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ASSESSMENT OF GENETIC VARIABILITY FOR LODGING RESISTANCE AND YIELD TRAITS IN DIVERSE RICE (*Oryza sativa* L.) GENOTYPES

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ABSTRACT

The field experiment was conducted during the *Rabi* 2024–2025 season at the Agricultural Research Station, Nellore, India to study the genetic variability, heritability, and genetic advance for lodging resistance and yield-related traits in a panel of 100 rice genotypes. Eleven key traits were evaluated viz., plant height, number of tillers per plant, culm thickness, culm diameter, panicle length, panicle weight, number of grains per panicle, grain yield per plant, section modulus, bending stress, and bending moment. Statistical analysis revealed significant genetic variation among the genotypes for all the studied traits. Traits such as panicle weight, number of grains per panicle, grain yield, section modulus, bending stress, and bending moment exhibited high genotypic and phenotypic coefficients of variation, indicating a broad range of variability. High heritability coupled with high genetic advance were observed for all the traits under study, suggesting the predominance of additive gene effects and the potential for effective improvement through pedigree method. These results highlight the importance of prioritizing high-heritability traits to accelerate genetic gains in breeding programs focused on enhancing lodging resistance and yield performance in rice.

KEYWORDS: Lodging resistance, variability, genetic advance, Rice, Bending moment.

INTRODUCTION

Rice (*Oryza sativa* L.) is the second most significant staple grain crop in the world after wheat. Rice serves as a primary source of calories for nearly half of the global population and holds a dominant position in terms of cultivation area and production, particularly in South and South-East Asian regions. However, yield losses due to various stresses, shrinking arable land, and rising population pose serious challenges. Climate change, with unseasonal rains and strong winds, further aggravates the problem by causing lodging, affecting both yield and quality. Proactive measures are needed to address these climate-induced stresses. Lodging is not only influenced by natural environmental factors but also by agronomic practices *viz.,* Excessive nitrogen application, inappropriate sowing dates and plant density, as well as factors like soil compaction and diseases such as sheath rot, significantly contribute to the risk of lodging (Zhang *et al*. 2014, 2016; Pan *et al*. 2019). Lodging can be categorized into three major types i.e., root lodging, bending type lodging, and breaking type lodging (Grafius and Brown 1954; Hirano *et al*. 2017). Upland-cultivated rice develops a weak root system leading to root lodging (Laosut m strength and for further improvement, knowledge of the genetic control of mechanisms that regulate culm strength is a prerequisite" (Badri *et al*. 2024).

The presence of adequate genetic variability is the fundamental pre-requisite to conduct any crop improvement programme. Therefore, it is essential to analyze the extent of variability within the species, understand the relationships among traits, and determine the contribution of each trait to enhancing rice productivity through breeding efforts (Khan *et al*. 2020). The genotypic coefficient of variation (GCV) indicates the extent of genetic variability and represents the inheritable component of trait variation. Genetic variability along with heritability estimates would provide the amount of genetic gain expected out of selection". Therefore, assessing variability is vital for establishing effective selection criteria aimed at enhancing culm strength and improving yield potential.

MATERIAL AND METHODS

A set of 100 rice genotypes were evaluated during 2024-25 rabi season at Agricultural Research Station (ARS), ANGRAU, Nellore, Andhra Pradesh, India. The genotypes were sown in the raised bed and transplanted into the main field 27 days after

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sowing with the spacing of 20 x 15 cm in Aplha Lattice Design. All the package of practices were followed for the good establishment of the crop. The genotypes were evaluated and observations were recorded on five randomly selected plants in each replication for morphological traits *viz.,* plant height (PH) (cm), tiller number (TN), culm thickness (CT) (mm), culm diameter (CD) (mm), section modulus (mm3), bending stress (BS) (Kg mm^{-2}), bending moment (BM) (g $stem^{-1}$), panicle length (PL) (cm), panicle weight (PW), number of grains per panicle (NGP), grain yield (GY). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed following the procedure outlined by Burton *et al.* 1952. The magnitude of variability was classified based on the criteria suggested by Sivasubramanian and Madhavamenon (1973). Broad-sense heritability (h^2) and genetic advance as a percentage of the mean (GAM) were estimated using the methods described by Lush 1940 and Johnson et al. 1955 respectively.

The following traits were determined as per Ookawa *et al.* 2010 and Badri *et al.* 2024

Culm diameter (CD) = $(a_1+b_1)/2$

Culm thickness (CT) = $[(a_1+b_1)/2] – [(a_2+b_2)/2]$

Section modulus (SM) = $\pi/32 \times (a_1\ 3b_1 - a_2\ 3b_2)/a_1$

Where, $a_1$is the outer diameter of the minor axis in an oval cross-section,

$b_1$is the outer diameter of the major axis in an oval cross-section.

a_2 is the inner diameter of the minor axis in an oval cross-section,

b_2 is the inner diameter of the major axis in an oval cross-section.

Bending stress (BS) = $(TR \div 40) \times (1000 \div TN)$

Bending moment at breaking (M) = Section modulus (SM) × Bending stress (BS)

Where; TR is the prostrate tester reading value (measure of pushing resistance) and TN is the tiller number. The prostrate tester (DIK-7400, Daiki Rika Kogyo Co. Ltd., Tokyo, Japan) was used to measure the pushing resistance of the culm.

RESULTS AND DISCUSSION

The identification of the key traits that can be used in crop improvement through various breeding techniques is extremely important. The observed variability, heritability estimates, and the strength and direction of trait associations, provide a clear understanding of the underlying genetic architecture. These findings form a robust basis for selecting desirable traits to enhance culm strength in rice breeding programs.

Analysis of variance for 11 lodging resistance and yield related traits revealed significant differences among the genotypes for all the traits under study, indicating the existence of greater variability among the genotypes. Such variability forms the foundation for effective selection in breeding programs.

The variability analysis indicated that PCV was consistently higher than GCV for all traits (Table 1), suggesting that phenotypic variation was influenced by both genetic and environmental factors. Plant height exhibited moderate variability (GCV: 19.37%, PCV: 19.52%), with very high heritability (98.50%) and high genetic advance as percent of mean (GAM: 39.61%), implying strong additive gene action and effective selection potential, in agreement with Srilakshmi et al. (2018), and Sahu *et al.* (2024). Similarly, number of tillers per plant showed moderate GCV (17.92%) and PCV (18.57%), high heritability (93.13%), and GAM (35.63%), supporting its improvement through selection, as observed by Akshay *et al.* (2022) and Arun *et al.* (2023). Culm thickness and culm diameter both recorded high genetic variability (GCV: 16.98% and 17.35%) and heritability (92.79% and 98.61%), with GAM values of 33.68% and 35.49%, respectively suggesting reasonable scope for improvement, as supported by Nomura *et al.* (2021), Silva *et al.* (2022) and Arun *et al.* (2023). The section modulus also showed high GCV (30.57%), heritability (99.16%), and GAM (62.70%), indicating the effectiveness of selection, which is in line with the observations of Akshay *et al.* (2024). Bending stress and bending moment exhibited high variability and heritability (95.34% and 98.14%), with respective GAM values of 51.23% and 104.16%, indicating potential for significant genetic gains, as reported by Akshay *et al.* (2024). Panicle length showed moderate GCV (12.59%),

Table 1. Estimates of Genetic variability parameters for lodging resistance and yield related traits in rice

S. No.	Character	Mean	Range		Coefficient of Variation (%)		Heritability in broad sense (h^2) (%)	GA	GA as percent of mean
			Min	Max	Genotypic	Phenotypic			
1.	Plant height (cm)	88.62	60.60	154.40	19.37	19.52	98.50	35.06	39.61
2.	No of tillers per plant^{-1}	14.76	9.42	28.80	17.92	18.57	93.13	5.26	35.63
3.	Culm thickness (mm)	1.01	0.56	1.64	16.98	17.62	92.79	0.34	33.68
4.	Culm diameter (mm)	5.25	2.87	7.64	17.35	17.47	98.61	1.86	35.49
5.	Panicle length (cm)	21.49	13.74	29.38	12.59	13.21	90.84	5.31	24.71
6.	Panicle weight (g)	2.86	1.12	6.36	37.66	38.04	98.01	2.20	76.81
7.	No of grains per panicle	137.49	37.00	283.80	38.18	38.46	98.54	107.34	78.07
8.	Grain yield per plant^{-1} **(g)**	17.58	5.21	36.96	40.06	40.54	97.64	14.34	81.55
9.	Section modulus (mm^3)	8.92	4.42	19.30	30.57	30.70	99.16	5.60	62.70
10.	Bending stress (kg mm^{-2})	15.89	8.65	29.30	25.47	26.09	95.34	8.14	51.23
11.	Bending moment (g stem^{-1})	148.32	51.38	437.37	51.04	51.52	98.14	154.49	104.16

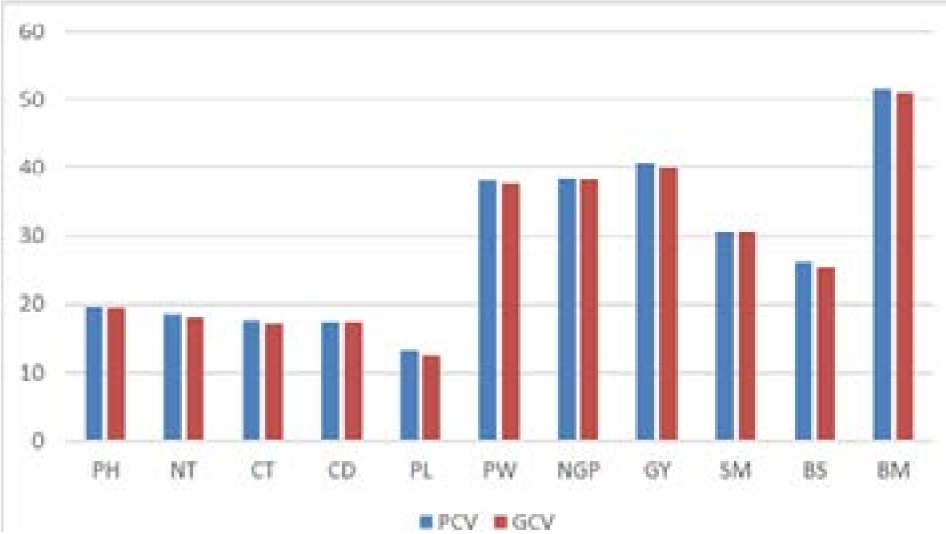

Fig 1. Phenotypiccoefficient of variation (PCV) and genotypic coefficient of variation (GCV) for 11 traits in Rice

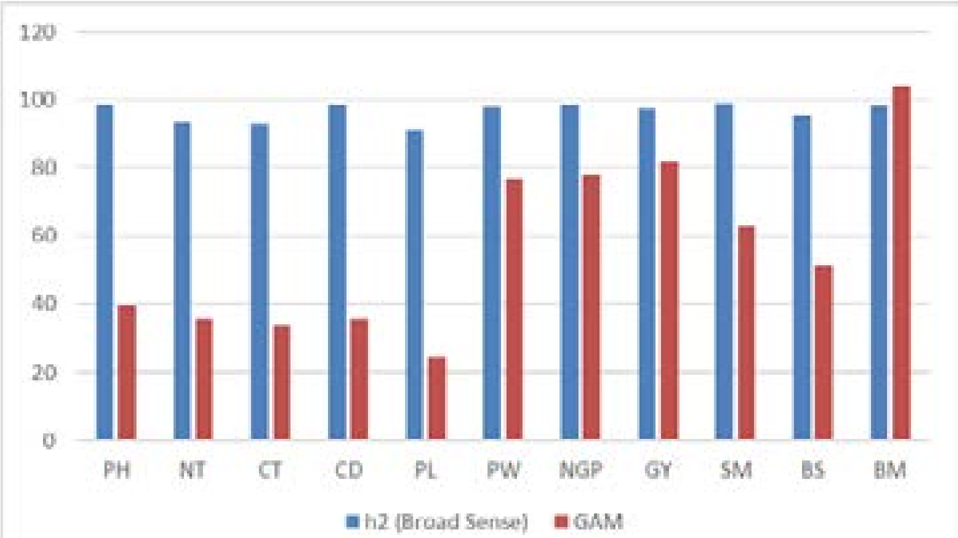

Fig. 2. Heritability (H_2bs) and genetic advance as percent of mean (GAM) for 11 traits in Rice

high heritability (90.84%), and GAM (24.71%), while Panicle weight and number of grains per panicle displayed high variability, with heritability estimates of 98.01% and 98.54%, and genetic advance as percent of mean values of 76.81% and 78.07%, respectively, suggesting considerable potential for selection gains. These results corroborate the findings of Hasan *et al*. (2022), Arun *et al*. (2023), and Harsharaj *et al*. (2024)Notably, grain yield per plant had the highest GCV (40.06%), PCV (40.54%), heritability (97.64%), and GAM (81.55%), indicating that it is largely controlled by additive gene action and can be improved efficiently through direct selection, accordance with Demeke *et al*. (2023) and Harsharaj *et al*. (2024). Overall, the combination of high heritability and high genetic advance observed for all the studied traits, indicates predominance of additive gene action, suggesting that direct selection would be highly effective in achieving genetic improvement, enhance genetic gain and accelerate progress in rice breeding programs.

The present study revealed substantial genetic variability, along with high heritability and notable genetic advance for several important lodging resistance and yield-related traits in rice. Traits such as culm thickness, culm diameter, section modulus, bending stress, bending moment, panicle weight, number of grains per panicle, and grain yield per plant were found to be under strong genetic control, indicating the effectiveness of direct selection for these traits in breeding programs. These findings offer valuable guidance for rice breeders in developing lodging-resistant and high-yielding varieties, thereby supporting sustainable rice cultivation and addressing the growing challenges of global food demand and resource limitations.

LITERATURE CITED

Akshay, M., Chandra, B.S., Devi, K.R and Hari, Y. 2022. Genetic variability studies for yield and its attributes, quality and nutritional traits in rice (*Oryza sativa* L.). *The Pharma Innovation Journal*. 11(5): 167-172.

Akshay, M., Krishna, L., Badri, J., Barbadikar, K. M. and Rao, D. S. 2024 Unraveling Promising Genetic Variability Associated with Strong Culm and Yield Parameters in Inter Sub-Specific Cross Derived Recombinant Inbred Lines in Rice (*Oryza sativa* L.). *International Journal of Plant & Soil Science*. 36(9): 700–711.

Ashikari, M., Sakakibara, H., Lin, S., Yamamoto, T., Takashi, T., Nishimura, A., Angeles, E.R., Qian, Q., Kitano, H. and Matsuoka, M. 2005. Cytokinin oxidase regulates rice grain production. *Science*. 309(5735): 741-745.

Arun, C., Jayalekshmy, V.G and Shahiba, A.M. 2023. Studies on PCV, GCV, Heritability, and Genetic Advance in Rice Genotypes for Yield and Yield Components. *International Journal of Plant & Soil Science*. 35(16): 324-330.

Badri, J., Padmashree, R., Anilkumar, C., Mamidi, A., Isetty, S.R., Swamy, A.V.S.R. and Sundaram, R.M. 2024. Genome-wide association studies for a comprehensive understanding of the genetic architecture of culm strength and yield traits in rice. *Frontiers in Plant Science.* 14: 1298083.

Burton GW. 1952. Quantitative inheritance in grasses. In proceedings of 6th International Grassland Congress, Pennsylvania State College, USA. 277-283.

Demeke, B., Dejene, T and Abebe, D. 2023. Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza Sativa* L.) genotypes at pawe, northwestern Ethiopia. *Cogent Food & Agriculture*. 9(1): 2157099.

Fan, C., Xing, Y., Mao, H., Lu, T., Han, B., Xu, C., Li, X. and Zhang, Q. 2006. GS3, a major QTL for grain length and weight and minor QTL for grain width and thickness in rice, encodes a putative transmembrane protein. *Theoretical and applied genetics*. 112: 1164-1171.

Grafius, J.E. and Brown, H.M. 1954. Lodging resistance in oats.

Harshraj, S., Ashutosh, Kumar., Harmeet, Singh, J., Bal, Krishna., Nilesh, T., Suhel, M and Pratiksha, P. 2024. Genetic variability, correlation and path-coefficient analysis for yield and yield attributing traits in aerobic rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 15(1): 226-232.

Hasan, N.A., Rafii, M.Y., Harun, A.R., Alı, N.S., Mazlan, N and Abdullah, S. 2022. Genetic analysis of yield and yield contributing traits in rice (*Oryza sativa* L.) BC_2F_3 population derived from MR264 × PS2. *Biotechnology & Biotechnological Equipment*. 36(1): 184-192.

Hirano, K., Okuno, A., Hobo, T., Ordonio, R., Shinozaki, Y., Asano, K., Kitano, H. and Matsuoka, M. 2014. Utilization of stiff culm trait of rice smos1 mutant for increased lodging resistance. *PLoS One*. 9(7): 96009.

Hirano, K., Ordonio, R.L. and Matsuoka, M. 2017. Engineering the lodging resistance mechanism of post-Green Revolution rice to meet future demands. *Proceedings of the Japan Academy, Series B.* 93(4): 220-233.

Huang, X., Qian, Q., Liu, Z., Sun, H., He, S., Luo, D., Xia, G., Chu, C., Li, J. and Fu, X. 2009. Natural variation at the DEP1 locus enhances grain yield in rice. *Nature genetics*. 41(4): 494-497.

Ikeda-Kawakatsu, K., Yasuno, N., Oikawa, T., Iida, S., Nagato, Y., Maekawa, M. and Kyozuka, J. 2009. Expression level of ABERRANT PANICLE ORGANIZATION1 determines rice inflorescence form through control of cell proliferation in the meristem. *Plant physiology*. 150(2): 736-747.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*. 47: 314-318

Khan, M.K., Pandey, A., Hamurcu, M., Hakki, E.E. and Gezgin, S. 2020. Role of molecular approaches in improving genetic variability of micronutrients and their utilization in breeding programs. *In Wheat and barley grain biofortification*. 27-52.

Laosutthipong, C., Seritrakul, P. and NaChiangmai, P. 2023. Lodging-related gene expression in upland rice varieties from Pala U Village, Thailand. *Int J Agric Technol*. 19(4): 1557–1590.

Lush, J.L. 1940. Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. *Journal of animal science*. 1940(1): 293-301.

Miura, K., Ikeda, M., Matsubara, A., Song, X.J., Ito, M., Asano, K., Matsuoka, M., Kitano, H. and Ashikari, M. 2010. OsSPL14 promotes panicle branching and higher grain productivity in rice. *Nature genetics*. 42(6): 545-549.

Nomura, T., Seki, Y., Matsuoka, M., Yano, K., Chigira, K., Adachi, S., Piñera-Chavez, F. J., Reynolds, M., Ohkubo, S and Ookawa, T. 2021. Potential of rice landraces with strong culms as genetic resources for improving lodging resistance against super typhoons. *Scientific reports*. 11(1): 15780.

Ookawa, T., Hobo, T., Yano, M., Murata, K., Ando, T., Miura, H., Asano, K., Ochiai, Y., Ikeda, M., Nishitani, R. and Ebitani, T. 2010. New approach for rice improvement using a pleiotropic QTL gene for lodging resistance and yield. *Nature communications.* 1(1): 132.

Pan, J., Zhao, J., Liu, Y., Huang, N., Tian, K., Shah, F., Liang, K., Zhong, X. and Liu, B. 2019. Optimized nitrogen management enhances lodging resistance of rice and its morpho-anatomical, mechanical, and molecular mechanisms. *Scientific reports*. 9(1): 20274.

Sahu, M., Chaudhari, P., Sao, P.K. and Javid S. 2024. Genetic variation among rice (*Oryza sativa* L) genotypes for yield and yield related traits. *International Journal of Farm Sciences*. 14(3-4): 108-110.

Shomura, A., Izawa, T., Ebana, K., Ebitani, T., Kanegae, H., Konishi, S. and Yano, M. 2008. Deletion in a gene associated with grain size increased yields during rice domestication. *Nature genetics*. 40(8): 1023-1028.

Silva, L.C., De Silva, Y.M.S.H.I.U., Rathnayake, H.R.M.C., Samarasinghe, W.R.C.P., Egodawatta, W.P.C., Senanayake, D.M.J.B., Bandara, J.M.S.V. and Wijesena, K.A.K. 2022. Selection of Culm Characteristics of Rice to Improve Lodging Resistance and Yield Components. *Tropical Agriculturist*. 170(2).

Sivasubramaniam, S. and Madhava Menon, P. 1973. Genotypic and phenotypic variability in rice. *Madras Agric J.* 12: 15-16

Song, X.J., Huang, W., Shi, M., Zhu, M.Z. and Lin, H.X. 2007. A QTL for rice grain width and weight encodes a previously unknown RING-type E3 ubiquitin ligase. *Nature genetics*. 39(5): 623-630.

Srilakshmi, P., Chamundeswari, N., Ahamed, L.M and Rao, S.V. 2018. Assessment of genetic variability studies in wet direct sown rice. *The Andhra Agricultural Journal*. 65(3): 555-560.

Terao, T., Nagata, K., Morino, K. and Hirose, T. 2010. A gene controlling the number of primary rachis branches also controls the vascular bundle formation and hence is responsible to increase the harvest index and grain yield in rice. *Theoretical and Applied Genetics*. 120: 875-893.

Zhang, W.J., Li, G.H., YANG, Y.M., Quan, L.I., ZHANG, J., LIU, J.Y., Shaohua, W.A.N.G., She, T.A.N.G. and DING, Y.F. 2014. Effects of nitrogen application rate and ratio on lodging resistance of super rice with different genotypes. *Journal of Integrative Agriculture*. 13(1): 63-72.