

International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(8): 2499-2502
www.biochemjournal.com
Received: 22-05-2026
Accepted: 28-06-2026

Saurav Vijaykumar Parbhanikar
MSc Student, Department of
Genetics and Plant Breeding,
VNMKV, College of Agriculture,
Latur, Maharashtra, India

Dr. Sandeep Govindappa Shinde,
Assistant Professor, Department of
Genetics and Plant Breeding,
Vasantrao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

Dr. Padmakar Balasaheb Wadikar
Associate Professor, Department of
Genetics and Plant Breeding,
VNMKV, College of Agriculture,
Latur, Maharashtra, India

Dr. Hirakant Vishwasrao Kalpande
Head, Department of Genetics and
Plant Breeding, Vasantrao Naik
Marathwada Krishi Vidyapeeth,
Parbhani, Maharashtra, India

Dr. Santosh Bhimrao Borgaonkar
Cotton Breeder, Cotton Research
Station Mehabub Baug, Vasantrao
Naik Marathwada Krishi
Vidyapeeth, Parbhani,
Maharashtra, India

Dr. Mahendra Shankarrao Dudhare
Associate Professor, Department of
Agricultural Microbiology,
VNMKV, Vilasrao Deshmukh
College of Agricultural
Biotechnology, Latur,
Maharashtra, India

Vijay Waman Panchal
MSc Student, Department of
Genetics and Plant Breeding,
VNMKV, College of Agriculture,
Latur, Maharashtra, India

Tejas Anant Narkhede
PhD Scholar, Department of
Genetics and Plant Breeding,
Vasantrao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

Corresponding Author:
Saurav Vijaykumar
Parbhanikar
MSc Student, Department of
Genetics and Plant Breeding,
VNMKV, College of
Agriculture, Latur,
Maharashtra, India

Dissecting yield associations through genotypic and phenotypic correlation and path analysis in upland rice

Saurav Vijaykumar Parbhanikar, Sandeep Govindappa Shinde, Padmakar Balasaheb Wadikar, Hirakant Vishwasrao Kalpande, Santosh Bhimrao Borgaonkar, Mahendra Shankarrao Dudhare, Vijay Waman Panchal and Tejas Anant Narkhede

DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i8Sab.9775>

Abstract

Grain yield is a complex trait, and correlation alone cannot distinguish direct effects from associations mediated through other characters. This study therefore evaluated genotypic and phenotypic correlations and partitioned them through path analysis in 40 upland rice genotypes grown in a randomized block design with three replications at Parbhani, Maharashtra, during Kharif 2025. Grain yield plant⁻¹ had significant positive genotypic and phenotypic correlations with tillers plant⁻¹ (0.956 and 0.664), panicle length (0.625 and 0.569), total spikelets panicle⁻¹ (0.846 and 0.818), grain length (0.440 and 0.437) and grain breadth (0.670 and 0.641). Days to 50% flowering was negatively correlated with yield at both levels (−0.203 and −0.202). Path analysis identified total spikelets panicle⁻¹ as the largest positive direct contributor at the genotypic (0.997) and phenotypic (0.584) levels, followed by grain breadth (0.826 and 0.721). Tiller number had a strong positive correlation with yield but a negative genotypic direct effect (−0.580), indicating mediation mainly through spikelet number, grain breadth and panicle length. Grain length likewise had positive correlations but negative direct effects. Test weight was not a useful yield criterion in this population, whereas length/breadth ratio had a positive direct effect but a weak negative total association. The results support simultaneous selection for spikelet-bearing capacity, grain breadth, adequate panicle length and productive tillering, with caution against selecting correlated traits in isolation. Because the analysis was conducted for one environment and the residual effect and standard errors were not provided in the source tables, the path coefficients should be validated in multi-environment trials.

Keywords: Upland rice, character association, genotypic correlation, phenotypic correlation, path analysis, spikelets, grain breadth, grain yield

Introduction

In rice, grain yield is assembled through the joint expression of phenology, plant architecture, tillering, panicle productivity and grain attributes. Simple correlation is useful for identifying traits that vary with yield, but a large correlation can arise from indirect effects through a third character. Path coefficient analysis addresses this limitation by partitioning an observed correlation into direct and indirect components, an approach introduced by Wright (1921) [4] and adapted for crop selection by Dewey and Lu (1959) [1].

Previous rice studies have shown that the most useful selection traits can differ among populations and environments. In upland rice, grains or spikelets per panicle, tillering and panicle traits have often been associated with yield (Seyoum *et al.*, 2012) [3], while recent work has emphasized the value of combining correlation, path coefficients and genetic parameters before defining selection criteria (Faysal *et al.*, 2022) [2]. The present paper focuses exclusively on character association and path analysis in the 40-genotype upland rice population evaluated at Parbhani.

2. Materials and methods

The trial was conducted during Kharif 2025 at the Experimental Farm of the Department of Genetics and Plant Breeding, College of Agriculture, VNMKV, Parbhani, Maharashtra,

India. Forty upland rice genotypes from CRRUS, Hazaribagh, and ICAR-IRRI, Hyderabad, were grown in a randomized block design with three replications. Each entry was planted in two rows in a 4.5 m × 1.20 m plot at 30 cm × 5 cm spacing. Five competitive plants per genotype per replication were used to derive plot-level means. Genotypic and phenotypic covariances were used to calculate correlation coefficients. Significance was assessed in the thesis using a t-test. Path coefficients were obtained by solving the simultaneous relationship $r_{i;y} = p_{i;y} + \sum r_{ij}p_{j;y}$, where $r_{i;y}$ is the correlation between trait i and yield, $p_{i;y}$ is the direct effect of trait i , and $r_{ij}p_{j;y}$ represents the indirect contribution through trait j . The present article reports the complete correlation and direct-effect values supplied in the thesis summary. Complete numerical tables were available for 11 traits; filled and unfilled spikelets described in the methods chapter were not reconstructed because their correlation and path coefficients were not supplied.

3. Results and discussion

3.1 Correlations with grain yield

Genotypic correlations with grain yield were generally stronger than phenotypic correlations, especially for tiller

number, panicle length and grain breadth. This pattern suggests that environmental variation attenuated the expression of several underlying genetic relationships. Tiller number had the strongest positive genotypic association with yield ($r = 0.956$), followed by total spikelets panicle⁻¹ (0.846) and grain breadth (0.670). At the phenotypic level, total spikelets panicle⁻¹ had the strongest positive association (0.818), followed by grain breadth (0.641) and tiller number (0.664).

Days to 50% flowering had a small but significant negative association with grain yield at both levels (−0.203 genotypic; −0.202 phenotypic), suggesting that earlier flowering may be advantageous in this moisture-limited production context. Days to maturity, plant height, test weight and length/breadth ratio were not meaningfully associated with yield. However, correlation should not be interpreted as causation: the high inter-trait association between tillers and total spikelets panicle⁻¹ ($r = 0.963$ at the genotypic level), and between tillers and panicle length (0.796), indicates substantial overlap among candidate selection traits.

Table 1: Genotypic and phenotypic correlations of component traits with grain yield plant⁻¹.

Trait	Genotypic r	Phenotypic r	Association with yield
Days to 50% flowering	-0.203	-0.202	Significant negative
Days to maturity	-0.072	-0.068	Negligible/weak
Plant height (cm)	-0.000	-0.000	Negligible/weak
Tillers plant ⁻¹	0.956	0.664	Significant positive
Panicle length (cm)	0.625	0.569	Significant positive
Total spikelets panicle ⁻¹	0.846	0.818	Significant positive
Test weight (g)	0.007	0.008	Negligible/weak
Grain length (mm)	0.440	0.437	Significant positive
Grain breadth (mm)	0.670	0.641	Significant positive
L/B ratio	-0.129	-0.115	Negligible/weak

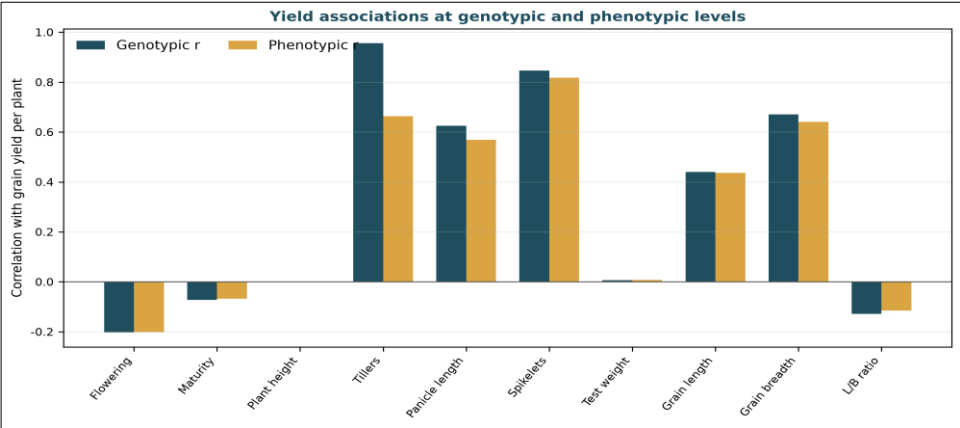


Fig 1: Original paired-bar visualization of the reported genotypic and phenotypic correlations with grain yield plant⁻¹

3.2 Direct and indirect effects revealed by path analysis

Total spikelets panicle⁻¹ had the largest positive direct effect on grain yield at both the genotypic (0.997) and phenotypic (0.584) levels. Grain breadth was the second most consistent direct contributor, with coefficients of 0.826 and 0.721. These direct effects agree with the positive correlations and support their use as primary selection criteria in this population. Panicle length also had a positive direct effect, although the phenotypic coefficient was small (0.025), indicating that its favourable association may operate mainly through panicle productivity.

The contrast between correlation and direct effect was particularly important for tiller number and grain length. Tiller number showed a very strong positive genotypic correlation with yield but a negative genotypic direct effect (−0.580); the thesis summary attributes its positive overall relationship chiefly to indirect effects through total spikelets panicle⁻¹ (0.960), grain breadth (0.511) and panicle length (0.197). Grain length had positive correlations with yield but negative direct effects at both levels (−0.294 genotypic; −0.359 phenotypic), indicating that its apparent yield benefit was mediated through other grain and panicle traits.

Therefore, selection for tiller number or grain length in isolation could be misleading. Test weight showed negligible correlations with yield and negative direct effects at both levels. Length/breadth ratio had positive direct effects but weak negative total correlations, demonstrating how opposing indirect effects can reverse the direction of a simple association. These

findings are biologically and statistically plausible for a population in which grain number, grain size and panicle structure compete for assimilates. They also echo the broader rice literature, where the most reliable yield criteria vary with genetic background and test environment (Seyoum *et al.*, 2012; Faysal *et al.*, 2022) ^[2, 3].

Table 2: Direct path coefficients for grain yield plant⁻¹

Trait	Genotypic direct effect	Phenotypic direct effect	Interpretation
Days to 50% flowering	-0.189	-0.167	Weak/negative yield criterion
Days to maturity	0.202	0.097	Consistent positive direct effect
Plant height (cm)	-0.073	-0.007	Weak/negative yield criterion
Tillers plant ⁻¹	-0.580	0.061	Correlation mainly indirect
Panicle length (cm)	0.248	0.025	Consistent positive direct effect
Total spikelets panicle ⁻¹	0.997	0.584	Consistent positive direct effect
Test weight (g)	-0.217	-0.094	Correlation mainly indirect
Grain length (mm)	-0.294	-0.359	Correlation mainly indirect
Grain breadth (mm)	0.826	0.721	Consistent positive direct effect
L/B ratio	0.498	0.478	Consistent positive direct effect

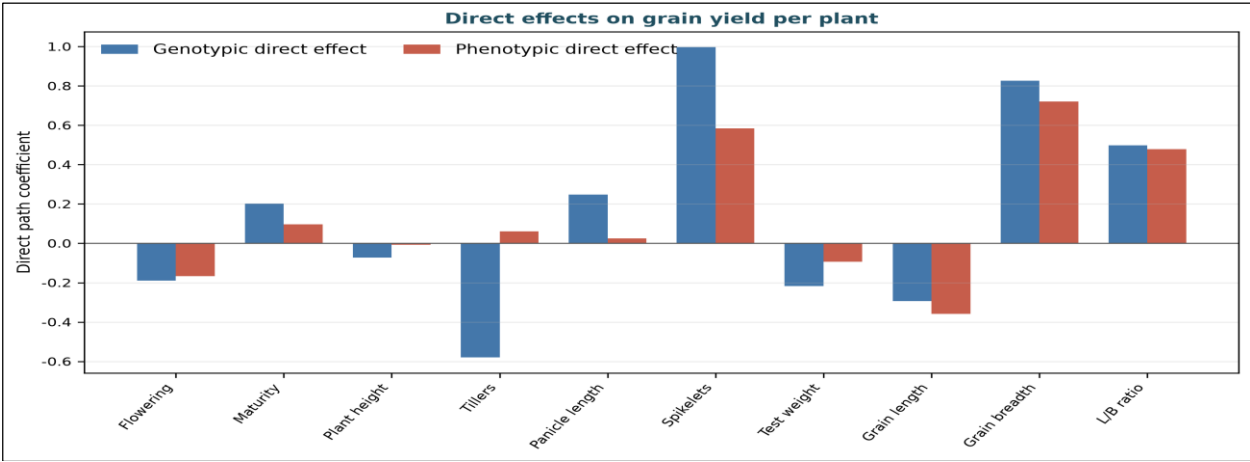


Fig 2: Original paired-bar visualization of genotypic and phenotypic direct effects on grain yield plant⁻¹

3.3 Selection model for upland rice yield improvement

The combined evidence supports a hierarchical selection model. Total spikelets panicle⁻¹ and grain breadth are the most dependable primary criteria because their correlations and direct effects are positive at both genetic and phenotypic levels. Panicle length is a complementary structural trait, while productive tillering should be retained only when it

results in productive panicles and higher spikelet-bearing capacity. Earlier flowering may be useful for drought escape, but it must be combined with adequate grain filling and acceptable grain quality. Test weight should not be prioritized as a yield criterion in this population unless quality objectives independently justify it.

Table 3: Evidence-based selection tiers for grain-yield improvement

Selection tier	Traits	Evidence-based rationale
Primary	Total spikelets panicle ⁻¹ ; grain breadth	Positive correlation and strong direct effects at both levels
Complementary	Panicle length; productive tillering	Favourable associations, but tiller effect is substantially indirect
Context dependent	Days to 50% flowering; grain length	Useful direction of association, but trade-offs and indirect effects require testing
Deprioritize for yield alone	Test weight; L/B ratio	Weak/negative overall association despite some heritable direct effects

4. Conclusions

Correlation and path analysis revealed that grain yield in the evaluated upland rice population was most directly associated with total spikelets panicle⁻¹ and grain breadth. Tiller number was strongly correlated with yield, but its negative genotypic direct effect showed that the association was primarily indirect through panicle productivity and grain breadth. Grain length showed the same general pattern of positive correlation but negative direct contribution. The breeding implication is to select for a coordinated phenotype

rather than for a single correlated trait: high spikelet-bearing capacity, favourable grain breadth, adequate panicle length, and sufficient productive tillering under a suitable flowering duration. The results are population- and environment-specific. The trial was conducted in one season and one location, and the source summary did not provide residual effects, standard errors of path coefficients or multicollinearity diagnostics. These should be reported in the final journal analysis, ideally using the original plot-level data and multi-

environment validation. Until then, the coefficients should be treated as strong hypotheses for selection, not universal causal estimates.

References

1. Dewey DR, Lu KH. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*. 1959;51:515-518. DOI:10.2134/agronj1959.00021962005100090002x.
2. Faysal ASM, Ali L, Azam MG, Sarker U, Ercisli S, Golokhvast KS, Marc RA. Genetic variability, character association, and path coefficient analysis in transplant Aman rice genotypes. *Plants*. 2022;11(21):2952. DOI:10.3390/plants11212952.
3. Seyoum M, Alamerew S, Bantte K. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *Journal of Plant Sciences*. 2012;7:13-22. DOI:10.3923/jps.2012.13.22.
4. Wright S. Correlation and causation. *Journal of Agricultural Research*. 1921;20:557-585.