



Exploration of Genetic Variability and Trait Association for Root Architecture Related Traits under Aerobic Conditions in Rice (*Oryza sativa* L.)

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Abstract

In this study, we performed exploration of genetic variability for root architecture related traits in a mapping population derived from TI-128×BPT 5204, such as length, volume, fresh and dry weight, in influencing nutrient and moisture uptake during 60 days after sowing under aerobic conditions at three diverse environments for the selection of desirable lines. The variance analysis, revealed significant variations ($p \leq 0.005$) for all studied traits, indicating a broader sense of genetic variability for selection purposes. Significant positive correlation was recorded between all the traits under study. The rice lines *viz.*, TB 1, TB4, TB 8, TB 24, TB 51, TB 67 and TB 107 exhibited comparatively higher RL, RV and RDW, than all the checks used in the present study. The identified lines exhibiting better root architectural traits can benefit in developing a suitable DSR cultivar with better adaptability and performance under dry direct seeded rice conditions.

Keywords: Aerobic rice, root, DDSR, genetic variability, correlation.

Introduction

Rice (*Oryza sativa* L.) stands as the primary food source for billions in developing nations, flourishing across diverse environments in terms of latitude, altitude, and topography, all with varying water availability. Despite its global significance irrigated rice cultivation is known for its inefficient water usage, requiring 3,000 to 5,000 liters of water to yield just one kilogram of grain. Startlingly, rice commands a substantial 85% share of the 70-80% of freshwater used in agriculture globally (Pathak *et al.*, 2011, Kommana *et al.*, 2023). Predictions sound an alarm, with around 39 million hectares of irrigated rice in Asia alone potentially facing yield reductions due to water scarcity (Tuong and Bouman, 2003, Reddy *et al.*, 2022). The forthcoming decades are poised for a critical shift toward more sustainable agricultural practices that integrate environmental well-being

and socio-economic considerations. Therefore, transitioning from the conventional transplanted puddled rice (TPR) to alternative systems that enhance water productivity without compromising yields is a prudent choice. This kind of shift in rice cultivation is needed to cope with water scarcity as well as to maintain the groundwater table (Phule *et al.*, 2019). One such system is direct-seeded rice (DSR), which not only reduces water consumption and labour needs but also bolsters resource efficiency, productivity, and mitigates greenhouse gas emissions. In recent years, DSR has gained prominence as the primary rice cultivation method in developed countries and has been adopted in more than 25% of global rice cultivation areas (Kumar and Ladha, 2011). Overall, DSR offers numerous benefits, including substantial savings in water and labor expenses, improved crop



rotation possibilities, and reduced greenhouse gas emissions (Corton *et al.*, 2000). DSR, in particular, makes efficient use of early-season monsoons in regions with limited moisture. Compared to TPR, the DSR system uses 60.3% less non-renewable energy and exhibits an average energy-use efficiency of 7.3 compared to 4.4 for TPR (Panda *et al.*, 2021).

Roots serve as the primary sensory and adaptive organs in response to various environmental stresses, including drought, flooding, salinity, and mineral deficiencies. An extensive root system helps support above ground plant growth by enabling better water and nutrient absorption from the soil, ultimately leading to higher yields (Padmashree *et al.*, 2022). Surprisingly, most breeding efforts have traditionally focused on improving above ground plant characteristics, largely neglecting root traits that contribute to nutrient acquisition efficiency (NAE), often due to limited awareness and inadequate screening methods. Unfortunately, these valuable root traits have been inadvertently disregarded or even selected against in the context of intensive agriculture. Tailoring root architecture to suit the requirements of DSR presents a promising opportunity to overcome adaptability and yield limitations. This approach could yield genotypes that thrive in DSR conditions, outperforming those suited for TPR (Sandhu *et al.*, 2021). The widespread acceptance and adoption of DSR, as well as the development of suitable rice varieties, hinge on overcoming the challenges associated with breeding varieties that thrive in low-water conditions and offer sufficient nutrient availability. In this study, we conducted a phenotypic evaluation of 150 Recombinant Inbred Lines (RILs) over 60 Days After Sowing (DAS) at three diverse locations under aerobic conditions, with a focus on traits related to root architecture.

Materials and Methods

The experimental material comprised of mapping population (150 lines, TB1 to TB150) developed through the crossing of selected mutant line (TI-

128) as the female parent with best root related traits (seedling vigour index, root length, root volume) and the wild type (BPT 5204) as the male parent. The Mapping population (F_7) comprised of 150 RILs were evaluated at three locations (ICAR-IIRR, Hyderabad (E_1), AHRS, Kathalagere, KSNUAHS Shivamogga (E_2), RARS, Karjat (E_3)) for root architecture related traits under aerobic conditions during *rabi* 2022. To evaluate the lines for root architecture related traits under aerobic conditions, the experiment was laid out in augmented block design with five blocks, wherein, each block consisted of 30 lines along with the parents (TI-128 and BPT-5204) and six checks (Sahabgadhyan, MAS 946-1, Sabita, TI-112, TI-3 and TI-17) were randomized in each block. Each RIL was sown in two-meter length line at a spacing of 20cm \times 15cm. Agronomic practices were followed as recommended for aerobic rice cultivation, for the first four weeks after sowing (WAS), lines were irrigated once in three days for two to three hours. From the fifth week, irrigation was provided 2-3 times a week for two hours to reach field capacity. The seeds were directly sown and 15 days after sowing extra seedlings were thinned to maintain a single plant per hill. Timely weeding was performed, and the field was maintained as per the agronomic practices with need-based irrigation.

Randomly three plants in each line were carefully uprooted by carefully pulling them out from the soil without damaging the roots (destructive sampling). The roots were washed manually using a high-pressure water pump and observations were recorded for root architecture related traits *viz.*, root length (RL), shoot length (SL), total plant length (TPL), root fresh weight (RFW), shoot fresh weight (SFW), total fresh weight (TFW), root dry weight (RDW), shoot dry weight (SDW), total dry weight (TDW), and root volume (RV). The analysis of variance, genetic variability parameters and correlation were carried out in R studio (version 3.5.2) using R-scripts for statistical analysis (Aravind *et al.*, 2019).



Results and Discussion

Analysis of variance (ANOVA) for root architecture related traits

The Mean Sum of Squares (MSS) for the root architecture related traits under aerobic conditions in the mapping population during *rabi* 2022 is presented in (Table 1). The ANOVA revealed that the MSS of test genotypes versus checks was highly significant

at $p < 0.05$ for all the traits under investigation. Highly variable traits are preferred in breeding programmes for maximizing the genetic base (Barde *et al.*, 2021). The MSS due to test genotypes exhibited highly significant differences at $p < 0.05$ for all the traits under investigation across three diverse locations, revealing that sufficient variability was present in the mapping population.

Table 1: Analysis of variance for root architectural related traits in RILs under aerobic condition during *rabi* 2022

Source	Location	d. f.	RL	SL	TPL	RFW	SFW	TFW	RDW	SDW	TDW	RV
Treatment	EI	157	1.64**	14.28**	19.82**	123.42**	591.24**	1024.12**	13.24**	57.28**	109.24**	228.26**
	EII		1.58**	15.24**	20.18**	130.28**	586.28**	1041.28**	14.28**	54.12**	107.28**	231.42**
	EIII		1.69**	16.22**	20.93**	126.47**	604.72**	1055.72**	15.46**	61.33**	112.93**	236.28**
Check	EI	7	1.68**	87.42**	78.12**	1010.32**	2042.36**	4230.28**	124.24**	218.24**	476.24**	556.82**
	EII		1.72**	86.28**	76.54**	1024.28**	2100.28**	4310.24**	130.54**	216.22**	472.24**	550.28**
	EIII		1.98**	95.89**	81.41**	1045.20**	2179.20**	4440.53**	127.78**	221.02**	484.23**	548.26**
Test genotypes	EI	149	1.28**	10.26**	14.24**	76.28**	412.26**	712.26**	8.62**	48.24**	72.42**	124.28**
	EII		1.32**	10.46**	13.26**	71.14**	421.58**	734.28**	8.84**	42.24**	74.26**	126.24**
	EIII		1.48**	11.98**	16.68**	75.22**	438.93**	740.45**	9.20**	44.52**	78.91**	132.22**
Test vs. Check	EI	1	1.36**	87.14**	222.28**	1228.24**	13284.28**	21364.28**	154.28**	1242.24**	2326.28**	1284.22**
	EII		1.28**	88.24**	216.24**	1324.24**	13862.24**	22328.24**	158.36**	1342.28**	2428.24**	1324.24**
	EIII		1.41**	91.42**	230.01**	1330.79**	14286.17**	24337.49**	162.70**	1448.96**	2582.72**	1266.28**
Block	EI	4	7.41	56.28	74.26	163.28	1242.28	1324.26	44.22	112.24	124.24	110.28
	EII		5.12	52.48	68.28	142.24	1366.48	1412.28	43.24	121.28	126.28	108.26
	EIII		6.12	58.64	79.54	154.32	1382.38	1426.38	38.26	116.26	132.24	104.22
Residuals	EI	28	0.48	15.32	19.22	86.24	62.24	42.28	12.26	25.24	42.22	31.26
	EII		0.56	16.84	18.24	76.32	74.28	54.26	11.24	28.34	44.26	32.48
	EIII		0.32	14.26	17.28	79.30	54.32	52.26	12.38	22.26	38.28	30.22

EI- ICAR-IIRR, Hyderabad, EII- AHRS, Kathalagere, KSNUAHS, Shivamogga, EIII-RARS, Karjat

RL- Root length (cm), SL- Shoot length (cm), TPL- Total Plant length (cm), RFW, Root fresh weight (g), SFW- Shoot fresh weight (g), TFW- Total fresh weight (g), RDW- Root dry weight (g), SDW- Shoot dry weight (g), TDW- Total dry weight (g), RV- Root volume (cm³)

Genetic variability parameters

The results of genetic variability parameters *viz.*, range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability and genetic advance as per cent mean were analyzed to estimate the extent and magnitude of genetic variation for root architecture related traits in mapping population. The mean

performance for the traits showed a wide range of variation for most of the characters studied and the findings of the present experiment are given in (Table 2). The heritability of broad-sense (h^2 bs) was divided into three categories: high (above 60%), medium (30%–60%), and low (less than 10%) (Robinson *et al.*, 1949). GAM is also divided into three



Table 2: Estimation of genetic variability parameters for root architectural related traits in RILs under aerobic condition during *Rabi* 2022

Traits	Location	Range		Mean	CV (%)	Genetic variability		h ² (bs) (%)	GAM
		Min	Max			GCV (%)	PCV (%)		
RL	EI	4.33	28.33	16.49	4.05	12.68	12.71	96.24	51.20
	EII	5.83	26.23	15.23	4.03	13.20	13.21	97.12	51.82
	EIII	5.89	24.24	14.81	4.97	13.90	14.10	97.26	52.40
SL	EI	19.90	53.23	31.77	5.20	10.82	10.86	94.12	45.28
	EII	22.97	44.13	31.81	5.33	10.16	10.24	93.26	46.24
	EIII	21.28	41.28	32.20	5.46	10.74	10.78	93.19	47.52
TPL	EI	24.40	62.83	40.25	7.59	9.18	9.72	97.12	39.28
	EII	29.00	53.87	41.04	6.76	9.26	9.64	94.28	41.26
	EIII	27.26	50.52	41.01	7.10	9.97	9.98	96.72	40.54
RFW	EI	5.70	60.30	23.11	8.04	13.22	13.24	95.24	57.26
	EII	10.24	63.20	24.32	8.81	13.82	13.86	94.24	57.40
	EIII	6.67	60.86	23.43	9.49	14.05	14.12	95.98	58.20
SFW	EI	16.20	125.10	58.73	12.12	35.42	36.42	94.12	57.26
	EII	15.12	127.12	58.48	13.77	36.28	37.12	93.88	59.28
	EIII	13.01	125.60	58.36	11.86	37.53	37.58	94.92	62.38
TFW	EI	23.8	175.5	81.84	9.88	38.24	38.68	85.28	51.28
	EII	25.96	171.40	82.80	11.25	37.26	37.88	84.26	52.24
	EIII	23.79	176.56	81.78	10.86	36.50	36.50	84.62	53.44
RDW	EI	1.91	20.97	7.73	4.05	36.28	36.33	93.12	32.68
	EII	3.40	21.06	8.08	4.03	35.29	35.31	94.04	32.88
	EIII	2.33	21.28	8.19	4.97	35.87	35.92	94.18	32.98
SDW	EI	5.06	39.09	18.35	5.20	36.28	36.42	76.28	66.24
	EII	3.26	37.61	16.56	8.33	34.26	34.28	74.26	67.28
	EIII	4.14	40.00	18.58	7.46	37.53	38.52	75.24	68.24
TDW	EI	7.56	56.10	26.08	7.59	32.28	33.52	82.24	26.54
	EII	6.86	52.32	24.64	6.76	31.26	32.28	84.26	25.24
	EIII	7.91	57.82	26.78	9.10	33.70	33.82	87.24	27.28
RV	EI	8.24	31.92	18.26	8.04	34.24	35.28	97.42	35.24
	EII	7.26	30.28	17.28	9.81	35.12	25.42	97.26	36.28
	EIII	7.28	32.24	17.36	9.49	35.87	36.82	98.12	36.94

EI- ICAR-IIRR, Hyderabad, EII- AHRS, Kathalagere, KSNUAHS, Shivamogga, EIII-RARS, Karjat

RL- Root length (cm), SL- Shoot length (cm), TPL- Total Plant length (cm), RFW, Root fresh weight (g), SFW- Shoot fresh weight (g), TFW- Total fresh weight (g), RDW- Root dry weight (g), SDW- Shoot dry weight (g), TDW- Total dry weight (g), RV- Root volume (cm³).

categories: high (>20%), medium (10–20%), and low) (below 10%) (Johnson *et al.*, 1955). High GCV and PCV coupled with high heritability and GAM were observed for the traits *viz.*, shoot length, root length, shoot fresh weight, root fresh weight, total fresh weight, shoot dry weight, root dry weight, total dry weight and root volume. Moderate to high GCV

and PCV coupled with high heritability and GAM were observed for total plant length and low GCV and PCV coupled with high heritability and high GAM. The narrow magnitude of difference between phenotypic and genotypic coefficients of variations was recorded for characters such as shoot length, root length, shoot fresh weight, root fresh weight,



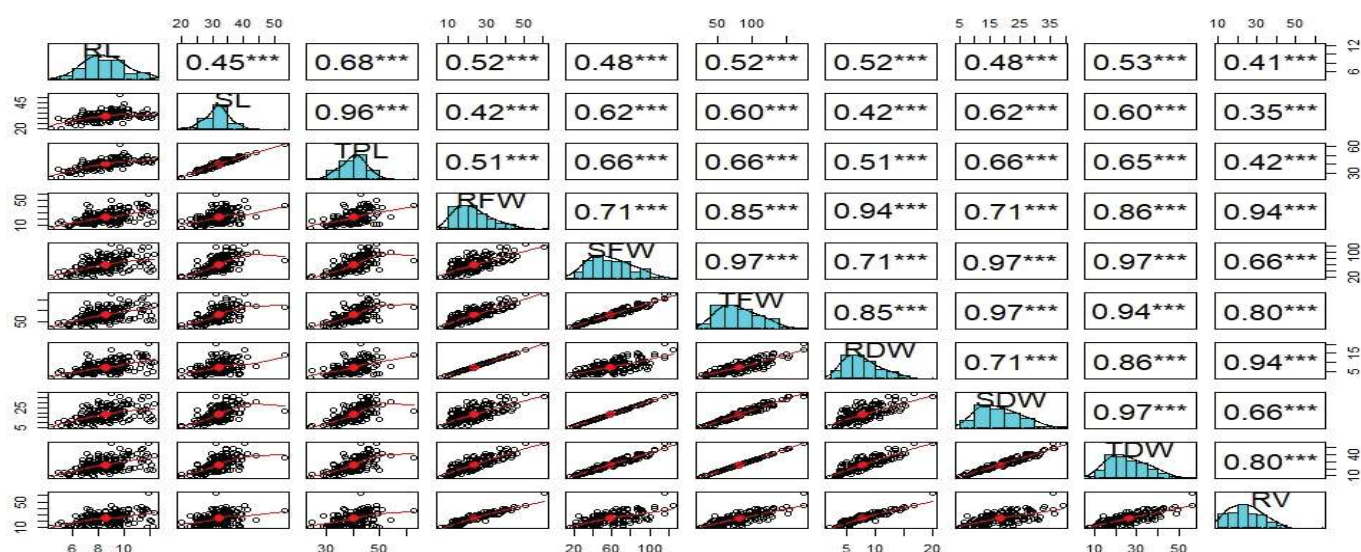
total fresh weight, shoot dry weight, total dry weight and root volume indicating the limited influence of environment in the expression of these characters. Selection based on the phenotypic performance of these characters would be effective in bringing about considerable genetic improvement. The narrow difference between GCV and PCV implies that most features are less influenced by the environment. The heritability estimates for a given trait determine the reliability of the phenotypic value. As a result, high heritability aids in the efficient selection of a specific trait, hence, quantitative trait genetic analysis is critical for breeding programmes. Our results are in accordance with the results of Koshle *et al.*, (2020) and Singh *et al.*, (2017) observed high heritability and GAM for the traits *viz.*, shoot length, root length, root to shoot length ratio, shoot fresh weight, root fresh weight, total fresh weight, root to shoot fresh weight ratio, shoot dry weight, root dry weight, total dry weight and root to shoot dry weight ratio and concluded that such characters would be considered for selection.

Estimates of correlation coefficients

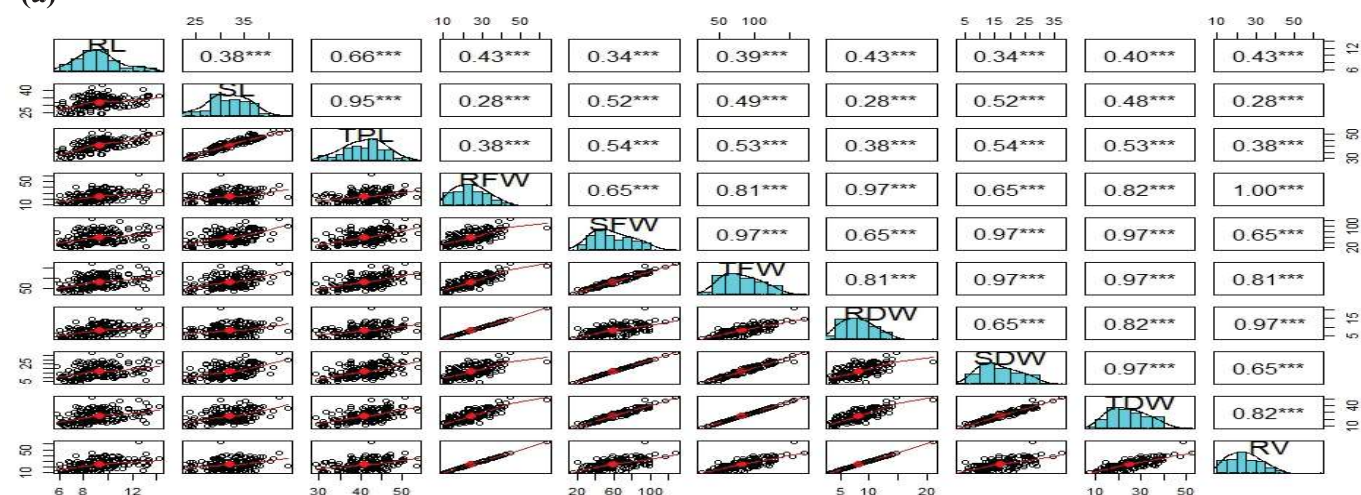
Correlation studies were carried out to know which parameters contributed to the maximum for root architecture traits and the details of the results are given in graphical representation of **(Figure 1)**. Root length exhibited the highest positive significant correlation with total plant length, total fresh weight, shoot fresh weight, shoot length, total dry weight, root volume, root dry weight and shoot dry weight. The shoot length exhibited the highest positive significant correlation with total plant length, root to shoot length ratio, root fresh weight, total dry weight, shoot fresh weight and shoot dry weight. Total plant length exhibited the highest positive significant correlation with shoot fresh weight, total fresh weight, shoot dry weight, total dry weight, root dry weight, root fresh weight and root volume. Root

to shoot length ratio exhibited the highest positive significant correlation with root fresh weight, root to shoot fresh weight ratio, root dry weight, total fresh weight, total dry weight, root to shoot dry weight ratio and root length per volume, tiller number per plant with shoot fresh weight and total fresh weight with root dry weight and root average diameter. Shoot fresh weight showed a positive significant association with total fresh weight, root fresh weight, shoots dry weight, total dry weight and root dry weight. Root fresh weight exhibited the highest positive significant correlation with total fresh weight, shoot dry weight, total dry weight, root dry weight, root to shoot fresh weight ratio and root to shoot dry weight ratio. Total fresh weight showed a positive significant correlation with total dry weight, shoot dry weight, root dry weight and root length per volume. Results are in accordance with the results of Sandhu *et al.*, (2019) who observed a positive significant correlation between shoot fresh weight, total fresh weight, shoot dry weight, total dry weight, root dry weight, root fresh weight and root volume with root length. Subudhi *et al.*, (2015) also reported the similar results.

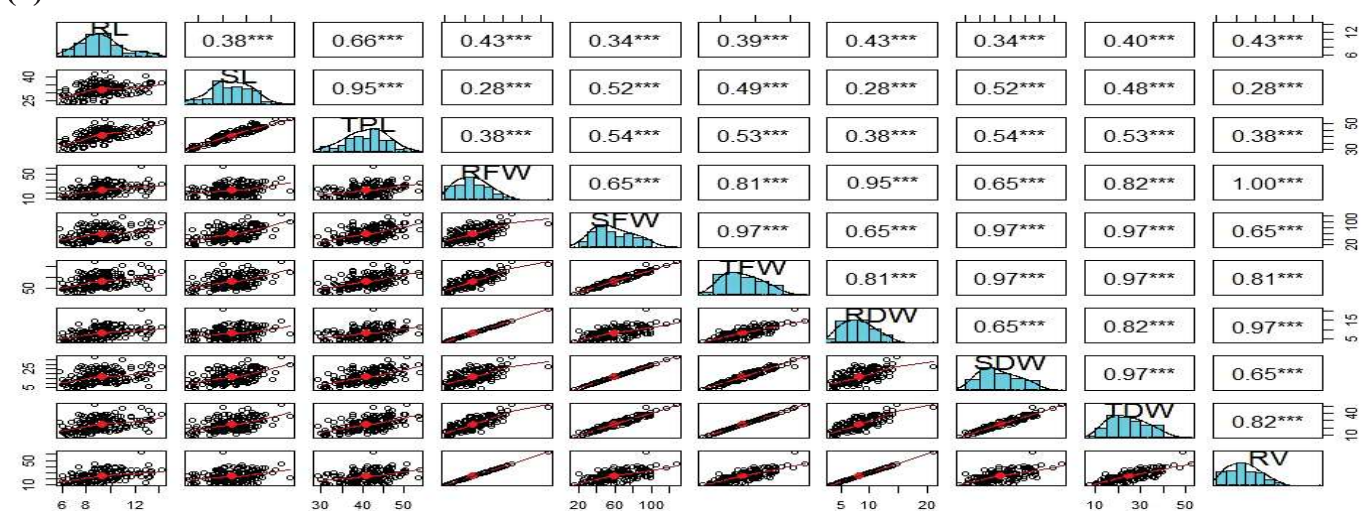
The positive and significant correlation among component traits indicated that these related traits could be used in combination for selection or initial phenotyping for seedling vigour. The root-related traits play a crucial role in nutrient acquisition, adaptation and need to be concentrated along with the yield-attributing traits (Padmashree *et al.*, 2023). Rice roots had an impact on plant growth and grain yield, which was highly connected to root dispersion as well as to root morphology (Yang, 2011). It has been reported that the uppermost layer (0–20 cm) of rice roots is crucial for moisture and nutrient absorption, which could improve the rate of grain filling, and, subsequently, the grain weight (Ishimaru *et al.*, 2017).



(a)



(b)



(c)

Figure 1: Graphical representation of correlation coefficients for root architectural traits in RILs at 60 DAS stage under polyhouse condition during Rabi 2022 (a) ICAR-IIRR, Hyderabad, (b) AHRs, Kathalagere, (c) RARS, Karjat



The rice lines TB 1, TB4, TB 8, TB 24, TB 51, TB 67 and TB 107 than the checks Sahabhabidhan, MAS 946-1, Sabita, TI-112, TI-3, TI-17. TB 1, TB 4 reported higher RL, TB 24 and TB 51 recorded higher RL and RV than the checks. These lines with the superior potential of RL and RV have a strong inherent genetic ability for performance under aerobic conditions. Root length and Root volume are important components of root architecture that are essential for survival in complex soil conditions, under deep sown conditions and primarily responsible for better adaptability and performance under DDSR, and are desirable for developing hybrid varieties for direct seeded genotypes with wide adaptability. Identifying the ideal root architecture and breeding new varieties with efficient root architecture has great potential to improve resource-use efficiency and grain yield, especially under DSR direct seeded genotypes with wide adaptability.

Conclusion

The current study was aimed to explore the root architectural related traits in rice RILs and their manifestation under water-limited conditions. We hypothesized that the variability in root architecture related traits in the RILs could be a breeding resource for improving genotypic performance under limited water conditions. We anticipate that the information will allow rice breeders to determine and select genotypes at the seedling stage. The identified lines with better root traits can be used to breed for water limiting or DDSR conditions.

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Authors' contribution

The study was planned by KMB, phenotyping the panel and analysis was done by KMB, VR, NDM, WBD, MB, PSP, MK, AAH; supervision and timely inputs were given by DB, GC, AMS, DBM, SKM, UTN, KCM; critically edited the manuscript KMB, LR.

References

- Aravind J, Shankar MS, Wankhede DP and Kaur V. 2019. Analysis of Augmented Randomised Complete Block Designs. *The Journal of Statistical Theory and Applications*, 21(4): 186-199.
- Barde MA, Mohammed MS, Oyekunle M, Usman IS and Shaahu A. 2021. Estimation of genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) Genotypes. *Magnesium (Mg²⁺)*, 4(1): 5-90.
- Corton TM, Bajita JB, Grospe FS, Pamplona RR, Asis CA, Wassmann R, Lantin RS and Buendia LV. 2000. Methane emission from irrigated and intensively managed rice fields in Central Luzon (Philippines). *Nutrient Cycling in Agrosystems*, 3(1): 58.
- Ishimaru T, Qin J, Sasaki K, Fujita D, Gannaban RB, Lumanglas PD, Simon EVM, Ohsumi A, Takai T and Kondo M. 2017. Physiological and morphological characterization of a high-yielding rice introgression line, YTH183, with genetic background of *Indica* Group cultivar, IR 64. *Field Crops Research*, 213: 89-99.
- Johnson HW, Robinson HF and Comstock RE. 1955. Estimates of genetic and environmental variability in soybean. *Journal of Agronomy*, 47(7): 314-318.
- Kommana M, Reddy DM, Amarnath K, Naik MV, Withanawasam DM, Bommisetty R, Maneesha K, Bhargavi M, Eragam A, Reddy BB and Sudhakar P. 2023. Identification of genomic regions governing moisture and heat stress tolerance employing association mapping in rice (*Oryza sativa* L.). *Molecular Biology Reports*, 50(2): 1499-515.



- Koshle R, Sarawgi AK, Sharma B, Parikh M and Ware S. 2020. Assessment of genetic variability for early seedling vigour, yield and its contributing traits in early duration genotypes of rice under direct seeded condition. *Journal of Pharmacology and Phytochemistry*, 9(6): 1225-1229.
- Kumar V and Ladha JK. 2011. Direct Seeding of Rice. Recent Developments and Future Research Needs. *Advances in Agriculture*, 1(2): 111.
- Padmashree R, Barbadikar KM, Magar ND, Balakrishnan D, Loksha R, Gireesh C, Siddaiah AM, Madhav MS, Ramesha YM, Bharamappanavara M and Phule AS. 2023. Genome-wide association studies in rice germplasm reveal significant genomic regions for root and yield-related traits under aerobic and irrigated conditions. *Frontiers in Plant Science*, 1(1): 14.
- Padmashree R, Nakul DM, Kalyani MB, Amol Phule, Honnappa, Senguttuvel P, Sheshu Madhav Maganti, Anantha MS, Divya Balakrishnan, Gireesh C, Manasa V and Loksha R. 2022. Phenotypic evaluation of seedling vigour-related traits in a set of rice lines. *Journal of Rice Research*, 15(1): 1-8.
- Panda S, Majhi PK, Anandan A, Mahender A, Veludandi S, Bastia D, Guttala SB, Singh SK, Saha S and Ali J. 2021. Proofing direct-seeded rice with better root plasticity and architecture. *International Journal of Molecular Sciences*, 22(11): 6058. <https://doi.org/10.3390/ijms22116058>.
- Pathak H, Tewari AN, Sankhyan S, Dubey DS, Mina U, Singh VK and Jain N. 2011. Direct-seeded rice: Potential, performance and problems-A review. *Current Advances in Agricultural Sciences*, 3(2): 77-88.
- Phule AS, Barbadikar KM, Maganti SM, Senguttuvel P, Subrahmanyam D, Babu MP and Kumar PA. 2019. RNA-seq reveals the involvement of key genes for aerobic adaptation in rice. *Scientific reports*, 9(1): 5235, <https://doi.org/10.1038/s41598-019-41703-2>.
- Reddy V, Mahantashivayogayya K, Diwan JR, Tembhumne BV and Pramesh D. 2022. Assessment of genetic stability of medium slender rice genotypes for yield traits using AMMI model and GGE biplot methodology over different locations of Karnataka. *International Journal of Environment and Climate Change*, 12(7): 67-75.
- Robinson HF, Comstock RE and Harvey PH. 1949. Estimates of heritability and degree of dominance in corn. *Journal of Agronomy*, 41(8): 353-359.
- Sandhu N, Yadav S, Kumar Singh V and Kumar A. 2021. Effective crop management and modern breeding strategies to ensure higher crop productivity under direct seeded rice cultivation system: A review. *Agronomy*, 11(7): 1264(1-25). <https://doi.org/10.3390/agronomy11071264>.
- Sandhu N, Yadav RB, Chaudhary B, Prasai H, Iftexharuddaula K, Venkateshwarlu C, Annamalai A, Xangsayasane P, Battan KR, Ram M and Cruz MTS. 2019. Evaluating the performance of rice genotypes for improving yield and adaptability under direct seeded aerobic cultivation conditions. *Frontiers in Plant Science*, 10: 159-172.
- Singh UM, Yadav S, Dixit S, Ramayya PJ, Devi MN, Raman KA and Kumar A. 2017. QTL hotspots for early vigor and related traits under dry direct-seeded system in rice (*Oryza sativa* L.). *Frontiers in Plant Science*, 8:286.
- Subudhi PK, Leon TD, Singh PK, Parco A, Cohn MA and Sasaki T. 2015. A chromosome segment substitution library of weedy rice for genetic dissection of complex agronomic and domestication traits. *PloS one*, 10(6): 1-22.
- Tuong TP and Bouman BAM. 2003. Rice production in water scarce environments. 2003. In *Water Productivity in Agriculture: Limits and Opportunities for Improvement*. CABIPublishing: Wallingford, UK, 2(2): 10-18.
- Yang, JC. 2011. Relationships of rice root morphology and physiology with the formation of grain yield and quality and the nutrient absorption and utilization. *Scientia Agricultura Sinica*, 44(1): 36-46.