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GENETIC VARIABILITY AND TRAIT ASSOCIATIONS FOR GRAIN YIELD IN RICE (*Oryza sativa* L.)

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ABSTRACT

The present investigation on grain yield traits in rice (*Oryza sativa* L.) was carried out using a biparental population derived from the cross of 'DRR Dhan 48' and 'Moudamani'. The study primarily focused on evaluating genetic variability and the association among morpho-agronomical traits influencing grain yield. Analysis of variance revealed significant variability among the lines for most traits, except panicle number per plant and spikelet fertility during the wet season 2024, whereas all traits showed significant variation during the dry season 2025. High genotypic and phenotypic coefficients of variation were recorded for grain number, panicle weight, panicle number and tiller number. High heritability coupled with high genetic advance as percent of mean was observed for grain number, panicle weight and panicle number, while panicle length, test weight and plant height exhibited high heritability with moderate genetic advance. Correlation analysis indicated that grain yield had a significant positive association with panicle weight, spikelet fertility, panicle number, and tiller number during the wet season 2024, and with panicle weight, grain number, and spikelet fertility during the dry season 2025. The strong and consistent association of grain yield with panicle weight, spikelet fertility, grain number, and panicle number suggests that these traits can be effectively utilized as selection criteria for improving grain yield in rice.

Key words: Biparental population, Correlation, Genetic advance as percent of mean, Heritability, Spikelet fertility, Genetic variability, Morpho-agronomical traits

Introduction

Rice has been a major component of food security in the present moment and in the future. The entire area under rice production in the world was estimated as 168 million hectares, and production was estimated to reach 532.87 million tons in 2023-24 (<https://www.statista.com/Agriculture-market-intelligence-centre>, PJTAU). India ranks second after China in rice production, with about 123.815 million metric tons produced from 45.152 million hectares of cultivated land and an average productivity of 2,742 kg/ha. In Telangana, rice is grown on 4.525 million hectares, producing 16.025 lakh tons, with an average productivity of 3,541 kg/ha. Yield is a multifactorial trait governed by numerous minor and major genes that are

influenced by environmental conditions and gene-gene interactions. Phenotypic selection is the essence of conventional breeding and may be driven by environmental conditions and hence it becomes hard to correctly select high yielding genotypes.

Understanding the relationship between yield and these component traits is essential for identifying the characters that play a decisive role in determining productivity. To achieve this, breeders employ different selection strategies aimed at isolating promising genotypes with favourable combinations of traits. In fact, phenotypic selection based on key morphological and grain quality traits has proven effective in recovering elite parent phenotypes (Singh *et al.*, 2022; Kumar *et al.*, 2018). The

objectives of the study were to assess the genetic variability for yield and yield-related traits in rice and to study the correlation among grain yield and its contributing traits.

Material and Methods

The study was conducted using a biparental population derived from the cross DRR Dhan 48 × Moudamani during the wet season of 2024 and the dry season of 2025. A total of ten traits were evaluated, days to 50% flowering (DFF), plant height (PH), panicle length (PL), tiller number (TN), panicle number (PN), grain number (GN), single plant yield (SPY), panicle weight (PW), test weight (TW) and spikelet fertility (SF). The data were analyzed using analysis of variance (ANOVA), genetic variability parameters, and correlation analysis in R software. Genetic variability parameters, including genotypic and phenotypic coefficients of variation, heritability and genetic advance were estimated, while correlation analysis was performed to assess the association among yield and yield-contributing traits.

Results and Discussion

Analysis of variance (ANOVA)

Analysis of variance (ANOVA) is one of the most reliable statistical methods used to detect variability within experimental material. In the present study, during wet season 2024, the mean sum of squares (MSS) of treatment adjusted (Table 1) revealed significant variation among the lines for most traits, except for panicle number

Table 1: Analysis of variance (ANOVA) for yield-related traits in the mapping population derived from the cross DDR Dhan 48 × Moudamani during wet season 2024.

Source	Block	TR	TC	TVC	RD
DF	4	201	4	197	16
DFF	48.65**	31.02 **	60.46 **	30.43 **	1.36
PH(cm)	266.62**	67.08 **	58.34 **	67.26 **	2.91
PL(cm)	8.82 **	4.76 **	45.26 **	3.93 **	0.73
TN	6.93 ^{ns}	5.63 ^{ns}	25.34 **	5.23 ^{ns}	2.77
PN	2.32 ^{ns}	4.82 *	16.34 **	4.59 *	1.74
PW(g)	2.73 **	2.26 **	4.43 **	2.22 **	0.04
SPY(g)	96.13 **	20.71 **	82.89 **	19.44 **	4.08
GN	573.89**	2011.20**	1462.66**	2022.34**	48.26
SF (%)	19.10 **	3.82 ^{ns}	38.75 **	3.11 ^{ns}	3.49
TW(g)	10.20 **	5.83 **	37.85 **	5.18 **	1.40

TR: Treatment; TC: Treatment: Check;
TVC: Test vs. Check; RD: Residuals
Significance at 5% level (P <= 0.05);
**Significance at 1% level ** P <= 0.01.
d.f- Degrees of freedom, DFF- Days to 50% flowering,
PH- Plant height (cm), PL- Panicle length(cm), TN- Tiller
number, PN- Panicle number, PW- Panicle weight(g),
SPY (GY)- Grain yield (g), GN- Grain number per panicle,
SF- Spikelet fertility (%), TGW (TW)- Test weight (g)

per plant and spikelet fertility. Similarly, the MSS of test genotypes and test genotypes versus checks were highly significant for all the evaluated traits, excluding panicle number per plant and spikelet fertility. During dry season 2025 all the traits showed significance, the MSS of test genotypes and test genotypes versus checks were also highly significant (Table 2), with spikelet fertility being significant as well. These results indicate that the population possesses considerable variability in yield traits, making it highly suitable for further genetic research. Moreover, there is ample of scope for the selection of superior transgressive segregants for desirable yield-

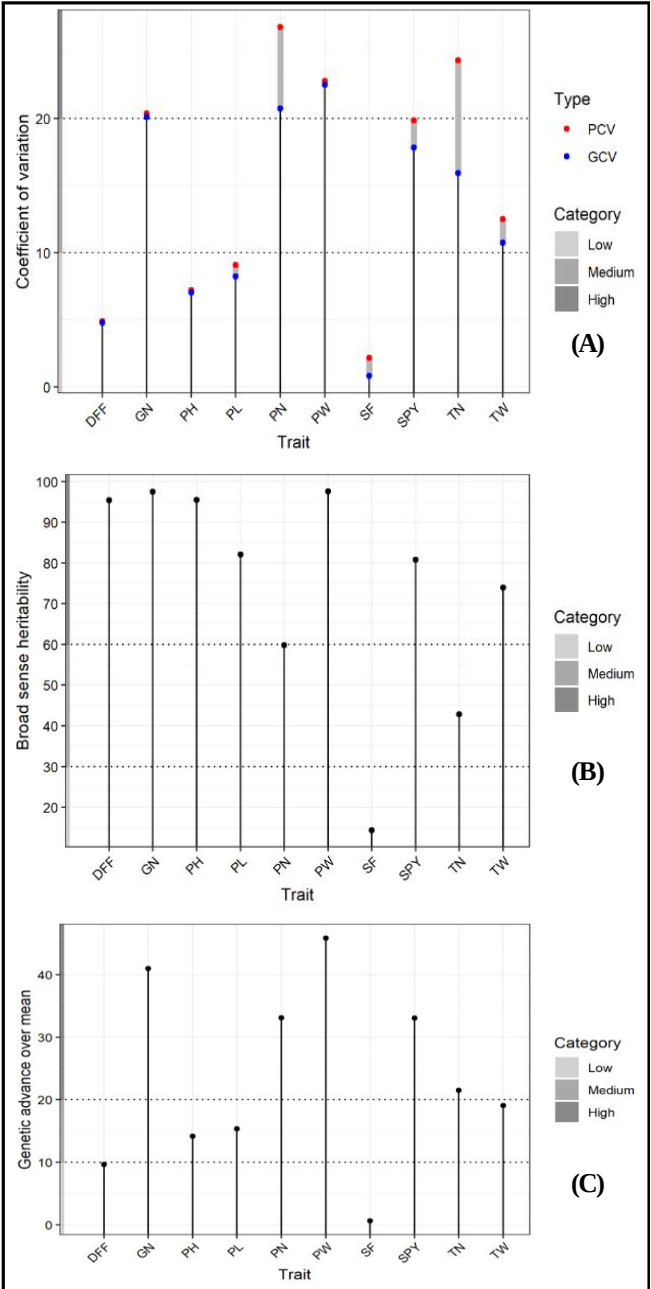


Fig. 1: Graphical representation of a) PCV, GCV, b) heritability (broad sense) and c) genetic advance as percent of mean for the yield traits.

Table 2: Analysis of variance (ANOVA) for yield-related traits in the mapping population derived from the cross DDR Dhan 48 × Moudamani during dry season 2025..

Source	Block	TR	TC	TVC	RD
DF	4	201	4	197	16
DFF	8.90 **	37.31 **	140.70 **	35.22 **	0.87
PH(cm)	108.04 **	52.71 **	65.44 **	52.45 **	1.44
PL(cm)	14.67 **	4.09 **	20.52 **	3.76 **	0.10
TN	46.77 **	5.07 **	6.60 **	5.04 **	0.87
PN	11.43 **	3.07 *	4.06 *	3.05 *	1.14
PW(g)	5.64 **	1.97 **	2.58 **	1.96 **	0.05
SPY(g)	83.50 **	27.78 **	73.36 **	26.86 **	1.20
GN	6512.33**	1720.89**	1273.36**	1729.98**	15.24
SF (%)	58.51 **	8.57 **	48.30 **	7.76 *	3.04
TW(g)	7.92 **	4.66 **	52.10 **	3.69 **	0.13

TR: Treatment; TC: Treatment: Check;

TVC: Test vs. Check; RD: Residuals

Significance at 5% level (P ≤ 0.05);

**Significance at 1% level ** P ≤ 0.01.

d.f- Degrees of freedom, DFF- Days to 50% flowering, PH- Plant height (cm), PL- Panicle length(cm), TN- Tiller number, PN- Panicle number, PW- Panicle weight(g), SPY (GY)- Grain yield (g), GN- Grain number per panicle, SF- Spikelet fertility (%), TGW (TW)- Test weight (g)

related traits, which can be utilized in the development of high-yielding rice varieties. Therefore, conducting a detailed analysis of genetic variability is crucial before initiating any crop improvement program, as it guides the choice of appropriate selection methods.

Variability Studies

The estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) for the studied traits revealed clear differences in the extent of genetic variability among the genotypes (Table 3). During wet season 2024, PCV ranged from 2.02 (SF) to 26.80 (PN), while the GCV ranged from 0.82 (SF) to 20.73 (PN) (Fig. 1) relatively high GCV and PCV were recorded for GN, PW, PN and TN, similarly Ubarhande *et al.*, (2025) observed high GCV and PCV for SPY indicating substantial genetic diversity indicating a broad spectrum of genetic variation and considerable potential for improvement through selection. Moderate GCV and PCV were observed for PL, TW, and PH, whereas DFF exhibited low variability, signifying its relative stability and minimal genetic variation. Similar to our studies, Deepika *et al.*, (2021) also reported low GCV and PCV for DFF. Akshay *et al.*, (2022) also observed high GCV and PCV for GN. Williams *et al.*, (2021) reported moderate GCV and PCV test weight.

The heritability estimates ranged from 42.83% (TN) to 97.60% (PW), reflecting that most of the studied traits

are largely governed by genetic factors with limited environmental influence. High heritability coupled with high genetic advance as a percentage of the mean (GAM) was observed for GN, PW, and PN. Similarly, Akshay *et al.*, (2022) also observed high heritability coupled with high genetic advance as percent of mean for grain number per panicle suggesting a predominance of additive gene action and indicating that simple selection methods would be effective for improving these traits. PL, TW and PH displayed high heritability with moderate GAM, Girish *et al.*, (2006) reported that plant height, test weight exhibited

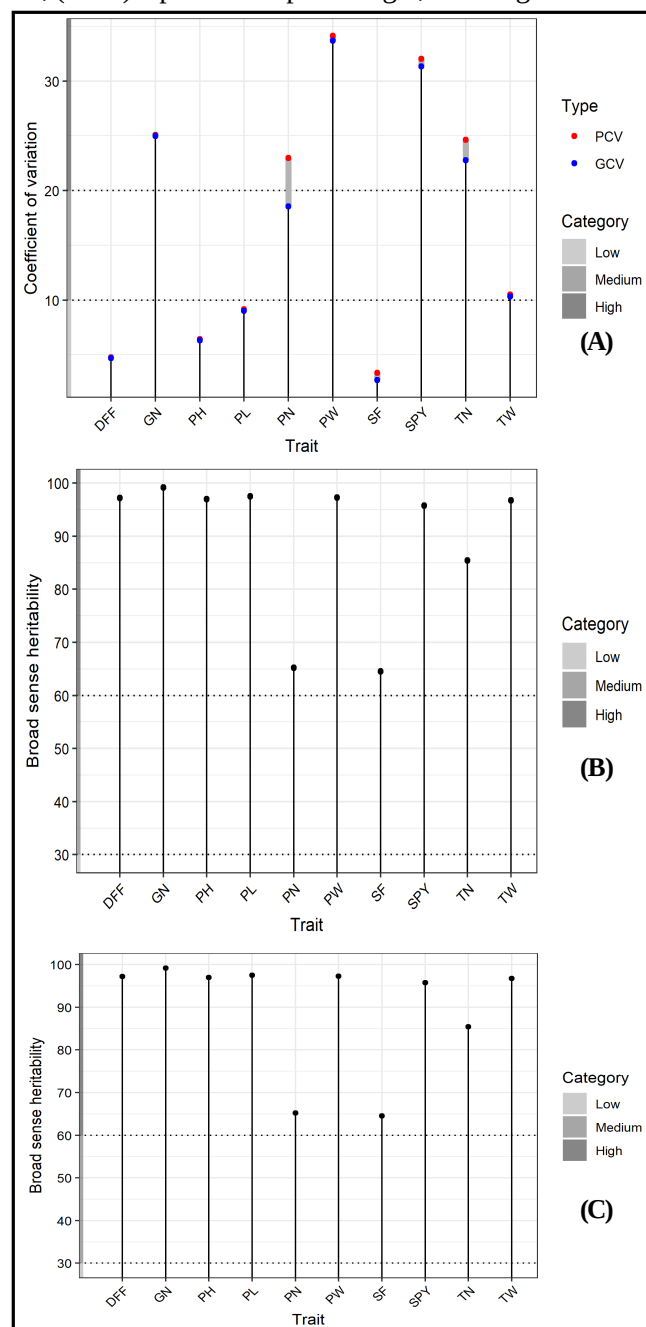
**Fig. 2:** Graphical representation of a) PCV, GCV, b) heritability (broad sense) and c) genetic advance as percent of mean for the yield traits.

Table 3: Variability parameters in mapping population from DRR Dhan 48 and Moudamini during wet season 2024.

Trait	MEAN	GCV	PCV	Heritability	GAM
DFF	111.03	4.78	4.89	95.39	9.63
PH	111.14	7.03	7.2	95.44	14.17
PL	22.19	8.23	9.08	82.03	15.37
TN	9.05	15.91	24.31	42.83	21.48
PN	7.77	20.73	26.8	59.84	33.08
PW	5.67	22.5	22.77	97.6	45.85
SPY	23.23	17.84	19.84	80.81	33.08
GN	216.37	20.11	20.37	97.52	40.98
SF	91.12	0.82	2.02	14.38	0.64
TW	18.59	10.74	12.48	73.97	19.05

a higher value of heritability and genetic advance in a RIL population. implying the influence of both additive and non-additive genetic effects. In contrast, TN exhibited moderate heritability with medium GAM, indicating a possible environmental influence on trait expression.

The small difference between PCV and GCV for most traits DFF, PH, PL, PW, GN and TW indicates that the environmental impact is minimal, thus making phenotypic selection effective for improving these traits. The combined presence of high variability, heritability, and genetic advance for crucial yield components such as GN, PW and PN highlights that these traits are largely controlled by additive genes and can be enhanced through direct selection. Overall, the study underscores that improvement in grain yield can be efficiently achieved by selecting for key yield-contributing traits like GN, PW, and PN, which play a major role in determining the yield potential of rice genotypes.

The analysis of genotypic and phenotypic coefficients of variation (GCV and PCV) showed noticeable variation across the evaluated traits, indicating substantial genetic diversity within the population (Table 4). During dry season 2025, PCV ranged from 3.33 (SF) to 34.14 (PW), whereas GCV values varied from 2.68 (SF) to 33.67 (PW) (Fig. 2). Traits such as PW, SPY, GN, TN and PN displayed high GCV and PCV, reflecting broad genetic variability and suggesting ample opportunity for effective selection and improvement of these yield-related traits. Moderate variability was recorded for PL, TW and PH, while DFF and SF exhibited low GCV and PCV, implying that these traits are relatively stable and less influenced by genetic factors.

Heritability values ranged from 64.55% (SF) to 99.19% (GN) and the genetic advance as percent of mean (GAM) ranged from 4.44% (SF) to 68.52% (PW). The combination of high heritability and high GAM observed for PW, SPY, GN and TN indicates that these traits are

Table 4: Variability parameters in mapping population from DRR Dhan 48 and Moudamini during dry season 2025.

Trait	MEAN	GCV	PCV	Heritability	GAM
DFF	117.28	4.71	4.78	97.21	9.58
PH	107.44	6.33	6.42	96.98	12.85
PL	21.84	9.03	9.14	97.51	18.39
TN	9.94	22.77	24.64	85.4	43.4
PN	7.87	18.55	22.97	65.24	30.92
PW	4.11	33.67	34.14	97.3	68.52
SPY	16.5	31.32	32.01	95.72	63.22
GN	172.5	24.96	25.06	99.19	51.29
SF	87.88	2.68	3.33	64.55	4.44
TW	18.74	10.32	10.49	96.75	20.94

largely governed by additive gene action, making selection based on phenotypic performance highly effective. Traits like PL, PH, TW, and DFF showed high heritability with moderate GAM, Girish *et al.*, (2006) reported that plant height, test weight exhibited a higher value of heritability and genetic advance in a RIL population suggesting a mix of additive and non-additive genetic effects, whereas PN exhibited moderate heritability along with high GAM, implying that genetic improvement through direct selection is possible.

The narrow gap between PCV and GCV for most of the evaluated traits DFF, PH, PL, PW, GN, TW and SF suggests that the influence of environmental factors is minimal, indicating that these traits are primarily controlled by genetic factors. This further implies that selection based on phenotype can be effectively utilized for genetic improvement.

Overall, the study highlights that traits like GN, PW, SPY and TN are under strong genetic control and can be efficiently enhanced through selection strategies exploiting additive genetic variation. Conversely, traits such as DFF and SF exhibited limited variability, indicating the need for alternative breeding approaches for their improvement. Therefore, the high variability, heritability and genetic advance estimates obtained in this study reaffirm the existence of broad genetic diversity and the scope for effective phenotype-based selection in rice breeding programs aimed at yield improvement.

Correlation studies of grain yield traits in rice

Improvement in one character may lead to enhancement of other positively associated traits, whereas traits with negative associations may decline. The correlation plot depicted the linkage between grain yield and its contributing traits. During wet season 2024 the grain yield exhibited a significant positive correlation with PW, SF, PN and TN. Varanasi *et al.*, (2023) reported

that GY had a significant positive correlation with DFF, TN, PN and TW. DFF exhibited a significant positive correlation with GN and a significant negative correlation with PL and PW.

Plant height exhibited a highly significant positive correlation with panicle length, a significant negative correlation with spikelet fertility. Panicle length exhibited a highly significant positive correlation with plant height and significant negative correlation with days to 50% flowering and spikelet fertility. Number of tillers per plant exhibited a highly significant positive correlation with panicle number, a significant correlation with grain yield and significant negative correlation with grain number and days to 50% flowering. Panicle number showed a highly significant positive correlation with number of tillers per plant, a significant positive correlation with grain yield. Panicle weight exhibited a highly significant positive correlation with grain number, a significant positive correlation with grain yield, test weight and spikelet fertility.

Grain number showed a highly significant positive correlation with spikelet fertility and panicle weight, a significant positive correlation with days to 50% flowering and a significant negative correlation with number of tillers per plant. Test weight showed a significant positive

correlation with panicle weight.

During dry season 2025 (Fig. 4) grain yield exhibited a highly significant positive correlation with panicle weight, grain number, spikelet fertility and highly significant negative correlation with number of tillers per plant. Varanasi *et al.*, (2023) reported that grain yield had a significant positive correlation with days to 50% flowering, number of tillers per plant, panicle number and test weight. Days to 50% flowering exhibited a significant positive correlation with plant height. Plant height exhibited a highly significant positive correlation with panicle length and panicle weight, a significant correlation with spikelet fertility, grain number and days to 50% flowering. Panicle length exhibited a highly significant positive correlation with plant height and number of tillers per plant, significant correlation with panicle number, panicle weight and test weight. Number of tillers per plant exhibited a highly significant positive correlation with panicle number and panicle length, a highly significant negative correlation with spikelet fertility and grain yield, a significant negative correlation with panicle weight and grain number. Panicle number showed a highly significant positive correlation with number of tillers per plant, a significant positive correlation with panicle length and a significant negatively correlation with spikelet fertility. Panicle weight exhibited

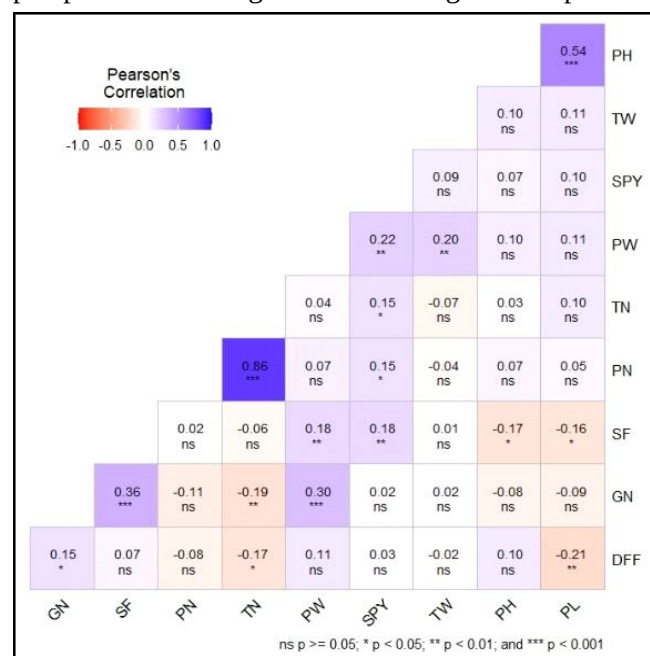


Fig. 3: Graphical representation of correlation coefficients among yield traits in bi-parental population derived from DRR Dhan 48 and Moudamani during wet season 2024. DFF- Days to 50% flowering, PH- Plant height (cm), PL- Panicle length(cm), TN- Tiller number, PN- Panicle number, PW- Panicle weight(g), SPY (GY)- Grain yield (g), GN- Grain number per panicle, SF- Spikelet fertility (%), TGW (TW)- Test weight (g).

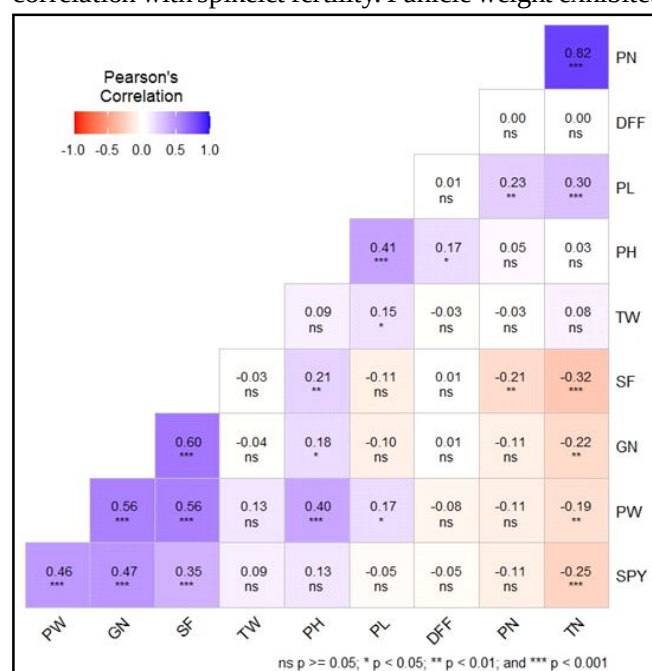


Fig. 4: Graphical representation of correlation coefficients among yield traits in bi-parental population derived from DRR Dhan 48 and Moudamani during dry season 2025. DFF- Days to 50% flowering, PH- Plant height (cm), PL- Panicle length(cm), TN- Tiller number, PN- Panicle number, PW- Panicle weight(g), SPY (GY)- Grain yield (g), GN- Grain number per panicle, SF- Spikelet fertility (%), TGW (TW)- Test weight (g).

a highly significant positive correlation with grain number, spikelet fertility, panicle weight and plant height, a significant positive correlation with panicle length and a significant negative correlation number of tillers per plant. Grain number showed a highly significant positive correlation with spikelet fertility, panicle weight and single plant yield a significant positive correlation with plant height and a significant negative correlation with number of tillers per plant. Test weight showed a significant positive correlation with panicle length.

The correlation analysis across both seasons revealed that grain yield in the mapping population is strongly influenced by yield-contributing traits such as panicle weight, spikelet fertility, grain number, and panicle number, while traits like tiller number often showed a negative association with yield, particularly in dry season 2025. The variation in correlation trends between wet season and dry season highlights the influence of environmental factors on trait relationships. Overall, traits including panicle weight, spikelet fertility and grain number consistently exhibited positive correlations with grain yield, making them reliable indicators for indirect selection in yield improvement. This suggests that targeting these traits in breeding programs would be more effective than direct selection for grain yield alone.

Conclusion

The biparental population exhibited considerable genetic variability for yield and yield-related traits across wet and dry seasons. High GCV, PCV, heritability and genetic advance observed for grain number, panicle weight, and panicle number indicated the predominance of additive gene action and the effectiveness of direct selection. Correlation analysis revealed that panicle weight, spikelet fertility, grain number, and panicle number were consistently and positively associated with grain yield. Therefore, these traits can be effectively utilized as reliable selection criteria for improving grain yield in rice breeding programs.

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