99 | 105.5 | 14.6 | 21.3 | 29.3 | 1.1 | 138.7 | 71.4 | 63.2 | 21 | 7.4 | 2.4 | 1.4 |
| 18 | 78 | 101 | 99.7 | 17.5 | 24.2 | 24.4 | 1.3 | 231.8 | 36.5 | 84.4 | 40.4 | 7.8 | 2.4 | 2 |
| 19 | 84 | 95 | 108.6 | 23.1 | 26.6 | 30.5 | 1.4 | 283.2 | 33.2 | 87.2 | 64.2 | 7.1 | 2.1 | 1.8 |
| 20 | 85 | 88 | 95.9 | 18.5 | 27.5 | 34.6 | 1.3 | 158.1 | 21.3 | 89.3 | 54.5 | 7.3 | 2.2 | 2.1 |
| 21 | 86 | 103 | 110.3 | 19.4 | 17.1 | 32.2 | 1.2 | 171.2 | 11.4 | 89.4 | 61.5 | 7.5 | 2.3 | 2 |
| 22 | 100 | 100 | 99.1 | 23.7 | 24.8 | 22.8 | 1.1 | 290 | 14.2 | 91.8 | 45.4 | 7.6 | 2 | 1.6 |
| 23 | 117 | 88 | 101.1 | 24.2 | 23.8 | 26.2 | 1.1 | 292.8 | 26 | 94.8 | 68.4 | 6.9 | 2.5 | 2.2 |
| 24 | 119 | 88 | 103 | 18.7 | 23.4 | 26.4 | 1 | 274.7 | 51.7 | 80.2 | 55.6 | 7.5 | 2.2 | 2 |
| 25 | 122 | 86 | 102.9 | 20.7 | 24.3 | 33.3 | 1.1 | 274.7 | 51 | 87.8 | 58.9 | 7.1 | 2.2 | 1.7 |
| 26 | 143 | 97 | 98.2 | 23.2 | 23.5 | 25.9 | 1 | 189 | 33.5 | 89.2 | 51.4 | 6.9 | 2 | 1.8 |
| 27 | 147 | 100 | 105.7 | 15.3 | 24.4 | 22.2 | 1 | 237.6 | 18.2 | 94.3 | 60.2 | 7.4 | 2.4 | 1.9 |
| 29 | 148 | 98 | 103.2 | 17.2 | 26.6 | 35.1 | 1.1 | 291.3 | 32.5 | 87.4 | 58.4 | 7.4 | 2.4 | 1.6 |
| 29 | 150 | 87 | 98.1 | 21.8 | 25.7 | 28.3 | 1.2 | 261.3 | 28.6 | 86.1 | 59 | 7.2 | 2.3 | 1.9 |
| 30 | 153 | 82 | 99.6 | 15.1 | 22.6 | 21 | 1.1 | 178.2 | 8 | 100 | 58.1 | 7.7 | 2.4 | 2.1 |
| 31 | 162 | 100 | 105.2 | 12.2 | 21.8 | 22 | 1.1 | 249.7 | 23.9 | 91.7 | 40.6 | 7.7 | 2.5 | 2.1 |
| Range | | 75 - 105 | 79.2 - 110.3 | 12.2 - 31.5 | 17.1 - 28 | 18.2 - 35.1 | 0.9 - 1.4 | 55.2 - 308.5 | 7.8 - 71.4 | 63.2 - 100.6 | 21 - 68.4 | 6.7-7.8 | 2 - 2.6 | 0.8 - 2.2 |
| Mean | | 91.90 | 100.49 | 18.77 | 23.59 | 26.10 | 1.15 | 211.56 | 31.46 | 86.57 | 49.86 | 7.41 | 2.30 | 1.88 |
| Standard Error | | 1.75 | 1.07 | 0.79 | 0.44 | 0.80 | 0.02 | 10.93 | 3.21 | 1.64 | 2.70 | 0.06 | 0.03 | 0.05 |
| CD (P = 0.05) | | 3.57 | 2.18 | 1.62 | 0.90 | 1.64 | 0.05 | 22.32 | 6.55 | 3.35 | 5.51 | 0.11 | 0.06 | 0.10 |
| CD (P = 0.01) | | 4.80 | 2.93 | 2.18 | 1.21 | 2.21 | 0.06 | 30.06 | 8.82 | 4.51 | 7.42 | 0.15 | 0.08 | 0.14 |
| **ASD16** | | 83 | 101.8 | 12.8 | 25.4 | 31.2 | 1.2 | 222.6 | 33.4 | 83 | 44.4 | 7.1 | 2.7 | 2.4 |
| **12 x 9-7-6-12-3-45** | | 101 | 102.1 | 29.6 | 22.4 | 23 | 1.4 | 121.4 | 20.9 | 93.2 | 42.5 | 7.8 | 2.1 | 1.7 |

DFF: Days to fifty percent flowering, PH: Plant height, NPT: Number of productive tillers per plant, PL: Panicle length, FLL: Flag leaf length, FG: Number of filled grains per plant, CG: Chaffy grains per panicle, SF: Spikelet fertility percentage, HSW: Hundred grain weight, SPY: Grain yield per plant, GL: Grain length, GW: Grain width.

Table 3. Genetic variability analysis for biometrical traits in $F_2$ and $F_3$ generation

| Characters | $F_2$ generation | | | | $F_3$ generation | | | |
|---|---|---|---|---|---|---|---|---|
| | PCV | GCV | Heritability | GAM | PCV | GCV | Heritability | GAM |
| Days to fifty percent flowering | 9.18 | 8.96 | 95.28 | 18.03 | 10.58 | 10.44 | 97.36 | 5.46 |
| Plant height (cm) | 7.38 | 6.76 | 84.03 | 12.77 | 5.90 | 5.45 | 85.22 | 9.08 |
| Number of productive tillers per plant | 32.27 | 31.66 | 96.26 | 64 | 23.49 | 22.88 | 94.86 | 10.41 |
| Panicle length (cm) | 9.076 | 8.497 | 87.64 | 16.38 | 10.39 | 7.83 | 56.76 | 12.89 |
| Flag leaf length (cm) | 57.48 | 55.06 | 98.52 | 34.67 | 17.13 | 16.30 | 90.54 | 13.51 |
| Number of filled grains per panicle | 26.95 | 26.87 | 87.38 | 55.18 | 28.76 | 28.74 | 99.85 | 5.35 |
| Number of chaffy grains per panicle | 66.26 | 65.94 | 47.03 | 39.19 | 56.79 | 56.26 | 98.15 | 37.92 |
| Spikelet fertility (%) | 9.85 | 9.85 | 94.93 | 20.29 | 10.55 | 10.40 | 97.24 | 5.32 |
| Single plant yield (g) | 45.72 | 45.71 | 90.96 | 94.14 | 30.15 | 29.93 | 98.58 | 13.03 |

The $F_2$ generation exhibited positive skewness for the number of productive tillers per panicle (0.82), flag leaf length (0.51), flag leaf width (0.17), and the number of chaffy grains per panicle (0.92) (Table 4). Conversely, negative skewness was evident for days to fifty percent flowering (-0.37), plant height (-1.70), panicle length (-1.00), the number of filled grains per panicle (-0.44), single plant yield (-1.46), grain length (-0.36), grain width (-0.13), and hundred seed weight (-2.27). In the $F_3$ generation, negative skewness was observed for days to fifty percent flowering (-0.42), plant height (-1.47), panicle length (-0.50), the number of filled grains per panicle (-0.48), spikelet fertility (-1.04), single plant yield (-1.47), grain length (-0.34), grain width (-0.18), and hundred seed weight (-2.20). Additionally, positive skewness was seen for the number of productive tillers per panicle (0.61), flag leaf length (0.46), flag leaf width (0.21), and the number of chaffy grains per panicle (0.90). In the $F_2$ generation (**Fig. 1**), a leptokurtic curve was observed for plant height (5.03), the number of productive tillers per panicle (1.19), panicle length (1.55), single plant yield (1.98), and hundred seed weight (8.27), whereas a platykurtic curve was observed for days to fifty percent flowering (-1.14), flag leaf length (-0.59), flag leaf width (-0.59), the number of filled grains per panicle (0.28), the number of chaffy grains per panicle (0.35), spikelet fertility (0.48), grain length (-0.11), and grain width (-0.15). In the $F_3$ generation (**Fig. 2**), the traits plant height (4.66), single plant yield (2.01), and hundred seed weight showed a leptokurtic curve, and the number of filled grains per panicle (0.02) showed a mesokurtic curve. Additionally, a platykurtic curve was observed for days to fifty percent flowering (-1.11), the number of productive tillers per panicle (0.65), panicle length (0.52), flag leaf length (-0.77), flag leaf width (-0.51), the number of chaffy grains per panicle (0.26), spikelet fertility (0.99), grain length (-0.93), and grain width (-0.45).

In both the $F_2$ and $F_3$ generations, positively skewed and platykurtic curves were observed for the number of productive tillers per plant, indicating that it is governed by a large number of genes with dominance-based gene interaction. Consequently, intense selection is needed to achieve faster genetic gains in these traits. Hosagoudar and Shashidhar (2018) and Harijan *et al*., (2021) reported similar results for days to flowering, the number of tillers, days to maturity, and yield per plant. Additionally, Seeli *et al*., (2021) observed similar findings for days to fifty percent flowering and the number of chaffy grains per panicle. Negatively skewed and leptokurtic curve was observed for plant height and hundred seed weight indicating the presence of complementary gene interaction in both $F_2$ and $F_3$ generation.

The parent-progeny regression analysis revealed a significant association between the traits in both the $F_2$ and $F_3$ generations (**Table 5 & Fig. 3**), with all traits showing highly significant regression coefficients ($p < 0.01$). Notably, the number of productive tillers per plant exhibited the highest regression coefficient (1.05), followed by the number of chaffy grains per panicle (1.00), single plant yield (0.99), the number of filled grains per panicle (0.98), days to fifty percent flowering (0.95), flag leaf length (0.95), hundred seed weight (0.94), and spikelet fertility (0.93). Similar findings have been reported in drought studies by Seeli *et al*., (2021) and Blessy *et al*. (2022), as well as in studies on single plant yield by Anilkumar and Ramalingam (2011), days to 50% flowering, plant height, and the number of productive tillers by Kavithamani *et al*., (2013), and panicle length by Lalitha *et al*., (2018). Higher regression values indicate a stronger genetic influence and less impact from environmental factors (Palanisamy, 2018). The results of this study suggest that these traits were less affected by the environment, and that selection based on their phenotypes in these generations was heritable.

All the traits analyzed in this study showed highly significant correlation coefficients. Intergenerational correlation studies are essential in assessing the extent to which the genetic potential of a trait is passed on to future generations. In this research, the analysis of

Table 4. Skewness and Kurtosis values for yield and yield contributing traits in $F_2$ and $F_3$ progenies

| Traits | $F_2$ generation | | $F_3$ generation | |
|---|---|---|---|---|
| | Skewness | Kurtosis | Skewness | Kurtosis |
| DFF | -0.37 | -1.14 | -0.42 | -1.11 |
| PH | -1.70** | 5.03** | -1.47** | 4.66** |
| NPT | 0.82 | 1.19 | 0.61 | 0.65 |
| PL | -1.00* | 1.55 | -0.5 | 0.52 |
| FLL | 0.51 | -0.59 | 0.46 | -0.77 |
| FLW | 0.17 | -0.54 | 0.21 | -0.51 |
| FG | -0.44 | 0.28 | -0.48 | 0.02 |
| CG | 0.92* | 0.35 | 0.90* | 0.26 |
| SF | -1.04* | 0.48 | -1.04* | 0.99 |
| SPY | -1.46** | 1.98 | -1.47** | 2.01** |
| GL | -0.36 | -0.11 | -0.34 | -0.93 |
| GW | -0.13 | -0.15 | -0.18 | -0.45 |
| HSW | -2.27** | 8.27** | -2.20** | 7.60** |

*, ** Significant at 5% and 1% respectively. DFF: Days to fifty percent flowering, PH: Plant height, NPT: Number of productive tillers per plant, PL: Panicle length, FLL: Flag leaf length, FG: Number of filled grains per plant, CG: Chaffy grains per panicle, SF: Spikelet fertility percentage, HSW: Hundred grain weight, SPY: Grain yield per plant, GL: Grain length, GW: Grain width.

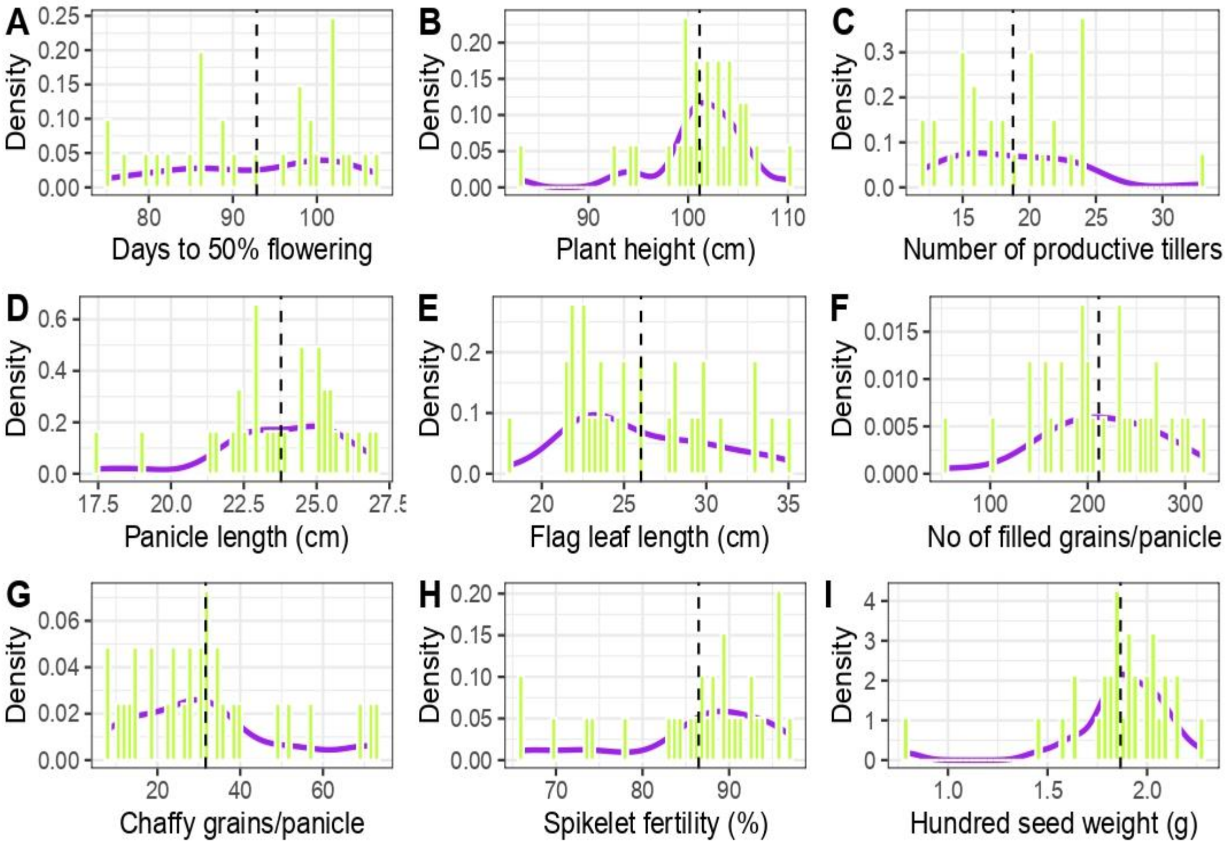
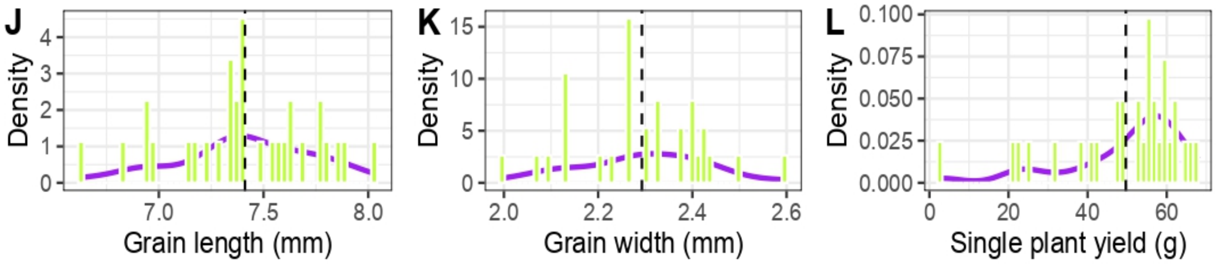


Fig. 1. Frequency distribution of biometrical traits in $F_2$ generation

https://doi.org/10.37992/2023.1403.103

Fig. 1. Continued..



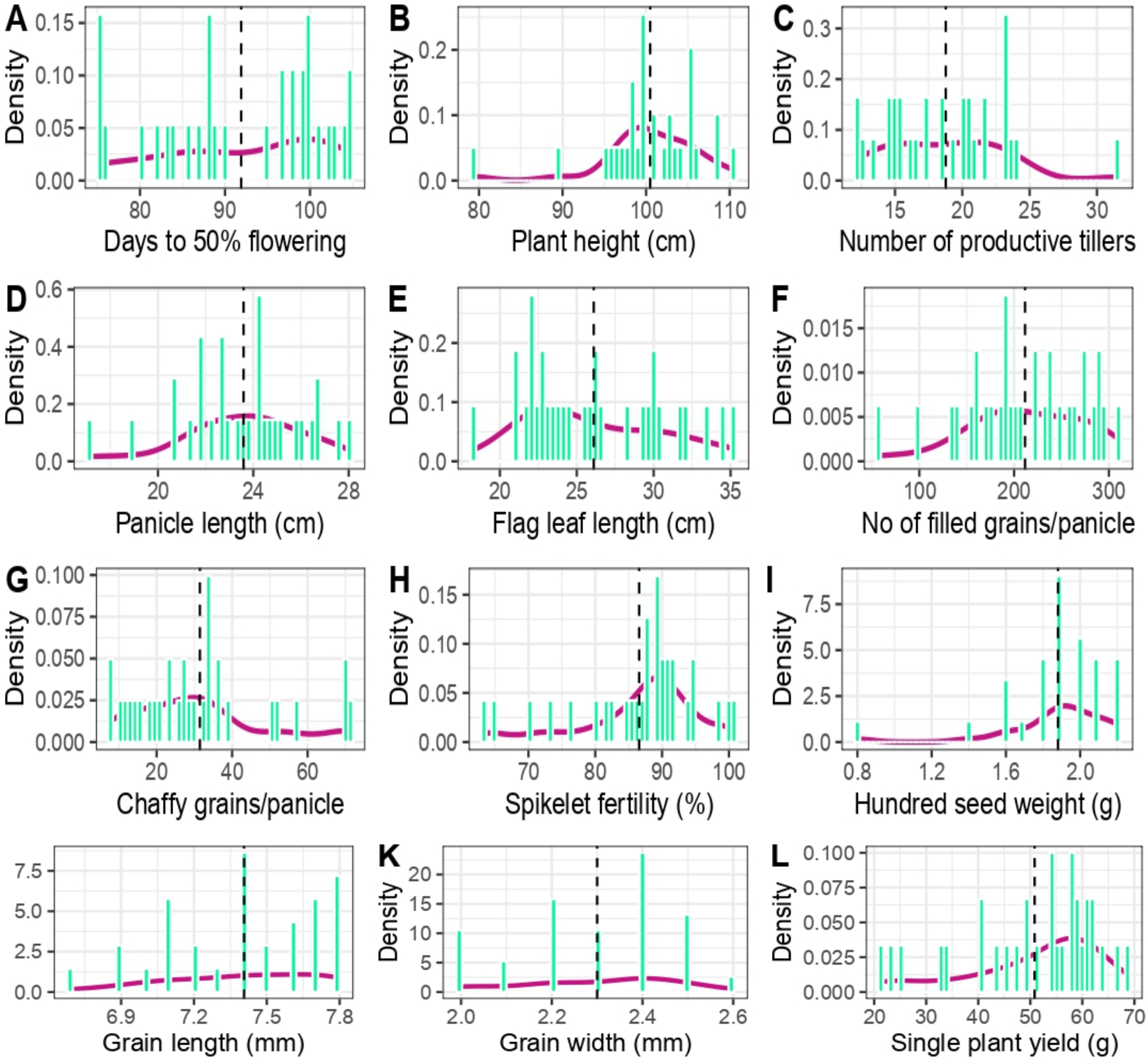


Fig. 2. Frequency distribution of biometrical traits in $F_3$ generation

**Table 5. Intergenerational correlation and regression values for the yield and yield contributing traits in $F_2$ and $F_5$ progenies**

| Traits | Correlation coefficient | Regression coefficient | Heritability |
|---|---|---|---|
| DFF | 0.96** | 0.95** | 49.72 |
| PH | 0.89** | 0.74** | 42.12 |
| NPT | 0.99** | 1.05** | 53.08 |
| PL | 0.95** | 0.84** | 43.5 |
| FLL | 0.98** | 0.95** | 48.2 |
| FG | 0.99** | 0.98** | 49.54 |
| CG | 0.99** | 1** | 50.53 |
| SF | 0.95** | 0.93** | 48.8 |
| SPY | 0.99** | 0.99** | 49.88 |
| GL | 0.81** | 0.88** | 54 |
| GW | 0.93** | 0.76** | 40.76 |
| HSW | 0.98** | 0.94** | 48.26 |

*, ** Significant at 5% and 1% respectively. DFF: Days to fifty percent flowering, PH: Plant height, NPT: Number of productive tillers per plant, PL: Panicle length, FLL: Flag leaf length, FG: Number of filled grains per plant, CG: Chaffy grains per panicle, SF: Spikelet fertility percentage, HSW: Hundred seed weight, SPY: Grain yield per plant, GL: Grain length, GW: Grain width.

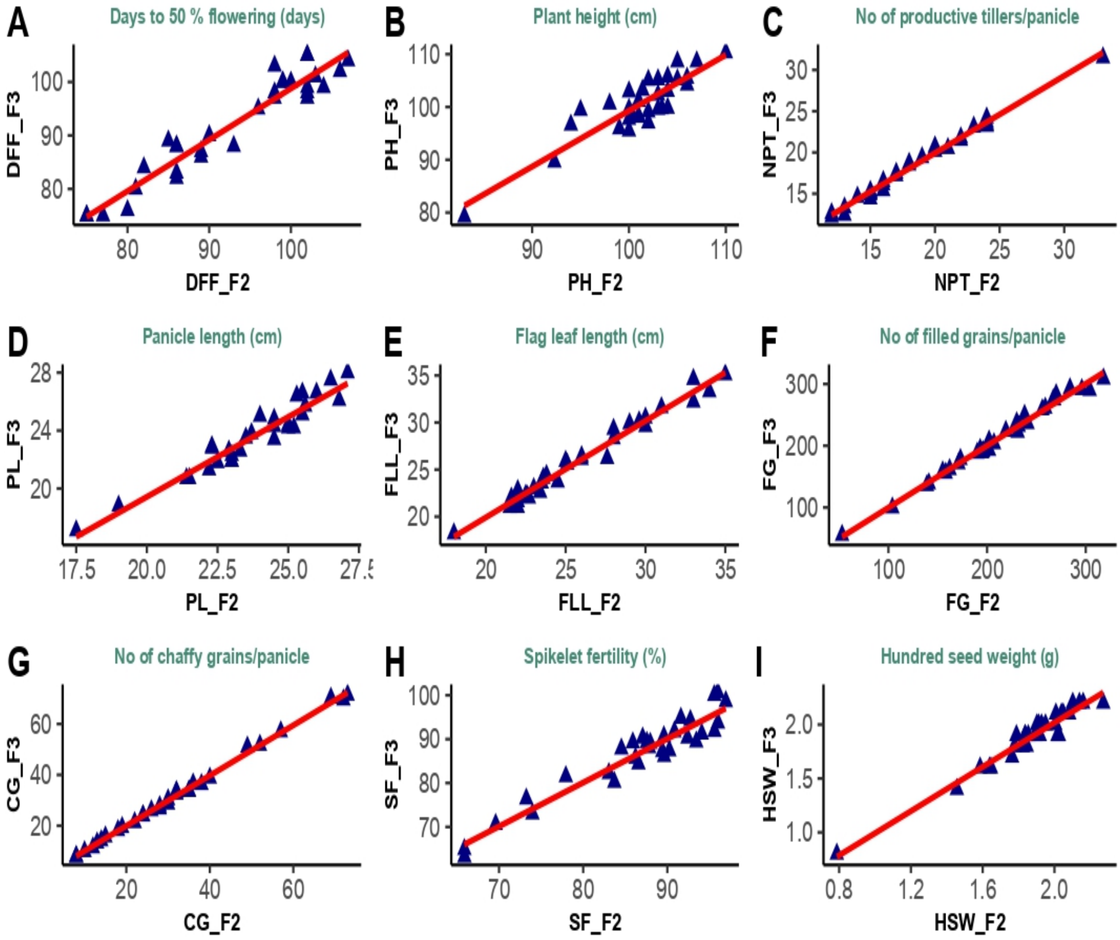
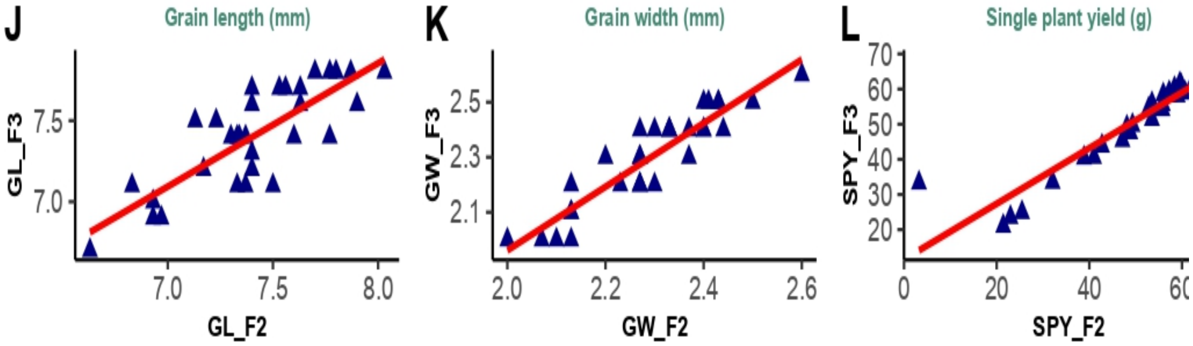


Fig. 3. Parent offspring regression for the quantitative traits

https://doi.org/10.37992/2023.1403.103

**Fig. 3. Continued..**



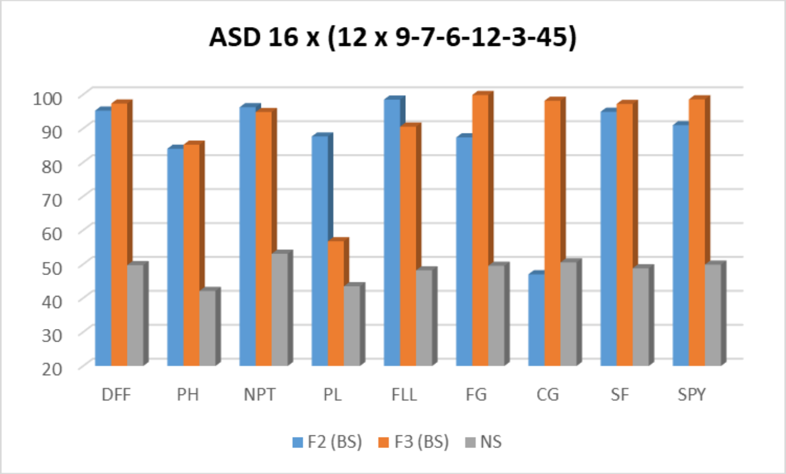


**Fig. 4. Comparison of broad sense and narrow sense heritability for yield and yield contributing traits of the cross**

BS: Broad sense heritability; NS: Narrow sense heritability. DFF: Days to fifty percent flowering, PH: Plant height, NPT: Number of productive tillers per plant, PL: Panicle length, FLL: Flag leaf length, FG: Number of filled grains per plant, CG: Chaffy grains per panicle, SF: Spikelet fertility percentage, SPY: Grain yield per plant.

intergenerational correlation revealed strong correlations among four traits: number of productive tillers per plant (0.99), number of filled grains per panicle (0.99), number of chaffy grains per panicle (0.99), and single plant yield (0.99). Additionally, flag leaf length and hundred seed weight exhibited a significant intergenerational correlation of 0.98, followed by spikelet fertility (0.95) and days to fifty percent flowering (0.96). Savitha and Kumari (2015) and Seeli *et al*., (2021) reported similar positive and significant findings for plant height, the number of filled grains per panicle, hundred grain weight, and panicle length. Similarly, Govintharaj *et al*., (2018) observed significant correlations for the number of productive tillers, panicle length, and single plant yield.

According to Kaler *et al*., (2022), traits with high broad sense and narrow sense heritability demonstrated greater prediction accuracy in plant breeding programs. In both the $F_2$ and $F_3$ generations, traits such as Days to fifty per cent flowering, plant height, number of productive tillers per panicle, flag leaf length, number of filled grains per panicle, spikelet fertility, and single plant yield exhibited high broad sense heritability (**Table 3**). However, when estimating narrow sense heritability using parent progeny regression analysis, these same traits that showed high broad sense heritability displayed only moderate narrow sense heritability percentages (**Fig. 4**), specifically days to fifty percent flowering (49.72%), plant height (42.12%), number of productive tillers per plant (53.08%), flag leaf length (48.20%), number of filled grains per panicle (49.54%), spikelet fertility (48.8%), and single plant yield (49.88%) (**Fig. 4**). To increase the effectiveness of selecting traits in a breeding program, one should consider the narrow sense heritability of the traits because relying solely on broad sense heritability may not be effective. While broad sense heritability provides an overall estimate of the genetic influence on trait variation, encompassing both additive and non-additive genetic effects, narrow sense heritability specifically focuses on the additive genetic effects. These additive genetic effects are the ones that can be reliably passed on from parents to offspring. Traits with high narrow sense heritability have a stronger genetic basis, making them more predictable and responsive to selection. Therefore, selecting individuals based on narrow sense heritability will lead to more effective improvements in those traits, as it targets the portion of genetic variation that can be passed on to future generations.

Scientific evidence suggests that utilizing an improved variety as a donor source is expected to result in a lower incidence of undesirable linkage drag compared to using wild or landrace varieties as donors (Das and Rao, 2015;Pradhan *et al*., 2015;Pradhan *et al*., 2016;Das *et al*., 2018;Pandit *et al*., 2021;Barik *et al*., 2023). Hence, it is of utmost importance to assess the segregating generations resulting from these crosses to achieve improved submergence tolerance while maintaining the high-yield potential of the varieties. The evaluated lines can be further advanced through backcrossing and subsequently released as a variety in flood-prone areas in India. Alternatively, they can be employed within a breeding pipeline to incorporate submergence tolerance into other prominent varieties.

## REFERENCES

Ali, A.-H.A., Abdel-Khalek, S.M., Emira, A.B. and Aboulila, A.A. 2023. Molecular profiling of some blast resistance genes and analysis of physiological variability in rice plants produced by anther culture and hybridization. *Physiological and Molecular Plant Pathology,* **126:** 102051. [Cross Ref]

Anilkumar, C.V. and Ramalingam, J. 2011. Parent progeny regression analysis in F2 and F3 generations of rice. *Electronic Journal of Plant Breeding,* **2:** 520-522.

Barik, S.R., Moharana, A., Pandit, E., Behera, A., Mishra, A., Mohanty, S.P., Mohapatra, S., Sanghamitra, P., Meher, J., and Pani, D.R. 2023. Transfer of Stress Resilient QTLs and Panicle Traits into the Rice Variety, Reeta through Classical and Marker-Assisted Breeding Approaches. *International Journal of Molecular Sciences,* **24:** 10708. [Cross Ref]

Blessy, V., Murugan, E., Suresh, R., Gnanamalar, R., Kumar, S.V. and Kanchana, S. 2022. Parent progeny regression analysis for yield and yield contributing traits in F3 and F4 generations in rice (*Oryza sativa* L.). *International Journal of Bio-resource and Stress Management*,**13:** 1021-1028. [Cross Ref]

Das, G. and Rao, G. 2015. Molecular marker assisted gene stacking for biotic and abiotic stress resistance genes in an elite rice cultivar. *Frontiers in plant science,* **6:** 698. [Cross Ref]

Das, G., Rao, G.J., Varier, M., Prakash, A. and Prasad, D. 2018. Improved Tapaswini having four BB resistance genes pyramided with six genes/QTLs, resistance/tolerance to biotic and abiotic stresses in rice. *Scientific reports,* **8:** 2413. [Cross Ref]

Govintharaj, P., Manonmani, S. and Robin, S. 2018. Variability and genetic diversity study in an advanced segregating population of rice with bacterial blight resistance genes introgressed. *Ciência e Agrotecnologia,* **42:** 291-296. [Cross Ref]

Grafius, J. 1959. Heterosis in Barley 1. *Agronomy Journal,* **51:** 551-554. [Cross Ref]

Harijan, Y., Katral, A., Mahadevaiah, C., Biradar, H., Hadimani, J. and Hittalmani, S. 2021. Genetic analysis of reciprocal differences for yield and yield attributing traits in segregating populations of rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry,* **10:** 614-621.

Hosagoudar, G. and Shashidhar, H. 2018. Studies on variability and frequency distribution of yield and yield related traits in F2 population of rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci*., **7:** 2048-2052. [Cross Ref]

Kaler, A.S., Purcell, L.C., Beissinger, T. and Gillman, J.D. 2022. Genomic prediction models for traits differing in heritability for soybean, rice, and maize. *BMC plant biology,* **22:** 1-11. [Cross Ref]

Kavithamani, D., Robin, S., Manonmani, S. and Mohanasundaram, K. 2013. Character association and parent progeny regression studies for yield in the segregating generations of TGMS rice lines. *ORYZA-An International Journal on Rice,* **50:** 45-51.

Lalitha, R., Anand, G., and Arunachalam, P. 2018. Parent progeny regression analysis on yield & yield component characters in advanced breeding lines in rice (*Oryza sativa* L.). *Green Farming,* **9:** 615-617.

Lingaiah, N. (2018). Variability studies in F2 population of Rice (*Oryza sativa* L.). *International Journal of Agriculture Sciences, ISSN***,** 0975-3710.

Manojkumar, D., Srinivas, T., Rao, L.S., Suneetha, Y., Sundaram, R. and Kumari, V.P. 2022. Study of genetic variability and trait associations in F2 Population of YH3 x AKDRMS 21-54 intra-specific cross of rice.

Nyquist, W.E. and Baker, R. 1991. Estimation of heritability and prediction of selection response in plant populations. *Critical reviews in plant sciences,* **10:** 235-322. [Cross Ref]

Palanisamy, S. 2018. Genetic analysis of biofortification of micronutrient breeding in rice (*Oryza sativa* L.). *Rice Crop: Current Developments* 17. [Cross Ref]

Pandit, E., Pawar, S., Barik, S.R., Mohanty, S.P., Meher, J. and Pradhan, S.K. 2021. Marker-assisted backcross breeding for improvement of submergence tolerance and grain yield in the popular rice variety 'Maudamani'. *Agronomy,* **11,**:1263. [Cross Ref]

Pradhan, S.K., Nayak, D.K., Mohanty, S., Behera, L., Barik, S.R., Pandit, E., Lenka, S. and Anandan, A. 2015. Pyramiding of three bacterial blight resistance genes for broad-spectrum resistance in deepwater rice variety, Jalmagna. *Rice,* **8:** 1-14. [Cross Ref]

Pradhan, S.K., Nayak, D.K., Pandit, E., Behera, L., Anandan, A., Mukherjee, A.K., Lenka, S. and Barik, D.P. 2016. Incorporation of bacterial blight resistance genes into lowland rice cultivar through marker-assisted backcross breeding. *Phytopathology,* **106:** 710-718. [Cross Ref]

Renuprasath, P., Ganesan, N.M., Bama, K.S., Boominathan, P., and Suresh, R. 2023. Variability and association analysis for yield and yield contributing traits in early segregating backcross population in Rice (*Oryza sativa* L.).

Riyanto, A., Hidayat, P., Suprayogi, Y., and Haryanto, T.a.D. 2023. Diallel analysis of length and shape of rice using Hayman and Griffing method. *Open Agriculture* 8**,** 20220169. [Cross Ref]

Savitha, P. and Kumari, R.U. 2015. Studies on skewness, kurtosis and parent progeny regression for yield and its related traits in segregating generations of rice. *ORYZA-An International Journal on Rice,* **52:** 80-86.

Seeli, F., Manonmani, S., Pushpam, R., and Raveendran, M. 2021. Parent progeny regression analysis in segregating generations of drought QTLs pyramided rice lines (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, **12:** 1178-1188. [Cross Ref]

Setter, T., Ellis, M., Laureles, E., Ella, E., Senadhira, D., Mishra, S., Sarkarung, S. and Datta, S. 1997. Physiology and genetics of submergence tolerance in rice. *Annals of Botany,* **79,** 67-77. [Cross Ref]

Singh, K.S., Suneetha, Y., Kumar, G.V., Rao, V.S., Raja, D.S., and Srinivas, T. 2020. Variability, correlation and path studies in coloured rice. *Int J Chem Stud,* **8**:2138-2144. [Cross Ref]

Smith, J., and Kinman, M.L. 1965. The Use of Parent-Offspring Regression as an Estimator of Heritability 1. *Crop Science,* **5:** 595-596. [Cross Ref]

Solanke, C.A., Patel, P., and Patel, P.K. 2023. Heritability and genetic advance for yield and quality traits in aromatic rice (*Oryza sativa* L.) genotypes.

Swapnil, K.P., Chakraborty, M., Singh, D., Kumari, P., and Ekka, J.P. 2020. Genetic variability, correlation and path coefficient studies in F2 generation of rice (*Orzya sativa* L.). *International Journal of Chemical Studies,* **8:** 3116-3120. [Cross Ref]

Visscher, P.M., Hill, W.G., and Wray, N.R. 2008. Heritability in the genomics era—concepts and misconceptions. *Nature reviews genetics*, **9:** 255-266. [Cross Ref]

Viswabharathy, S., Thulasinathan, T., Subburaj, S., Seeli, F.D.P., Ayyenar, B., Kambale, R., Mohanavel, V., Rajagopalan, V.R., Manickam, S. and Jeyakumar, P. 2023. Harnessing parent-offspring regression analysis to develop high-yielding submergence tolerant lines of *Oryza sativa* L. *Electronic Journal of Plant Breeding,* **14:** 675-686. [Cross Ref]