

MORPHOPHYSIOLOGICAL TRAIT PROFILING AND MULTIVARIATE CHARACTERIZATION OF RICE (*ORYZA SATIVA* L.) GENOTYPES FOR GRAIN YIELD

Vipul G. Baldaniya¹, Ajay V Narwade², Mayur R. Thesiya³, Jasmee R. Patel^{4*}, Pathik B. Patel⁵

¹Assistant Professor, Plant Physiology, K. K. Institute of Agricultural Sciences and Research, Ganpat University, Mehsana, Gujarat-384012, India

²Professor and Head, Department of Plant Physiology, Navsari Agricultural University, N. M. College of Agriculture, Navsari, Gujarat-396450, India

³Assistant Professor, Department of Plant Pathology, B.A. College of Agriculture, Anand Agricultural University, Anand, Gujarat-388110, India

^{4*}Assistant Professor, Department of Plant Pathology, Junagadh Agricultural University, Junagadh, Gujarat-362001, India.

⁵Principal and Dean, Navsari Agricultural University, N. M. College of Agriculture, Navsari, Gujarat-396450, India

*Corresponding Author: Jasmee R. Patel, Email: drjasmee@gmail.com

ABSTRACT

Rice is the largest cereal crop in the world. Increased rice productivity depends on canopy development, physiological traits, photosynthetic activity, phenology, sink formation and assimilate partitioning. A field experiment was conducted at Navsari Agricultural University, Gujarat, India, during the Kharif seasons of 2020 and 2021 to evaluate 20 rice genotypes in a randomized block design with three replications. Various morpho-physiological, phenological and yield-related traits were recorded. Pooled means identified IET-28705 as the most consistently superior genotype, recording the highest leaf area (70.13 cm²), leaf area index (0.234), net photosynthetic rate (44.30 $\mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$), stomatal conductance (0.446 mol H₂O m⁻² s⁻¹), transpiration rate (5.73 mmol H₂O m⁻² s⁻¹), tiller number (18.93 plant⁻¹), panicle length (30.42 cm), test weight (26.68 g), grain yield (26.63 g plant⁻¹) and harvest index (49.13%). At the genotype level, grain yield showed strong positive correlation with tiller number ($r=0.965$), LAI ($r=0.957$), leaf area ($r=0.956$), photosynthetic rate ($r=0.952$), stomatal conductance ($r=0.929$), transpiration rate ($r=0.922$) and panicle length ($r=0.854$). A parsimonious three-predictor regression model explained 94.6% of the variation in pooled grain yield ($R^2=0.946$; adjusted $R^2=0.936$); path analysis identified tiller number as the largest direct contributor (0.844), followed by harvest index (0.157). The hierarchical clustering separated the genotypes into four phenotypic groups, with IET-28705, IET-28701, IET-28696 and IET-28704 forming a high-performance cluster. These integrated results support the use of canopy, gas-exchange and sink traits for better genotype identification.

KEYWORDS: Rice, morpho-physiological traits, yield, correlation, path analysis, hierarchical clustering

INTRODUCTION

Rice (*Oryza sativa* L.) is the world's largest cereal crop and is eaten as a staple by approximately 90% of people in Southeast Asia, Africa and Latin America. Rice is an everyday dietary staple in many countries and is mostly consumed by humans, with more than half of the world's population depending on it as their main source of carbohydrates. Rice is regarded as one of the primary dietary crops (20%) among the cereals. Asian countries are expected to account for more than 70% of the predicted growth in the consumption of rice worldwide. Rice is grown in almost 120 countries around the world, but China and India account for more than half of the world's rice production. In the world, rice cultivation uses 155 million hectares of land and produces 596 million tonnes of output and productivity. India used 47 thousand hectares of land for rice cultivation, which was second in terms of production after China [1].

Rapid population increase and economic development, on the other hand, were exerting pressure on food production to expand. To meet the growing world population, which is estimated to be 10 billion by the end of this century, an increase in rice production per unit area is necessary. The consumption of milled rice in the world is currently at 480 million metric tons (MMT) per year, with over 85% of it being consumed for human consumption. About half of the world's rice consumption is consumed by China and India [2].

Yield and yield characteristics in many field crops are complex, regulated by a variety of genes, and heavily influenced by environmental factors. For any reproduction effort, it is more advantageous to identify genotypes based on divergence studies. In rice seed production, measuring genetic diversity among groups or clusters is crucial to selecting the best parents. [3]. The global population's growth is leading to an increase in the need for crop production. The production of grains has undergone changes due to technology-assisted agriculture, hybrid varieties, and gene selection for increased productivity and adaptability.

Although numerous studies have evaluated rice genetic variability, comparatively few have integrated leaf development, gas exchange, phenology, biomass partitioning and yield attributes in the same set of genotypes under the agro-ecological conditions of South Gujarat. Therefore, the present investigation was undertaken to quantify variation among rice genotypes for major morpho-physiological and yield-related traits and to identify genotypes with a favourable combination of traits for future rice improvement.

MATERIALS AND METHODS

2.1. Experimental Site.

The experiment was conducted during the Kharif seasons of 2020 and 2021 at the research farm of Navsari Agricultural University, Navsari, Gujarat, India (20.9248° N, 72.9079° E). The experimental location falls within the heavy-rainfall zone-I (agro-ecological situation III) of south Gujarat.

2.2. Plant Material

Twenty rice genotypes obtained from the Main Rice Research Centre, Navsari Agricultural University, were evaluated using a randomized block design (RBD) with three replications. The genotypes were GNR-4, GR-15, Lalkada, NVSR-6158, IET-25453, IET-25470, IET-24336, IET-27170, IET-26375, Chittimuthyalu, IET-28690, IET-28691, IET-28694, IET-28695, IET-28696, IET-28701, IR-64, BPT-5204, IET-28704 and IET-28705. All these genotypes were collected from the Main Rice Research Centre, Navsari Agricultural University, Navsari, Gujarat.

2.3. Experimental Setup and Sowing

Following land preparation, 21-day-old seedlings were transplanted during the second week of July at two seedlings per hill with 20 cm × 15 cm row-to-row and plant-to-plant spacing. The crop was harvested during the fourth week of October. All genotypes were subjected to the same field management practices within each experimental season. Detailed information on fertilizer rates, irrigation schedule, weed and pest management, plot dimensions and meteorological conditions should be inserted from the original field records before submission.

2.4. Evaluation of Parameters

Five representative hills from the interior rows of each plot were selected for recording morphological and yield-related observations. Plant height, leaf area, leaf area index, tillers plant⁻¹, panicle length, days to 50% flowering, days to maturity, test weight, straw yield plant⁻¹, grain yield plant⁻¹ and harvest index were recorded.

Leaf area was estimated using the length × maximum-width method: LA = K × L × W, where LA is leaf area, L is leaf length, W is maximum leaf width and K is the correction factor (0.75). Leaf area index (LAI) was calculated as leaf area per unit ground area.

Total dry matter was determined from five randomly selected plants harvested at ground level at crop maturity. Samples were oven-dried at 60 ± 10 °C for 48 h and weighed. Biological yield was calculated as the sum of grain yield and straw yield. Harvest index was calculated as the ratio of grain yield to biological yield, expressed as a percentage [6].

$$\text{Harvest Index} = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

Biological yield = Grain yield + Straw yield

Net photosynthetic rate, stomatal conductance and transpiration rate were measured using a CI-340 handheld photosynthesis system (CID Bio-Science). The units are reported using standard gas-exchange conventions as μmol CO₂ m⁻² s⁻¹ for photosynthetic rate, mol H₂O m⁻² s⁻¹ for stomatal conductance and mmol H₂O m⁻² s⁻¹ for transpiration rate. The measurement growth stage, leaf position, time of measurement and chamber/environmental settings were not specified in the supplied manuscript and should be added from the experimental records.

Data from each season were subjected to analysis of variance (ANOVA) following Gomez and Gomez (1984). Differences among genotype means were assessed using the critical difference (CD) at the 5% significance level when the F-test was significant. Pooled means across the two seasons were used to summarize genotype performance. To complement the univariate ANOVA, an exploratory multivariate analysis was conducted using pooled genotype means (n=20). Pearson correlation coefficients were calculated between grain yield and the other measured traits. A parsimonious multiple linear regression model was fitted with grain yield plant⁻¹ as the dependent variable and three predictors - tillers plant⁻¹, harvest index and test weight - as explanatory variables. These variables were selected to represent sink number and biomass partitioning while maintaining acceptable multicollinearity; variance inflation factors (VIFs) were calculated for the selected predictors. Standardized regression coefficients were interpreted as direct path coefficients and the residual path coefficient was calculated as √(1-R²). Hierarchical clustering was performed using Ward's minimum-variance method on standardized pooled values of the 15 measured traits. Because the multivariate analyses were based on genotype means rather than plot-level observations, correlation, regression and path coefficients were treated as genotype-level exploratory relationships rather than independent replication-based tests. The complete genotype × year inferential analysis should be conducted from the original plot-level data before final submission if those data are available.

RESULTS

Study of rice morpho-physiological parameters and statistical analysis

Significant genotypic variation was observed for plant height, leaf area and leaf area index (Table 1). Across seasons, IR-64 was the tallest genotype, with pooled plant height of 125.98 cm, whereas IET-28695 was the shortest (94.34 cm). Leaf area varied markedly among genotypes. IET-28705 recorded the highest pooled leaf area (70.13 cm²), followed by IET-28701 (65.88 cm²), while NVSR-6158 had the lowest value (40.02 cm²). The corresponding LAI values ranged from 0.133 in NVSR-6158 to 0.234 in IET-28705, indicating substantial differences in canopy development.

The comparatively large leaf area and LAI of IET-28705 suggest greater potential for canopy light interception and carbon assimilation. Similar genotypic variation in leaf and physiological traits has been documented in diverse rice germplasm, supporting the importance of canopy architecture as a component of yield potential.

Table 1. Genotypic variation in plant height, leaf area and leaf area index during 2020, 2021 and pooled analysis.

Genotype s	Plant height			Leaf area			Leaf area index		
	2020	2021	Pool ed	2020	2021	Pool ed	2020	2021	Pool ed

GNR-4	100.22 ± 6.6	98.69 ± 6.83	99.4 ± 5	45.48 ± 4.3	43.46 ± 1.8	44.4 ± 7	0.152 ± 0.01	0.145 ± 0.01	0.14 ± 8
GR-15	119.80 ± 8.2	115.14 ± 6.0	117.47	48.57 ± 6.1	44.33 ± 6.3	46.4 ± 5	0.162 ± 0.02	0.148 ± 0.02	0.15 ± 5
Lalkada	113.59 ± 6.4	114.06 ± 2.6	113.83	41.97 ± 2.9	42.82 ± 1.7	42.4 ± 0	0.140 ± 0.01	0.143 ± 0.01	0.14 ± 1
NVSR-6158	121.54 ± 9.2	119.60 ± 5.6	120.57	40.41 ± 2.0	39.63 ± 2.3	40.0 ± 2	0.135 ± 0.01	0.132 ± 0.01	0.13 ± 3
IET-25453	117.86 ± 7.9	116.68 ± 6.2	117.27	45.84 ± 5.3	42.63 ± 4.2	44.2 ± 3	0.153 ± 0.02	0.142 ± 0.01	0.14 ± 7
IET-25470	113.99 ± 7.2	115.47 ± 6.2	114.73	50.75 ± 2.4	49.68 ± 1.5	50.2 ± 2	0.169 ± 0.01	0.166 ± 0.01	0.16 ± 7
IET-24336	108.42 ± 8.1	117.23 ± 6.3	112.83	60.14 ± 0.7	60.02 ± 3.1	60.0 ± 8	0.200 ± 0.01	0.200 ± 0.01	0.20 ± 0
IET-27170	109.10 ± 7.1	110.39 ± 6.4	109.75	41.86 ± 2.3	42.94 ± 1.4	42.4 ± 0	0.140 ± 0.01	0.143 ± 0.01	0.14 ± 1
IET-26375	119.33 ± 4.5	121.36 ± 6.6	120.34	44.14 ± 2.9	44.39 ± 2.5	44.2 ± 6	0.147 ± 0.01	0.148 ± 0.01	0.14 ± 8
Chittimuth yalu	110.63 ± 7.2	113.51 ± 4.8	112.07	46.22 ± 3.7	46.09 ± 2.7	46.1 ± 6	0.154 ± 0.01	0.154 ± 0.01	0.15 ± 4
IET-28690	106.60 ± 5.7	105.45 ± 5.0	106.03	42.59 ± 2.6	41.83 ± 3.8	42.2 ± 1	0.142 ± 0.01	0.139 ± 0.01	0.14 ± 1
IET-28691	106.85 ± 2.7	106.70 ± 5.8	106.78	47.92 ± 2.5	44.02 ± 3.4	45.9 ± 7	0.160 ± 0.01	0.147 ± 0.01	0.15 ± 3
IET-28694	111.37 ± 7.7	112.01 ± 6.7	111.69	52.95 ± 4.6	52.10 ± 2.6	52.5 ± 3	0.177 ± 0.01	0.174 ± 0.01	0.17 ± 5
IET-28695	93.47 ± 7.1	95.21 ± 7.9	94.34	50.61 ± 1.8	49.66 ± 2.1	50.1 ± 4	0.169 ± 0.01	0.166 ± 0.01	0.16 ± 7
IET-28696	120.52 ± 6.7	120.74 ± 7.3	120.63	62.57 ± 4.8	60.73 ± 5.0	61.6 ± 5	0.209 ± 0.02	0.202 ± 0.02	0.20 ± 5
IET-28701	110.40 ± 6.2	111.18 ± 6.2	110.79	65.68 ± 1.8	66.08 ± 1.9	65.8 ± 8	0.219 ± 0.01	0.220 ± 0.01	0.22 ± 0
IR-64	126.18 ± 7.3	125.79 ± 6.2	125.98	51.17 ± 1.4	49.15 ± 2.1	50.1 ± 6	0.171 ± 0.01	0.164 ± 0.01	0.16 ± 7
BPT-5204	97.66 ± 5.4	96.62 ± 6.4	97.14	53.18 ± 1.7	54.00 ± 1.9	53.5 ± 9	0.177 ± 0.01	0.180 ± 0.01	0.17 ± 9
IET-28704	103.02 ± 4.2	101.15 ± 6.7	102.08	62.44 ± 4.8	59.83 ± 3.6	61.1 ± 4	0.208 ± 0.02	0.199 ± 0.01	0.20 ± 4
IET-28705	105.32 ± 5.8	105.88 ± 6.1	105.60	69.66 ± 3.2	70.59 ± 3.0	70.1 ± 3	0.232 ± 0.01	0.235 ± 0.01	0.23 ± 4
S Em ±	5.36	4.48	3.49	2.38	2.25	1.64	0.0074	0.0075	0.0054
CD at 5 %	15.35	12.82	9.84	6.82	6.44	4.62	0.023	0.021	0.015
CV (%)	8.38	6.98	7.71	8.06	2.76	7.92	8.06	7.76	7.92
YT: S Em ±	4.94			2.32			0.007		
YT: CD at 5 %	NS			NS			NS		

Show significant differences among genotypes were also observed for photosynthetic rate, stomatal conductance and transpiration rate (Table 2). IET-28705 exhibited the highest pooled photosynthetic rate ($44.30 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$), stomatal conductance ($0.446 \text{ mol H}_2\text{O m}^{-2} \text{ s}^{-1}$) and transpiration rate ($5.73 \text{ mmol H}_2\text{O m}^{-2} \text{ s}^{-1}$). IET-28701, IET-28704, IET-28696 and IET-24336 also showed comparatively high gas-exchange performance. In contrast, NVSR-6158 recorded the lowest pooled photosynthetic rate ($25.41 \mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$) and stomatal conductance ($0.324 \text{ mol H}_2\text{O m}^{-2} \text{ s}^{-1}$), whereas Lalkada showed the lowest transpiration rate ($3.22 \text{ mmol H}_2\text{O m}^{-2} \text{ s}^{-1}$).

The consistency of high photosynthetic activity and stomatal conductance in IET-28705 across both seasons is significant because variation in these traits can influence carbon acquisition and biomass formation. Contemporary rice studies similarly report substantial genotypic variation in gas exchange and demonstrate associations between physiological performance, biomass and grain yield.

Table 2. Genotypic variation in net photosynthetic rate, stomatal conductance and transpiration rate during 2020, 2021 and pooled analysis.

	Photosynthesis rate	Stomatal conductance	Transpiration rate
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Genotypes	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
GNR-4	34.02 ± 3.54	35.42 ± 1.57	34.72	0.355 ± 0.02	0.359 ± 0.01	0.357	3.64 ± 0.22	3.59 ± 0.09	3.62
GR-15	35.59 ± 0.80	34.29 ± 2.42	34.94	0.357 ± 0.01	0.360 ± 0.01	0.359	4.33 ± 0.19	4.24 ± 0.06	4.29
Lalkada	31.45 ± 0.87	32.30 ± 0.96	31.88	0.343 ± 0.02	0.337 ± 0.01	0.340	3.27 ± 0.18	3.18 ± 0.72	3.22
NVSR-6158	25.28 ± 1.06	25.53 ± 0.97	25.41	0.324 ± 0.01	0.324 ± 0.01	0.324	3.33 ± 0.08	3.39 ± 0.07	3.36
IET-25453	34.41 ± 1.58	33.79 ± 2.32	34.10	0.357 ± 0.03	0.354 ± 0.03	0.356	3.70 ± 0.02	3.63 ± 0.12	3.67
IET-25470	37.71 ± 2.69	36.63 ± 2.31	37.17	0.360 ± 0.03	0.357 ± 0.02	0.359	3.90 ± 0.04	3.87 ± 0.10	3.88
IET-24336	39.51 ± 3.30	40.20 ± 1.25	39.85	0.380 ± 0.02	0.378 ± 0.01	0.379	5.24 ± 0.44	5.12 ± 0.09	5.18
IET-27170	27.00 ± 0.78	28.39 ± 1.46	27.70	0.337 ± 0.02	0.335 ± 0.02	0.336	3.24 ± 0.06	3.25 ± 0.06	3.25
IET-26375	33.49 ± 2.20	32.84 ± 1.50	33.16	0.351 ± 0.01	0.346 ± 0.02	0.349	3.62 ± 0.10	3.60 ± 0.04	3.61
Chittimut hyalu	34.53 ± 3.22	33.19 ± 1.29	33.86	0.355 ± 0.02	0.357 ± 0.02	0.356	3.89 ± 0.10	3.76 ± 0.04	3.82
IET-28690	31.92 ± 3.37	33.01 ± 2.21	32.47	0.351 ± 0.03	0.345 ± 0.04	0.348	3.61 ± 0.30	3.45 ± 0.18	3.53
IET-28691	35.49 ± 1.80	34.19 ± 1.53	34.84	0.354 ± 0.02	0.358 ± 0.01	0.356	4.23 ± 0.25	4.12 ± 0.19	4.18
IET-28694	38.99 ± 1.81	40.35 ± 1.31	39.67	0.366 ± 0.02	0.360 ± 0.03	0.363	5.07 ± 0.11	5.02 ± 0.41	5.04
IET-28695	37.31 ± 2.39	38.25 ± 2.21	37.78	0.360 ± 0.03	0.351 ± 0.02	0.356	4.57 ± 0.63	4.50 ± 0.40	4.54
IET-28696	42.34 ± 0.99	41.31 ± 2.74	41.83	0.383 ± 0.04	0.384 ± 0.03	0.383	5.31 ± 0.33	5.32 ± 0.36	5.32
IET-28701	43.79 ± 5.55	43.19 ± 2.77	43.49	0.428 ± 0.01	0.434 ± 0.03	0.431	5.55 ± 0.32	5.49 ± 0.08	5.52
IR-64	38.71 ± 1.41	36.56 ± 3.52	37.64	0.364 ± 0.02	0.362 ± 0.01	0.363	3.92 ± 0.16	3.86 ± 0.21	3.89
BPT-5204	39.34 ± 1.88	40.20 ± 1.84	39.77	0.375 ± 0.02	0.371 ± 0.01	0.373	5.12 ± 0.30	5.06 ± 0.20	5.09
IET-28704	43.35 ± 2.78	42.91 ± 2.59	43.13	0.388 ± 0.03	0.401 ± 0.02	0.395	5.40 ± 0.36	5.31 ± 0.08	5.36
IET-28705	45.05 ± 2.85	43.55 ± 4.72	44.30	0.446 ± 0.03	0.445 ± 0.03	0.446	5.77 ± 0.17	5.69 ± 0.18	5.73
S Em ±	1.82	1.64	1.22	0.017	0.016	0.012	0.19	0.17	0.13
CD at 5 %	5.21	4.69	3.45	0.050	0.047	0.034	0.54	0.50	0.36
CV (%)	8.64	7.81	8.24	8.21	7.83	8.02	7.47	7.09	7.29
YT: S Em ±			1.73			0.017			0.18
YT: CD at 5 %			NS			NS			NS

Genotypes differed substantially in days to 50% flowering, tiller number and panicle length (Table 3). IR-64 was the earliest genotype, reaching 50% flowering in 63.83 days, whereas IET-28705 was the latest (105.67 days), followed closely by GNR-4 (106.83 days). IET-28705 produced the greatest number of tillers (18.93 plant⁻¹) and the longest panicles (30.42 cm), while NVSR-6158 produced the fewest tillers (9.27 plant⁻¹) and IET-27170 had the shortest panicles (19.32 cm).

Table 3. Genotypic variation in days to 50% flowering, tillers plant⁻¹ and panicle length during 2020, 2021 and pooled analysis.

Genotypes	50% flowering			Tillers per plant			Length of panicle		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
GNR-4	107.00 ± 1.6	106.67 ± 1.2	106.83	11.33 ± 0.3	11.67 ± 1.1	11.50	19.27 ± 0.4	19.53 ± 0.6	19.40
GR-15	101.67 ± 1.2	103.33 ± 2.0	102.50	12.67 ± 0.6	12.40 ± 0.4	12.53	21.87 ± 0.3	21.87 ± 0.3	21.87

Lalkada	81.33 ± 1.2	80.67 ± 1.7	81.00	10.47 ± 0.7	10.93 ± 0.3	10.70	22.83 ± 3.3	21.63 ± 2.4	22.23
NVSR-6158	75.00 ± 1.6	75.00 ± 2.4	75.00	9.13 ± 0.3	9.40 ± 0.7	9.27	21.65 ± 1.4	20.76 ± 2.3	21.21
IET-25453	90.00 ± 2.2	92.00 ± 1.6	91.00	11.80 ± 0.3	11.13 ± 0.8	11.47	23.82 ± 1.1	24.37 ± 0.5	24.10
IET-25470	93.00 ± 1.6	93.67 ± 2.0	93.33	12.93 ± 0.7	13.00 ± 0.3	12.97	24.25 ± 0.4	24.17 ± 0.2	24.21
IET-24336	93.67 ± 1.7	92.00 ± 1.6	92.83	14.53 ± 1.1	14.67 ± 1.2	14.60	26.21 ± 0.6	26.35 ± 1.7	26.28
IET-27170	90.00 ± 0.8	88.67 ± 2.5	89.33	9.33 ± 0.3	9.93 ± 0.7	9.63	19.12 ± 0.4	19.52 ± 0.9	19.32
IET-26375	97.33 ± 1.7	94.67 ± 1.2	96.00	11.80 ± 0.3	10.53 ± 1.2	11.17	22.93 ± 2.4	23.38 ± 0.3	23.15
Chittimuthyalu	97.33 ± 1.7	98.33 ± 2.0	97.83	11.87 ± 0.4	12.33 ± 0.5	12.10	24.63 ± 2.2	22.75 ± 0.8	23.69
IET-28690	98.67 ± 0.9	100.33 ± 2.0	99.50	11.13 ± 0.4	11.27 ± 1.2	11.20	20.68 ± 0.8	21.17 ± 0.7	20.92
IET-28691	90.00 ± 1.6	93.00 ± 1.6	91.50	13.20 ± 0.4	13.53 ± 0.8	13.37	23.96 ± 1.3	28.30 ± 1.2	26.13
IET-28694	91.00 ± 1.6	90.00 ± 1.6	90.50	14.07 ± 1.3	13.93 ± 0.5	14.00	25.70 ± 0.4	25.16 ± 0.6	25.43
IET-28695	99.67 ± 1.2	103.33 ± 2.0	101.50	12.47 ± 0.7	12.87 ± 0.7	12.67	24.15 ± 1.1	24.73 ± 1.3	24.44
IET-28696	90.33 ± 2.1	91.33 ± 1.2	90.83	14.87 ± 0.2	15.60 ± 0.7	15.23	27.40 ± 1.3	26.34 ± 0.9	26.87
IET-28701	92.33 ± 2.1	90.33 ± 1.2	91.33	18.07 ± 1.0	18.80 ± 0.2	18.43	29.26 ± 0.9	27.05 ± 1.1	28.16
IR-64	63.33 ± 1.2	64.33 ± 2.0	63.83	13.67 ± 0.4	12.73 ± 0.4	13.20	25.40 ± 0.6	25.19 ± 0.5	25.30
BPT-5204	86.67 ± 1.2	87.67 ± 2.0	87.17	12.87 ± 1.0	13.67 ± 0.4	13.27	21.29 ± 0.4	21.46 ± 0.3	21.37
IET-28704	86.67 ± 1.2	87.67 ± 1.2	87.17	17.07 ± 0.3	16.87 ± 0.2	16.97	28.30 ± 0.8	27.81 ± 1.4	28.06
IET-28705	104.67 ± 1.2	106.67 ± 1.2	105.67	19.13 ± 0.6	18.73 ± 0.4	18.93	30.27 ± 0.6	30.57 ± 0.6	30.42
S Em ±	1.12	1.29	0.85	0.46	0.52	0.35	0.94	0.79	0.61
C D at 5 %	3.20	3.69	2.40	1.33	1.49	0.98	2.69	2.25	1.73
CV (%)	2.11	2.43	2.28	6.13	6.82	6.49	6.75	5.66	6.23
YT: S Em ±	YT: S Em ±	YT: S Em ±	1.21			0.49			0.18
YT: CD at 5 %	YT: CD at 5 %	YT: CD at 5 %	NS			NS			NS

Total dry matter, days to maturity and test weight also varied among genotypes (Table 4). IR-64 accumulated the greatest pooled total dry matter (35.72 g plant⁻¹), whereas IET-28695 accumulated the least (21.10 g plant⁻¹). GNR-4 required the longest time to maturity (134.67 days), while NVSR-6158 was the earliest to mature (108.33 days). IET-28705 had the highest pooled test weight (26.68 g), followed by IET-26375 (26.10 g) and IET-28696 (25.68 g).

Table 4. Genotypic variation in total dry matter per plant, days to maturity and test weight during 2020, 2021 and pooled analysis.

Genotypes	Total dry matter per plant			Days to maturity			Test weight		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
GNR-4	21.22 ± 2.6	21.56 ± 1.6	21.39	133.33 ± 2.2	136.00 ± 1.6	134.67	16.19 ± 0.2	16.22 ± 0.4	16.21
GR-15	29.38 ± 2.3	28.96 ± 1.2	29.17	125.33 ± 1.2	124.33 ± 1.2	124.83	20.70 ± 0.3	20.76 ± 0.6	20.73
Lalkada	27.57 ± 2.4	27.29 ± 2.0	27.43	116.00 ± 1.7	116.00 ± 2.0	116.00	17.31 ± 0.4	17.09 ± 0.3	17.20
NVSR-6158	30.49 ± 2.6	29.77 ± 2.2	30.13	107.00 ± 1.6	109.67 ± 2.2	108.33	14.72 ± 0.4	14.54 ± 0.4	14.63
IET-25453	28.56 ± 2.9	29.10 ± 3.3	28.83	125.67 ± 1.2	126.00 ± 3.3	125.83	20.99 ± 0.5	21.58 ± 0.9	21.29

IET-25470	27.60 ± 1.1	28.31 ± 0.3	27.96	116.33 ± 1.7	117.67 ± 0.3	117.00	19.58 ± 1.2	21.85 ± 1.1	20.72
IET-24336	27.78 ± 3.3	26.69 ± 3.1	27.23	124.00 ± 1.2	125.33 ± 3.1	124.67	19.82 ± 0.3	19.84 ± 0.5	19.83
IET-27170	25.41 ± 2.6	25.41 ± 2.0	25.41	119.33 ± 1.7	119.00 ± 2.0	119.17	16.08 ± 0.5	16.31 ± 0.7	16.19
IET-26375	29.49 ± 2.6	29.85 ± 1.5	29.67	127.33 ± 1.2	125.00 ± 1.5	126.17	25.93 ± 1.2	26.26 ± 1.1	26.10
Chittimuthyalu	27.15 ± 1.2	26.14 ± 0.4	26.64	127.33 ± 0.9	128.00 ± 0.4	127.67	18.31 ± 0.4	18.44 ± 0.2	18.38
IET-28690	25.33 ± 1.9	23.71 ± 2.1	24.52	120.67 ± 0.9	121.67 ± 2.1	121.17	17.97 ± 1.1	20.64 ± 0.6	19.30
IET-28691	25.54 ± 2.6	25.37 ± 1.9	25.46	112.00 ± 1.6	113.67 ± 1.9	112.83	17.62 ± 0.2	17.61 ± 0.5	17.61
IET-28694	26.81 ± 1.5	27.09 ± 1.0	26.95	112.67 ± 1.2	111.33 ± 1.0	112.00	21.06 ± 0.6	21.29 ± 0.8	21.17
IET-28695	20.94 ± 2.4	21.26 ± 4.5	21.10	121.67 ± 1.2	121.00 ± 4.5	121.33	18.78 ± 0.5	19.23 ± 0.2	19.00
IET-28696	31.34 ± 3.8	31.51 ± 2.5	31.42	112.67 ± 1.7	114.00 ± 2.5	113.33	25.80 ± 0.2	25.57 ± 0.8	25.68
IET-28701	25.78 ± 3.2	25.57 ± 3.0	25.68	114.33 ± 1.2	113.33 ± 3.0	113.83	21.92 ± 0.5	21.46 ± 0.6	21.69
IR-64	35.05 ± 3.0	36.40 ± 2.4	35.72	107.67 ± 0.8	109.67 ± 2.4	108.67	22.04 ± 0.6	22.35 ± 0.4	22.20
BPT-5204	21.15 ± 3.2	21.73 ± 4.3	21.44	114.67 ± 1.2	114.00 ± 4.3	114.33	15.87 ± 0.5	15.69 ± 0.6	15.78
IET-28704	24.47 ± 3.9	24.00 ± 4.8	24.24	108.67 ± 1.2	109.67 ± 4.8	109.17	25.59 ± 0.7	24.91 ± 0.3	25.25
IET-28705	25.14 ± 4.5	25.35 ± 2.0	25.25	125.67 ± 1.7	125.33 ± 2.0	125.50	27.56 ± 0.2	25.80 ± 1.4	26.68
S Em ±	0.89	1.06	0.69	1.39	1.31	0.96	1.20	1.06	0.80
CD at 5 %	2.56	3.04	1.95	3.98	3.76	2.69	3.45	3.03	2.26
CV (%)	5.78	6.87	6.34	2.03	1.91	1.97	10.32	8.99	9.68
YT: S Em ±	YT: S Em ±	YT: S Em ±	0.98			1.35			1.13
YT: CD at 5 %	YT: C.D. at 5 %	YT: CD at 5 %	NS			NS			NS

Substantial genotypic variation was observed for straw yield, grain yield and harvest index (Table 5). IET-24336 produced the highest pooled straw yield (28.73 g plant⁻¹), whereas GR-15 produced the lowest (20.00 g plant⁻¹). Grain yield ranged from 13.84 g plant⁻¹ in NVSR-6158 to 26.63 g plant⁻¹ in IET-28705. The latter also showed the highest harvest index (49.13%), indicating efficient partitioning of accumulated biomass towards grain production. IET-28696 (22.65 g plant⁻¹) and IET-28704 (22.33 g plant⁻¹) were the next best genotypes for grain yield.

Table 5. Genotypic variation in straw yield per plant, grain yield per plant and harvest index during 2020, 2021 and pooled analysis.

Genotypes	Straw yield per plant			Grain yield per plant			Harvest index		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
GNR-4	22.99 ± 0.6	23.66 ± 0.4	23.32	16.57 ± 0.4	16.98 ± 0.2	16.77	41.89 ± 0.5	42.19 ± 0.9	42.04
GR-15	19.66 ± 0.9	20.33 ± 0.9	20.00	18.95 ± 0.1	18.93 ± 0.5	18.94	49.07 ± 1.1	48.17 ± 1.1	48.62
Lalkada	20.09 ± 0.7	20.76 ± 0.8	20.43	14.98 ± 0.3	15.51 ± 0.5	15.25	42.73 ± 0.3	43.40 ± 0.8	43.06
NVSR-6158	20.35 ± 1.1	21.02 ± 1.2	20.69	13.68 ± 0.2	13.99 ± 0.2	13.84	40.18 ± 1.0	40.31 ± 1.7	40.24
IET-25453	20.67 ± 1.0	22.89 ± 1.5	21.78	16.79 ± 1.0	17.56 ± 0.7	17.17	44.72 ± 0.5	44.27 ± 3.4	44.49
IET-25470	26.32 ± 1.4	26.99 ± 1.7	26.66	19.78 ± 1.0	20.05 ± 1.1	19.92	42.90 ± 2.5	42.86 ± 2.2	42.88
IET-24336	28.39 ± 1.3	29.06 ± 1.0	28.73	20.89 ± 1.2	21.25 ± 1.7	21.07	42.40 ± 2.5	42.58 ± 1.3	42.49
IET-27170	19.76 ± 0.9	20.43 ± 0.7	20.10	14.68 ± 0.8	14.51 ± 0.8	14.59	42.64 ± 2.6	41.34 ± 1.1	41.99

IET-26375	20.32 ± 0.8	20.99 ± 1.0	20.66	16.49 ± 0.7	17.26 ± 0.7	16.87	44.79 ± 0.9	46.09 ± 2.2	45.44
Chittimuthyalu	26.50 ± 0.6	27.17 ± 0.9	26.84	17.04 ± 0.7	17.54 ± 0.5	17.29	39.09 ± 0.7	39.81 ± 1.8	39.45
IET-28690	20.42 ± 0.5	21.09 ± 0.3	20.75	15.78 ± 0.4	16.18 ± 0.5	15.98	43.62 ± 1.3	43.84 ± 0.6	43.73
IET-28691	21.76 ± 1.7	22.43 ± 2.0	22.09	19.42 ± 0.6	18.37 ± 0.	18.89	47.12 ± 2.2	44.00 ± 3.1	45.56
IET-28694	21.92 ± 1.2	23.99 ± 1.1	22.95	20.63 ± 0.4	20.90 ± 0.1	20.77	48.49 ± 1.1	46.88 ± 1.1	47.69
IET-28695	22.35 ± 1.3	23.02 ± 1.5	22.68	18.59 ± 0.6	18.13 ± 0.8	18.36	45.42 ± 1.0	43.62 ± 1.0	44.52
IET-28696	23.66 ± 0.6	24.33 ± 0.2	24.00	22.36 ± 0.5	22.93 ± 0.1	22.65	48.57 ± 1.2	49.11 ± 0.8	48.84
IET-28701	25.04 ± 0.8	26.04 ± 0.6	25.54	23.91 ± 0.2	24.07 ± 0.3	23.99	48.84 ± 0.9	48.19 ± 0.7	48.51
IR-64	22.14 ± 1.2	22.81 ± 0.7	22.48	20.62 ± 0.3	20.41 ± 0.5	20.52	48.24 ± 1.2	47.07 ± 1.0	47.66
BPT-5204	22.62 ± 0.8	23.29 ± 0.5	22.95	20.80 ± 0.3	20.76 ± 0.3	20.78	47.89 ± 0.9	47.10 ± 0.9	47.49
IET-28704	24.13 ± 1.3	25.68 ± 2.8	24.91	22.19 ± 0.3	22.46 ± 0.7	22.33	47.92 ± 1.0	46.87 ± 3.5	47.40
IET-28705	27.16 ± 1.6	28.23 ± 2.6	27.69	26.52 ± 0.3	26.75 ± 0.1	26.63	49.40 ± 1.8	48.86 ± 2.7	49.13
S Em ±	0.69	0.66	0.48	0.73	0.68	0.50	0.97	1.64	0.96
C D at 5 %	1.98	1.89	1.35	2.08	1.95	1.40	2.78	4.71	2.69
CV (%)	5.26	4.81	5.04	6.61	6.15	6.38	3.72	6.36	5.20
YT: S Em ±	YT: S Em ±	YT: S Em ±	0.68			0.70			1.35
YT: CD at 5%	YT: CD at 5 %	YT: CD at 5 %	NS			NS			NS

2.5. Genotype-level correlation, regression, path analysis and clustering

The pooled genotype means revealed strong positive associations between grain yield and several source- and sink-related traits (Table 6 and Figure 1). The strongest correlations were observed with tillers plant⁻¹ (r=0.965), LAI (r=0.957), leaf area (r=0.956), net photosynthetic rate (r=0.952), stomatal conductance (r=0.929) and transpiration rate (r=0.922). Panicle length (r=0.854), harvest index (r=0.754), straw yield (r=0.680) and test weight (r=0.662) also showed positive associations with grain yield. Plant height (r=-0.125), total dry matter (r=-0.014) and days to maturity (r=-0.163) showed weak associations, while days to 50% flowering was weakly positive (r=0.144). The close relationships among leaf area, LAI and gas-exchange traits indicate that high-yielding genotypes tended to possess a coordinated source-sink phenotype rather than superiority in a single attribute.

Table 6. Pearson correlation coefficients between pooled genotype traits and grain yield per plant.

Trait	r	Direction/strength
Tillers per plant	0.965	positive
Leaf area index	0.957	positive
Leaf area	0.956	positive
Photosynthesis rate	0.952	positive
Stomatal conductance	0.929	positive
Transpiration rate	0.922	positive
Length of panicle	0.854	positive
Harvest index	0.754	positive
Straw yield per plant	0.680	positive
Test weight	0.662	positive
Days to maturity	-0.163	negative
50% flowering	0.144	positive
Plant height	-0.125	negative
Total dry matter per plant	-0.014	negative

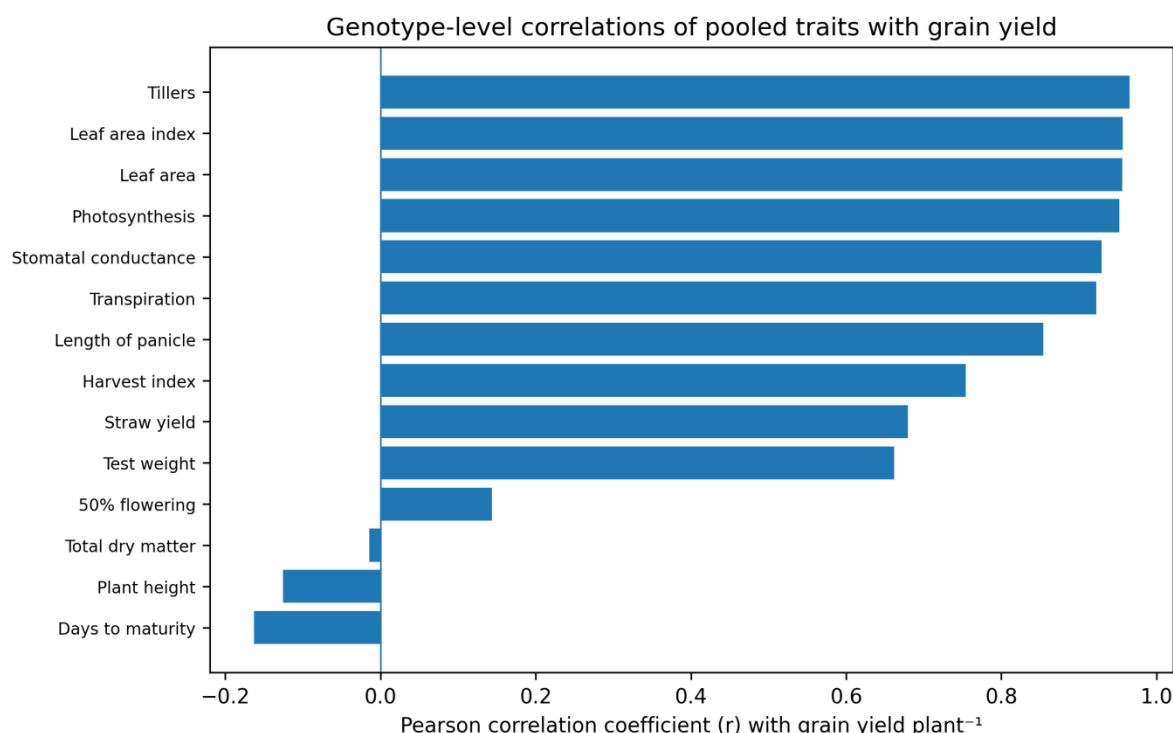


Fig. 1: Genotype-level Pearson correlations of pooled traits with grain yield per plant.

A parsimonious multiple regression model was fitted using tillers per plant, harvest index and test weight as predictors. The three-predictor model explained 94.6% of the variation in pooled grain yield ($R^2 = 0.946$; adjusted $R^2 = 0.936$; $F = 93.78$, $P < 0.001$). The predictor set was deliberately restricted to reduce multicollinearity among the highly associated source and sink traits; variance inflation factors were 2.20, 2.21 and 1.96 for tillers, harvest index and test weight, respectively. Tiller number showed the dominant standardized regression coefficient and direct path effect (0.844), whereas harvest index contributed a smaller positive direct effect (0.157) and test weight had a negligible direct effect (0.019). The residual path coefficient was 0.232, indicating that the selected predictors accounted for most of the genotype-level variation in the pooled dataset.

Table 7. Parsimonious multiple regression and path coefficients for pooled grain yield per plant.

Predictor	Standardized β / direct path	t	P	VIF	Total indirect effect
Tillers per plant	0.844	9.823	3.518e-08	2.20	0.121
Harvest index	0.157	1.825	0.08668	2.21	0.597
Test weight	0.019	0.233	0.8188	1.96	0.643
Model residual /	$R^2=0.946$, adjusted $R^2=0.936$	$F=93.78$	<0.001		

A recursive path model using the same five predictors was derived from the pooled correlation matrix. Direct effects are equivalent to the standardized partial regression coefficients for this model.

Trait	Direct path coefficient	Total indirect effect
Tillers per plant	0.510	0.455
Photosynthesis rate	0.343	0.609
Length of panicle	0.064	0.790
Test weight	-0.008	0.670
Harvest index	0.121	0.633

Residual path coefficient = 0.200. The largest direct effects were from tiller number (0.510) and photosynthetic rate (0.343), whereas test weight had a near-zero direct effect after accounting for the other predictors.

Hierarchical clustering based on standardized values of all 15 traits produced four phenotypic groups (Table 8 and Figure 2). Cluster I comprised IET-28696, IET-28701, IET-28704 and IET-28705 and represented the group with the most favourable overall performance. Cluster II included eight genotypes with intermediate and heterogeneous performance, whereas Cluster III contained Lalkada, NVSR-6158, IET-27170 and IET-28690. Cluster IV comprised GR-15, IET-25453, IET-26375 and IR-64, reflecting a distinct multivariate phenotype that included the early-flowering IR-64.

Table 8. Ward hierarchical clustering of 20 rice genotypes based on standardized pooled traits.

Cluster	Genotypes
Cluster 1	IET-28696, IET-28701, IET-28704, IET-28705
Cluster 2	GNR-4, IET-25470, IET-24336, Chittimuthyalu, IET-28691, IET-28694, IET-28695, BPT-5204
Cluster 3	Lalkada, NVSR-6158, IET-27170, IET-28690
Cluster 4	GR-15, IET-25453, IET-26375, IR-64

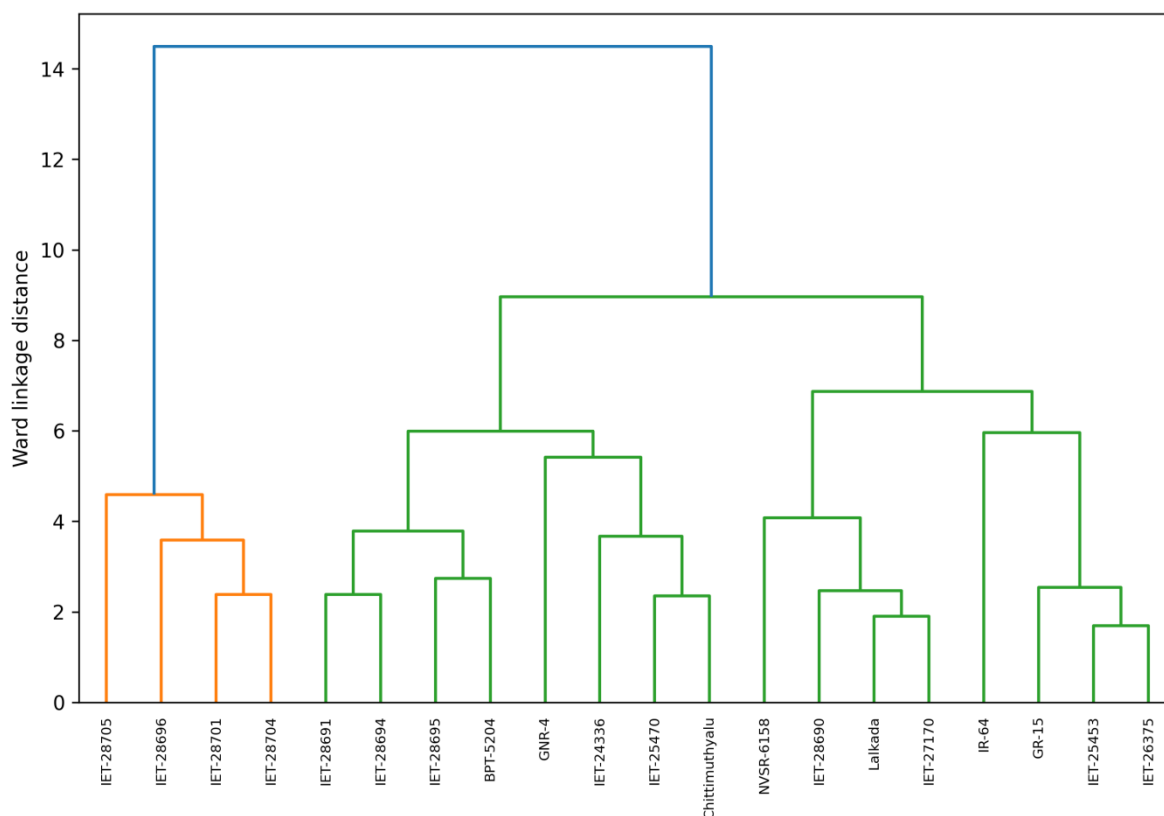


Fig. 2: Ward hierarchical dendrogram of the 20 rice genotypes based on pooled morpho-physiological and yield-related traits.

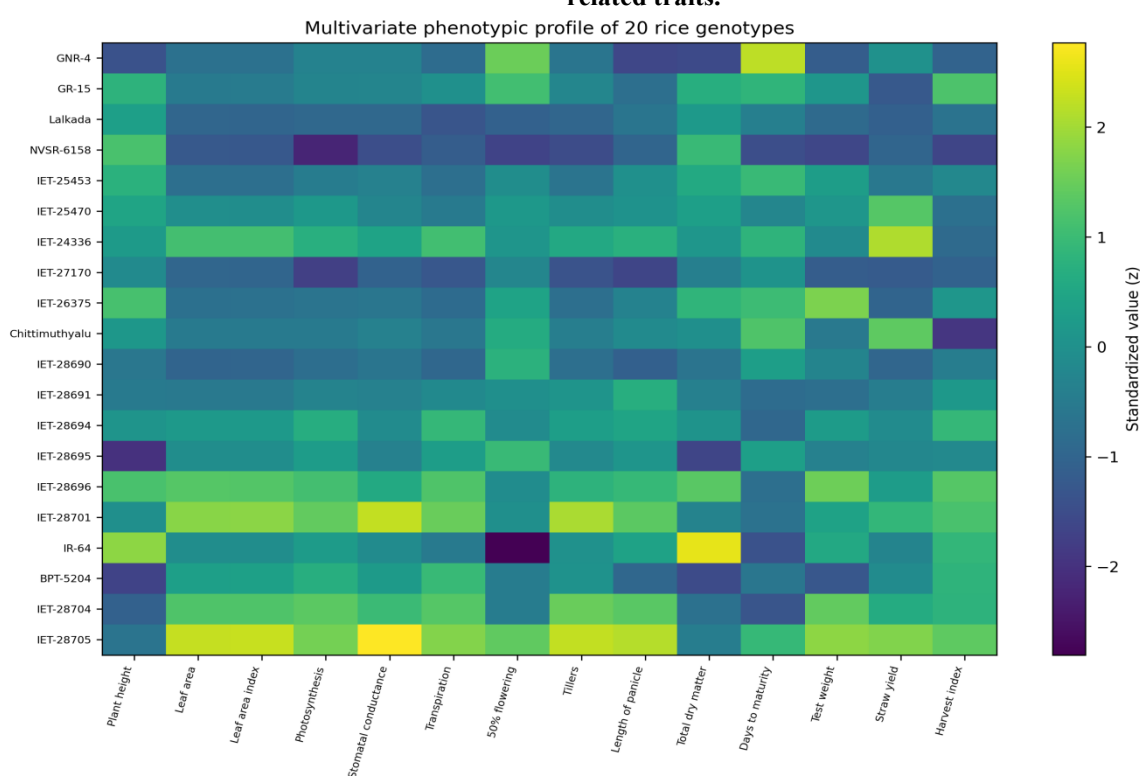


Fig. 3: Heatmap of standardized pooled values across the 15 measured traits.

The multivariate analyses strengthened the interpretation obtained from the univariate genotype comparisons. The exceptionally high genotype-level correlations of grain yield with tiller number, LAI, leaf area and photosynthetic rate indicate that yield differences were closely aligned with both canopy development and source activity. Because these traits were also strongly intercorrelated, a parsimonious regression model was used rather than entering the full set of predictors simultaneously. The low VIF values for tiller number, harvest index and test weight supported a more stable predictor set, and tiller number showed the largest direct effect on grain yield. This result emphasizes the importance of productive sink number in distinguishing high-yielding genotypes, while the positive direct contribution of harvest index indicates the additional importance of efficient biomass partitioning.

The weak direct effect of test weight after accounting for tiller number and harvest index indicates that grain weight alone contributed little independent information to grain yield within the selected model. Its moderate positive simple correlation with grain yield nevertheless suggests that heavier grains may accompany favourable yield phenotypes, although this relationship was largely shared with other yield components. The distinction between simple association and direct contribution is important for breeding decisions: traits with strong direct effects, such as tiller number in the present analysis, may be more informative selection criteria, whereas traits with strong indirect associations can serve as complementary indicators of a favourable plant phenotype.

The ward clustering provided an supplementary phenotypic perspective. The grouping of IET-28705 with IET-28701, IET-28696 and IET-28704 is consistent with the superior pooled performance of these genotypes for several yield-associated traits and supports their consideration as a promising high-performance group. In contrast, the separation of IR-64 into Cluster IV reflects its distinctive early flowering and high total dry matter profile. Thus, clustering can help breeders identify both superior groups and phenotypically contrasting material that may be useful for broadening the breeding pool.

DISCUSSION

The observed variation in plant height among the genotypes is consistent with the quantitative nature of plant architecture and its dependence on genetic background and environmental conditions [8, 9, 10]. Plant height can influence biomass accumulation, canopy structure and lodging risk; therefore, its optimum value rather than maximum value is generally desirable in breeding populations. The present genotypes covered a broad height range, demonstrating useful phenotypic diversity for selection.

Leaf area and LAI are important determinants of canopy development because they influence the interception of incident radiation and the assimilatory capacity of the crop. IET-28705 combined the largest leaf area and LAI with the highest photosynthetic rate, suggesting that its superior canopy development was accompanied by greater physiological activity [11, 12]. Studies of diverse rice materials have similarly reported substantial variation in leaf area, gas exchange and biomass traits, emphasizing the value of integrated phenotyping [10, 13].

Photosynthetic rate, stomatal conductance and transpiration varied substantially among the genotypes. The superior gas-exchange performance of IET-28705, particularly its higher photosynthetic rate and stomatal conductance, provides a plausible physiological basis for its greater biomass production and grain yield [12, 14, 15]. Genetic variation in photosynthetic capacity in rice has been linked to differences in stomatal and mesophyll conductance, while field studies have shown that high-yielding genotypes can maintain comparatively higher photosynthetic activity and favourable source traits [16].

Phenology and reproductive architecture also contributed to differences among genotypes. IR-64 was markedly early-flowering and early maturing, demonstrating its value where short-duration production is required [17]. In contrast, IET-28705 had a longer growth duration but also produced more tillers, longer panicles and heavier grains [18, 19]. This combination indicates that the longer vegetative and reproductive duration in IET-28705 was associated with greater sink development and grain production under the conditions of the experiment [20, 21].

The high grain yield of IET-28705 was accompanied by high tiller number, long panicles, high test weight, high leaf area, high gas-exchange rates and a high harvest index [27, 23]. This combination is more informative than any single trait because grain yield is the integrated outcome of source strength, sink size and assimilate partitioning. Recent work on contrasting rice genotypes likewise supports the role of photosynthesis and source-sink relationships in determining yield potential [8, 28, 29, 30].

Importantly, the present study is an evaluation under the prevailing Kharif environment at Navsari and should not be interpreted as evidence of broad adaptation without multi-location testing. Genotype $\times$ environment interaction can alter the ranking of rice genotypes; therefore, IET-28705 should be validated across seasons, locations and representative management environments before being advanced as a broadly adapted cultivar or donor parent.

CONCLUSION

The 20 rice genotypes show considerable diversity in morphological, physiological, phenological and yield-related traits. IET-28705 genotype most consistently favourable, combining high canopy development and gas-exchange activity with superior tillering, panicle length, test weight, grain yield and harvest index. At the genotype level, grain yield was highly strongly correlated with tiller number, LAI, leaf area and photosynthetic rate. A parsimonious regression model using tiller number, harvest index and test weight explained 94.6% of the variation in pooled grain yield, and path analysis identified tiller number as the strongest direct contributor. Ward clustering further grouped IET-28705 with IET-28701, IET-28696 and IET-28704 as a high-performance phenotypic cluster. Collectively, these results support an integrated selection strategy emphasizing sink development, canopy function and efficient biomass partitioning. Because the multivariate analyses were derived from pooled genotype means, their interpretation is exploratory; replication-level validation and multi-environment testing are required before claims of stability, broad adaptation, or breeding superiority are made.

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Conflicts of Interest

The authors declare that they have no conflict of interest.

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