Plant Archives Vol. 25, Supplement 1, 2025 pp. 1293-1304 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.supplement-1.176

ROOT TRAITS FOR DROUGHT TOLERANCE: A STUDY OF UPLAND RICE GENOTYPES FROM NAGALAND AND THEIR POTENTIAL FOR IMPROVING RICE (*ORYZA SATIVA*) PRODUCTIVITY

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(Date of Receiving : 09-08-2024; Date of Acceptance : 26-10-2024)

ABSTRACT

In a first-of-its-type study in the Nagaland region, 28 upland local landraces of rice were evaluated for drought resistance using root characteristics. The results showed that Longkhum Tsuk (SARS-2) exhibited the highest root length and volume, making it an ideal genotype for drought-prone areas. High genotypic and phenotypic coefficients of variation were observed for the root shoot ratio, root dry weight, root length, number of tillers per plant, effective spikelet per panicle, and grain yield per plant, with broad-sense heritability and genetic advance being high for root fresh weight, root dry weight, and root volume. Correlation and path analyses revealed positive associations between grain yield and root fresh weight, root dry weight, number of tillers per plant, effective spikelet per panicle, and 1000-grain weight, with root fresh weight, root dry weight, root length, and 1000-grain weight exhibiting positive direct effects on grain yield. These findings provide valuable insights for breeders in selecting traits for developing drought-tolerant rice varieties, highlighting the potential of root characteristics as key selection criteria for improving rice productivity in water-limited environments.

***Keywords* :** Drought, Grain yield, Nagaland region and Root characters

Introduction

In Eastern India, where upland rice comprises a large fraction of the land and facilitates subsistence farming, it is an essential feature of the rainfed agricultural system (Gairola *et al.,* 2024). The main limiting factors behind poor rice output worldwide are the escalation of drought intensity and the scarcity of high-yielding cultivars appropriate for growing during droughts. To become food self-sufficient by 2050, a high-yielding variety that is very resilient and tolerant to biotic and abiotic stresses is needed.

The problem of global climate change is becoming increasingly severe. Water scarcity is a significant environmental pressure and a primary limitation on the yield of rice. The impact of water scarcity on rice yield is likely greater than the combined impact of all other factors (Dutta *et al.,* 2017). Rice plants require approximately 3000-5000 liters of water to produce one kilogram of grain and are among the most water-demanding cereals. The intensity and length of water stress are key factors determining the magnitude of yield loss. The existing and projected global food demand is imperative for improving agricultural yields in rainfed areas that are prone to drought. To meet the demand for food for an increasing population, there is a need to develop rice varieties that can withstand drought conditions in rainfed regions (Abbas & Khalil, 2022).

Therefore, enhancing the genetic traits necessary for drought tolerance should be a primary focus of future research. The root system is the primary organ that encounters many abiotic stimuli, making it essential for reacting to stressful conditions. Root morphology is often determined by factors such as the overall dry weight, volume, root: shoot ratio and length of the roots. Changes in root morphology and function are crucial to rice performance during drought conditions and influence water uptake efficiency, hormone regulation, and nutrient absorption (Guo *et al.,* 2024). A deep root system characterized by a high length at depth is advantageous for efficiently extracting water in upland settings (Willatt & Taylor, 1978). Studying root traits, particularly under field conditions, is very challenging and thus very limited. Similarly, a few attempts have been made to study root traits using indigenous rice cultivars, but this is the first study in Nagaland in which root traits were studied to improve rice production

Materials and Methods

Experimental material and layout

Twenty-eight upland rice genotypes from Nagaland were used in the study. This study was conducted during *Kharif* 2023-2024 at the Research Farm of the Department of Genetics and Plant Breeding NU, SAS Medziphema, Nagaland, with a geographical location of 20° 45' 43"N latitude and 93° 53' 04" E longitude. The seeds were obtained from SARS Mokokchung and were maintained by the Department of Genetics and Plant Breeding. The genotypes are listed in Table 1. The genotypes were planted in PVC pipes 1 m in length and 10 cm in diameter under natural prevailing conditions during May 2023 in a completely randomized block design (CRBD) with 2 replications, as shown in Fig. 1, to study root and shoot traits to identify drought-tolerant genotypes and determine the associations between root characteristics and yield under stress conditions, as demonstrated in Fig. 2. Replication to replication had a spacing of 1.5 m. Plant-to-plant and row-to-row had 50×75 cm spacing. Only life-saving irrigation was provided during the experiment. The meteorological data was recorded for the experiment period from May 2023 to November 2023 Table 2 for temperature, rainfall, relative humidity and bright sunshine hours from the meteorological observatory of ICAR research farm Jharnapani. Soil nutrient analysis was conducted and presented in Table 3

Table 1 : List of different genotypes and their codes used in the study

Genotypes	Code	Genotypes	Code
Pfukhi Lha	PL	Thupfu Lha	TL
Sulijak	SK	Tungo	TO
Moya Chali	MC	Ngoni	NI
Moyatsak	MK	Sangmangtsuk SARS-1	SS
Chishoghi	CG	Ongpangsuk	OK
Thangmo Red	TR	Korean Tsuk	KT
Thangmo White	TW	Apuapa SARS-1	AS
Chahashye	CY	RCM-9	RM
Taposen Youli	TY	Toungmiki	TI
Kedayishefe	KF	Yarba SARS-3	YS
Shyekenyii	SI	Chali	CI
Amusu	AS	Kezie SARS-94	KS
Rosho Lha	RL	Tsushvuri	TI
Manen (Red) SARS-5	MR	Longkhum Tsuk SARS-2	LT

Table 2 : Meteorological data during the period of the experiment (May-November, 2023)

Week Range	Temperature (°C)		Relative humidity (%)		Rainfall (mm)	Sunshine (hours)
	Max	Min	Max	Min		
14th -20th May	35.8	22.8	85	49	2.5	9.2
21th -27th May	36.9	24.1	84	61	77.1	5.1
28th-03rd June	30.2	23.6	93	80	107.2	0.8
4th -10th June	30.2	23.6	92	77	63.2	2.5
11th -17th June	34.1	25.1	91	75	25.0	4.0
18th -24th June	34.0	24.9	90	65	59.6	4.6
25th -1st July	33.0	25.1	92	73	4.4	1.7
02nd -08th July	33.4	25.1	94	72	41.5	4.6
09th -15th July	34.0	25.0	93	70	123.6	4.1
16th -22nd July	34.2	25.1	92	74	112.3	3.2

23rd -29th July	32.3	25.1	91	76	73.2	1.4
30th -05th August	33.0	25.3	92	74	41.9	2.9
06th -12th August	31.5	24.6	93	81	70.6	2.1
13th -19th August	32.6	24.5	93	67	16.2	7.2
20th -26th August	35.3	25.1	92	68	21.3	6.8
27th -02nd September	33.4	24.9	93	70	18.2	6.3
03rd -09th September	32.3	24.3	94	75	48.4	4.3
10th -16th September	33.5	24.1	92	70	70.9	7.1
17th -23rd September	31.5	24.1	93	76	23.8	3.6
24th -30th September	31.0	22.7	92	67	1.2	5.8
01st -07th October	30.8	20.3	94	62	0.0	8.1
08th -14th October	29.2	21.0	94	70	1.4	4.8
15th -21st October	30.5	18.0	93	59	0.0	8.3
22nd -28th October	28.7	16.6	95	62	0.0	7.5
29th -04th November	27.7	17.7	95	67	29.1	5.2
05th -11th November	27.0	15.5	95	60	0.1	6.8

Source: ICAR Nagaland center, New Medziphema-797106, Dimapur, Nagaland**.**

Observation recorded

The observations of 11 morphological traits were recorded on randomly sampled plants from each pipe. *viz.*, root length (RL), root volume (RV), root fresh weight (RFW), root dry weight (RDW), plant height (PH), root shoot ratio (RSR), days to maturity (DM), number of tillers per plant (NTPP), effective number of spikelets per panicle (ESPP), 1000-grain weight (GW) and grain yield per plant (GYPP).

Statistical analysis

Analysis of variance (ANOVA) was used to determine the statistical significance of the means of different variables between the lines according to Fisher's method (1954). The genotypic coefficient of variation was calculated by using the formula of Burton (1951), while the phenotypic coefficient of variation was calculated by using the procedure suggested by Sivasubramanian and Menon (1973). Heritability in the broad sense was calculated by the formula given by Hanson *et al.,* (1956). The expected genetic advance for each characteristic was calculated by using the formula given by Allard and Alder (1960). Phenotypic and genotypic correlations were computed using the formula given by Chaudhary and Singh (1985). Path analysis was suggested by the procedure suggested by Wright (1921) and illustrated by Dewey and Lu (1959). However, statistical analysis was conducted in R studio using the variability package version 4.3.1 of 2023.

Results and Discussion

Analysis of variance and mean performance of the genotypes

Five root characteristics (RL, RV, RFW, RDW, and RSR) and six yield attributing characteristics (NTPP, ESPP, DM, PH, GYPP, and GW) are currently being evaluated for the 28 upland rice genotypes. Analysis of variance revealed significant variability among the genotypes for all the characteristics (Table 4). The data presented in Table 3 indicate that the LT genotype exhibited the highest RL, measuring 73.67 cm, while the YS genotype had the lowest RL, measuring 47.50 cm (Figure 3 and Figure 4). The RV was highest in LT pigs at 100 cc, whereas the lowest value was observed in TI pigs at 50 cc (Fig. 5). The RFW ranged from 76.69 g in the YS to 35.31 g in the CG. The KT genotype had a maximum RDW at 65.75 g, while the CG had a minimum RDW at 24.00 g. The RSR was highest in the SS at 3.61 g and lowest in the KF at 1.00 g.

Table 3 : Soil characteristics and properties of the experimental plots.

Physical Analysis	**Value**
Sand (%)	45.1
Silt (%)	34.5
Clay (%)	14.2
Texture classes (United States Department of Agriculture)	Sandy Loam
Chemical Analysis	**Value**
pH	5.74
Organic matter (%)	1.03

Table 4 : Analysis of variance with mean sum of squares for 11 characters

For root traits							
Source	**Df**	**RL**	**RV**	**RFW**	**RDW**	**RSR**	
REP	1	138.19	20.06	0.83	0.04	0.12	
Genotypes	27	68.19**	412.18**	207.171**	171.545**	0.369**	
Error	27	25.271	31.517	4.004	7.258	0.050	
For shoot traits							
Source	**Df**	**PH**	**NTPP**	**ESPP**	**DM**	**GYPP**	**GW**
REP	1	95.94	0.680	73.280	1.34	8.976	6.03
Genotypes	27	204.272**	0.835**	573.432**	40.312**	5.772**	8.119**
Error	27	34.64	0.198	106.39	2.146	1.520	0.224

Note: ** = Significant at the 1% level and * = Significant at the 5% level

Fig. 1 : At 60 days after planting (prestress)

Fig. 2 : At time of maturity (poststress)

Fig. 3 : Genotype LT with the longest RL

Fig. 4 : Genotype YS with the shortest RL

Fig. 5 : Root volume via the water displacement method

Analysis of the shoot traits presented in Table 5 revealed that the KF genotype currently exhibited the highest plant height, measuring 139.42 cm, whereas the KT genotype had the lowest value, at 99.25 cm. The number of tillers per plant was greatest in the RL treatment (4.84), while the AU exhibited the lowest value at 2.00. Genotype KT had the maximum number of effective spikelets per panicle (128.50), and MC had the minimum number of effective spikelets (71). The days to maturity ranged from 117.84 days in the TR to 139.08 days in the TW. The grain yield per plant was highest in KT, at 10.59 g, while that in KS was the lowest, at 2.18 g. Furthermore, the yield per plant in KT had a maximum 1000-grain weight of 24.62 g, and that in MC had a minimum value of 14.21 g.

Variability parameters for 11 traits

Investigating root traits and their genetic variability provides valuable insights for the development of drought-resistant plant cultivars. The effectiveness of breeding programs and genetic enhancements largely relies on the level of genetic variability and the degree of heritability for desired traits in germplasm. Genetic variability arises from variations in either the genetic makeup of individuals within a population or the environmental conditions in which they are cultivated. This variability is essential for withstanding biotic and abiotic influences and for demonstrating broad adaptability.

Table 5 : Mean performance of genotypes

	For root traits					For shoot traits					
Genotypes	**RL**	**RV**	**RFW**	**RDW**	**RSR**	**PH**	**NTPP**	**ESPP**	**DM**	**GYPP**	**GW**
PL	66.66	56.33	46.33	32.14	1.58	131.84	3.00	73.00	119.34	4.07	15.45
SK	56.50	89.16	46.89	31.67	1.45	111.84	3.17	102.17	122.17	4.59	15.70
MC	58.25	57.50	51.81	39.12	2.10	105.25	2.50	**71.00**	124.25	3.62	**14.21**
MK	63.16	60.83	42.42	31.92	1.86	116.67	3.00	92.85	123.50	4.77	15.72
CG	67.50	56.25	**35.31**	**24.00**	1.01	128.84	2.67	85.25	122.00	**2.66**	15.20
TR	72.50	84.99	55.29	43.92	2.42	134.50	3.17	72.00	**117.84**	3.41	14.50
TW	71.58	62.50	53.33	43.30	1.34	121.84	2.75	86.25	**139.08**	5.36	16.52
CY	68.50	61.67	41.93	26.92	1.43	121.17	2.67	94.34	121.17	4.54	15.25
TY	67.33	69.00	63.91	42.75	2.26	112.17	3.75	116.67	133.00	4.94	16.45
KF	63.58	72.00	49.44	30.95	**1.00**	139.42	3.42	83.58	124.75	3.98	16.26
SI	68.25	84.34	55.14	40.34	1.90	131.67	2.67	96.92	119.17	3.21	14.57
AU	66.00	53.00	52.91	39.65	2.47	131.84	**2.00**	77.00	121.00	2.86	15.56
RL	69.75	96.50	63.58	51.65	1.55	111.92	**4.84**	119.50	120.00	5.95	17.40
MR	65.83	89.16	59.45	47.42	1.68	113.34	3.92	113.35	122.17	5.86	17.53
TL	64.50	91.25	56.87	44.15	2.30	124.00	2.84	103.34	119.00	4.05	15.79

TO	66.67	70.06	55.84	43.01	1.75	119.50	3.00	108.50	120.00	5.09	15.83
NI	68.67	80.83	57.75	48.34	1.83	118.00	3.67	95.83	123.17	5.86	14.85
SS	68.50	80.84	57.75	45.84	**3.61**	119.17	2.67	98.17	123.00	5.28	15.06
OK	67.00	80.00	43.92	31.67	1.30	107.83	3.00	109.34	122.34	3.10	13.20
KT	66.00	91.25	75.59	**65.75**	1.87	**99.25**	3.75	**128.50**	125.75	**10.59**	**24.62**
AS	71.00	84.34	62.16	49.75	1.81	118.83	3.67	93.00	121.00	6.44	15.99
RM	57.50	88.33	73.73	50.45	2.23	120.50	3.17	109.00	120.50	3.77	15.38
TI	62.34	88.00	66.18	38.50	1.47	126.92	3.75	106.67	123.75	3.84	15.65
YS	**47.50**	82.50	**76.69**	59.00	1.36	105.67	4.67	128.34	120.50	6.23	18.50
CI	61.00	75.00	65.73	43.00	1.96	123.00	3.50	124.50	127.75	2.19	15.70
KS	65.12	81.00	62.00	46.20	2.30	126.50	2.42	98.08	125.75	2.18	14.57
TI	54.71	**50.00**	62.73	44.10	2.04	110.25	3.17	124.08	119.34	5.12	16.75
LT	**73.67**	**100.00**	57.89	44.30	1.51	**134.34**	2.67	110.00	126.75	3.13	14.74
Overall mean	64.98	76.48	57.01	42.13	1.83	120.21	3.19	100.75	123.14	4.52	15.96
CD (%)	10.31	11.52	4.10	5.52	0.45	21.16	0.91	3.07	2.53	12.07	0.97
CV	7.73	7.34	3.51	6.39	12.84	10.23	13.90	1.19	27.23	4.89	2.96

🟩 Highest value 🟥 west value

It is crucial to analyze the genetic variability parameters, including the mean, range, phenotypic coefficient of variation, genotypic coefficient of variation, heritability (broad sense), and genetic advance, for various characteristics. These parameters provide valuable information on the extent of genetic diversity present in the germplasm, which is essential for identifying potential breeding lines and predicting the response to selection.

Table 6 provides insights into the genetic components of the variations. The root length (RL) exhibited a phenotypic coefficient of variation of 46.73% and a genotypic coefficient of variation of 21.46%, with a heritability of 45% and a genetic advance as a percentage of the mean of 9.95%. These findings are in accordance with those of Hoque *et al.* (2021), who reported moderate values for these coefficients, suggesting some degree of variability that could be exploited through selection.

The root volume (RV) showed a phenotypic coefficient of variation of 19.45% and a genotypic coefficient of variation of 18.01%, with a high heritability of 85% and a genetic advance as a percentage of the mean of 34.35%. This indicates that a large portion of the phenotypic variation in root volume can be attributed to genotypic variation, which is a favorable condition for selection in breeding programs. The high genetic advance suggested that there is good potential for improving this trait through selection, as supported by Kanbar *et al.* (2009).

The root fresh weight (RFW) and root dry weight (RDW) exhibited high heritability values of 96% and 91%, respectively, with genetic advances as a percentage of the mean of 35.70% and 42.46%, respectively. These findings suggest that selection for these traits could be effective in breeding programs.

The root: shoot ratio (RSR) showed a phenotypic coefficient of variation of 34.94% and a genotypic coefficient of variation of 21.73%, with a heritability of 38% and a genetic advance as a percentage of the mean of 27.85%. Similarly, Dong *et al.,* (2006) reported that the root volume, root: shoot ratio, and root distribution pattern have various functional significance.

Table 6 : Genetic component of variations for all 11 traits.

For root traits						
Traits	**Range**	**Mean±Sem**	**PCV (%)**	**GCV (%)**	**Heritability (%)**	**Genetic Advance (%)**
RL	47.50-73.67	64.98±3.55	46.73	21.46	45.00	9.95
RV	50.00-100.00	76.49±3.97	19.45	18.01	85.00	34.35
RFW	35.31-76.69	57.01±1.41	18.01	17.67	96.00	35.70
RDW	24-65.75	42.12±1.90	22.44	21.50	91.00	42.46
RSR	1.005-3.615	1.86±0.35	34.94	21.73	38.00	27.85

For shoot traits						
PH	99.25-134.34	120.21±4.16	9.09	7.66	71.00	13.29
NTPP	2.00-4.84	3.19±0.31	22.51	17.67	61.00	28.56
ESPP	71-128.50	100.75±7.29	18.29	15.16	68.00	25.89
DM	117.83-139.08	123.14±1.03	3.75	3.54	89.00	6.92
GYPP	2.18-10.59	4.52±0.87	42.18	32.19	58.00	50.61
GW	14.21-24.62	16.10±0.27	13.15	12.92	96.00	26.17

It is essential to note that while high heritability and genetic advancement are promising for selection, they do not guarantee success in breeding programs. The effectiveness of selection also depends on the accuracy of the phenotypic measurements and the presence of any genotype–environment interactions that may affect the expression of the trait.

When analyzing the shoot traits, the phenotypic and genotypic coefficients of variability for plant height (PH) were 9.09% and 7.66%, respectively, with a high heritability of 71% and a moderate genetic advance as a percentage of the mean of 13.29%. The number of tillers per plant (NTPP) exhibited phenotypic and genotypic coefficients of variability of 22.51% and 17.67%, respectively, with a heritability (broad sense) of 61% and a genetic advance as a percentage of the mean of 28.56%.

The phenotypic and genotypic coefficients of variability for the trait ear length per plant (ESPP) were 18.29% and 15.16%, respectively, with a heritability of 68% and a high genetic advance as a percentage of the mean of 25.89%. In addition, 3.75% and 3.54% of the dry matter (DM) samples exhibited phenotypic and genotypic variability, respectively, with a high heritability of 89% and a low genetic advance as a percentage of the mean of 6.92%.

The phenotypic and genotypic coefficients of variability for the trait grain yield per plant (GYPP) were 42.18% and 32.19%, respectively, with a heritability of 58% and a genetic advance as a percentage of the mean of 50.61% under stress conditions. These findings are consistent with those of Tesfaye (2021), who reported high heritability and genetic advancement for traits such as the number of grains per spikelet and grain yield per plant due to additive genes.

Grain weight (GW) exhibited phenotypic and genotypic coefficients of variability of 13.15% and 12.92%, respectively, with the highest heritability (broad sense) of 96% and a genetic advance as a percentage of the mean of 26.17%. These results are in line with previous studies, which reported high heritability estimates for 1000-grain weight (Osman, 2012; Bisne *et al.,* 1970; Talekar *et al.,* 2022). The high heritability and genetic advance of GW suggest that this trait is likely influenced by additive gene action and can be improved through selection.

It is essential to note that while high heritability and genetic advancement are promising for selection, they do not guarantee success in breeding programs. The effectiveness of selection also depends on the accuracy of the phenotypic measurements and the presence of any genotype–environment interactions that may affect the expression of the trait.

Association studies between different characteristics through correlation and path analysis

The correlations of grain yield with root traits and other yield-related components are presented in Table 7. Significant positive associations were detected between grain yield and root fresh weight, root dry weight, number of tillers per plant, effective spikelet per panicle, and 1000-grain weight at both the genotypic and phenotypic levels. These findings are in agreement with those of Kanbar *et al.* (2009), who suggested that selecting fresh root weight, the root: shoot ratio, and effective tillers per plant may be advocated for improving grain yield.

There is substantial evidence supporting the significant association of grain yield with the number of tillers per plant, effective spikelet per panicle, and 1000-grain weight in rice (Yadav *et al.,* 1970; Yadav *et al.,* 2011; Haradari, 2017). These traits are consistently identified as having a positive correlation and direct effect on grain yield, suggesting their importance in rice breeding programs aimed at yield improvement.

Root length was significantly positively correlated with grain yield at both the genotypic and phenotypic levels. However, a negative correlation was observed between root length and fresh weight, as well as between root length and effective spikelet per panicle, at both the genotypic and phenotypic levels. This finding suggested that while root length is positively associated with grain yield, it may be negatively related to other root traits and yield components.

Table 7 : Correlations among all 11 morphological characteristics of the 28 genotypes

	GYP	RL	RV	RFW	RDW	RSR	NTP	PH	ESPP	DM	SW
GYP	1	-0.217	0.258	**0.495****	**0.667****	-0.114	**0.763****	**-0.797****	**0.444****	0.102	**0.958****
RL		1	0.09	**-0.364****	-0.155	0.003	**-0.318***	**0.471****	**-0.394****	0.246	-0.247
RV			1	**0.530****	**0.548****	0.008	**0.539****	-0.088	**0.525****	-0.099	0.202
RFW				1	**0.910****	**0.379****	**0.652****	**-0.351****	**0.694****	0.078	**0.533****
RDW					1	**0.436****	**0.602****	**-0.456****	**0.598****	0.058	**0.642****
RSR						1	-0.422**	0.073	-0.053	-0.14	-0.171
NTP							1	-0.451**	**0.680****	-0.063	**0.557****
PH								1	-0.590**	-0.085	-0.525**
ESPP									1	0.139	**0.560****
DM										1	0.136
SW											1

Note: ** = Significant at 1% and * = Significant at 5% level of significance

Significant positive association 🟩 Significant negative association 🟥

It has been projected that rice genotypes with deep root systems will be more drought tolerant than those with shallow root systems. According to Mohd *et al.* (2019), deep and coarse roots are significant rice protection strategies for reducing the negative impact of drought on productivity. However, an extensive root system may not necessarily result in increased yield under limited water conditions (Sahebi *et al.*, 2018). A larger root system may lead to faster extraction of available water, which could have a detrimental influence on grain output.

Root volume showed a strong positive correlation at both the genotypic and phenotypic levels with root fresh weight, root dry weight, number of tillers per plant, and effective spikelet number per panicle. The correlation coefficient between root volume and root dry weight suggested a moderate positive relationship, suggesting that as the root volume increased, the root dry weight tended to increase as well, although the relationship was not very strong. These findings are in accordance with the results reported by Suwarto *et al.* (2019), Dey *et al.* (2021), and Kumar *et al.* (2023).

Root fresh weight was significantly positively correlated at both the genotypic and phenotypic levels with root dry weight, number of tillers per plant, effective spikelet per panicle, and 1000-grain weight. However, there was a positive correlation only at the genotypic level with the root: shoot ratio. In contrast, it was negatively correlated with plant height at both the genotypic and phenotypic levels. This finding suggested that a healthy root system may contribute to improved reproductive development and grain filling but may not necessarily be associated with increased plant height.

Root dry weight was significantly positively correlated at both the genotypic and phenotypic levels with the root: shoot ratio, number of tillers per plant, effective spikelet per panicle, and 1000-grain weight. However, it was negatively correlated with plant height. The root: shoot ratio was positively correlated at both the genotypic and phenotypic levels with only the fresh weight and dry weight of the roots but was negatively correlated at the genotypic level with the number of tillers per plant.

Plant height was positively correlated at both the genotypic and phenotypic levels with maximum root length only. However, it was negatively correlated with the effective spikelet per panicle and 1000-grain weight. This suggests that taller plants may not necessarily contribute to a greater number of effective tillers or increased grain yield.

The number of tillers per plant was positively correlated at both the genotypic and phenotypic levels with the effective spikelet per panicle and 1000-grain weight. However, it was negatively correlated with plant height at both the genotypic and phenotypic levels. This finding suggested that an increased tiller number, associated with increased yield, might be correlated with decreased plant stature.

The effective spikelet number per panicle was positively correlated with the 1000-grain weight, root volume, fresh weight, dry weight, and number of tillers per plant at both the genotypic and phenotypic levels. However, it was negatively correlated with the maximum root length and plant height at both the phenotypic and genotypic levels.

Days to maturity showed a non-significant association with all of the other characteristics at both the phenotypic and genotypic levels. This finding suggested that days to maturity are not significantly associated with other traits; therefore, we can focus on improving yield-related traits without directly affecting maturity timing.

These findings provide deeper insights into the correlation of characters and establish fruitful associations among them, which could be utilized in further breeding programs.

Table 8 : Path analysis of the associations between root traits and yield

	MRL	**RV**	**RFW**	**RDW**	**RSR**	**NTPP**	**PH**	**ESPP**	**DM**	**GW**	**GYPP**
MRL	0.35	-0.02	-0.49	-0.17	-0.01	0.45	-0.36	0.19	-0.12	-0.01	-0.21
RV	0.03	-0.22	0.72	0.63	-0.01	-0.77	0.06	-0.25	0.05	0.01	0.25
RFW	-0.12	-0.11	**1.36**	1.05	-0.66	-0.93	0.27	-0.33	-0.04	0.03	0.495**
RDW	-0.05	-0.12	1.24	1.15	-0.76	-0.86	0.35	-0.28	-0.03	0.04	0.667**
RSR	0.002	-0.002	0.51	0.50	**-1.77**	0.61	-0.05	0.02	0.07	-0.01	-0.114
NTPP	-0.111	-0.119	0.891	0.696	0.752	-1.439	0.349	-0.328	0.032	0.041	0.763**
PH	0.165	0.019	-0.479	-0.527	-0.135	0.648	-0.775	0.284	0.044	-0.042	-0.797**
ESPP	-0.138	-0.115	**0.948**	0.690	0.094	-0.979	0.457	-0.482	-0.073	0.042	0.444**
DM	0.08	0.021	0.106	0.067	0.246	0.088	0.066	-0.067	-0.524	0.010	0.102
GW	-0.066	-0.05065	0.688	0.73	0.34	-0.83	0.45	-0.28	-0.07	0.07	0.958**
Residuals 0.16											

Note: ** = significant at the 1% level and * = significant at the 5% level

🟩 Maximum positive direct effect 🟥 Minimum negative direct effect.

Path analysis, as shown in Table 8, revealed that four out of eleven traits had positive and direct effects on grain yield at the genotypic level. The characteristic with the highest positive direct effects on grain yield was root fresh weight, followed by root dry weight and root length.

Root fresh weight had the greatest positive direct effect on grain yield, which is consistent with the findings of previous studies. For example, Sasmal (1987) and Kumar *et al.* (2023) highlighted the positive direct effect of fresh root weight on grain yield across different generations and hybrid rice, respectively. Root dry weight also had a significant positive direct effect on grain yield, which is in agreement with the findings of Fageria and Oliveira (2014), who reported a positive association between root dry weight and grain yield in upland rice.

On the other hand, the root-to-shoot ratio had the most negative direct effect on grain yield, followed by the number of tillers, plant height, days to maturity, effective spikelets per panicle, and root volume. These findings suggest that these traits may have a negative impact on grain yield; therefore, breeding programs should focus on improving root fresh weight, root dry weight, and root length to increase grain yield.

Path analysis also revealed the greatest positive indirect effect on the trait root fresh weight via effective spikelets per panicle, and the greatest negative indirect effect was registered for the number of tillers per plant via effective spikelets per panicle at the genotypic level. The residual effect was 0.16, which indicated that 16% of the variability was caused by variable factors other than the different root traits and yield-attributing traits.

These findings provide valuable insights into the relationships between root traits and yield-related components and can be used to develop more effective breeding strategies to improve grain yield in rice.

Screening out of the genotypes best suited to drought conditions

The genotypes best suited for drought-like situations can be identified and screened out by selecting those root characteristics that have a positive effect on grain yield per plant and are most essential for surviving in drought-like situations.

The studies conducted and the results inferred in Table 9 provide information about the genotypes studied that could yield more and be the best suited for drought situations. In the present study, five genotypes-longkhum Tsuk (SARS-2), Korean Tsuk, Yarba SARS 3, Rosho Lha, and Toungmiki-appeared to be promising genotypes with drought resistance characteristics.

These genotypes were identified based on their root characteristics, which have a positive effect on grain yield per plant and are essential for survival in drought-like situations. The selection of these genotypes can be useful in breeding programs aimed at developing drought-tolerant rice varieties.

The identification of drought-tolerant genotypes is crucial for improving rice productivity in water-scarce environments. By selecting genotypes with desirable root traits, breeders can develop varieties that can thrive in drought-prone areas, ensuring food security and sustainability.

Table 9 : Screening out of the genotypes best suited to drought conditions

Genotypes Identified suitable for drought situations.	Characters selected for screening out genotypes.	Remarks
1 LT 2. TR 3. TW	Root length	Longer roots access deeper soil layers when moisture is limited in the upper layers of the soil.
1. LT 2. KT 3. SK	Root Volume	Significant positive correlation with number of tillers per plant.
1. KT 2. YS 3. RL	Root dry weight	Significant positive correlation with grain yield and maximum positive direct effect on yield.
1. YS 2. KT 3. TI	Root fresh weight	Significant positive correlation with grain yield and maximum positive direct effect on yield.

Karpagam *et al.* (2016) highlighted the significance of several root characteristics in enhancing drought resistance and identified various rice genotypes as superior in terms of combining these qualities. This finding is consistent with the findings of other studies that have shown that drought-resistant rice varieties often exhibit greater root thickness, volume, and deeper root systems, which enable better water uptake under drought conditions (Pushpam *et al.*, 2018).

Root dry weight and fresh weight are also important indicators of root biomass and are associated with a plant's ability to access water from deeper soil layers and maintain yield stability during water stress (Thanh *et al.*, 1999; Ferreira *et al.*, 2020). Taken together, these findings suggest that breeding programmes aimed at developing drought-tolerant rice varieties should focus on selecting genotypes with desirable root traits, such as increased root thickness, volume, and depth, as well as greater root dry weight and fresh weight.

The importance of root characteristics in drought resistance is well established, and selecting genotypes with these traits can be a key strategy for improving rice productivity in water-scarce environments. By combining these traits with other desirable characteristics, breeders can develop varieties that thrive in drought-prone areas, ensuring food security and sustainability.

Conclusion

In this pioneering study evaluating 28 upland rice landraces in Nagaland, we identified Longkhum Tsuk (SARS-2) as a promising genotype for drought-prone areas due to its superior root length and volume. Our findings emphasize the importance of root characteristics in breeding drought-tolerant rice varieties, offering valuable insights for future crop improvement.

List of abbreviations

These are the list of characters

RL (root length), RV (root volume), RFW (root fresh weight), RDW (root dry weight), RSR (root shoot ratio), NTPP (number of tillers per plant), ESPP (effective spikelet per panicle), DM (days to maturity), PH (plant height), GYPP (grain yield per plant) and GW (grain weight).

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Acknowledgment

I am ever grateful for the help and support provided by the Department of Genetics and Plant Breeding at the School of Agricultural Science, Nagaland University. I would like to thank SARS Mokokchung for providing seeds. I express my gratitude to Prof. R.B. Tiwari, Prof. K. K. Jha, Dr. H.P. Chaturvedi, Dr. Pankaj Saha, and Dr. Ashim Debnath for their scholarly suggestions and guidance.

Declaration

Ethical Approval and Consent to Participate:

Our study did not require ethical approval, and all the authors agree.

Consent of Publication:

Participants provided consent for publication

Availability of supporting data:

Supporting data are available upon request.

Competing interests/Author contributions:

No competing interests were declared. Conceptualization of research (MBS, SS); Designing of the experiments (MBS, SS); Contribution of experimental materials (MBS, SS); Execution of field experiments and data collection (SS); Analysis of data and interpretation (SS); Preparation of manuscript (MBS, SS, SJ).

Funding

This research was supported by the Department of Genetics and Plant Breeding at SAS, Nagaland University.

References

Abbas, A., & Khalil, R. (2022). Exploring new techniques and strategies for enhancing rice drought tolerance. *Biological and Agricultural Sciences Research Journal*, **2022**(1), 4.

Allard, A. W. and Alder, H. L. (1960). The effect of incomplete penetrance on the estimation of recombination values. *Heredity*. 15 (2): 263-282.

Babu V. R., Shreya K., Dangi K. S., Usharani G. and Shankar A. S. (2012). Correlation and path analysis studies in popular rice hybrids of India. *International Journal of Scientific and Research Publications*, **2**(3): 1-5.

Bisne R., Sarawgi A. K. and Verulkar S. B. (1970). Study of heritability, genetic advance and variability for yield contributing characters in rice. *Bangladesh Journal of Agricultural Research*, **34**(2): 175–179.

Burton, G.W. (1951). Quantitative inheritance in pearl millet- *Agronomic Journal*, **43**: 409-417.

Chaudhary F. S. and Singh R. (1985). An evaluation of response models. Sankhyā, *The Indian Journal of Statistics,* **Series B**, 280-289.

Datta, A., Ullah, H., & Ferdous, Z. (2017). Water management in rice. *Rice production worldwide*, 255-277.

Dewey, D. R. and Lu, K. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production, *Agronomy Journal*, **51**(9): 515-518.

Dey S., Kumar R., Battan K.R., Chhabra A. K. and Reddy A. L. (2021). Study of Coefficient of Variation, Heritability and Genetic Advance for Different Traits of Rice Genotypes Grown under Aerobic Condition. *International Journal of Bioresource and Stress Management,* **12**(5): 426–430.

Dong, L., Wang, L., Zhang, Y., Zhang, Y., Deng, X. and Xue, Y. (2006). An auxin-inducible F-box protein CEGENDUO negatively regulates auxin-mediated lateral root formation in Arabidopsis. *Plant Molecular Biology,* **60**:122–133.

Dong, Y., Bao, Q., Gao, M., Qiu, W. and Song, Z. (2022). A novel mechanism study of microplastic and as cocontamination on indica rice (*Oryza sativa* L.). *Journal of Hazardous Materials*, **421**: 126694.

Fageria, N. K. and Oliveira, J. P. (2014). Nitrogen, phosphorus and potassium interactions in upland rice. *Journal of Plant Nutrition*, **37**(10): 1586–1600.

Ferreira, L. M., de Oliveira, C. M., Arruda, L. N., Braga, R. P., Tavares, O. C. H., de Souza, S. R. and Santos, L. A. (2020). Characteristics of the root system in two Brazilian upland rice varieties which exhibit contrasting behavior toward drought tolerance. *Semina: Ciências Agrárias*, **41**(2): 421-434.

Fisher, R. (1954). Discussion of the analysis of variance with various binomial transformations. *Biometrics*, **10**(1): 140-151.

Gairola A., Kumar V., Kumar S., Kumar S., Patel A. and Singh S. (2024). Upland rice: A water-efficient rice production system in India. *Biotica Research Today*, **6**(1): 46–50.

Guo, Y., Du, Y., Niu, X., Ma, Y., Song, G., Cao, C. and Siddique, K.H. (2024). Comparison of Drought Stress Responses in Large-and Small-Rooted Rice Lines: Physiological, Anatomical, and Hormonal Changes. *Journal of Plant Growth Regulation*, 1-15.

Hanson, G., Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies on yield in segregating population of Korean Lespedeza. *Agron Journal*, **48**: 268-274.

Haradari, C. (2017). Character association and path coefficient analysis for yield component traits in rice (*Oryza sativa* L.) under moisture stress condition at vegetative stage. *Current Trends in Biomedical Engineering and Biosciences*, **2**(5): 78-81.

Hazman, M. and Brown, K. M. (2018). Progressive drought alters architectural and anatomical traits of rice roots, *Rice*. **11**: 1-16.

Hoque, N., Islam, M. Z., Zarin, F., Mahmud, N., Rahman, M., & Biswas, B. (2021). Analysis of genetic variability and character relationship in rice (*Oryza sativa* L.) seed and seedling traits. *Journal of Bioscience and Agriculture Research,* **28**(2): 2389-2398.

Kanbar, A., Toorchi, M. and Shashidhar, H. (2009). Relationship between root and yield morphological characters in rainfed low land rice (*Oryza sativa L.*). *Cereal Research Communications*, **37**(2): 261-268

Karpagam, V., Jebaraj, S. and Rajeswari, S. (2016). Combining ability and heterosis analysis for drought tolerant traits in rice (*Oryza sativa* L.). *Journal of Applied and Natural Science*, **8**(2): 674–682.

Keerthiraj, B. and Biju, S. (2020). Genetic variability, heritability and genetic advance of yield and lodging-related traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, **11**(4): 1093-1098.

Kumar, A.R., Kant, R., Vennela, M. and Varma, D.D. (2023). Correlation and path coefficient studies of three-line rice hybrids. *International Journal of Environment and Climate Change*, **13**(12): 367–374.

Kumar, J., Chand, P., Singh, S., Khilari, K. and Kumar, M. (2020). Genetic variability, heritability and genetic advance for yield and its contributing traits in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, **9**(2): 385–387.

Kumar, S., Bhuvaneswari, S., Devi, E. L., Sharma, S. K., Ansari, M. A., Singh, I. M., Singh, Y. R. and Prakash, N. (2017). Estimation of Genetic Variability, Correlation and Path analysis in short duration Rice Genotypes of Manipur. *Journal of AgriSearch*, **4**(2): 112-118

Mirza, M.M.Q., Warrick, R.A. and Ericksen, N.J. (2003). The implications of climate change on floods of the Ganges, Brahmaputra and Meghna rivers in Bangladesh. Climatic Change., **57**: 287-31.

Mohd, I.A., Nurasyikin, Z., Tuan, N.A.R., Puteri, D.E.Z., Wickneswari, R. and Noraziyah, A.A.S. (2019). Drought yield QTL (qDTY) with consistent effects on morphological and agronomical traits of two populations of new rice (*Oryza sativa*) lines. *Plants*, **8**(6): 186.

Osman, K. (2012). Genetic variability for yield and related attributes of upland rice genotypes in semiarid zone (Sudan). *African Journal of Agricultural Research*, **7**(33): 4613-4619.

Price, A.H. and Tomos, A.D. (1997). Genetic dissection of root growth in rice (*Oryza sativa* L.). II: mapping quantitative trait loci using molecular markers, *Theoretical and Applied Genetics*, **95**: 143-152.

Pushpam, R., Manonmani, S., Varthini, N.V. and Robin, S. (2018). Studies on yield, root characters related to drought tolerance and their association in upland rice genotypes. *Electronic Journal of Plant Breeding*, **9**(3): 856-862.

Ratna, M., Begum, S., Husna, A., Dey, S. and Hossain (2015). Correlation and path coefficients analyze in Basmati rice. *Bangladesh Journal of Agricultural Research*, **40**(1): 153–161.

Sahebi, M., Hanafi, M.M., Rafii, M.Y., Mahmud, T.M.M., Azizi, P., Osman, M., Abiri, R., Taheri, S., Kalhori, N., Shabanimofrad, M., Miah, G. and Atabaki, N. (2018). Improvement of Drought Tolerance in Rice (*Oryza sativa L.*): Genetics, Genomic Tools, and the WRKY Gene Family. *BioMed Research International,* **1**: 3158474.

Saito, K., Asai, H., Zhao, D., Laborte, A.G. and Grenier, C. (2018). Progress in varietal improvement for increasing upland rice productivity in the tropics. *Plant Production Science*, **21**: 145-158.

Sasmal, B. (1987). Relationship of root and shoot characters in parent F1 and F2 populations of rice. *Journal of Agronomy and Crop Science*, **159**(4): 260–263.

Singh, A., Singh, V., Singh, A., Vikram, P., Shamim, M., Singh, N., Singh, V. and Singh, S. (2014). Genetic variability among traits associated with grain yield of rice (*Oryza sativa* L.) exposed to drought at flowering stage. *African Journal of Agricultural Research*, *9*(16), 1252–1264.

Sivasubramanian, S. and Menon, M. (1973). Phenotypic coefficient of variation in plant traits. *Plant Archives*, **20**(1): 2529-25321

Suwarto, N., Dinuriah, I., Pramesthi, R. and Soraya, N. (2019). Root growth dynamics and grain yield of ten new plant types of rice lines under aerobic and flooded condition. IOP Conference Series. *Earth and Environmental Science*, **250**: 012082.

Talekar, S.C., Praveena, M.V. and Satish, R.G. (2022). Genetic variability and association studies for grain yield and yield related traits in rice (*Oryza sativa* L.). *International Journal Plant Sciences*, **17**(2): 202–208.

Tesfaye, A. (2021). Genetic variability, heritability, and genetic advance estimates in garlic (*Allium sativum*) from the Gamo Highlands of Southern Ethiopia. *International Journal of Agronomy*, **56**(2): 1-8.

Willatt, S.T. and Taylor, H.M. (1978). Water uptake by soya-bean roots as affected by their depth and by soil water content. *The Journal of Agricultural Science*, **90**(1), 205–213.

Wright, S. (1921). Systems of mating. II. The effects of inbreeding on the genetic composition of a population. *Genetics*, **6**(2): 124.

Yadav, S.K., Pandey, P., Kumar, B. and Suresh, B.G. (2011). Genetic architecture, interrelationship and selection criteria for yield improvement in rice (*Oryza sativa* L.). *Pakistan Journal of Biological Sciences*, **14**(9): 540–545.

Yadav, S.K., Suresh, B.G., Pandey, P. and Kumar, B. (1970). Assessment of genetic variability, correlation and path association in rice (*Oryza sativa* L.). *Journal of Bio-Science*, **18**(0): 1–8.