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Research Note

Morphological characterization of strong culm traits and their association with yield performance in rice (*Oryza sativa* L.)

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Abstract
Lodging resistance is an important characteristic for enhancing the productivity and stability of rice (*Oryza sativa*). This study assessed the genetic variability of 81 rice germplasm lines from southern India, focusing on 12 traits contributing for culm structure and yield. A field experiment was conducted in a randomized block design, and the recorded phenotypic data were analysed employing descriptive statistics, variability estimates, correlation analysis, and Principal Component Analysis. The findings revealed high genotypic coefficient of variation and phenotypic coefficient of variation, along with high heritability and genetic advance for culm length of fourth internode, section modulus of fourth internode, and single plant yield. These results indicate strong genetic control and the potential for effective selection for culm traits. Additionally, SPY showed strong positive correlations with the number of productive tillers and hundred seed weight. Plant height, culm length, and culm thickness also exhibited strong correlations with section modulus of fourth internode, highlighting their importance in lodging resistance. The PCA identified three major components that explained 56.16% of the total variability, with culm related traits and yield traits being key contributors. These findings highlight the significance of culm morphology traits in breeding programs and provide valuable insights for parental line selection to enhance rice productivity and develop non-lodging cultivars.

Keywords: rice, culm strength, genetic variability, correlation, PCA

Rice (*Oryza sativa*) is one of the most significant staple foods in the world and provides vital nutrition to almost half of the world's population. An essential component of meals, especially in Asia, Africa, and parts of Latin America, rice is grown in a wide range of conditions, from tropical to temperate (Khush,2005). It is a crop that millions of people depend on because of its adaptability and importance in everyday meals (Olagunju *et al*.,2021). In cereal crops, environmental factors and morphological (structural) characteristics affect lodging. Lodging in rice refers to when the rice plants bend or fall over, usually due to the weight of the mature grains or external factors like wind and rain. This can have a major impact on rice yields and the overall quality of the harvested crop (Yao *et al.,*2011; Zhang *et al*.,2013). Lodging is a significant issue for many crops, particularly cereals, because of the stem's hollow shape. A low-density hollow foam core supports the nearly entirely dense elements that make up the rice stem, which can be thought of as an exterior shell (Zhdanov *et al*.,2020). Thick skin fiber cells make up the mechanical tissue layer that makes up the outer shell, while parenchymal tissue reinforced by vascular bundles makes up the foam core. If lodging, which is defined as bending to the stem's prostrate look, is not adequately controlled, crop output can be reduced by 80% (Foulkes *et al*.,2011; Muhammad *et al.,*2020). The final quality of grain is negatively impacted by lodging during the ripening stage, which can result in mold infestation, pest carryover, lower nutrient content, and poor cooking quality.

Measurements of lodging resistance in cereals have been made using culm lodging traits, including increased primary culm height (culm length fourth), plant height, single plant yield, culm wall thickness, internode diameter, pith thickness, internode length, and section modulus. (Zhang *et al.,*2016; Olagunju *et al.,*2021). Larger culm diameters and thicker walls are typically better for lodging resistance. A prior study has found that there are two types of lodging for cereal plants *ie* stem lodging and root lodging (Sterling *et al.,*2003). While stem lodging describes the bending or breaking of the lower culm internodes as a result of severe bending strain at the higher internodes, root lodging occurs when whole and unbroken culms lean from the crown because their root anchorage in the ground fails. The new primary focus for enhancing lodging resistance and grain yield is strengthening the stems of the lower internodes of rice plants, as stem strength, or the bending or breaking strength of the culm, is crucial for stem lodging resistance, especially for the basal internodes of crops (Islam *et al.,*2007; Zhang *et al*.,2010). The purpose of this study is to examine the diversity of morphological traits related to culm strength and their effect on yield.

A field experiment was conducted during the *Kharif* , 2024 at Karunya Institute of Technology and Sciences, Coimbatore. A total of 81 rice genotypes gathered from different locations in Tamil Nadu and Kerala were used for the study. The experiment was laid out in a Randomized complete block design in three replications following a spacing of 20 × 20 cm and a row length of 2 m. Observations were recorded from five plants that were chosen at random from each replication for culm morphology traits and yield. Observations on the number of productive tillers (NP), Plant Height (PH), Total Culm Length (CL), Culm Length Fourth internode (CLF), Culm Thickness (CT), Culm Diameter (CD), and Pith Thickness (PT) were recorded at 20 days after the heading of the genotype. Section modulus fourth internode (SMF) was calculated using the formula proposed by Ookawa *et al.,* 2014. Observations on Panicle Length (PL), Panicle Weight (PW), Hundred Seed Weight (HSW), and Single Plant Yield (SPY) were recorded after harvest.

The mean data were subjected to Analysis of Variance (ANOVA) to examine the genotype differences. Descriptive statistics, genetic variability and heritability studies, and correlation analysis between various traits, and Principal Component Analysis (PCA), were conducted to group the genotypes based on performance for culm morphology traits and yield traits using the STAR tool (Statistical Tool for Agricultural Research). Variability estimates such as phenotypic variation (PV), genotypic variation (GV), environmental variation (EV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2_{BS}), and genetic advance as a percentage of the mean (GAM) were calculated. GCV and PCV were calculated using the formula described by (Burton and Devane 1953). The range of variation was classified as high (> 20%), moderate (10-20%), and low (<10%), based on the criteria proposed by Sivasubramaniam and Madhavamenon, 1973. Broad-sense heritability (h^2_{BS}) was estimated by taking the ratio of genotypic variance to total variance (Lush, 1949 and Hanson *et al*.,1956), and it was expressed as a percentage. According to Robinson *et al.* (1949), heritability estimates were categorized into high (> 60%), moderate (30-60%), and low (0-30%). GAM was calculated and similarly classified as high (> 20%), moderate (10-20%), and low (< 10%), following the guidelines provided by (Johnson *et al.,*1955).

Analysis of variance for culm morphology and yield traits revealed significant differences (**Table 1)** among the genotypes**.** The *per se* performance of genotypes is presented in **Table 2**. The genotype *Vellakar* recorded a maximum value for PH (125.2 cm) and CL (104.7 cm). A high CLF (19.1 cm) and CT (5.9cm) was exhibited by KRG92 and *Prathyasa* respectively. Maximum value for CD and PT was recorded by CO 52 whereas high SMF was observed in the genotype *Mysore malli*. Previous studies have shown that thicker culms with larger diameters contribute to higher bending resistance, thereby reducing susceptibility to lodging (Ookawa and Ishihara, 1992). Shorter plants with reduced CL generally have a lower centre of gravity, enhancing their stability against lodging (Shah *et al.,* 2019). The genotype CO 51 recorded a high NP and ADT 38 exhibited maximum PL(28.7mm). High mean value for PW, HSW and SPY was recorded by CR1009*Sub 1*, TPS 3 and Sorna mashuri respectively. Low CV (<5 %) was observed for PH, CL, CLF and CT suggesting uniformity across genotypes, making them as promising traits for breeding lodging-resistant rice cultivars (Kashiwagi *et al.,* 2008; Hu *et al.,* 2023). SMF displayed the moderate variation (CV, 10.24%) followed by PT (CV, 8.38 %), which can be beneficial for breeding programs to select for improved lodging resistance and plant architecture (Kashiwagi and Ishimaru, 2004). The variations observed for these traits indicates significant genetic diversity among the rice genotypes. Traits with lower CV values can be targeted for stability, while traits with higher variation, such as SMF and PT, present opportunities for genetic enhancement (Peng *et al.,* 2008).

The analysis of genetic variability parameters, including GV, PV, EV, GCV, PCV, ECV, $h^2(BS)$, GA, and GAM, revealed significant variability among the traits studied in

Table 1. Analysis of variance for culm morphology and yield traits

	Mean sum of square		
Traits	**Genotype**	**Replication**	**Error**
Df	80	2	160
PH (cm)	185.92 *	123.40	11.40
CL (cm)	175.06*	30.97	6.89
CLF (cm)	48.42*	0.06	0.07
CT (mm)	2.05**	0.01	0.01
CD (mm)	64.86*	28.40	5.91
PT (mm)	73.60*	26.97	5.83
SMF (m^3)	77.73*	4.01	0.95
NP(no.)	51.33*	4.64	0.85
PL (cm)	35.86*	6.68	1.95
PW (g)	17.58*	6.87	1.43
HSW (g)	0.66**	0.09	0.01
SPY (g)	254.86**	23.85	3.77

* Significant at **$p < 0.05$**, ** Significant at **$p < 0.01$**

rice **(Table 3).** Traits such as CLF, SMF, NP, HSW, and SPY exhibited high GCV and PCV values, indicating substantial genetic variation. The minimal difference between GCV and PCV for these traits suggests a lower environmental influence, making them suitable for direct selection in breeding programs. The combination of high heritability and high GAM for CLF, CT, CD, PT, SMF, NP, PL, PW, HSW and SPY indicates strong additive gene action, making these traits ideal candidates for selection and genetic improvement. Other traits, such as PH and CL, showed high heritability and medium GAM, suggesting a mixed influence of genetic and environmental factors (Maurya *et al.*,2018). These findings are consistent with previous studies in rice, where traits associated with yield and structural stability exhibited high heritability and genetic advance, making them suitable for selection-based improvement (Akinwale *et al.,* 2011). The low environmental variance (EV) for most traits indicates that the genotypes are relatively stable in the given environmental conditions.

Correlation coefficient measures the relationship between two variables, whether that relationship arises from genetic linkage, pleiotropy, or environmental factors (Saran *et al*., 2023; Vengatesh and Govindarasu, 2018). Correlation among the culm and yield traits are represented in **Fig.1**(values not shown). One of the most notable findings is the strong positive association between PH and CL (0.96**), suggesting that taller plants tend to have longer culms and selecting for PH may directly influence culm elongation, which can affect lodging susceptibility. This relationship reflects an interconnected genetic and physiological basis for plant stature and culm elongation, aligning with previous studies (Chigira *et al.,* 2020). Traditional rice landraces generally exhibit increased plant height with longer culms, which may reduce lodging resistance. However, certain genotypes, such as 'Monster Rice 1,' maintain strong lodging resistance despite their height (Mullangie *et al.,* 2024). This suggests that strategic hybridization could improve lodging resistance while preserving desirable plant height characteristics (Sanni *et al.,* 2012). CT exhibited positive correlation with PH (0.17**) and CL (0.18**), implying that plants with thicker culms can potentially support more structural integrity, thereby enhancing overall mechanical support. Furthermore, CD showed a strong correlation with PT (0.94**), underscoring the structural contributions of culm anatomy to plant productivity. Thicker culms with greater pith thickness may provide robust support and improved nutrient conduction, favouring tiller development and subsequently enhancing yield. These findings align with reports from (Zhang *et al*., 2016 and Chigira *et al*.,2020). Similarly a high positive correlation was identified between CT and SMF (0.79**), emphasizing the structural role of the culm in providing mechanical strength. This relationship suggests that thicker culms are associated with a higher section modulus, indicative of bending strength and improved lodging resistance. The moderate positive correlation of CT with PH and SMF further highlights the importance of culm architecture (CT, PT, CD) in supporting taller plants. Similar results have been observed in rice (Kashiwagi *et al.,* 2008; Deshabandu *et al*., 2024) and Kodo millet (Sreeja *et al*., 2014). Regarding yield components, SPY displayed significant positive correlations with the NPT (0.65**) and HSW (0.58**), as well as with PH and CL (0.15*). These relationships underscore the importance of productive tillers and heavier seeds in enhancing overall yield. Positive associations between HSW and NP or PH suggest that improving both traits could lead to yield gains

Table 2. Overall mean value for culm morphology and yield traits

S.No	Genotype name	PH (cm)	CL (cm)	CLF (cm)	CT (mm)	CD (mm)	PT (mm)	SMF (m^3)	NP (no.)	PL (cm)	PW (g)	HSW (g)	SPY (g)
G1	Aanai Komban	93.6	76.0	11.1	3.0	34.0	25.0	5.6	20.2	17.2	16.4	2.2	44.6
G2	ADT 45	99.0	80.5	14.2	3.2	42.0	33.1	6.1	19.0	**17.0**	20.1	2.4	36.7
G3	Amman Ponni	93.1	75.3	9.3	3.1	39.0	30.5	5.4	10.5	20.0	19.4	1.9	24.8
G4	Arumpatham Kuruvai	95.3	76.8	7.5	3.1	32.0	23.3	**1.0**	20.8	21.0	18.3	2.6	41.3
G5	ASD 16	116.0	96.7	17.2	**2.8**	**28.0**	**19.2**	5.6	13.8	22.3	20.1	2.6	36.8
G6	Chinnar	96.1	79.0	12.3	3.8	45.0	34.3	8.3	11.5	18.3	19.4	1.8	26.6
G7	CO 51	96.7	76.8	10.2	4.2	38.0	27.0	10.1	**25.5**	25.3	20.1	1.8	35.5
G8	CO 52	**90.7**	**69.8**	17.2	3.0	**52.0**	**42.8**	6.5	12.4	26.4	21.1	2.2	40.0
G9	CO 53	105.6	84.5	16.3	3.9	44.0	32.8	10.6	12.0	20.4	23.4	2.2	37.9
G10	CO 54	105.5	88.9	7.4	2.9	40.0	31.0	5.8	15.4	18.6	20.4	2.3	42.5
G11	CO 55	95.5	78.6	13.3	3.1	35.0	26.0	5.8	10.8	18.3	22.4	2.2	27.5
G12	CR1009*Sub 1*	106.9	88.8	11.2	3.2	48.0	38.8	6.8	17.4	19.4	**25.5**	2.4	43.6
G13	JGL	111.2	91.4	16.3	4.1	35.0	23.6	9.9	17.4	21.0	20.1	2.3	39.5
G14	Kalasar	103.1	84.7	18.0	2.9	40.0	32.4	4.2	8.6	26.0	19.8	**1.2**	13.9
G15	Karudan Samba	115.6	97.0	**5.5**	4.1	39.0	27.8	9.9	11.8	22.4	19.0	2.5	25.6
G16	Karumkuruvai	111.7	94.2	13.2	2.9	42.0	34.6	3.9	16.4	24.1	20.4	2.3	41.4
G17	Karuppu Kavuni	96.6	78.3	17.1	3.1	35.0	25.6	6.7	20.2	23.8	16.3	2.8	46.8
G18	Keerai Samba	107.1	89.7	12.3	4.0	33.0	21.7	9.8	13.8	28.3	15.4	2.2	28.6
G19	Kichili Samba	113.9	96.9	11.3	2.9	47.0	37.8	6.2	14.8	24.7	15.4	2.3	45.7
G20	Kollan Samba	117.6	97.7	9.0	3.9	32.0	21.4	8.9	17.5	28.3	17.0	1.5	24.6
G21	Kothamalli Samba	96.3	79.1	9.2	3.8	38.0	26.8	12.5	19.8	24.6	17.3	1.8	41.2
G22	Kottaram Samba	101.3	84.6	18.2	4.0	44.0	32.7	11.3	14.3	18.9	15.0	2.0	26.5
G23	Kulipadichan	117.0	96.4	16.2	5.1	47.0	33.2	26.1	20.8	18.5	17.3	2.6	37.9
G24	Kullakar	96.5	79.3	17.3	2.9	37.0	29.5	4.1	19.1	19.3	18.1	2.1	25.7
G25	Kuttakar	95.5	77.8	14.3	**2.8**	39.0	31.6	3.8	17.7	22.4	17.3	2.6	36.6
G26	Kuzhaiyadi Samba	105.6	88.3	7.5	3.6	41.0	27.7	22.1	13.5	22.7	18.3	2.4	27.5
G27	Mapillai Samba	107.2	90.9	18.2	4.1	40.0	28.6	15.2	15.5	22.6	17.6	2.6	26.9
G28	Milagu Samba	112.7	95.1	14.3	4.0	31.0	19.7	10.9	18.7	24.1	20.5	2.1	31.5
G29	Navara	114.8	96.1	18.1	3.9	34.0	23.0	9.5	17.5	22.4	20.3	2.3	34.4
G30	Norungan	104.7	87.1	7.5	3.9	38.0	26.9	9.8	22.3	28.6	19.8	2.6	46.8
G31	Poongar	104.2	85.3	9.3	2.9	38.0	29.2	5.1	17.8	24.9	19.3	2.4	35.8
G32	Rajae Samba	116.1	96.9	13.4	3.0	31.0	22.1	5.7	24.5	26.3	18.5	2.4	36.4
G33	Rakthasali	104.4	87.7	8.1	4.0	45.0	34.0	9.1	14.6	28.4	17.1	2.3	28.8
G34	Seeraga Samba	117.9	96.5	17.0	5.1	37.0	23.9	12.9	16.6	26.7	15.3	2.6	18.6
G35	Sithiraikar	114.6	96.3	12.2	4.0	36.0	24.9	9.5	17.1	24.7	20.2	2.4	34.4
G36	Sivapu Kavuni	111.2	95.1	17.3	3.0	39.0	29.9	5.3	20.5	23.1	16.2	2.6	44.8
G37	Sorna mashuri	109.7	93.0	10.3	3.0	44.0	36.2	3.8	21.5	23.7	22.4	2.8	**47.5**
G38	Thanga Samba	107.2	90.3	18.2	3.9	48.0	39.0	5.5	14.7	18.6	19.8	1.9	31.5
G39	Thooyamalli	99.9	83.0	9.4	3.0	35.0	26.0	5.4	19.6	18.9	20.3	2.6	33.8
G40	TPS 3	96.2	79.1	18.2	4.0	38.0	26.8	9.5	24.7	19.4	22.1	**2.9**	45.5
G41	TPS 5	117.0	98.7	17.3	3.7	40.0	26.6	22.0	23.0	19.5	21.4	2.8	44.6
G42	Vellakar	**125.2**	**104.7**	16.4	4.0	41.0	29.9	13.6	10.4	19.0	19.9	2.1	26.5

Table 2. Continued...

S.No	Genotype name	PH (cm)	CL (cm)	CLF (cm)	CT (mm)	CD (mm)	PT (mm)	SMF (m^3)	NP (no.)	PL (cm)	PW (g)	HSW (g)	SPY (g)
G43	ADT 53	99.3	81.5	9.3	3.8	38.0	27.6	11.7	14.5	21.6	22.1	2.3	21.3
G44	BABTLA	97.6	78.9	9.2	**2.8**	34.0	27.0	2.7	13.2	24.7	23.9	2.1	17.5
G45	ADT 38	95.6	77.8	10.0	3.8	37.0	26.0	9.3	15.8	**28.7**	25.4	1.3	27.6
G46	Super ponni 43	94.9	77.7	18.0	3.1	47.0	38.3	5.3	14.1	26.7	19.8	1.8	**10.9**
G47	IR50	99.0	83.0	17.0	3.0	48.0	39.0	5.5	14.5	26.5	20.2	1.8	22.8
G48	Gundu	98.1	80.1	16.0	3.9	34.0	22.7	10.5	12.3	24.6	22.4	1.7	28.3
G49	RLR	100.0	83.3	8.0	3.6	48.0	34.9	19.2	9.5	25.8	21.1	1.6	18.3
G50	LLR	99.0	82.1	11.5	**2.8**	41.0	32.0	5.6	10.8	22.0	20.5	1.8	30.5
G51	Nootri pathu	96.0	77.8	11.0	3.2	40.0	30.6	7.3	13.2	25.4	19.8	1.9	17.6
G52	Renjini	104.8	86.0	17.1	3.0	41.0	31.9	6.1	13.6	23.1	23.8	1.3	15.5
G53	Pavithra	102.9	85.7	16.1	4.9	38.0	26.7	10.9	13.8	19.3	21.4	2.3	22.5
G54	Makom	95.9	77.9	7.1	4.8	37.0	25.8	11.1	10.6	20.1	19.8	1.4	26.8
G55	Mysore malli	93.9	76.3	12.8	5.2	41.0	26.7	**29.7**	11.3	21.3	17.3	1.5	17.5
G56	KRG74	105.7	90.4	10.4	3.6	37.0	27.8	20.4	8.4	28.3	19.3	1.4	20.5
G57	KRG75	97.4	78.2	16.0	2.9	38.0	27.7	6.7	8.2	21.0	17.5	1.6	16.8
G58	KRG76	114.4	95.9	17.6	2.9	41.0	30.5	4.2	**7.7**	18.9	20.0	1.3	18.6
G59	KRG77	104.8	86.5	5.7	2.9	44.0	32.3	5.1	13.4	19.2	16.9	1.6	29.8
G60	KRG 78	109.0	90.6	13.0	3.8	40.0	33.2	8.9	10.4	19.6	15.3	1.5	22.5
G61	KRG79	93.7	76.0	13.2	3.1	43.0	30.8	7.1	8.3	18.0	17.3	1.7	20.8
G62	KRG80	95.6	77.9	9.3	**2.8**	37.0	34.1	6.1	9.1	25.0	18.0	1.5	25.5
G63	KRG81	98.0	79.7	9.6	3.7	41.0	26.2	9.4	12.4	26.4	21.0	1.4	15.3
G64	KRG82	95.3	77.7	19.0	2.9	35.0	32.0	6.3	11.0	28.4	20.7	2.7	28.3
G65	IG 18	106.2	88.4	15.7	3.9	37.0	23.8	14.0	10.5	28.1	23.1	2.3	17.7
G66	KRG 84	114.0	95.8	7.6	4.0	40.0	25.9	9.5	11.0	18.4	18.3	1.6	33.5
G67	ARB6072	109.4	90.8	14.3	4.8	35.0	28.8	10.6	13.0	17.1	19.3	2.4	39.8
G68	Jcl nel	110.8	95.9	10.5	5.1	37.0	21.9	13.3	11.8	17.6	18.4	1.7	21.5
G69	Prathyasa	95.2	77.5	17.2	**5.9**	31.0	23.9	13.3	10.9	17.4	21.7	1.3	25.3
G70	PISINI	95.6	78.7	18.3	4.9	39.0	19.8	10.5	11.8	22.0	19.9	1.9	35.5
G71	KRG88	104.2	87.0	6.2	4.9	37.0	26.0	10.8	13.2	25.4	18.0	2.0	25.8
G72	KRG89	114.5	97.1	13.1	3.7	42.0	25.7	10.6	13.8	23.1	18.6	1.8	39.5
G73	KRG90	103.9	85.3	17.8	3.9	40.0	30.8	10.2	10.4	19.3	19.3	1.7	25.8
G74	KRG 91	94.3	77.1	6.1	4.9	45.0	27.0	12.9	11.6	23.1	24.1	**1.2**	20.8
G75	KRG92	96.0	78.0	**19.1**	4.9	41.0	33.8	10.4	13.5	22.0	22.1	1.7	30.5
G76	KRG93	112.6	94.1	16.2	3.9	35.0	30.0	9.0	13.4	25.4	**14.9**	**1.2**	20.5
G77	KRG94	104.7	86.6	17.2	3.8	35.0	24.3	8.0	14.0	26.7	19.0	1.5	34.9
G78	KRG95	107.9	89.3	14.2	4.9	44.0	22.0	13.2	14.6	21.4	15.8	1.9	35.5
G79	KRG112	104.6	87.2	7.4	3.6	39.0	30.9	19.2	16.8	24.9	17.3	1.5	30.0
G80	KRG101	103.9	86.0	18.1	3.9	38.0	28.2	9.0	14.0	17.4	15.9	2.5	28.7
G81	KRG102	103.8	86.0	12.0	4.9	42.0	30.6	3.8	14.0	26.7	18.2	2.4	20.0
	MEAN	103.9	86.0	13.2	3.7	39.2	28.8	9.5	14.7	22.6	19.4	2.0	30.0
	CD 5%	5.44	4.23	0.45	0.16	3.92	3.89	1.57	1.49	2.25	1.93	0.20	3.13
	CV %	3.25	3.05	2.12	2.25	6.80	8.38	10.24	6.31	6.19	6.16	6.17	6.47

Table 3. Variability estimates for culm morphology and yield traits

Trait	GV	PV	EV	GCV (%)	PCV (%)	ECV (%)	Heritability (h^2BS)	GA	GAM (%)
PH	58.17	69.57	11.40	7.33	8.02	3.24	83.2	14.36	13.82
CL	56.05	62.95	6.89	8.70	9.22	3.05	89.4	14.55	16.92
CLF	16.12	16.19	0.07	30.50	30.58	2.12	99.1	8.24	62.69
CT	0.68	0.69	0.01	17.93	18.08	2.24	98.3	1.69	36.66
CD	19.65	25.57	5.91	11.30	12.89	6.20	76.4	8.00	20.40
PT	22.59	28.42	5.83	16.49	18.49	8.37	79.1	8.73	30.29
SMF	25.59	26.54	0.94	53.14	54.12	10.23	96.6	10.23	97.50
NP	16.82	17.68	0.85	27.99	28.69	6.31	95.1	8.24	56.25
PL	11.30	13.26	1.95	14.88	16.11	6.18	85.2	6.39	28.30
PW	5.38	6.82	1.43	11.96	13.46	6.18	78.5	4.24	21.88
HSW	0.21	0.23	0.01	22.98	23.79	6.16	93.2	0.92	45.72
SPY	83.69	87.47	3.77	30.46	31.14	6.47	95.7	18.43	61.38

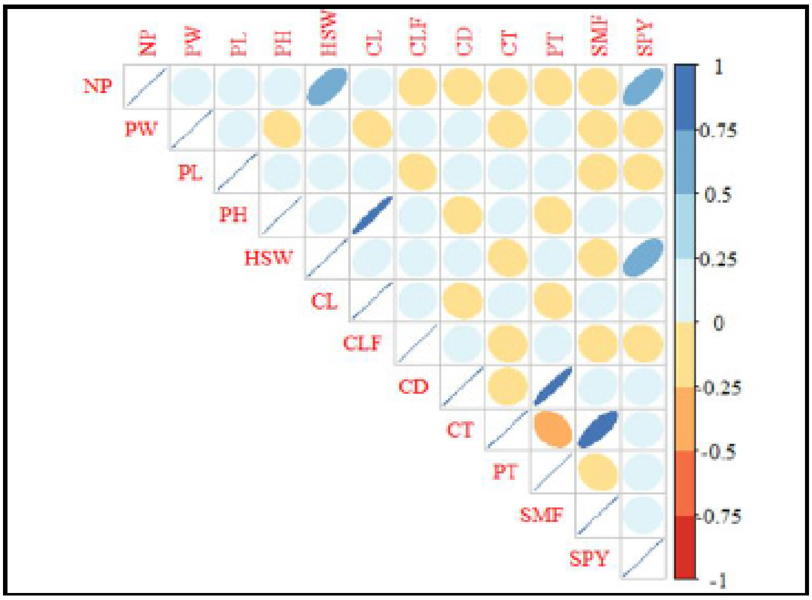

Fig.1. Correlation among culm morphology traits associated with yield-attributing traits for the rice genotypes. Blue indicates a positive correlation, red indicates a negative correlation, and the ellipse shape represents strength.

while maintaining an optimal plant height for structural support. Similar findings have been reported by multiple researchers (Mau *et al.,* 2017; Sanni *et al.,* 2012; Gautam and Shrestha 2023; Deshabandu *et al*., 2024). On the other hand, some notable negative correlations were detected. PW negatively correlated with PH (-0.18**), possibly indicating a resource allocation trade-off, where taller plants do not necessarily invest as much in (PW). Similarly, HSW negatively correlated with CT (-0.13*), while CT was inversely associated with PT (-0.34**), indicating that increased culm thickness may come at the expense of pith content, which could affect flexibility and biomass distribution. Additionally, PT was negatively correlated with PH (-0.16**) and SMF (-0.19**), suggesting that pith composition may influence culm strength and mechanical properties. These findings underscore the intricate interplay between culm traits and yield-attributing factors, highlighting the importance of achieving structural and agronomic balance simultaneously in plant breeding programs. Optimizing CT and pith content, for instance, could be crucial for improving both yield and resistance to lodging. Overall, this analysis provides valuable insights into the genetic and phenotypic relationships governing plant architecture and yield attributes.

Principal Component Analysis (PCA) is a widely used statistical technique for analyzing complex germplasm data, reducing high-dimensional datasets into a smaller set of uncorrelated principal components (Jegadeeswaran *et al.,* 2017). This transformation simplifies data interpretation, especially when observed traits are strongly correlated. In this study, PCA was performed using twelve quantitative traits to assess their relative importance in capturing genetic variation. The scree plot **(Fig. 2)** revealed that three principal components (PC1, PC2, and PC3) had eigenvalues greater than 1 (PC1: 2.8, PC2: 2.2, PC3: 1.8), together explaining 56% of the total variance **(Table 4)**. The PCA analysis of twelve traits identified key dimensions that explain the variability within the dataset **(Fig.3)**. PC1 accounts for approximately 23.4% of the total variation, with the strong positive loadings were observed for these traits in the principal component score matrix **(Fig. 3),** with values of PT (0.33), CD (0.26), and PW (0.17). Similar findings were reported by Al-Daej *et al*. (2023) and Chakma *et al*. (2012). PC2 explains an additional 18.1% of the total variation, primarily influenced by SPY (0.40), HSW (0.42), NP (0.39), and PT (0.29). PC3 contributes 14.61% of the variation, driven mainly by the NP (0.12), PW (0.12), and PL (0.10). Thus, PC1, representing structural traits and PW, exhibited the greatest variability**.** The PCA biplot **(Fig. 4)** illustrated the distribution of genotypes and traits across the first two principal components, highlighting significant variability for traits such as HSW, SPY, NP, PH, CL, and CT, which had the longest vectors. In contrast, CLF and PL exhibited shorter vectors, indicating a more uniform distribution among genotypes. These results coincide with findings of Yadav *et al*. (2017), and Reddy *et al*. (2019) regarding CD, CT and PH. Several genotypes showed superior performance across various traits **(Fig 4)**, genotype G36 (*Sivapukavuni*) excelled in HSW, SPY, and NPT; genotypes 'KRG112 (G79),' 'CO 53(G9),' and 'ADT 45(G2)' performed notably well in SMF and CT; and genotype 'CO 53(G9)' demonstrated exceptional performance in PT further reinforcing its value for maintaining culm integrity. These genotypes offer valuable insights for targeted breeding programs aimed at trait improvement.

In the context of progressive changes in environmental conditions and related unforeseen occurrences, genetic diversity may act as a repository for numerous unique features. The significant variability and association observed across key culm morphology traits such as

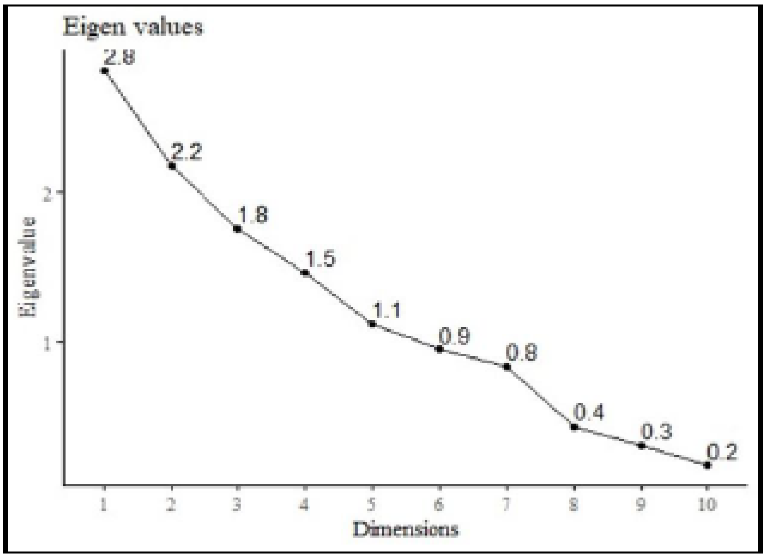

Fig. 2. Scree plot showing the Eigen values of the PCs

Table 4. Eigenvalues and percent of variation of principal component axes

Principal components	Eigen values	Percentage of variation	Cumulative percentage
PC1	2.81	23.43	23.43
PC2	2.20	18.11	41.54
PC3	1.80	14.61	56.16
PC4	1.46	12.17	68.32
PC5	1.12	9.30	77.62
PC6	0.94	7.86	85.48
PC7	0.83	6.93	92.41

Principal component scores

PCs	NP	PW	PL	PH	HSW	SPY	CL	CLF	CD	CT	PT	SMF
PC12	0	0	0	0	0	0	0	0	-0.67	0.2	0.71	0.07
PC11	0.01	0.01	0	-0.71	-0.01	0	0.71	0.02	0	0	0	0
PC10	-0.07	0.01	0.04	0.01	-0.19	0.21	0.01	0	-0.14	-0.68	0	0.68
PC9	-0.69	0.02	0.18	-0.03	0.06	0.65	-0.02	0.11	-0.06	0.12	-0.07	-0.16
PC8	0.35	0.14	0.02	0.11	-0.8	0.38	0.08	0.04	0.03	0.1	0.02	-0.21
PC7	0.21	-0.34	0.56	-0.15	0.01	-0.04	-0.16	0.68	0.02	0.08	-0.01	0.11
PC6	-0.02	-0.9	-0.18	-0.12	-0.14	0.1	-0.1	-0.3	-0.02	-0.07	0.02	-0.12
PC5	0.01	0.01	0.78	0.11	0	-0.08	0.12	-0.58	0.09	-0.06	0.11	-0.06
PC4	0.27	0.11	-0.03	-0.4	0.14	0.34	-0.39	-0.29	0.16	0.41	0	0.43
PC3	0.13	0.13	0.1	-0.28	0	-0.05	-0.28	-0.11	-0.64	-0.17	-0.52	-0.28
PC2	0.39	0.07	-0.04	-0.05	0.43	0.4	-0.06	0.05	0.14	-0.46	0.3	-0.41
PC1	-0.32	0.17	0.01	-0.45	-0.32	-0.3	-0.45	0.01	0.26	-0.23	0.33	-0.2

Fig.3. Score matrix showing the contribution of twelve quantitative traits across different principal components (PCs). Colour intensity represents the strength and direction of correlation, with green indicating positive and red indicating negative contributions.

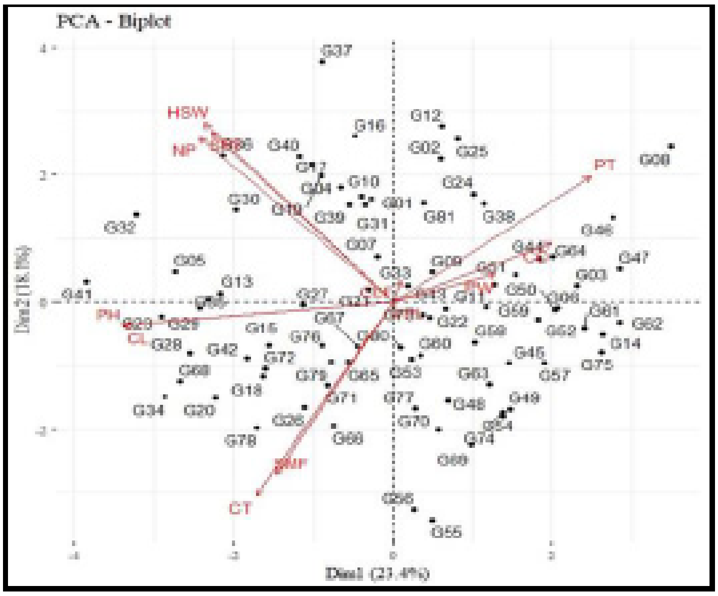

Fig. 4. PCA biplot of PC 1 and PC 2 showing the relationship among the traits

culm thickness, culm diameter and section modulus of fourth internode underscores the potential for genetic enhancement through selective breeding. Correlation and PCA analyses identified primary contributors to genetic variation, highlighting their role in determining overall culm characteristics. This research establishes a basis for subsequent genetic and molecular investigations focused on creating high-yield, non-lodging rice varieties suited diverse agro-climatic conditions.

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