

PHENOTYPIC CHARACTERIZATION OF MULTI-PARENT ADVANCED BREEDING LINES FOR SUBMERGENCE TOLERANCE IN RICE (*ORYZA SATIVA* L.)

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ABSTRACT

Submergence is one of the major abiotic stresses limiting rice production in flood-prone ecosystems, causing substantial yield losses. The present study was undertaken to assess genetic variability and identify submergence-tolerant, high-yielding rice genotypes among multiparent advanced generation intercross (MAGIC) lines. A field experiment was conducted during kharif 2023 at the Zonal Agricultural and Horticultural Research Station (ZAHRS), Shivamogga, using 50 MAGIC lines along with eight check varieties in a randomized complete block design with two replications. Analysis of variance revealed significant differences among genotypes for all the traits under both submergence and non-submergence conditions, indicating the presence of considerable genetic variability. Submergence tolerance screening was performed by subjecting the genotypes to complete submergence for 14 days, including the national tolerant check Swarna Sub1, the local tolerant check Hemavathi, and the susceptible check Jyothi. Survival percentage and stem elongation percentage were recorded seven days after de-submergence, and genotypes were evaluated according to the International Rice Research Institute (IRRI) standard evaluation system. Genetic variability and character association analyses revealed substantial variation among the genotypes and significant positive associations of grain yield with several yield-contributing traits. Two MAGIC lines exhibited consistent superiority under both submergence and normal conditions by recording higher grain yield and survival percentage than the check varieties. These promising genotypes can be utilized in future breeding programmes and subjected to multi-location trials and genomic selection for the development of submergence-tolerant, high-yielding rice cultivars.

KEYWORDS: character association; genetic variability; grain yield; MAGIC lines; rice; stem elongation; submergence tolerance; survival percentage.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food for more than half of the world's population and plays a vital role in ensuring global food and nutritional security. It is cultivated across diverse agro-ecological regions under irrigated, rainfed, upland, lowland, deep-water, and tidal wetland ecosystems, reflecting its remarkable adaptability to different production environments (1,2). Despite its wide cultivation, rice productivity is severely constrained by several abiotic stresses, including drought, salinity, heat, cold, and flooding, the frequency and intensity of which are increasing due to climate change (3). Among these, flooding and complete submergence have emerged as major challenges in rainfed lowland rice ecosystems, particularly in South and Southeast Asia, where erratic rainfall, river overflow, and cyclonic events frequently inundate rice fields during the cropping season (4).

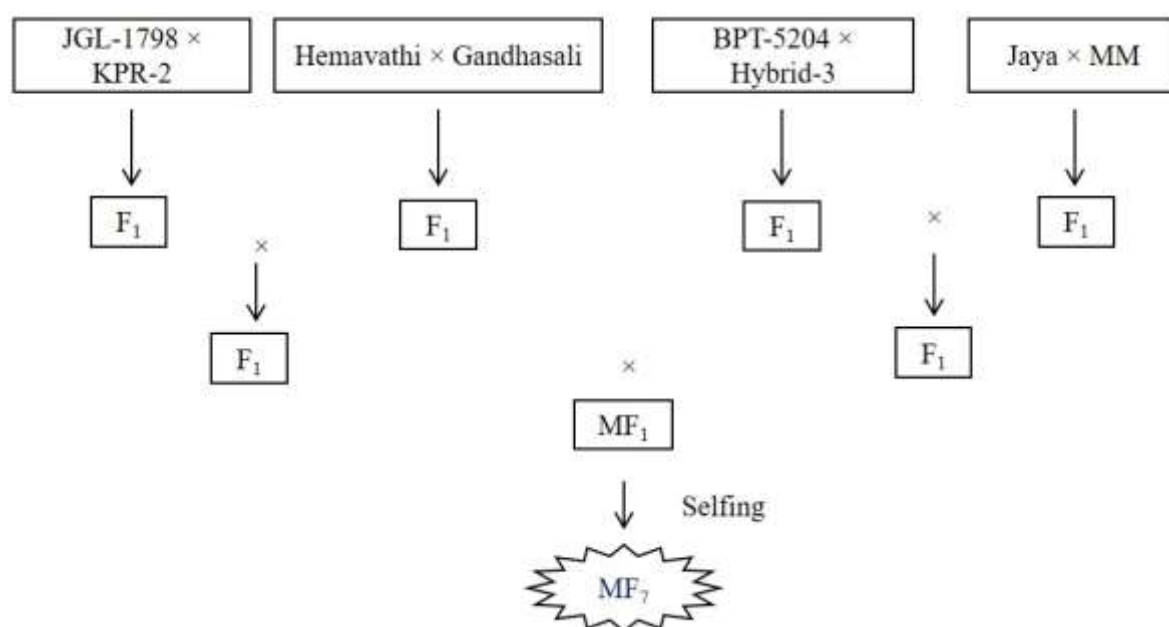
Submergence is recognized as one of the most destructive abiotic stresses limiting rice production, ranking after drought and salinity in terms of its impact on productivity (5). Approximately 15-20 million hectares of rice-growing areas worldwide are prone to seasonal flooding, resulting in substantial yield losses each year. In India, flood-prone ecosystems account for a significant proportion of the rice-growing area, where complete submergence lasting from several days to two weeks often causes severe crop mortality and economic losses (6). India's rice production currently exceeds 120 million tonnes; however, demand is projected to increase substantially by 2050 owing to population growth and changing consumption patterns. Therefore, improving rice productivity under flood-prone environments has become a major breeding priority (7).

Rice possesses several adaptive mechanisms that enable it to survive under flooded conditions. The formation of aerenchyma facilitates internal oxygen transport from shoots to roots, allowing plants to withstand temporary oxygen deficiency. However, prolonged complete submergence severely restricts gas exchange and light

penetration, resulting in reduced photosynthesis, depletion of carbohydrate reserves, excessive stem elongation, chlorophyll degradation, and ultimately plant death if the stress persists beyond the tolerance threshold (8). Genotypes carrying submergence tolerance genes such as Sub1 suppress excessive elongation growth, conserve energy reserves, and exhibit higher survival and better recovery following de-submergence than susceptible cultivars (9). Consequently, identifying new sources of submergence tolerance remains an important objective in rice improvement programmes.

The development of climate-resilient rice varieties requires access to genetically diverse breeding materials possessing superior agronomic performance and stress tolerance. Multi-parent Advanced Generation Inter-Cross (MAGIC) populations have emerged as valuable genetic resources because they combine favorable alleles from multiple founder parents through repeated intercrossing, resulting in greater genetic recombination, broader allelic diversity, and improved mapping resolution compared with conventional biparental populations (10). MAGIC populations facilitate the identification of novel quantitative trait loci (QTLs), enable precise phenotypic and genetic analyses, and provide elite breeding lines suitable for direct utilization in crop improvement programmes. Their enhanced genetic diversity also increases the probability of identifying superior recombinants with high yield and multiple stress tolerance (11).

Phenotypic characterization forms the foundation of any breeding programme by quantifying the extent of genetic variability, estimating genetic parameters, and identifying superior genotypes for selection. Evaluation of breeding lines under both normal and submergence conditions provides valuable information on survival percentage, stem elongation, recovery ability, yield, and yield-related traits, thereby facilitating the identification of stable and high-performing genotypes suitable for flood-prone environments. Furthermore, studies on genetic variability,



heritability, and character association assist breeders in selecting traits that contribute most effectively to grain yield under stress conditions (12).

Therefore, the present investigation entitled "Phenotypic Characterization of Multi-parent Advanced Breeding Lines for Submergence Tolerance in Rice (*Oryza sativa* L.)" was undertaken to evaluate MAGIC breeding lines for submergence tolerance under field conditions, assess the magnitude of genetic variability and character association for yield and related traits, and identify superior genotypes with enhanced survival and grain yield for their potential utilization in future rice breeding programmes targeting flood-prone ecosystems (**Plate. 1**).

2. MATERIALS AND METHODS

2.1 Experimental site and plant materials

The present investigation was conducted during the kharif 2023 season at the Zonal Agricultural and Horticultural Research Station (ZAHRS), College of Agriculture, Shivamogga, Karnataka, India. The experimental material consisted of 50 Multi-parent Advanced Generation Inter-Cross (MAGIC) breeding lines (MF₇ generation) developed through a series of intercrosses involving eight founder parents (**Table.1**) and maintained at the Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga. The MAGIC population was developed to broaden the genetic base and facilitate the identification of superior recombinants for agronomic and stress tolerance traits. In addition to the MAGIC lines, eight check varieties-JGL-1798, KPR-2, BPT-5204, Hemavathi, Gandhasali, Jaya, Mysore Mallige, and Swarna Sub1 were included for comparison. Swarna Sub1 served as the national check for submergence tolerance, Hemavathi as the local tolerant check, and Jyothi as the susceptible check during submergence screening.

2.2 Experimental design and crop management

The experiment was laid out in a Randomized Complete Block Design (RCBD) with 58 genotypes (50 MAGIC lines and eight checks) and two replications. Seeds of all genotypes were sown in a wet-bed nursery during the kharif 2023 season. Twenty-one-day-old seedlings were transplanted manually under two experimental conditions: (i) a submergence screening field and (ii) a normal control field (**Plate. 2**). Seedlings were transplanted at a spacing of 20 cm × 15 cm (row × plant spacing). In the submergence experiment, seedlings were also established in polythene bags filled with soil to facilitate physiological observations. All recommended agronomic practices, including irrigation, nutrient management, weed control, and plant protection measures, were uniformly followed to ensure a healthy crop stand throughout the experimental period.

2.3 Screening for submergence tolerance

Submergence tolerance was evaluated by subjecting one-week-old established seedlings to complete submergence under 50-60 cm of water for 14 consecutive days. After the treatment period, the field was de-submerged and the crop was allowed to recover under normal conditions. Standard crop management and plant protection measures were followed during the recovery period.

The number of surviving hills was recorded 15 days after de-submergence, and survival percentage was calculated using the following formula:

$$\text{Survival Percentage (\%)} = \frac{\text{Number of surviving hills after de-submergence}}{\text{Number of hills before submergence}} \times 100$$

The genotypes were classified according to the (13) Standard Evaluation System based on survival percentage:

SES Score	Survival (%)	Reaction
1	91–100	Highly tolerant
3	81–90	Tolerant
5	51–80	Moderately tolerant
7	11–50	Susceptible
9	<10	Highly susceptible

2.4 Recording of physiological traits

Observations on physiological traits were recorded from five randomly selected plants in each genotype, and the mean values were used for statistical analysis.

2.4.1 Survival percentage

Survival percentage was determined 15 days after de-submergence using the formula described above, and genotypes were classified according to the (13) Standard Evaluation System.

2.4.2 Stem elongation (%)

Plant height was recorded immediately before submergence and again immediately after 14 days of complete submergence. Stem elongation was expressed as the percentage increase in plant height during the submergence period using the following equation:

$$\text{Stem Elongation (\%)} = \frac{\text{Plant height after submergence} - \text{Plant height before submergence}}{\text{Plant height before submergence}} \times 100$$

2.5 Recording of agronomic and yield-related traits

Agronomic and yield-related observations were recorded under both submergence and non-submergence (control) conditions using five randomly selected and tagged representative plants from each genotype in each replication. The mean values of these observations were used for statistical analysis. Data were recorded on days to 50% flowering, days to physiological maturity, plant height (cm), number of tillers per plant, panicle length (cm), number of filled grains per panicle, panicle fertility (%), test weight (1000-grain weight, g), grain length/breadth (L/B) ratio, and grain yield per plant (g). Days to 50% flowering and days to physiological maturity were recorded on a plot basis. Plant height was measured from the soil surface to the tip of the panicle, excluding awns, at physiological maturity. The number of tillers per plant was determined by counting both productive and unproductive tillers. Panicle length was measured from the flag leaf node to the tip of the panicle, excluding awns. The number of filled grains per panicle was determined by counting filled grains from five representative panicles and calculating their average. Panicle fertility was estimated as the percentage of filled grains relative to the total number of spikelets per panicle. Test weight was recorded as the weight of 1000 fully developed grains using an electronic balance. Grain length, breadth, and the length-to-breadth (L/B) ratio were measured using an Indosaw Grain Analyser 4.0. Grain yield per plant was calculated as the average grain weight obtained from the five sampled plants and expressed in grams.

2.6 Statistical analysis

The recorded data were subjected to analysis of variance (ANOVA) appropriate for a Randomized Complete Block Design to determine the significance of genotypic differences. Estimates of genetic variability were

computed following standard biometrical procedures. Genotypic and phenotypic correlation coefficients among yield and yield-related traits were estimated according to the method proposed by (14) using variance and covariance components.

The genotypic and phenotypic correlation coefficients were calculated as:

$$r_g = \frac{Cov_g(x, y)}{\sqrt{\sigma_g^2(x) \times \sigma_g^2(y)}}$$

$$r_p = \frac{Cov_p(x, y)}{\sqrt{\sigma_p^2(x) \times \sigma_p^2(y)}}$$

where r_g and r_p represent genotypic and phenotypic correlation coefficients, respectively; Cov_g and Cov_p denote genotypic and phenotypic covariance between traits; and σ_g^2 and σ_p^2 represent the corresponding genotypic and phenotypic variances.

All statistical analyses were performed using R statistical software (Version 4.1). The significance of correlation coefficients was tested using the procedure described by (15) at 5% and 1% probability levels with $(n - 2)$ degrees of freedom. Correlation coefficients exceeding the corresponding tabulated values were considered statistically significant.

3. RESULTS AND DISCUSSION

3.1 Screening of rice genotypes for submergence tolerance under field conditions

Fifty Multi-parent Advanced Generation Inter-Cross (MAGIC) breeding lines along with eight check varieties (JGL-1798, KPR-2, Hemavathi, Gandhasali, BPT-5204, Mysore Mallige, Jaya, and Swarna Sub1) were evaluated for submergence tolerance during kharif 2023 under field conditions at ZAHRS, Shivamogga. Twenty-one-day-old seedlings were transplanted in the submergence field, and complete submergence stress (50–60 cm water depth) was imposed seven days after transplanting for a period of 14 days. Following de-submergence, stem elongation was recorded immediately, while survival percentage was assessed 15 days after de-submergence. The survival percentage was used to classify the genotypes according to the Standard Evaluation System (SES) for Rice developed by (13). Considerable variation was observed among the evaluated genotypes for survival under complete submergence, indicating the existence of substantial genetic variability for submergence tolerance. Based on survival percentage, only the national tolerant check Swarna Sub1 obtained an SES score of 1 (highly tolerant). Four genotypes, including the local tolerant check Hemavathi, recorded an SES score of 3, indicating tolerance to submergence. Twenty-two genotypes were classified as moderately tolerant (SES score 5), while thirty-one genotypes were categorized as susceptible (SES score 7). None of the evaluated genotypes fell under the highly susceptible (SES score 9) category. The distribution of genotypes across different SES classes is presented in (Table. 2).

Although survival percentage is considered the principal criterion for evaluating submergence tolerance, stem elongation was also assessed as an important physiological parameter because certain genotypes exhibited relatively lower survival despite showing minimal leaf injury after de-submergence. Therefore, both survival percentage and stem elongation were considered together to identify superior genotypes with enhanced tolerance. Based on these parameters, together with grain yield under stress conditions, six promising genotypes were identified, of which three exhibited high tolerance, while the remaining three were moderately tolerant to submergence. Notably, two MAGIC lines outperformed the tolerant check Hemavathi by recording higher survival percentage, optimum stem elongation, and superior grain yield under submergence stress. Genotypes recording more than 80 % survival with an SES score of 3 were considered tolerant and may serve as valuable genetic resources for developing submergence-tolerant rice cultivars through breeding programmes.

Significant variation was also observed for stem elongation among the evaluated genotypes. The highest stem elongation percentage was recorded in Mysore Mallige, followed by Gandhasali and ML-2-6-9-1-28-14, whereas the lowest stem elongation was observed in Swarna Sub1, followed by ML-1-7-8-1-7-12 and ML-1-1-2-1-39-15. The present findings indicated that genotypes exhibiting moderate stem elongation coupled with higher survival percentage performed better under prolonged submergence than those showing excessive elongation. Excessive stem elongation under flooded conditions accelerates the depletion of stored non-structural carbohydrates required for maintenance, recovery, and grain production, ultimately reducing plant survival and yield. In contrast, genotypes with restrained elongation conserve energy reserves, resulting in improved recovery and productivity following de-submergence. These observations are consistent with the quiescence strategy associated with Sub1-mediated submergence tolerance, in which suppression of excessive elongation enhances survival and post-submergence recovery. The results obtained in the present investigation are in agreement with earlier reports by (16-24), who also reported that rice genotypes possessing submergence tolerance exhibit higher survival rates, controlled stem elongation, and better grain yield under complete submergence stress. These findings further confirm that combining survival percentage with physiological traits such as stem elongation provides a more

reliable assessment of submergence tolerance and facilitates the identification of superior breeding lines for developing climate-resilient rice varieties.

3.2 Genetic variability among multi-parent advanced breeding lines for grain yield and associated traits under submergence and control conditions

3.2.1 Analysis of variance for growth, yield and yield attributes

Analysis of variance (ANOVA) revealed highly significant ($P < 0.01$) differences among the 50 MAGIC breeding lines and eight check varieties for all ten growth, yield, and yield-related traits under both submergence and control conditions (**Table 3**), indicating the presence of substantial genetic variability in the experimental material. The wide range observed for each trait further confirmed the existence of considerable phenotypic diversity, thereby providing ample scope for effective selection. Similar observations have been reported by (25-27). Estimates of the mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (H^2), and genetic advance as percentage of mean (GAM) are presented in (**Table 4**).

3.2.2 Genetic variability parameters

Considerable variation in genetic parameters was observed among the studied traits under both submergence and control conditions (**Table 4**). Under submergence, days to 50% flowering ranged from 115 to 136 days with a mean of 124.94 days, recording low PCV (4.77%) and GCV (4.64%) despite very high heritability (94.48%) and low GAM (9.28%). Similarly, under control conditions, the trait ranged from 95 to 123 days with low PCV (5.79%) and GCV (5.53%) and high heritability (91.20%), indicating limited genetic variability and restricted scope for improvement through direct selection. Days to maturity exhibited a wider range under submergence (116-175 days) with a mean of 140.45 days, moderate PCV (10.74%) and GCV (10.49%), high heritability (95.42%), and high GAM (21.11%), suggesting predominance of additive gene action. Under control conditions, however, the lower PCV (4.90%) and GCV (4.61%) coupled with high heritability (88.47%) and low GAM (8.93%) indicated comparatively less genetic variability.

Plant height ranged from 72–112 cm under submergence and 94-156 cm under control conditions. The trait recorded low to moderate variability, with PCV and GCV values of 9.15% and 7.75% under submergence and 12.09% and 10.16% under control, respectively. High heritability (71.81% under submergence and 70.63% under control) coupled with moderate GAM (13.53% and 17.59%, respectively) suggested moderate effectiveness of selection. Number of tillers per plant exhibited substantial variation, ranging from 4.33 to 23.00 under submergence and 8.00 to 27.77 under control conditions. Under submergence, the trait recorded high PCV (26.40%) but moderate GCV (14.53%) with relatively low heritability (30.30%) and moderate GAM (16.48%), indicating considerable environmental influence. In contrast, under control conditions, high PCV (22.81%) and GCV (20.07%) together with high heritability (77.37%) and GAM (36.36%) suggested greater genetic control and good prospects for selection.

Among the yield-contributing traits, panicle length varied from 11.20 to 26.00 cm under submergence and 12.00 to 29.74 cm under control conditions. The trait recorded moderate PCV (12.73%) but low GCV (8.28%) under submergence, whereas under control it exhibited higher PCV (20.38%) and GCV (16.12%) with high heritability (62.59%) and GAM (26.27%). Number of filled grains per panicle showed considerable variability, ranging from 130.00 to 441.05 under submergence and 148.98 to 459.67 under control. High PCV (31.19%) and moderate GCV (18.88%) under submergence, together with high PCV (28.35%) and GCV (23.36%) under control, accompanied by high GAM (23.54% and 39.64%, respectively), indicated the predominance of additive gene effects and the effectiveness of direct selection.

Panicle fertility ranged from 44.00-96.00% under submergence and 68.92-96.30% under control conditions. Low PCV (7.20%) and GCV (6.47%) with high heritability (80.81%) and moderate GAM (11.99%) under submergence suggested limited variability despite strong genetic control, whereas under control the trait exhibited higher PCV (21.73%) than GCV (12.40%), indicating a greater influence of environmental factors. The length-to-breadth (L/B) ratio ranged from 2.38–4.78 under submergence and 2.50–5.60 under control. Moderate PCV (14.23%) and GCV (12.45%) with high heritability (76.62%) and GAM (22.46%) under submergence indicated good prospects for improvement, whereas comparatively lower GCV (9.28%) under control reflected reduced variability.

Test weight varied from 8.00 to 20.14 g under submergence and 11.73 to 20.40 g under control conditions. Moderate PCV (12.41% and 13.71%) and GCV (10.53% and 12.87%) with high heritability (72.04% and 88.13%) and GAM (18.42% and 24.89%) under both environments indicated that this trait is largely governed by additive gene action. Among all the traits evaluated, grain yield per plant exhibited the highest genetic variability. Under submergence, grain yield ranged from 12.30 to 38.00 g with a mean of 21.63 g, recording high PCV (35.50%) and GCV (31.48%), high heritability (78.66%), and high GAM (57.52%). Similarly, under control conditions, grain yield ranged from 21.00 to 64.55 g with a mean of 37.53 g, exhibiting high PCV (31.67%), GCV (27.39%), heritability (74.82%), and GAM (48.80%). The combination of high GCV, high heritability, and high genetic advance for grain yield and filled grains per panicle suggests that these traits are predominantly controlled by additive gene action and can be effectively improved through phenotypic selection.

Overall, grain yield per plant, number of filled grains per panicle, test weight, number of tillers per plant, and days to maturity exhibited favorable genetic parameters for selection, whereas days to 50% flowering and panicle fertility showed comparatively low genetic variability. These findings demonstrate that the MAGIC population

possesses abundant exploitable genetic diversity for developing high-yielding and submergence-tolerant rice cultivars. Similar results have been reported by (28-34) in rice.

3.2.3 Correlation among grain yield and yield-contributing traits under submergence and control conditions

Phenotypic correlation analysis was performed to determine the association between grain yield per plant and nine yield-attributing traits under both submergence and control conditions. The correlation coefficients are presented in (Fig. 1). The results revealed considerable variation in the magnitude and direction of association among the studied traits, indicating their differential contribution towards grain yield under stress and non-stress environments. Under submergence stress, grain yield per plant exhibited a strong positive and significant correlation with number of tillers per plant ($r = 0.709$), number of filled grains per panicle ($r = 0.705$), panicle fertility ($r = 0.512$), panicle length ($r = 0.250$) and length-to-breadth (L/B) ratio ($r = 0.205$). Test weight also showed a positive association with grain yield ($r = 0.169$), although the relationship was not significant. In contrast, days to 50% flowering ($r = -0.193$), days to maturity ($r = -0.191$) and plant height ($r = -0.245$) exhibited significant negative correlations with grain yield, indicating that early maturing and relatively shorter genotypes were more productive under submergence stress.

Similarly, under control conditions, grain yield per plant was significantly and positively associated with number of filled grains per panicle ($r = 0.718$), number of tillers per plant ($r = 0.682$), panicle length ($r = 0.429$), panicle fertility ($r = 0.398$) and test weight ($r = 0.351$). The L/B ratio showed a positive but non-significant association ($r = 0.161$). Conversely, days to 50% flowering ($r = -0.296$) and days to maturity ($r = -0.238$) were significantly and negatively correlated with grain yield, whereas plant height exhibited a weak, non-significant negative association ($r = -0.176$). Among the interrelationships of yield components, number of tillers per plant showed strong positive correlations with number of filled grains per panicle under both submergence ($r = 0.587$) and control ($r = 0.391$) conditions and was also positively associated with panicle length ($r = 0.277$ and 0.291) and panicle fertility ($r = 0.391$ and 0.192) under the respective environments. Likewise, number of filled grains per panicle exhibited significant positive associations with panicle length ($r = 0.304$ and 0.440), panicle fertility ($r = 0.282$ and 0.423), and test weight ($r = 0.219$ and 0.409) under submergence and control conditions, respectively. These positive associations indicate that improvement in these component traits is likely to result in enhanced grain yield.

Conversely, days to 50% flowering and days to maturity consistently showed significant negative correlations with number of tillers per plant, grain yield, and several yield-contributing traits across both environments, suggesting that delayed flowering and maturity adversely influenced productivity. Plant height also exhibited negative associations with most yield components, particularly number of tillers per plant ($r = -0.250$ and -0.206), number of filled grains per panicle ($r = -0.191$ and -0.010) and grain yield ($r = -0.245$ and -0.176) under submergence and control conditions, respectively. Overall, the correlation analysis demonstrated that number of tillers per plant, number of filled grains per panicle, panicle length, panicle fertility, and test weight were the major yield-contributing traits under both environments. Among these, number of tillers per plant and number of filled grains per panicle exhibited the strongest positive association with grain yield, indicating that these traits can serve as reliable indirect selection criteria for improving grain yield under both submergence and normal conditions. The present findings are in agreement with the reports of (35-45), who also reported significant positive associations of grain yield with tiller number, filled grains per panicle, panicle length, panicle fertility, and test weight in rice.

3.2.4 Genetic variability and character association for physiological traits under submergence conditions

3.2.4.1 Genetic variability of physiological traits

Genetic variability for the physiological traits associated with submergence tolerance was assessed in 50 MAGIC breeding lines along with eight check varieties under submerged conditions. The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability, and genetic advance as percentage of mean (GAM) are presented in (Table 5). Both physiological traits, namely survival percentage and stem elongation percentage, exhibited considerable genetic variability, indicating the existence of substantial scope for genetic improvement through selection. Survival percentage ranged from 13.27% to 92.60% with a mean of 52.78%. The trait exhibited high GCV (33.91%), high PCV (35.15%), very high broad-sense heritability (93.08%), and high GAM (67.39%), indicating the predominance of additive gene action and the effectiveness of direct phenotypic selection. Among the evaluated genotypes, the tolerant check Swarna Sub1 recorded the highest survival percentage (92.60%), whereas the susceptible check Mysore Mallige recorded the lowest survival (13.27%). Similar findings have been reported by (17-18, 21-23). Similarly, stem elongation percentage exhibited substantial variability, ranging from 23.27% to 81.25% with a mean value of 47.11%. The trait recorded high GCV (26.31%), high PCV (27.91%), high heritability (88.89%), and high GAM (51.11%), suggesting that stem elongation is also predominantly governed by additive genetic effects. The highest stem elongation was observed in Mysore Mallige (81.25%), whereas the lowest was recorded in the tolerant check Swarna Sub1 (23.27%). These results are in agreement with the findings of (23-25,46), who also reported high variability and heritability for survival percentage and stem elongation under submergence stress.

3.2.5 Character association of physiological traits with grain yield

Phenotypic correlation analysis was carried out to determine the association of physiological traits with grain yield under submergence conditions (**Table. 5**). The results indicated that survival percentage exhibited a strong positive and highly significant correlation with grain yield per plant ($r = 0.75$), demonstrating that improved plant survival following submergence directly contributed to higher productivity. Conversely, survival percentage showed a significant negative correlation with stem elongation percentage ($r = -0.50$), indicating that excessive stem elongation reduced the survival ability of rice plants under prolonged flooding (**Fig. 2**). In contrast, stem elongation percentage exhibited a significant negative correlation with grain yield per plant ($r = -0.32$) and survival percentage ($r = -0.50$). These findings suggest that excessive elongation under submerged conditions results in rapid depletion of stored carbohydrates required for post-submergence recovery, thereby reducing both survival and grain yield. Moderate suppression of stem elongation, as observed in tolerant genotypes such as Swarna Sub1, appears to enhance energy conservation and improve plant recovery following de-submergence. Overall, the present investigation demonstrated that survival percentage is the most important physiological trait contributing to grain yield under submergence stress, whereas stem elongation percentage showed an adverse relationship with both survival and productivity. Therefore, simultaneous selection for higher survival percentage and controlled stem elongation would be an effective breeding strategy for developing high-yielding, submergence-tolerant rice cultivars. These findings are consistent with those of (46-51), who reported similar relationships between physiological responses and submergence tolerance in rice.

4. CONCLUSION

The present study revealed significant genetic variability among 50 MAGIC breeding lines and eight check varieties evaluated under both submergence and normal conditions, indicating ample scope for genetic improvement of submergence tolerance in rice. Phenotypic screening identified one highly tolerant genotype (SES score 1; Swarna Sub1), four tolerant genotypes (SES score 3), 22 moderately tolerant genotypes (SES score 5), and 31 susceptible genotypes (SES score 7). The tolerant check Swarna Sub1 recorded the highest survival percentage (92.60%) with the lowest stem elongation (23.27%), whereas the susceptible check Mysore Mallige exhibited the lowest survival (13.27%) and highest stem elongation (81.25%). Genetic variability analysis revealed high heritability and genetic advance for important traits, including grain yield per plant ($H^2 = 78.66\%$; $GAM = 57.52\%$), survival percentage ($H^2 = 93.08\%$; $GAM = 67.39\%$), and stem elongation ($H^2 = 88.89\%$; $GAM = 51.11\%$), indicating the predominance of additive gene action and the effectiveness of phenotypic selection. Correlation analysis further demonstrated that grain yield was strongly and positively associated with number of tillers per plant ($r = 0.709$), number of filled grains per panicle ($r = 0.705$), panicle fertility ($r = 0.512$), and survival percentage ($r = 0.75$), while it was negatively associated with stem elongation ($r = -0.32$). Based on their superior survival, controlled stem elongation, and higher grain yield under submergence, two MAGIC breeding lines that outperformed the tolerant check Hemavathi were identified as promising candidates for multi-location evaluation, molecular characterization, and utilization in breeding programmes aimed at developing high-yielding, climate-resilient, and submergence-tolerant rice cultivars.

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Table 1: List of MF₇ MAGIC lines along with checks of rice taken for the experiment

Table 2: Top performing lines for submergence tolerance along with tolerant and susceptible checks.

Sl. No.	Genotypes	Sl. No.	Genotypes
M1	ML-1-1-2-1-38-24	M30	ML-1-9-12-1-9-13
M2	ML-1-1-2-1-39-15	M31	ML-1-10-1-1-43-19
M3	ML-1-1-3-1-9-2	M32	ML-1-10-2-1-14-24
M4	ML-1-1-4-1-10-7	M33	ML-1-11-4-1-29-16
M5	ML-1-1-5-1-36-12	M34	ML-1-11-4-1-46-17
M6	ML-1-2-5-1-41-25	M35	ML-1-11-11-1-15-19
M7	ML-1-3-1-1-4-3	M36	ML-1-15-2-1-3-12
M8	ML-1-3-2-1-25-11	M37	ML-1-15-2-1-47-18
M9	ML-1-3-3-1-23-18	M38	ML-1-15-14-1-11-13
M10	ML-1-3-6-1-6-5	M39	ML-1-15-15-1-5-11
M11	ML-1-3-7-1-13-9	M40	ML-1-15-16-1-26-19
M12	ML-1-3-8-1-19-19	M41	ML-1-15-19-1-51-14
M13	ML-1-5-2-1-4-21	M42	ML-1-15-20-1-20-19
M14	ML-1-5-3-1-40-14	M43	ML-1-15-21-2-12-17
M15	ML-1-5-4-1-53-4	M44	ML-2-5-5-1-11-15
M16	ML-1-5-6-1-8-17	M45	ML-2-5-14-1-12-23
M17	ML-1-5-8-1-50-13	M46	ML-2-5-15-1-27-21
M18	ML-1-6-6-2-33-27	M47	ML-2-6-9-1-28-14
M19	ML-1-7-3-1-31-19	M48	ML-2-7-3-1-2-19
M20	ML-1-7-5-1-42-28	M49	ML-2-7-5-1-34-17
M21	ML-1-7-8-1-7-12	M50	ML-2-10-4-1-26-32
M22	ML-1-7-8-1-30-23	C1	JGL-1798
M23	ML-1-8-2-1-54-21	C2	KPR-2
M24	ML-1-8-4-1-18-14	C3	Hemavathi (LC)
M25	ML-1-9-3-1-24-17	C4	Gandhasali
M26	ML-1-9-10-1-55-29	C5	BPT-5204
M27	ML-1-9-11-1-22-26	C6	Mysore mallige
M28	ML-1-9-11-1-44-23	C7	Jaya
M29	ML-1-9-12-1-21-8	C8	Swarna sub1 (NC)

Genotype	SRP	Score	SEP	GY
Swarna sub1 (NC)	92.60	1	23.27	23.50
ML-1-1-2-1-39-15	86.58	3	32.97	34.05
ML-1-7-8-1-7-12	83.77	3	31.85	35.00
Hemavathi (LC)	83.27	3	57.19	31.50
ML-1-3-2-1-25-11	82.17	3	51.35	24.52
ML-1-5-6-1-8-17	79.25	5	38.32	38.00
ML-1-2-5-1-41-25	77.00	5	32.14	30.50
ML-1-3-1-1-4-3	76.60	5	56.23	25.35
Gandhasali (SC)	18.97	7	69.09	18.80
Mysore mallige (SC)	13.27	7	81.25	15.80

Table 3: Analysis of variance for yield and its component characters in control and stress conditions during Kharif 2023.

D	=	Days to 50 <i>per cent</i> flowering	PF	=	Panicle fertility (%)	T	=	Test weight (g)
FF						W		
D	=	Days to maturity	PL	=	Panicle length (cm)	G	=	Grain yield per plant (g)
M						Y		
P	=	Plant height (cm)	L/B	=	Length/Breadth ratio			
H								
N	=	Number of tillers per plant	NF	=	Number of filled grains per panicle			
T			G					

Table 4: Estimation of mean, range and genetic parameters for yield and yield related characters in control and stress conditions during Kharif 2023.

Traits	Mean		Range				PCV (%)		GCV (%)		h^2_{sc} (%)		GAM (%)	
	Control	Stress	Minimum	Stress	Maximum	Stress	Control	Stress	Control	Stress	Control	Stress	Control	Stress
DFF	110.21	124.94	95	115	123	136	5.79	4.77	5.53	4.64	91.20	94.48	10.88	9.28
DM	139.62	140.45	125	116	156	175	4.90	10.74	4.61	10.49	88.47	95.42	8.93	21.11
PH	123.22	92.05	94	72	156	112	12.09	9.15	10.16	7.75	70.63	71.81	17.59	13.53
NT	18.86	9.70	8	4.33	27.77	23	22.81	26.40	20.07	14.53	77.37	30.30	36.36	16.48
PL	22.15	20.89	12	11.20	29.74	26	20.38	12.73	16.12	8.28	62.59	42.28	26.27	11.09
NFG	240.18	240.13	148.98	130	459.67	441.05	28.35	31.19	23.36	18.88	67.86	36.63	39.64	23.54
PF	85.47	77.83	68.92	44	96.30	96	21.73	7.20	12.40	6.47	32.57	80.81	14.58	11.99
LB	3.68	3.50	2.50	2.38	5.60	4.78	12.23	14.23	9.28	12.45	57.66	76.62	14.52	22.46
TW	16.01	15.76	11.73	8	20.40	20.14	13.71	12.41	12.87	10.53	88.13	72.04	24.89	18.42
GY	37.53	21.63	21	12.30	64.55	38.00	31.67	35.50	27.39	31.48	74.82	78.66	48.80	57.52

DF	=	Days to 50 <i>per cent</i> flowering	PF	=	Panicle fertility (%)	GC	=	Genotypic co-efficient of variation (%)
D	=	Days to maturity	PL	=	Panicle length (cm)	PCV	=	Phenotypic co-efficient of variation (%)
PH	=	Plant height (cm)	L/B	=	Length/Breadth ratio	h²_{bs}	=	Heritability in broad sense (%)
NT	=	Number of tillers per plant	NFG	=	Number of filled grains per panicle	GAM	=	Genetic advance as per cent of mean (%)
T	=	Test weight (g)	T	=	Test weight (g)			
W	=	Test weight (g)	W	=	Test weight (g)			
GY	=	Grain yield per plant (g)	GY	=	Grain yield per plant (g)			

Table 5: Estimation of physiological parameters for yield and yield related characters in submergence stress during Kharif 2023.

Traits	Mean	Minimum	Maximum	PCV (%)	GCV (%)	h ² (%)	GAM (%)
Survival percentage (%)	52.78	13.27	92.60	35.15	33.91	93.08	67.39
Stem elongation percentage (%)	47.11	23.27	81.25	27.91	26.31	88.89	51.11
Grain yield er plant (g)	21.63	12.30	38.00	35.50	31.48	78.66	57.52

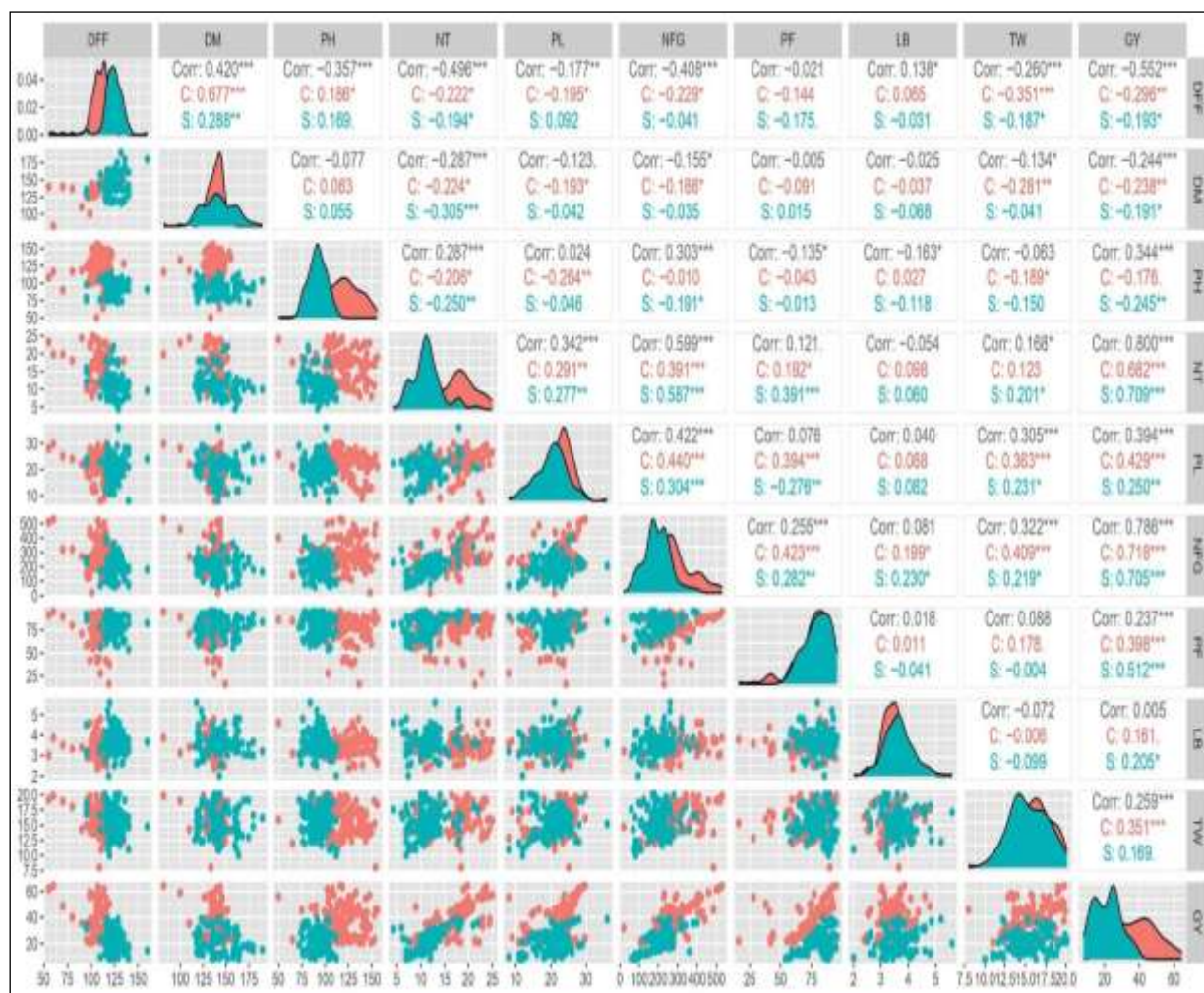


Figure 1: Phenotypic correlation among growth, yield and yield related characters of MAGIC lines of rice

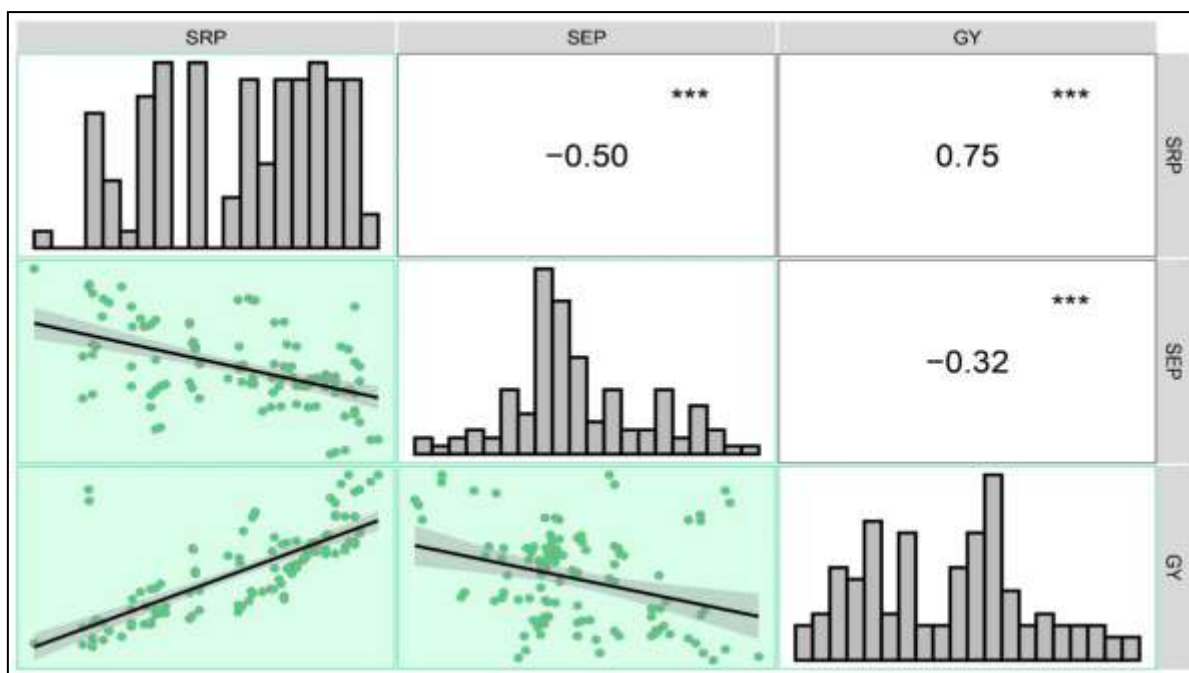


Figure 2: Phenotypic correlation among grain yield per plant and physiological traits for submergence tolerance.

SRP: Survival Percentage, **SEP:** Stem Elongation Percentage, **GY:** Grain yield per plant

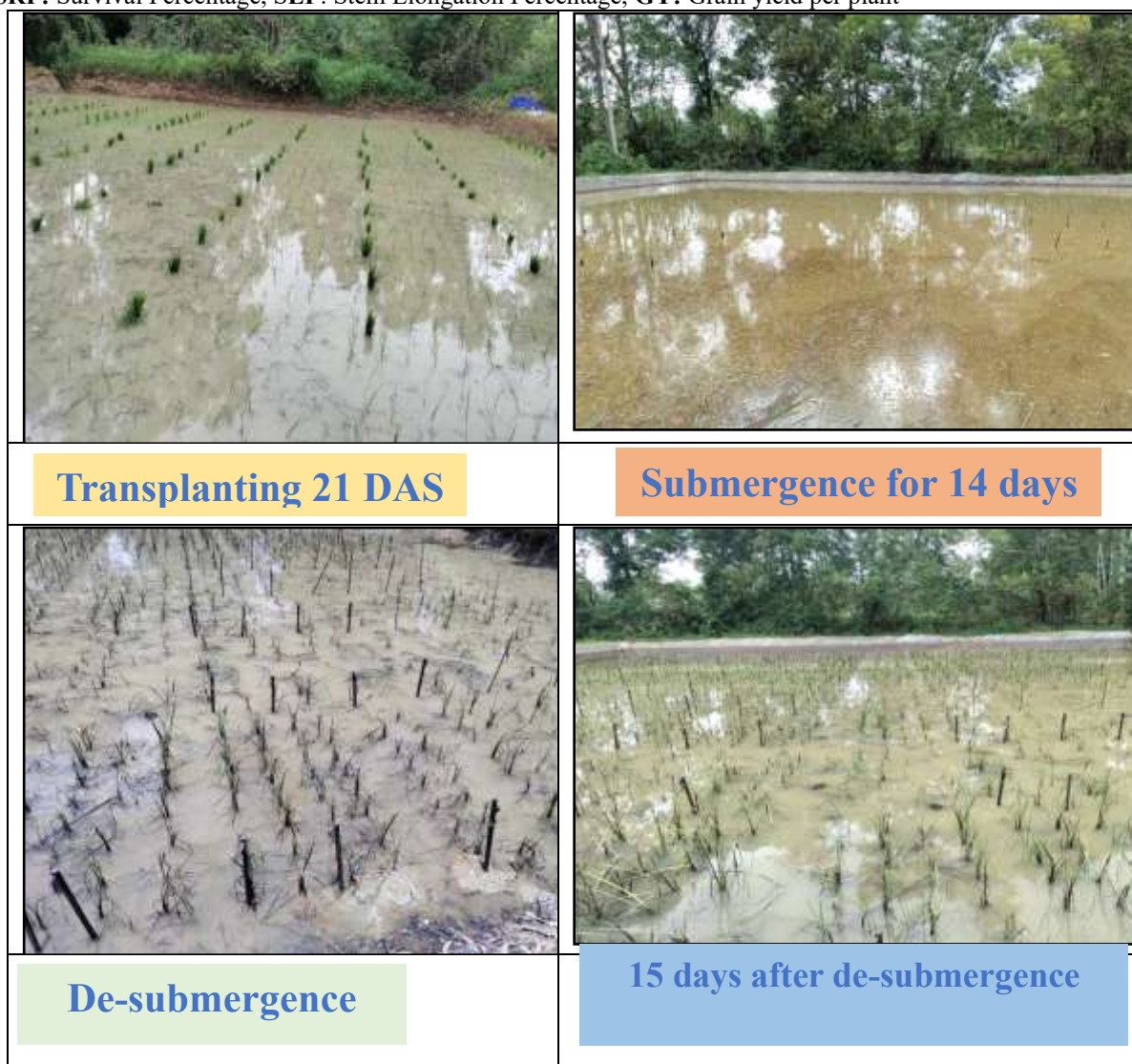


Plate 1. Stages of submergence screening in rice



STRESS



CONTROL

Plate 2: Comparative field conditions during submergence stress and control