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RESEARCH ARTICLE

Prediction of upland rice yield under drought stress using machine learning

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Abstract

Upland rice farming in Nagaland faces erratic rainfall and prolonged drought that severely limit productivity. We hypothesized that readily measurable phenotypic traits can reliably predict grain yield without molecular data. This study aimed to compare predictive performance of machine learning models; identify key phenotypic traits influencing yield; and develop a practical selection framework for regional breeding programs operating under resource constraints. Twenty eight indigenous upland rice (*Oryza sativa* L.) genotypes were evaluated under rainfed, drought conditions during the 2023–2024 kharif season using a completely randomized block design with two replications. Eighteen phenotypic traits encompassing root architecture, shoot morphology, phenological development and yield components were measured. Three supervised machine learning approaches-multiple linear regression (MLR), LASSO regression and Random Forest (RF)-were applied to predict grain yield per plant (GYPP). Specific root length (SRL), root dry weight (RDW) and test weight (TW) emerged as significant yield predictors across all three models. The MLR model achieved the highest accuracy (R^2 = 0.986; root mean square error [RMSE] = 0.296), while LASSO demonstrated superior generalization (cross-validated R^2 = 0.874; CV-RMSE = 0.342). Random Forest confirmed findings through nonlinear analysis (R^2 = 0.729). The convergence of traits across models validates their robustness. Phenotypic trait-based prediction provides a cost-effective approach for selecting drought-resilient genotypes without molecular data, offering practical value for resource-limited breeding programs in Nagaland and similar rainfed environments.

Keywords: drought stress; grain yield prediction; machine learning; phenotypic traits; random forest; rice genotypes

Introduction

Rice (*Oryza sativa* L.) is a staple food for over half the global population and remains critical for food security in India. In Nagaland, upland rice is extensively cultivated under rainfed conditions, where erratic rainfall and prolonged drought during critical growth stages such as tillering and flowering severely limit productivity and jeopardize smallholder farmer livelihoods (1). Identifying and developing drought-resilient, high-yielding genotypes adapted to this agroecological zone is essential for sustainable agriculture in this region.

Phenotypic traits such as root dry weight (RDW), specific root length (SRL), test weight (TW) and tiller number are readily measurable in field conditions and are strongly associated with drought tolerance (2). While classical linear regression has been traditionally employed in agronomic research to quantify trait-yield relationships, machine learning approaches such as LASSO regression and random forest offer advantages in managing multicollinearity and capturing nonlinear trait interactions (3). These models have shown strong predictive performance in various rice studies and are increasingly being used alongside classical regression methods (4). Notably, these models require only field-derived phenotypic data, making them ideal for resource-constrained breeding programs lacking molecular tools. However, few studies have compared the predictive ability of classical and modern modelling approaches specifically for upland rice adapted to rainfed, drought-prone environments like Nagaland, nor have most models been tailored to localized germplasm or specific stress conditions.

We hypothesized that readily measurable phenotypic traits under drought conditions can reliably predict grain yield without requiring molecular data. This study therefore aimed to: (a) compare predictive performance of Multiple Linear Regression (MLR), LASSO regression and random forest models; (b) identify key phenotypic traits predictive of grain yield; and (c) develop a practical selection framework for resource-constrained breeding programs in Nagaland.

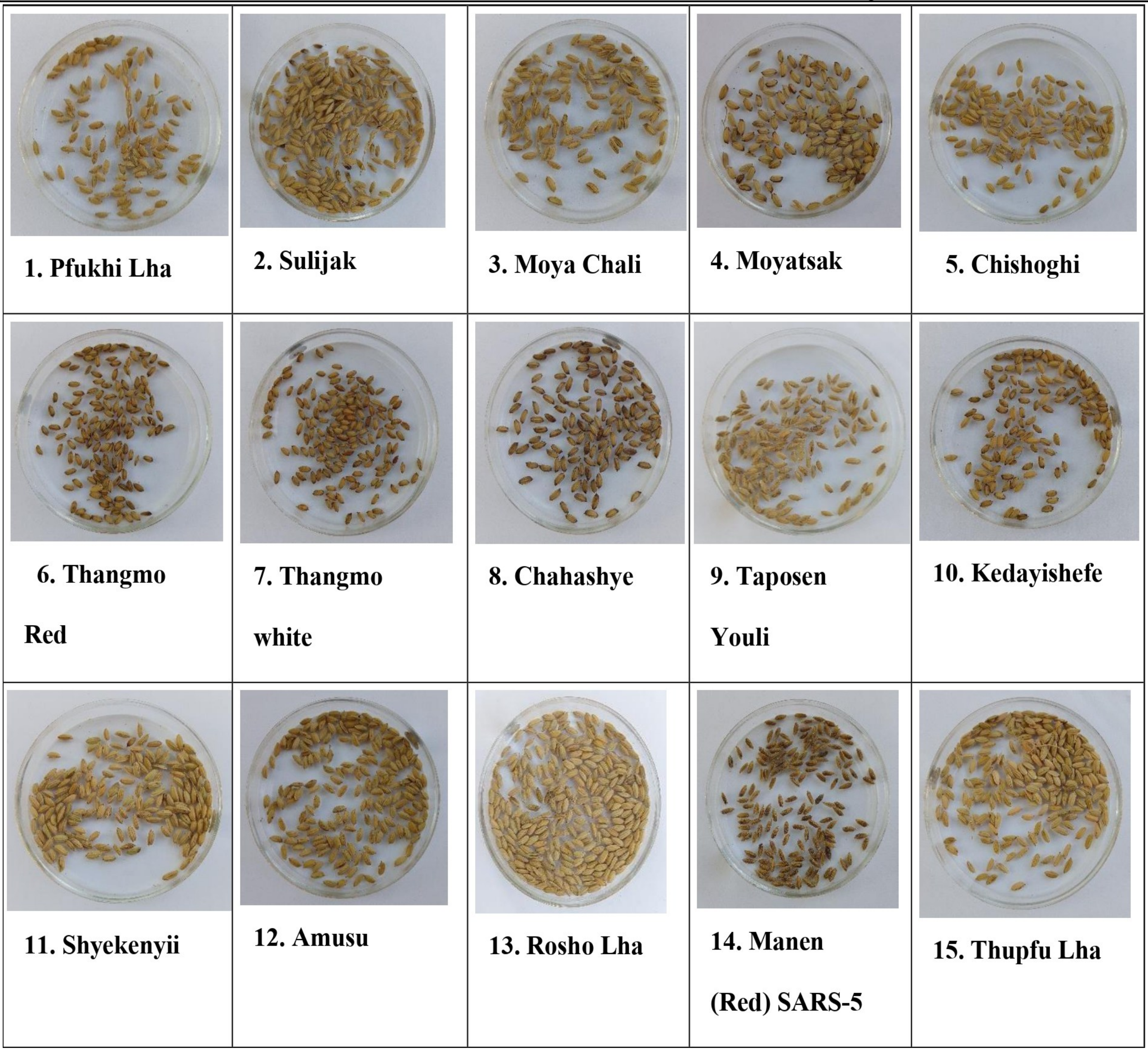
Materials and methods

Experimental material and location

Twenty eight indigenous upland rice (*Oryza sativa* L.) genotypes (Table 1 & Fig. 1) from Nagaland were selected based on their

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

Genotypes	Place of collection
Pfukhi Lha	State Agricultural Research Station (SARS), Mokokchung, Nagaland
Sulijak	SARS Mokokchung
Moya Chali	SARS Mokokchung
Moyatsak	SARS Mokokchung
Chishoghi	SARS Mokokchung
Thangmo Red	SARS Mokokchung
Thangmo White	SARS Mokokchung
Chahashye	SARS Mokokchung
Taposen Youli	SARS Mokokchung
Kedayishefe	SARS Mokokchung
Shyekenyii	SARS Mokokchung
Amusu	SARS Mokokchung
Rosho Lha	SARS Mokokchung
Manen (Red) SARS-5	SARS Mokokchung
Thupfu Lha	SARS Mokokchung
Tungo	SARS Mokokchung
Ngoni	SARS Mokokchung
Sangmangtsuk SARS-1	SARS Mokokchung
Ongpangsuk	SARS Mokokchung
Korean Tsuk	SARS Mokokchung
Apuapa SARS-1	SARS Mokokchung
RCM-9	SARS Mokokchung
Toungmiki	SARS Mokokchung
Yarba SARS-3	SARS Mokokchung
Chali	SARS Mokokchung
Kezie SARS-94	SARS Mokokchung
Tsushvuri	SARS Mokokchung
Longkhum Tsuk SARS-2	SARS Mokokchung



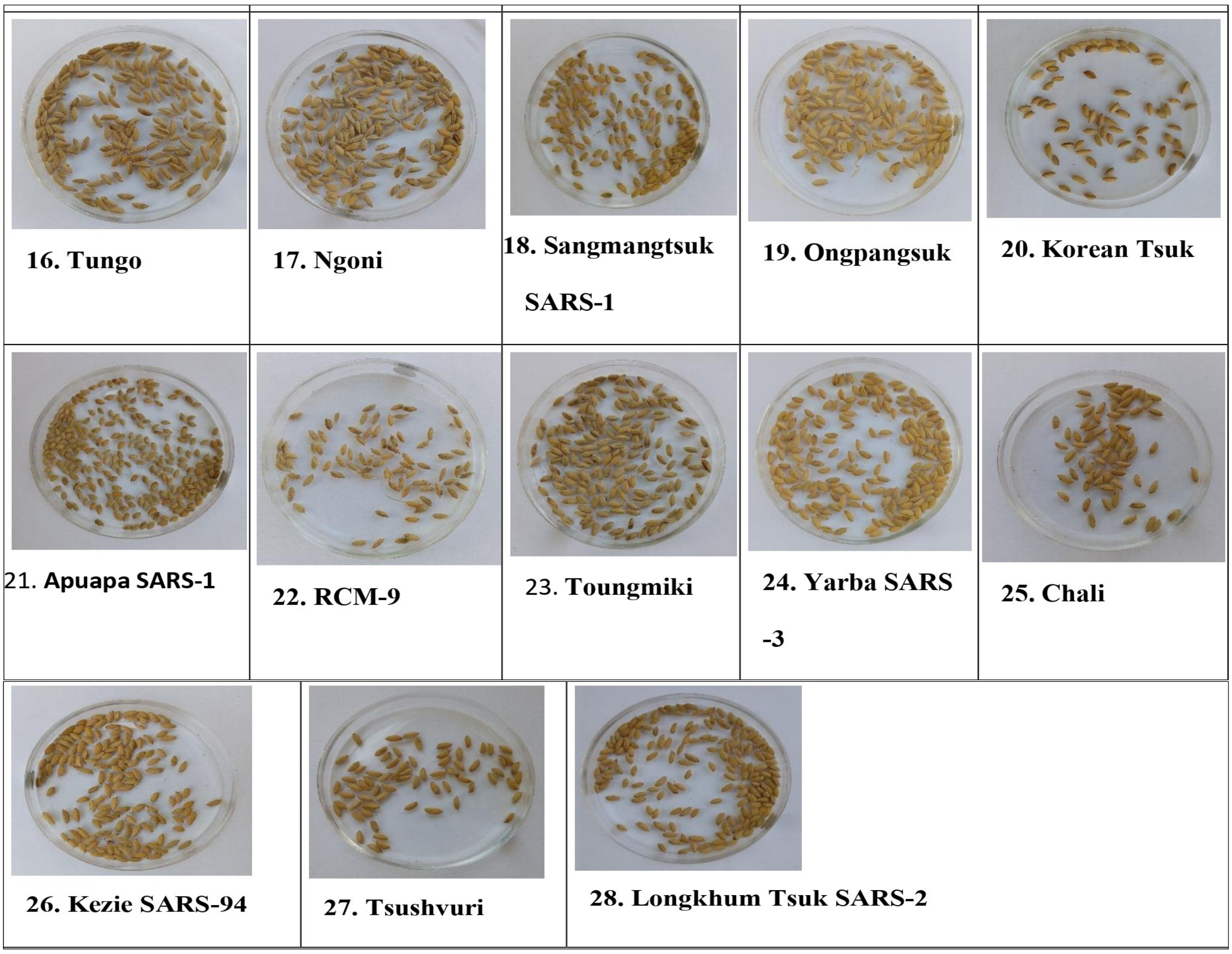


Fig. 1. Phenotypic variation among various genotypes used in research.

ecological significance and diversity under rainfed conditions. These genotypes were sourced from the State Agricultural Research Station (SARS), Mokokchung and maintained by the Department of Genetics and Plant Breeding, School of Agricultural Sciences, Nagaland University. The experiment was conducted during the Kharif season (2023–2024) at Nagaland University, Medziphema Campus (20°45′43″N, 93°53′04″E), which experiences natural rainfed conditions prone to drought stress.

Experimental design and phenotypic evaluation

The 28 genotypes were evaluated under rainfed conditions using a Completely Randomized Block Design (CRBD) with two replications. Each experimental plot measured 5.0 m × 4.0 m, comprising three rows with 12 plants per plot (four plants per row in PVC pipes), spaced 50 cm × 50 cm apart to promote root expansion and stress response development. Consistent cultural and agronomic practices were maintained throughout the experimental period to minimize environmental variation.

Eighteen phenotypic traits were measured on randomly selected plants: Root Traits [Maximum Root Length (MRL, cm), Root Volume (RV, cm^3), Root Fresh Weight (RFW, g), Root Dry Weight (RDW, g), Root-to-Shoot Ratio (RSR), Specific Root Length (SRL, cm/g)]; Shoot Traits [Plant Height (PH, cm), Shoot Length (SL, cm), Panicle Length (PL, cm), Number of Tillers per Plant (NTP), Number of Panicles per Plant (NPPP), Effective Number of Spikelets per Panicle (ESPP)]; Phenological Traits [Days to 50 % Flowering (DTF), Days to Maturity (DM)]; and Yield and Stress Traits [1000-Grain Weight (TW, g), Grain Yield per Plant (GYPP, g), Harvest Index (HI, %), Percentage Moisture Loss (% ML)]. All measurements followed standard procedures and average values per genotype across replications were used for statistical analysis.

Multicollinearity assessment

Before developing predictive models, the dataset was screened for missing values and outliers. Variance Inflation Factor (VIF) analysis was performed using the car package in R to evaluate multicollinearity among the 18 phenotypic predictors. Variables with VIF > 5.0 were flagged for redundancy. Pearson correlation coefficients were computed to identify trait pairs with r > 0.80, ensuring trait suitability for modelling.

Supervised learning models for yield prediction

All statistical analyses were conducted using R Studio (version 2024.12.1). Three supervised learning models were developed and compared to predict grain yield per plant (GYPP).

Multiple linear regression (MLR)

The MLR model identifies linear trait-yield relationships using the equation:

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_k X_k + \varepsilon \quad \text{(Eqn 1)}$$

Where Y is grain yield per plant (GYPP), β_0 is the intercept, β_i are regression coefficients for each phenotypic trait (X_i) and ε is the random error term. Regression coefficients were estimated using Ordinary Least Squares (OLS) and assessed for significance at α = 0.05 using two-tailed t-tests.

LASSO regression

LASSO (Least Absolute Shrinkage and Selection Operator) regression was implemented using the glmnet package with the penalty function:

$$\text{Minimize } [\Sigma_i{=}1^n (y_i - \hat{y}_i)^2 + \lambda \Sigma_{j=1}^{p} |\beta_j|] \quad \text{(Eqn 2)}$$

Where λ is the regularization parameter controlling feature selection and coefficient shrinkage. The optimal λ was selected via 10-fold cross-validation to minimize cross-validated error. This approach performs simultaneous regularization and variable selection, managing multicollinearity effectively.

Random forest regression

Random forest regression was implemented using the random forest package with 500 decision trees (ntree = 500) and 5 features evaluated at each split (mtry = 5). Variable importance was ranked using percentage increase in mean squared error (% IncMSE) and node purity increase (IncNodePurity). The model captures nonlinear trait interactions and provides robust variable rankings.

Model validation and performance assessment

Model performance was rigorously evaluated using 10-fold cross-validation through the caret package. Each model was trained on 80 % of data and validated on 20 %, a standard ratio in supervised learning. Bootstrap resampling with 1000 iterations generated 95 % confidence intervals for regression coefficients. Key performance metrics evaluated were: (1) coefficient of determination (R^2), (2) root mean square error (RMSE), (3) cross-validated R^2 (CV-R^2), (4) cross-validated RMSE (CV-RMSE) and (5) residual diagnostics. Model accuracies were compared to determine the most effective method for yield prediction and trait prioritization under drought stress conditions.

Results

Twenty-eight indigenous upland rice genotypes from Nagaland demonstrated significant phenotypic diversity when subjected to drought stress, as depicted in Fig. 1. Table 1 contains the list of genotypes evaluated along with their respective codes. Through multiple linear regression analysis, three phenotypic traits were identified as statistically significant positive predictors of grain yield per plant (GYPP) in upland rice under drought conditions (Table 2). SRL had the most substantial impact ($\beta = 35.09$, $p < 0.001$), followed by root dry weight (RDW; $\beta = 0.108$, $p < 0.001$) and test weight (TW; $\beta = 0.172$, $p < 0.001$).

Linear regression plots showing the relationships between GYPP and these three significant traits are displayed in Fig. 2, with the model accounting for 97.8 % of the yield variation (adjusted $R^2 = 0.978$). Diagnostic plots confirmed that the assumptions of normality, linearity and homoscedasticity were met for the multiple linear regression model (Fig. 3). Model validation demonstrated strong predictive performance, with a cross-validated R^2 of 0.891 and a CV-RMSE of 0.315. The assessment of multicollinearity revealed that all variance inflation factors were below 3.2 (mean VIF = 2.09), which is well under the critical threshold of 5.0 (Supplementary Table 1). Bootstrap resampling with 1000 iterations verified the stability of coefficients through narrow 95 % confidence intervals for all three significant predictors (Supplementary Table 2).

The Least Absolute Shrinkage and Selection Operator (LASSO) regression retained the same three traits as significant yield predictors with adjusted coefficients (Table 3 & 4). Specific root length remained the most influential predictor (SRL = 34.85), followed by root dry weight (RDW = 0.098) and test weight (TW = 0.172), while 15 non-informative traits were penalized towards zero. Cross-validation showed superior generalization performance for the LASSO model (CV-R^2 = 0.874; CV-RMSE = 0.342) with a lower overfitting index (0.049) compared to multiple linear regression (Supplementary Table 3).

Random forest regression further supported these findings by identifying SRL, RDW and TW as the most significant predictors based on both percentage increase in mean squared error (% IncMSE) and increase in node purity (Fig. 4). Trait importance scores from the random forest model demonstrated that the same three traits as evident from table 3 dominated across variable importance metrics. The consistent ranking of traits across

Table 3. Standardized regression coefficients of significant phenotypic traits (SRL, RDW, TW) influencing grain yield per plant in upland rice under drought conditions based on multiple linear regression analysis

Trait	Standardized Coefficient
SRL	0.68
RDW	0.55
TW	0.22

SRL= Specific root length, RDW= Root dry weight, TW= Test weight.

Table 2. Multiple linear regression model for predicting grain yield per plant (GYPP) in upland rice under drought stress (n = 56). Coefficient estimates are presented with significance levels (*$p < 0.05$, ** $p < 0.01$, *** $p < 0.001$*), multicollinearity diagnostics and bootstrap 95% confidence intervals. The model showed high explanatory power (adjusted $R^2 = 0.978$) and accuracy (CV-RMSE = 0.315)

Trait	Estimate	Std_Error	t_Value	P_Value	VIF	CI_Lower_95	CI_Upper_95	Std_Coefficient	Significance
SRL	35.091	3.516	9.981	<0.001	2.89	28.142	42.04	0.68	***
RDW	0.108	0.019	5.775	<0.001	2.67	0.071	0.146	0.55	***
TW	0.172	0.039	4.426	<0.001	1.87	0.095	0.249	0.22	***
MRL	0.018	0.012	1.473	0.153	2.34	-0.005	0.041	0.087	
RV	0	0.005	0.072	0.943	1.89	-0.009	0.01	0.005	
RFW	-0.012	0.018	-0.669	0.509	3.12	-0.047	0.023	-0.043	
RSR	0.097	0.105	0.921	0.365	1.45	-0.111	0.305	0.078	
NTP	0.021	0.129	0.166	0.87	1.78	-0.232	0.274	0.012	
PH	-0.013	0.01	-1.321	0.198	2.91	-0.033	0.007	-0.089	
ESPP	-0.002	0.005	-0.348	0.731	1.56	-0.011	0.007	-0.023	
DM	-0.001	0.014	-0.093	0.926	1.23	-0.029	0.027	-0.007	
DTF	-0.007	0.012	-0.616	0.543	2.45	-0.031	0.017	-0.045	
SL	-0.008	0.006	-1.415	0.169	2.03	-0.019	0.003	-0.098	
PL	0.015	0.022	0.674	0.506	1.67	-0.028	0.058	0.054	
NPPP	-0.054	0.067	-0.813	0.424	2.34	-0.186	0.078	-0.067	
HI	-0.947	11.364	-0.083	0.934	1.34	-23.221	21.327	-0.006	
ML	0.01	0.005	1.818	0.081	1.92	0	0.02	0.134	

MRL = Maximum root length, RV = Root volume, RDW = Root dry weight, RSR = Root-to-shoot ratio, NTP = Number of tillers per plant, PH = Plant height, ESPP = Effective spikelets per panicle, DM = Days to maturity, TW = 1000-grain weight, DTF = Days to 50% flowering, SL = Shoot length, PL = Panicle length, NPPP = Number of panicles per plant, SRL= Specific root length, HI= Harvest Index and ML= Percentage Moisture Loss.

Table 4. Coefficient estimates of phenotypic traits selected by LASSO regression for predicting grain yield per plant in upland rice under drought stress. Zero coefficients indicate traits excluded by the model during regularization

Trait	LASSO Coefficient
MRL	0.0199
RV	0
RFW	-0.0029
RDW	0.0984
RSR	0.0778
NTP	-0.0054
PH	-0.0134
ESPP	-0.0013
DM	-0.0034
TW	0.1717
DTF	-0.0079
SL	-0.0065
PL	0.0073
NPPP	-0.0324
SRL	34.8492
HI	0.4952
ML	0.0093
(Intercept)	-4.2678

MRL = Maximum root length, RV = Root volume, RDW = Root dry weight, RSR = Root-to-shoot ratio, NTP = Number of tillers per plant, PH = Plant height, ESPP = Effective spikelets per panicle, DM = Days to maturity, TW = 1000-grain weight, DTF = Days to 50% flowering, SL = Shoot length, PL = Panicle length, NPPP = Number of panicles per plant, GYPP = Grain yield per plant, SRL= Specific root length, HI= Harvest Index and ML= Percentage Moisture Loss.

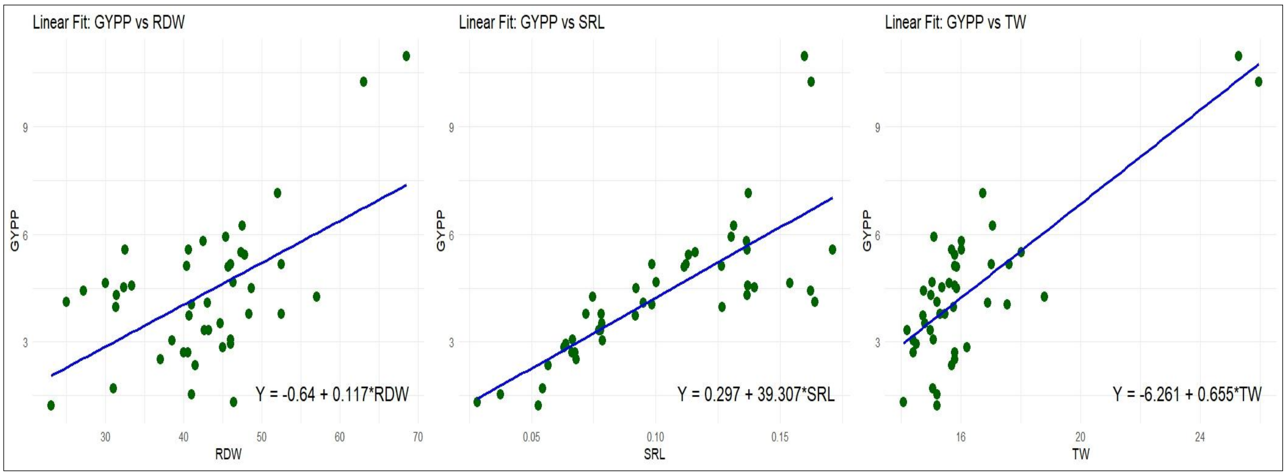


Fig. 2. Linear regression plots showing the relationship between grain yield per plant (GYPP) and three significant traits — Root Dry Weight (RDW), Specific Root Length (SRL) and Thousand-Seed Weight (TW).

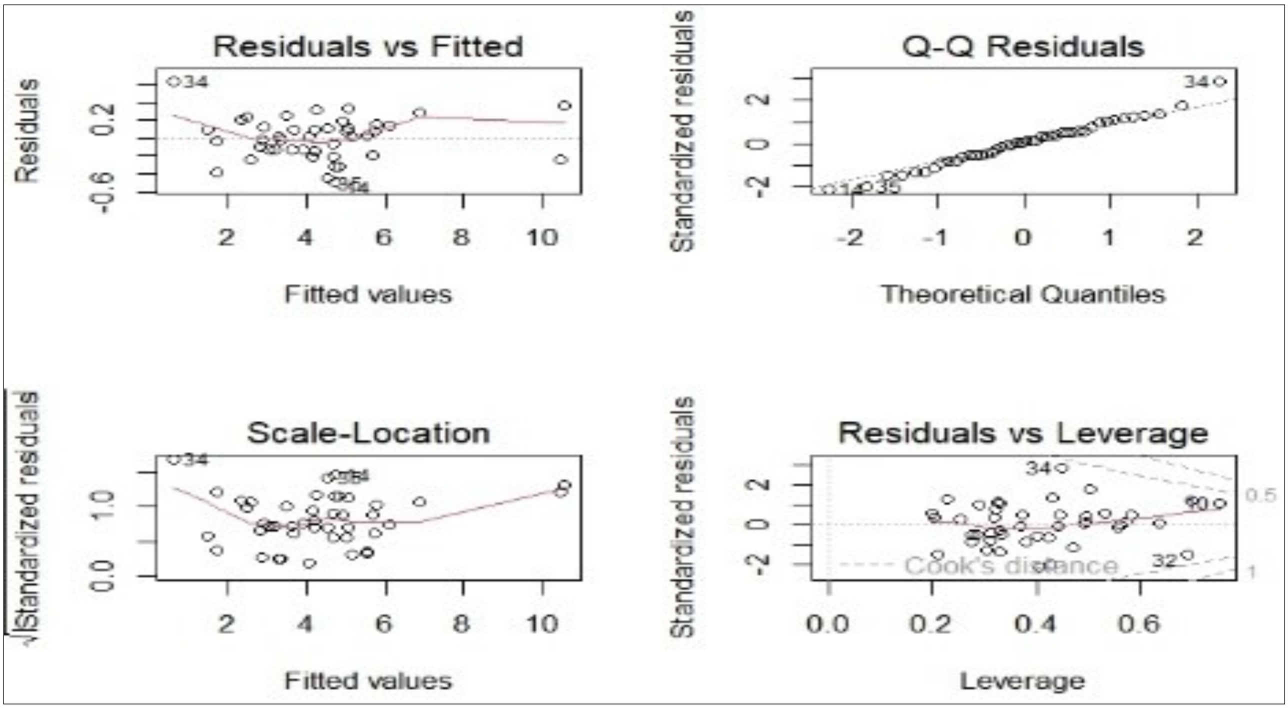
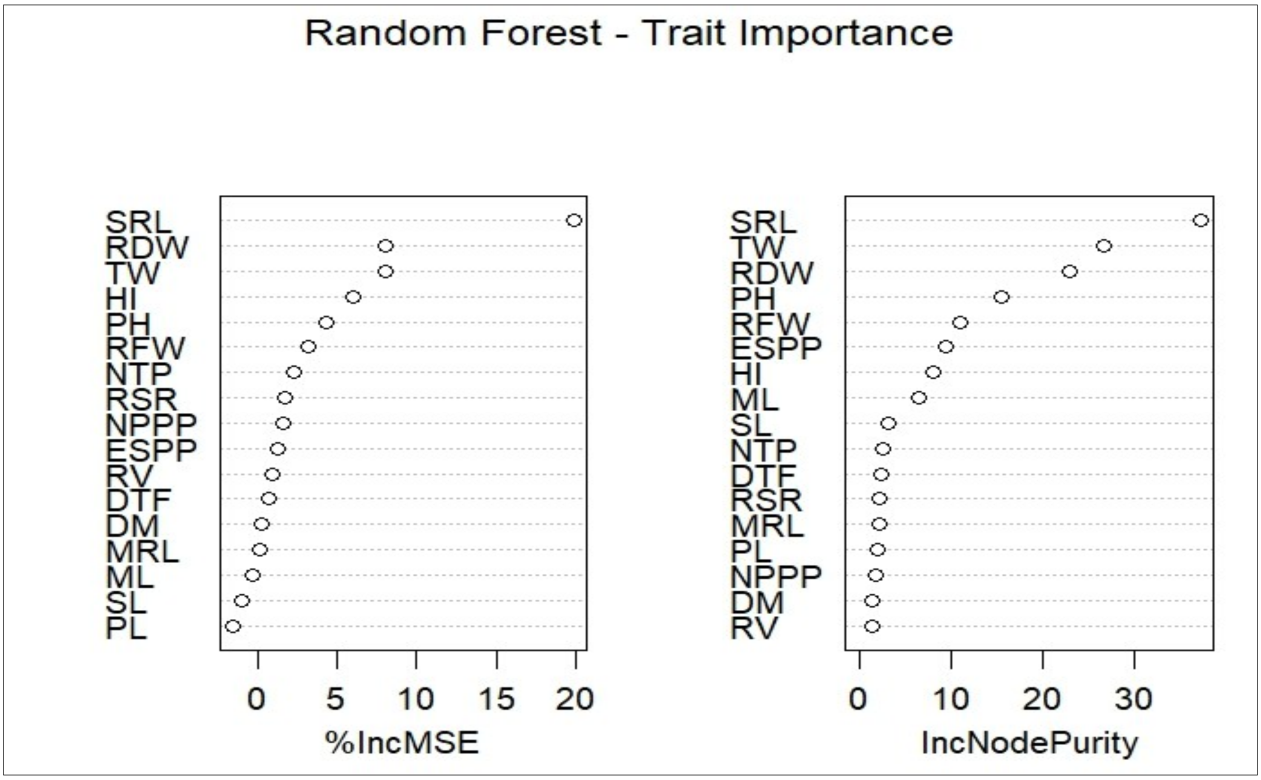


Fig. 3. Diagnostic plots of the multiple linear regression model showing residual patterns: (top left) residuals vs. fitted values, (top right) Q-Q plot for normality, (bottom left) scale-location plot for homoscedasticity and (bottom right) leverage vs. residuals.



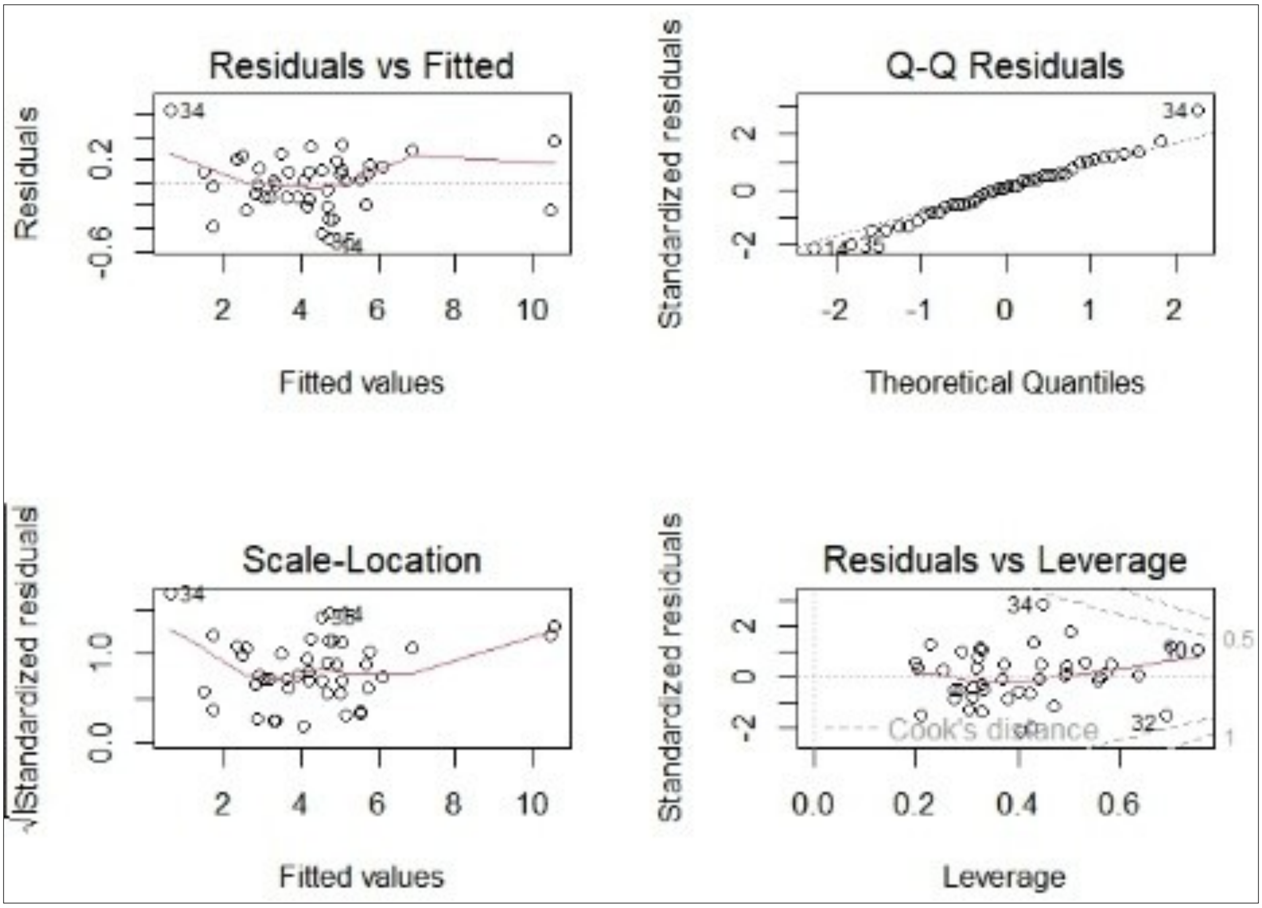


Fig. 4. Trait importance scores from the Random Forest model based on % IncMSE and IncNodePurity.

multiple linear regression, LASSO and random forest models provides strong evidence for the reliability of SRL, RDW and TW as selection indices for drought resilience in upland rice.

Discussion

RDW, TW and SRL emerged as crucial phenotypic traits that enhance yield under drought stress, with findings validated through multiple statistical approaches. Root dry weight indicates a plant's ability to develop a robust root system and improve deep soil water uptake, thereby maintaining yield stability during water scarcity (5). Test weight, which reflects grain size or density, positively affects yield by facilitating effective grain filling under drought conditions, highlighting efficient internal resource use during stress (6). Specific root length, which measures root length relative to biomass, represents a plant's ability to efficiently explore the soil for water and nutrients (7). A higher specific root length allows better access to soil moisture, supporting growth when water is limited. Most notably, SRL ($p < 0.001$) exhibited the largest effect size (coefficient = 35.09), suggesting that finer and longer roots per unit dry weight may provide a distinct advantage by enhancing soil penetration and water acquisition efficiency, a crucial trait for maintaining yield under rainfed, moisture-limited conditions. Collectively, these three traits highlight the physiological basis of yield resilience and represent promising targets for selection in upland rice breeding programs aimed at drought-prone environments.

In contrast, several traits demonstrated weak or insignificant contributions to yield prediction under the experimental conditions. Root fresh weight (RFW), number of tillers per plant (NTP), plant height (PH) and panicle length (PL) were not statistically significant, suggesting their contributions to yield were weak or inconsistent. Although maximum root length (MRL) and SL exhibited positive trends, they did not achieve statistical significance. These findings indicate that simple measures of root size may be less predictive than metrics reflecting root efficiency, such as SRL. The dominance of SRL as the primary predictor reflects its fundamental role in drought adaptation through enhanced soil exploration efficiency per unit root biomass investment (5). High SRL genotypes maximize water extraction capacity while minimizing carbon allocation to structural root tissues, a critical advantage under water-limited conditions. Root dry weight represents the absolute water uptake capacity, with larger root systems providing greater buffering against soil water depletion. Test weight integration as a key predictor indicates that drought tolerance encompasses not only water acquisition mechanisms but also grain filling efficiency under terminal stress, suggesting coordinated physiological responses spanning both vegetative and reproductive phases.

While this study demonstrates considerable potential for phenotypic trait-based yield prediction, several limitations warrant careful consideration. The single-season, single-location experimental design limits generalizability across diverse environmental conditions and years. Environmental heterogeneity within the experimental site, including micro-variations in soil moisture, fertility gradients and localized drought intensity, likely influenced trait-yield relationships but could not be quantified in the current design. The model's high R^2 value of 0.986 suggested that nearly 99 % of yield variation was accounted for by phenotypic traits; however, the large coefficient of SRL might dominate the model and multicollinearity could affect coefficient stability. Future investigations should incorporate environmental covariates such as volumetric soil water content, leaf water potential measurements, or normalized difference vegetation index (NDVI) to enhance model accuracy and biological interpretation. Multi-year and multi-location studies would strengthen the generalizability and reliability of these findings across Nagaland's diverse agroecological zones.

These findings align with earlier studies highlighting the significance of belowground traits in maintaining yield stability under drought conditions (2, 3). Previous researchers identified root dry weight and SRL as crucial predictors of upland rice yield using LASSO-based modeling (2). Similarly, another study demonstrated that test weight and root vigor traits possess strong predictive power in machine-learning-based yield estimation (3). The convergence of our results with previous research underscores the robustness and generalizability of SRL, RDW and TW as selection indices for drought resilience. Several traits, including root volume (RV), days to maturity (DM) and number of tillers per plant (NTP), diminished to insignificance in the LASSO-optimized prediction framework, highlighting their limited relevance for phenotypic selection under drought stress. This automated exclusion enhances model parsimony, allowing breeders to concentrate on fewer and more reliable performance indicators.

The random forest model effectively captured significant trait-yield relationships and demonstrated robust performance despite nonlinearity and multicollinearity among traits. Although the random forest model exhibited slightly lower predictive power (R^2 = 0.729) compared to the Multiple Linear Regression (R^2 = 0.986) and LASSO models, it offers the advantage of identifying complex, nonlinear interactions that linear methods might miss. This balance between interpretability and predictive performance makes Random Forest a valuable tool for trait prioritization and genotype ranking, particularly in phenotypically diverse datasets such as upland rice under drought stress. The consistency of trait rankings across all three statistical approaches—MLR, LASSO and Random Forest—provides strong evidence for the robustness of SRL, RDW and TW as reliable selection indices. This convergence validates the biological relevance of identified traits and strengthens confidence in their utility for genotype prioritization in breeding programs.

Overall, this analysis supports the use of root-based traits, particularly SRL and RDW, as core selection indices for drought resilience in upland rice breeding programs. The practical implication is that breeders can reliably select high-yielding, drought-adapted genotypes using simple, cost-effective field measurements without requiring molecular data or advanced technologies. This approach is especially beneficial for regional breeding programs operating under resource constraints, such as those in Nagaland, where access to genomic tools is limited. Integrating phenotypic trait-based selection with supervised machine learning provides a scalable, evidence-based strategy for developing climate-resilient rice varieties that can sustain productivity under increasingly erratic rainfall patterns.

Conclusion

This study demonstrates that three phenotypic traits SRL, RDW and TW reliably predict grain yield in upland rice under drought stress using machine learning approaches. These easily measurable, cost-effective traits provide a practical selection framework for breeding programs in resource-limited regions like Nagaland, eliminating the need for molecular data. The consistency of findings across multiple linear regression, LASSO and random forest models validates the robustness of these traits as reliable indices for drought resilience. Integrating phenotypic trait-based selection with supervised learning techniques offers a scalable, evidence-based strategy for developing climate-resilient rice varieties. This approach directly enhances climate-resilient agriculture in upland ecosystems while supporting food security and farmer livelihoods in moisture-limited agroecological zones.

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Authors' contributions

MBS and SS carried out conceptualization of the research, design of the experiments and contribution of experimental materials. Execution of field experiments and data collection, data analysis and interpretation and preparation of the manuscript were performed by SS. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

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