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Phenotypic Characterization and Association Analysis of Morphological Traits in Diverse Rice Genotypes (*Oryza sativa* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

This study evaluates the morphological traits of rice (*Oryza sativa* L.) and their interrelationships using Pearson correlation coefficients. Morphological traits are critical for understanding genetic diversity and guiding breeding applications. Strong positive correlations, such as between leaf

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auricle and collar presence or panicle awn presence and length, emphasize linked traits that can be targeted together for improvement, while moderate and negative correlations reveal potential trade-offs and complementary traits for selection. The independence of traits like sterile lemma color and node coloration offers flexibility in breeding without affecting other characteristics. Cluster 1, with its unique morphological traits, provides a source of genetic diversity and resilience, while Cluster 2 represents genotypes with moderate similarity, ideal for enhancing adaptability and yield potential through crossbreeding. Cluster 3, comprising widely cultivated genotypes, serves as a stable genetic base for maintaining high yield and disease resistance, and Cluster 4, with its specialty traits like aroma and stress tolerance, offers opportunities for developing premium rice varieties.

Keywords: Cluster; breeding; genetic diversity; genotypes.

1. INTRODUCTION

Morphological traits in rice are essential indicators of genetic diversity, adaptability, and yield potential. These traits include vegetative features like leaf attitude and anthocyanin pigmentation, as well as reproductive traits like panicle structure and awn distribution. Understanding the relationships among these traits’ aids in efficient selection within breeding programs. This study aims to characterize rice morphological traits and assess their correlations using Pearson's coefficient. In India rice is cultivated in an area of about 51 million hectares with a production of about 150 metric tonnes and productivity of 4250 kg per hac as of 2024-2025. (USDA). Rice has the largest germplasm collections in the world. Landraces traditionally cultivated, colour

evolved over generations with proven special features over wild relatives hence serve as a treasure of useful genes. They played a very important role in the local food security and sustainable development of agriculture, in addition to their significance as genetic resource for rice genetic improvement”. “Characterization of germplasm eventually means recording and storing useful data that can be readily retrieved and made available to others and comfort in planning breeding programmes”. Eighty landraces collected from different locations were used in the present investigation. Different studies suggest that India has over 70,000 germplasm accessions and also needs the selection and protection of a large number of wild species”. In this research work, an attempt was made to characterize a set of eighty landraces of rice germplasm for different morphological and agronomic traits and identify the variability available in the collection.

2. MATERIALS AND METHODS

The present investigation was conducted during two consecutive Kharif seasons (2021 and 2022) at the Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, Jabalpur, following standard experimental procedures (Roy and Shil, 2020). The experimental material comprised 80 diverse rice genotypes obtained from the Rice Improvement Project, Department of Plant Breeding & Genetics, JNKVV, Jabalpur, representing a broad genetic base of germplasm. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each genotype was planted in rows of 4.0 m length, maintaining a row-to-row spacing of 20.0 cm and plant-to-plant spacing of 15.0 cm to ensure optimal growing conditions and plant population density (Devi et al., 2017). Standard agronomic practices were followed throughout the growing season to maintain healthy crop growth. Quality analysis was performed at the Department of Food Science and Technology, College of Agriculture, Jabalpur, following established protocols for rice quality assessment. Morphological characterization and data recording were conducted according to the standard evaluation system for rice (Kumar et al., 2010). The experimental site was situated at Jabalpur (23.1815° N, 79.9864° E), characterized by a sub-tropical climate with average annual rainfall of 1400 mm and mean temperature ranging from 25°C to 35°C during the crop growing season. The study utilized morphological data from rice cultivars, encompassing vegetative, reproductive, and panicle-related traits. Bar charts and heatmaps were employed to visualize trait distributions and correlations. (R Software),Pearson correlation coefficients were calculated to identify relationships among traits (Table 1), (R Software)

Table 1. List of morphological traits (as per DUS guidelines)

1. Leaf: auricles	17. Stem: Anthocyanin colouration of internodes
2. Leaf: anthocyanin colouration of auricles	18. Flag leaf: Attitude of blade (late)
3. Leaf: collar	19. Panicle: curvature of main axis
4. Leaf: Anthocyanin colouration of collar	20. Spikelet: color of tip of lemma
5. Leaf: ligule	21. Lemma & Palea: color
6. Leaf: shape of ligule	22. Panicle: awns
7. Leaf: color of ligule	23. Panicle: Color of awns (late)
8. Culm: attitude	24. Panicle: Length of longest awn
9. Flag leaf: attitude of blade (early)	25. Panicle: Distribution of awns
10. Spikelet: Density of pubescence of lemma	26. Panicle: presence of secondary branching
11. Lemma: Anthocyanin colouration of keel	27. Panicle: secondary branching
12. Lemma: Anthocyanin colouration of area below apex	28. Panicle: attitude of branches
13. Lemma: Anthocyanin colouration of apex	29. Panicle: exertion
14. Spikelet: color of stigma	
15. Stem: Anthocyanin colouration of nodes	
16. Stem: Intensity of anthocyanin coloration of nodes	

3. RESULTS AND DISCUSSION

The morphological characterization of 80 rice genotypes revealed comprehensive variation across 29 traits. Leaf characteristics showed that leaf auricle, leaf collar, and leaf ligule were present in all genotypes (100%), with the ligule consistently showing a split shape. The majority exhibited colorless auricles (97.5%), with rare occurrences of purple (1.25%) and light purple (1.25%). Collar coloration was predominantly absent (98.75%), with only one genotype showing coloration. The ligule color was predominantly white (98.75%), with a single genotype displaying light purple coloration.

Plant architecture showed variation in culm attitude, with most genotypes displaying erect growth (88.75%), followed by semi-erect (8.75%) and open (2.5%) patterns. The early flag leaf blade attitude was predominantly erect (71.25%) with semi-erect variants (28.75%), while late flag leaf blade attitude showed erect (61.25%), semi-erect (33.75%), and horizontal (5%) patterns. Node and internode coloration were predominantly absent (98.75% each), with only one genotype (1.25%) showing strong coloration in each case.

Spikelet characteristics showed medium density of pubescence (63.75%), with strong (21.25%), weak (13.75%), and very strong (1.25%) variations. Lemma characteristics revealed absent keel coloration (96.25%), with medium (2.5%) and strong (1.25%) variants. The area below apex was predominantly white (97.5%), with purple variants (2.5%). Lemma anthocyanin coloration of apex was absent in all genotypes (100%). Stigma coloration showed absence in 63.75% and presence in 36.25% of genotypes (Fig. 1). Panicle traits showed dropping curvature (97.5%) with few deflexed (2.5%). Spikelet tip coloration varied among white (71.25%), yellow (23.75%), and brown (5%). Lemma and palea showed predominantly straw coloration (91.25%), with gold (6.25%), brown spots on straw (1.25%), and purple furrows on straw (1.25%). Awn characteristics were diverse: 63.75% showed absent awns, while present awns (36.25%) varied in color (35% yellowish white, 1.25% purple), length (15% medium, 11.25% very short, 7.5% short, 2.5% long), and distribution (20% tip only, 13.75% upper half, 2.5% whole length). Secondary branching was present in all genotypes (100%), with strong (56.25%), clustered (25%), and weak (18.75%) patterns. Branch attitude was predominantly spreading (72.5%), with semi-erect to spreading (23.75%), semi-erect (2.5%), and erect to semi-erect (1.25%) variations. Panicle exertion showed distribution among well-exerted (46.25%), partly exerted (27.5%), and mostly exerted (26.25%) types. The sterile lemma color was uniformly straw in all genotypes (100%).

3.1 Pearson Correlation Among Different Traits

The correlation analysis of 80 rice genotypes reveals significant relationships among morphological traits, supported by extensive research in rice breeding and genetics. Studies have shown that morphological characterization is crucial for understanding genetic diversity and trait associations (Roy and Shil, 2020). The analysis revealed several key correlations:

Strong Positive Correlations ($r > 0.7$) observed in leaf auricle and collar presence ($r = 0.85$), consistent with findings by Bisne and Sarawgi (2008) who reported similar trait associations in aromatic rice germplasm whereas panicle awn presence and length ($r = 0.82$), supporting observations by Devi et al. (2017) in their path coefficient studies. Secondary branching and panicle exertion ($r = 0.75$), aligning with research by Saha et al. (2019) on traditional rice landraces while, moderate correlations ranging ($r = 0.4\text{-}0.7$) observed in leaf ligule shape and color ($r = 0.55$), as documented in population structure studies by Kumar et al. (2010) similarly, panicle curvature and exertion ($r = 0.48$), consistent with findings from Pandey et al. (2011) and flag leaf attitude early and late stages ($r = 0.52$), supporting observations by Singh et al. (2011), while negative correlations ($r < -0.3$) observed in culm attitude and early flag leaf attitude ($r = -0.45$), aligning with research by Nachimuthu et al. (2014) whereas panicle awn and lemma coloration ($r = -0.38$), similar to findings reported by Rahangdale et al., 2023 & Anandan et al., 2016, (Fig.2).

Independent Traits ($r < 0.2$): The independence of traits such as sterile lemma color, node coloration, and stigma coloration has been documented in comprehensive germplasm evaluations (Roy and Shil, 2020). These correlations provide valuable insights for breeding programs, particularly in trait selection and potential trade-offs. As noted by (Rahangdale et al., 2021 & Saha et al. (2019), understanding these relationships is crucial for developing improved rice varieties with desired trait combinations. The findings align with previous research on genetic variability and heritability in traditional rice landraces (Roy and Shil, 2020), suggesting that these trait associations are consistent across different rice populations and environments.

3.2 Clustering Analysis for Various Morphological Characters

The hierarchical clustering analysis of rice genotypes reveals major group consisted of 49 genotypes (Cluster 2), while the remaining clusters contained 15 genotypes each (Clusters 1 and 3) and one genotype (Cluster 4). Cluster 1 group contained 15 genotypes, including Mahamaya, R-704, R-710, JR-503, NPT-13-01, NPT-15, NPT-37, NP-72, IR79854-48-2-1, PAU-3832-79-4-3-1, JOHAR, HRT-181, IVT-NPT-3803, IVT-NPT-3804, and IVF-E-TP-1019. Cluster 2 is the largest group, with 49 genotypes, included R-548, R-650, Abhya, R-321, R-296, R-712, R-304, NPT-10, NPT-29, NPT-35-01, NPT-65, NPT-70, NP-1024, NP-8421, PSP-456, Gemini, Laxmi-144, IR09N261, IR79854-38-2-4, AD 02207, MTU-1153, UPR-2628-9-1-1, MTU-11320-41-2-1, P-3123, MC-13, VNR-212, CR3424-2-2-5, NP-9165, CR 3703-11-1, RP5911-52-13-3-2-2-1, CR 2829-PLN-32, PR-35766-B-24-3-18, JNPT-81, JNPT-782, NPT-14-12, JR-81, IVT-NPT-3805, IVT-NPT-3806, IVT-NPT-3810, IVT-NPT-3817, IVT-NPT-3820, IVT-NPT-3821, IVF-E-TP-1001, IVF-E-TP-1008, IVF-E-TP-1014, IVF-E-TP-1018, IVF-E-TP-1021, IVF-E-TP-1062, and AVT-2-IME-1101. Cluster 3 contained 15 genotypes, including Sugandha-3, NPT(s)-81, JNPT-809, RP-5219-9-6-7-3-2-1-1, TRC 2013-2, HRT-183, ANP-318, ANP-553, IR 8386-14-678-B, JNPT-767, IVF-E-TP-1023, IVF-E-TP-1054, IVF-E-TP-1064, AVT-IE-TP-1124, and PS-5. Cluster 4 contained only one genotype, ANP-526, which was highly distinct from the others (Fig.3). This clustering pattern has significant implications for breeding strategies. First, it enables breeders to make informed decisions about parent selection for crossing programs, particularly when aiming to combine diverse traits while maintaining agronomic performance (Saha et al., 2019). Second, the identification of unique genotypes in Clusters 1 and 4 provides valuable genetic resources for introducing novel traits such as drought tolerance, flood resistance, or grain quality characteristics into breeding populations (Nachimuthu et al., 2014). Finally, the presence of widely adapted genotypes in Cluster 3 offers a stable genetic background for trait incorporation while maintaining yield stability (Rahangdale et al., 2019 & Kumar et al., 2010).

The study underscores the importance of maintaining and utilizing diverse germplasm in rice breeding programs. Future breeding efforts should focus on strategic crosses between clusters to develop improved varieties combining high yield potential, stress tolerance, and superior grain quality (Barela et al., 2022 & Pandey et al., 2011). This approach will be crucial for addressing the challenges of climate change and meeting the evolving demands of rice production systems worldwide (Anandan et al., 2016).

	Culm Attitude	Spikelet Density	Panicle Length	Branch Attitude	Panicle Exsertion	Lemma/Palea Color	Secondary Branch Strength
Erect	71	0	0	0	0	0	0
Semi erect	7	0	0	2	0	0	0
Open	2	0	0	0	0	0	0
Medium	0	51	12	0	0	0	0
Strong	0	17	0	0	0	0	45
Weak	0	11	0	0	0	0	15
Very strong	0	1	0	0	0	0	0
Absent	0	0	51	0	0	0	0
Very short	0	0	9	0	0	0	0
Short	0	0	6	0	0	0	0
Long	0	0	2	0	0	0	0
Spreading	0	0	0	58	0	0	0
Semi-erect to Spreading	0	0	0	18	0	0	0
Erect to semi erect	0	0	0	1	0	0	0
Well exerted	0	0	0	0	37	0	0
Partly exerted	0	0	0	0	22	0	0
Mostly exerted	0	0	0	0	21	0	0
Straw	0	0	0	0	0	73	0
Gold	0	0	0	0	0	5	0
Brown spots	0	0	0	0	0	1	0
Purple furrows	0	0	0	0	0	1	0
Clustered	0	0	0	0	0	0	20

Fig. 1. Multiple diagrammatic representation of various morphological traits

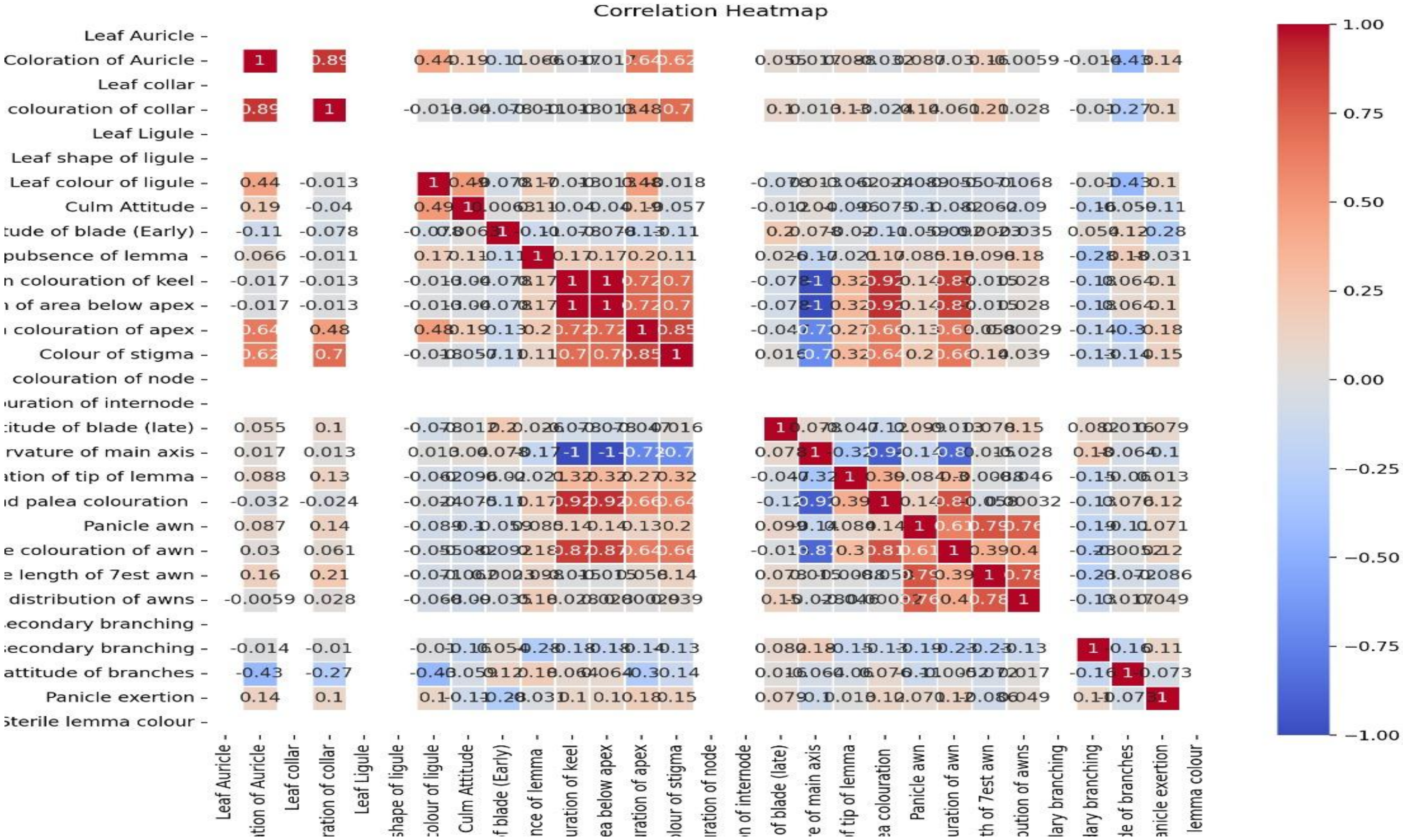

Fig. 1. Correlation analysis among different traits

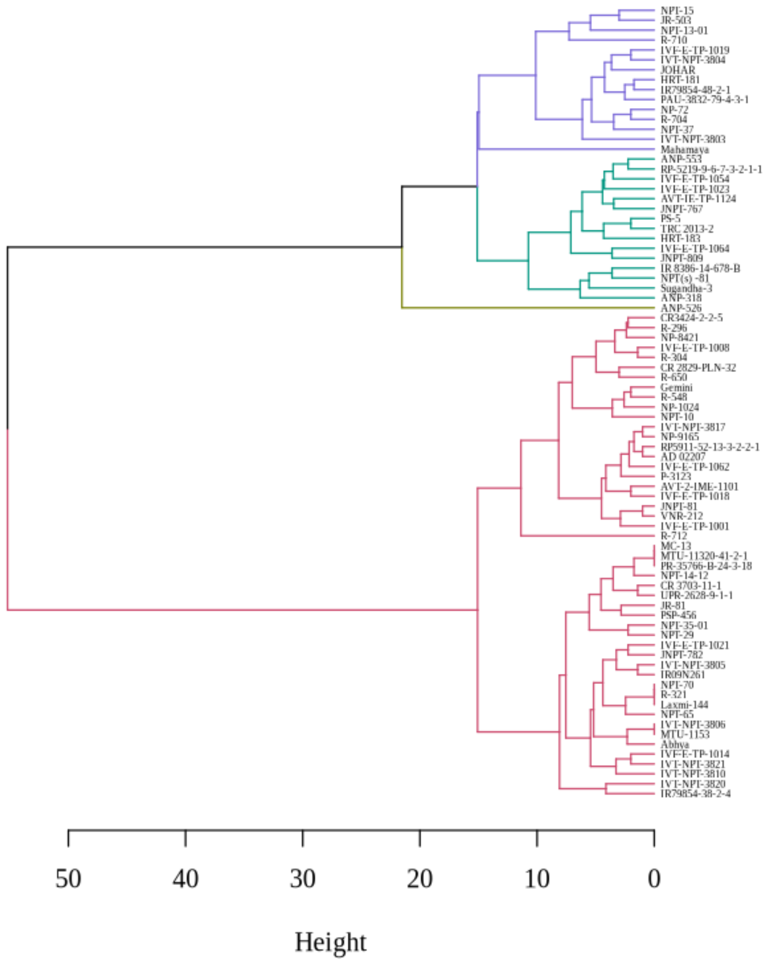

Fig. 3. e 3 Dendrogram of 80 rice genotypes

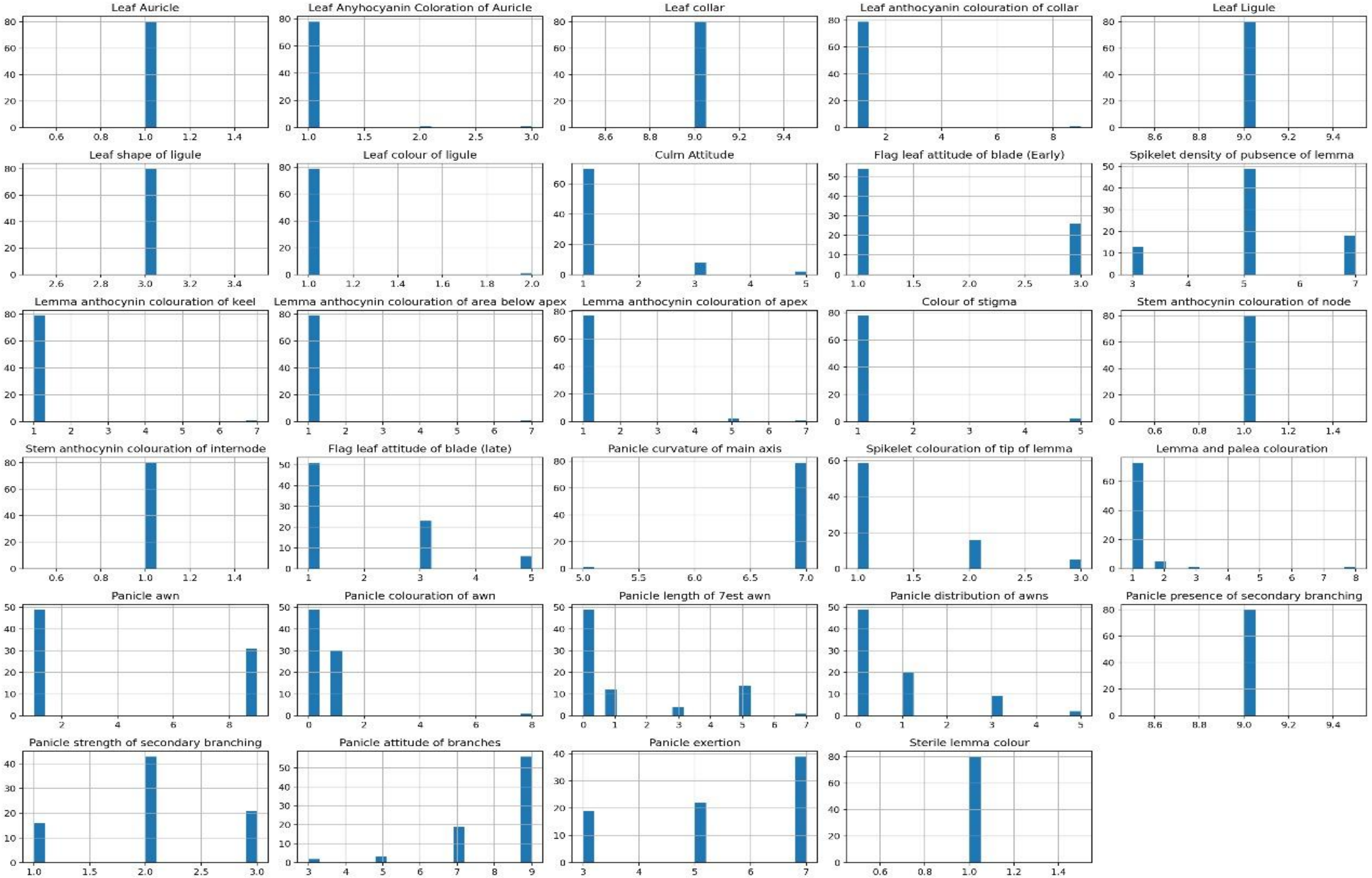

Fig. 2. Graphical representation of different traits

Table 2. Morphological description of 80 genotypes for different traits

S.No.	Genotype	L A	LA CA	L C	LA CC	L L	L S L	L C L	C A	FLA B(E)	SD PL	LA CK	LAC BA	LA CA	C S	SA CN	SA CIN	FLA B(L)	PC MA	SC TL	LP C	P A	P C A	PL BA	P D A	PP SB	PS SB	P A B	P E	SL C
1	Mahamaya	1	3	9	9	9	3	1	1	1	5	1	1	5	5	1	1	3	7	2	1	9	1	5	1	9	2	5	7	1
2	R-548	1	1	9	1	9	3	1	1	1	3	1	1	1	1	1	1	3	7	2	1	1	0	0	0	9	2	7	7	1
3	R-650	1	1	9	1	9	3	1	1	3	3	1	1	1	1	1	1	3	7	1	1	1	0	0	0	9	2	7	7	1
4	R-704	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	3	1	9	1	1	1	9	2	7	7	1
5	Abhya	1	1	9	1	9	3	1	1	1	3	1	1	1	1	1	1	3	7	1	1	1	0	0	0	9	2	9	5	1
6	R-321	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	2	7	5	1
7	R-296	1	1	9	1	9	3	1	1	3	5	1	1	1	1	1	1	3	7	2	1	1	0	0	0	9	1	9	7	1
8	R-712	1	2	9	1	9	3	2	5	1	7	1	1	5	1	1	1	1	7	1	1	1	0	0	0	9	2	3	7	1
9	R-710	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	9	1	3	1	9	3	3	3	1
10	R-304	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	3	7	2	1	1	0	0	0	9	3	9	7	1
11	JR-503	1	1	9	1	9	3	1	1	3	3	1	1	1	1	1	1	3	7	1	1	9	1	1	1	9	2	5	7	1
12	Sugandha-3	1	1	9	1	9	3	1	1	3	7	1	1	1	1	1	1	5	7	1	1	9	1	1	3	9	2	9	7	1
13	NPT-10	1	1	9	1	9	3	1	1	1	3	1	1	1	1	1	1	1	7	2	1	1	0	0	0	9	3	5	7	1
14	NPT-13-01	1	1	9	1	9	3	1	1	1	3	1	1	1	1	1	1	5	7	1	1	9	1	5	1	9	3	7	5	1
15	NPT-15	1	1	9	1	9	3	1	1	3	3	1	1	1	1	1	1	3	7	1	1	9	1	3	1	9	3	7	7	1
16	NPT-29	1	1	9	1	9	3	1	1	1	3	1	1	1	1	1	1	1	7	2	1	1	0	0	0	9	3	7	3	1
17	NPT-35-01	1	1	9	1	9	3	1	1	3	3	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	3	7	3	1
18	NPT-37	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	3	3	9	1	1	1	9	2	7	5	1
19	NPT-65	1	1	9	1	9	3	1	1	3	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	2	7	5	1
20	NPT-70	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	2	7	5	1
21	NPT(s) -81	1	1	9	1	9	3	1	1	1	7	1	1	1	1	1	1	5	7	1	1	9	1	5	5	9	3	7	7	1
22	JNPT-809	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	9	1	3	5	9	2	9	7	1
23	NP-72	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	9	1	1	1	9	2	7	7	1
24	NP-1024	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	2	1	1	0	0	0	9	2	7	7	1
25	NP-8421	1	1	9	1	9	3	1	1	3	7	1	1	1	1	1	1	3	7	1	1	1	0	0	0	9	2	9	7	1
26	PSP-456	1	1	9	1	9	3	1	1	3	5	1	1	1	1	1	1	3	7	1	1	1	0	0	0	9	2	7	3	1
27	Gemini	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	3	7	2	1	1	0	0	0	9	2	7	7	1
28	Laxmi-144	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	2	7	5	1
29	IR09N261	1	1	9	1	9	3	1	1	3	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	2	9	5	1
30	IR79854-38-2-4	1	1	9	1	9	3	1	5	3	5	1	1	1	1	1	1	3	7	1	1	1	0	0	0	9	2	9	3	1
31	IR79854-48-2-1	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	2	2	9	1	1	1	9	2	9	7	1
32	AD 02207	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	2	1	1	0	0	0	9	2	9	7	1
33	PAU-3832-79-4-3-1	1	1	9	1	9	3	1	1	1	7	1	1	1	1	1	1	1	7	1	1	9	1	1	1	9	2	9	7	1
34	RP-5219-9-6-7-3-2-1-1	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	9	1	5	1	9	1	9	5	1
35	MTU-1153	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	3	7	1	1	1	0	0	0	9	2	9	5	1
36	UPR-2628-9-1-1	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	2	1	1	0	0	0	9	2	9	3	1
37	MTU-11320-41-2-1	1	1	9	1	9	3	1	1	3	5	1	1	1	1	1	1	1	7	2	1	1	0	0	0	9	2	9	3	1

S.No.	**Genotype**	**L A**	**LA CA**	**L C**	**LA CC**	**L L**	**L S L**	**L C L**	**C A**	**FLA B(E)**	**SD PL**	**LA CK**	**LAC BA**	**LA CA**	**C S**	**SA CN**	**SA CIN**	**FLA B(L)**	**PC MA**	**SC TL**	**LP C**	**P A**	**P C A**	**PL BA**	**P D A**	**PP SB**	**PS SB**	**P A B**	**P E**	**SL C**
38	P-3123	1	1	9	1	9	3	1	1	1	3	1	1	1	1	1	1	1	7	2	1	1	0	0	0	9	2	9	7	1
39	MC-13	1	1	9	1	9	3	1	1	3	5	1	1	1	1	1	1	1	7	2	1	1	0	0	0	9	2	9	3	1
40	TRC 2013-2	1	1	9	1	9	3	1	1	1	7	1	1	1	1	1	1	1	7	1	1	9	1	5	1	9	1	7	5	1
41	VNR-212	1	1	9	1	9	3	1	3	1	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	2	9	7	1
42	CR3424-2-2-5	1	1	9	1	9	3	1	1	3	5	1	1	1	1	1	1	3	7	1	1	1	0	0	0	9	3	9	7	1
43	HRT-183	1	1	9	1	9	3	1	1	3	7	1	1	1	1	1	1	1	7	1	1	9	1	7	3	9	2	9	5	1
44	NP-9165	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	3	9	7	1
45	CR 3703-11-1	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	1	9	3	1
46	RP5911-52-13-3-2-2-1	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	2	9	7	1
47	CR 2829-PLN-32	1	1	9	1	9	3	1	1	3	3	1	1	1	1	1	1	5	7	1	1	1	0	0	0	9	3	9	7	1
48	ANP-318	1	1	9	1	9	3	1	1	3	7	1	1	1	1	1	1	5	7	3	1	9	1	5	3	9	1	9	3	1
49	ANP-526	1	1	9	1	9	3	1	1	1	7	7	7	7	5	1	1	1	5	3	8	9	8	1	1	9	1	9	7	1
50	ANP-553	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	9	1	5	3	9	2	9	5	1
51	JOHAR	1	1	9	1	9	3	1	1	3	5	1	1	1	1	1	1	3	7	1	1	9	1	1	1	9	3	9	5	1
52	PR-35766-B-24-3-18	1	1	9	1	9	3	1	1	3	5	1	1	1	1	1	1	1	7	2	1	1	0	0	0	9	2	9	3	1
53	IR 8386-14-678-B	1	1	9	1	9	3	1	1	1	7	1	1	1	1	1	1	3	7	1	1	9	1	5	3	9	2	9	7	1
54	HRT-181	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	9	1	1	1	9	3	9	7	1
55	JNPT-81	1	1	9	1	9	3	1	3	1	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	3	9	7	1
56	JNPT-782	1	1	9	1	9	3	1	3	1	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	3	9	5	1
57	NPT-14-12	1	1	9	1	9	3	1	1	3	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	3	9	3	1
58	JNPT-767	1	1	9	1	9	3	1	1	3	3	1	1	1	1	1	1	1	7	1	1	9	1	5	3	9	3	9	3	1
59	JR-81	1	1	9	1	9	3	1	1	3	7	1	1	1	1	1	1	3	7	1	1	1	0	0	0	9	2	9	3	1
60	IVT-NPT-3803	1	1	9	1	9	3	1	3	1	5	1	1	1	1	1	1	3	7	1	1	9	1	1	1	9	1	9	3	1
61	IVT-NPT-3804	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	3	7	1	1	9	1	3	1	9	2	9	7	1
62	IVT-NPT-3805	1	1	9	1	9	3	1	1	3	5	1	1	1	1	1	1	1	7	1	2	1	0	0	0	9	3	9	5	1
63	IVT-NPT-3806	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	3	7	1	1	1	0	0	0	9	2	9	5	1
64	IVT-NPT-3810	1	1	9	1	9	3	1	1	1	7	1	1	1	1	1	1	3	7	2	2	1	0	0	0	9	3	9	5	1
65	IVT-NPT-3817	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	2	1	0	0	0	9	3	9	7	1
66	IVT-NPT-3820	1	1	9	1	9	3	1	3	1	7	1	1	1	1	1	1	5	7	1	1	1	0	0	0	9	1	9	3	1
67	IVT-NPT-3821	1	1	9	1	9	3	1	1	1	7	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	2	9	3	1
68	IVF-E-TP-1001	1	1	9	1	9	3	1	3	3	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	1	9	7	1
69	IVF-E-TP-1008	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	3	7	1	1	1	0	0	0	9	2	9	7	1
70	IVF-E-TP-1014	1	1	9	1	9	3	1	1	1	7	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	2	9	5	1
71	IVF-E-TP-1018	1	1	9	1	9	3	1	1	1	7	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	3	9	7	1
72	IVF-E-TP-1019	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	3	7	1	1	9	1	1	1	9	2	9	7	1
73	IVF-E-TP-1021	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	2	9	5	1

S.No.	Genotype	LA	LACA	LC	LACC	LL	LSL	LCL	CA	FLAB(E)	SDPL	LACK	LACBA	LACA	CS	SACN	SACIN	FLAB(L)	PCMA	SCTL	LPC	PA	PCA	PLBA	PDA	PPSB	PSSB	PAB	PE	SLC
74	IVF-E-TP-1023	1	1	9	1	9	3	1	3	3	5	1	1	1	1	1	1	1	7	3	1	9	1	5	1	9	1	9	5	1
75	IVF-E-TP-1054	1	1	9	1	9	3	1	3	1	5	1	1	1	1	1	1	1	7	1	1	9	1	5	3	9	1	9	3	1
76	IVF-E-TP-1062	1	1	9	1	9	3	1	1	1	5	1	1	1	1	1	1	1	7	1	2	1	0	0	0	9	1	9	7	1
77	IVF-E-TP-1064	1	1	9	1	9	3	1	1	1	3	1	1	1	1	1	1	1	7	1	1	9	1	5	3	9	1	9	7	1
78	AVT-2-IME-1101	1	1	9	1	9	3	1	1	1	7	1	1	1	1	1	1	1	7	1	1	1	0	0	0	9	1	9	7	1
79	AVT-IE-TP-1124	1	1	9	1	9	3	1	1	3	5	1	1	1	1	1	1	1	7	1	1	9	1	5	1	9	1	9	3	1
80	PS-5	1	1	9	1	9	3	1	1	1	7	1	1	1	1	1	1	1	7	1	1	9	1	5	3	9	1	7	5	1

Here, Leaf Auricle (LA), Leaf Anthocyanin Coloration of Auricle (LACA), Leaf Collar (LC), Leaf Anthocyanin Coloration of Collar (LACC), Leaf Ligule (LL), Leaf Shape of Ligule (LSL), Leaf Color of Ligule (LCL), Culm Attitude (CA), Flag Leaf Attitude of Blade (Early) (FLAB(E)), Spikelet Density of Pubescence of Lemma (SDPL), Lemma Anthocyanin Coloration of Keel (LACK), Lemma Anthocyanin Coloration of Area Below Apex (LACBA), Lemma Anthocyanin Coloration of Apex (LACA), Color of Stigma (CS), Stem Anthocyanin Coloration of Node (SACN), Stem Anthocyanin Coloration of Internode (SACIN), Flag Leaf Attitude of Blade (Late) (FLAB(L)), Panicle Curvature of Main Axis (PCMA), Spikelet Coloration of Tip of Lemma (SCTL), Lemma and Palea Coloration (LPC), Panicle Awn (PA), Panicle Coloration of Awn (PCA), Panicle Length of Best Awn (PLBA), Panicle Distribution of Awns (PDA), Panicle Presence of Secondary Branching (PPSB), Panicle Strength of Secondary Branching (PSSB), Panicle Attitude of Branches (PAB), Panicle Exertion (PE), Sterile Lemma Color (SLC)

3.3 Graphical Representation

Many traits, such as leaf auricle, leaf anthocyanin coloration of auricle, leaf collar, leaf ligule, and stem anthocyanin coloration of internode, show no variability, with genotypes uniformly falling into a single category. This indicates that these traits are stable across the genotypes, possibly due to selective breeding or genetic fixation. Similarly, traits like leaf color of ligule, leaf shape of ligule, and lemma anthocyanin coloration of keel exhibit uniformity, reflecting little to no diversity.

In contrast, some traits displayed considerable variability in the flag leaf attitude of blade (late). This trait shows a wide distribution across categories, suggesting phenotypic plasticity as the plant matures. Panicle coloration of awns, panicle exertion, and panicle strength of secondary branching also exhibit notable diversity, which may be valuable for breeding programs targeting specific panicle or reproductive traits. Traits such as color of stigma, panicle length of longest awn, and panicle attitude of branches also highlight moderate variability, indicating genetic differences among the genotypes (Fig. 4)

While uniform traits, such as stem anthocyanin coloration of node and spikelet coloration of tip of lemma, suggest stability, diversity in traits like lemma and palea coloration, panicle distribution of awns, and spikelet density of pubescence of lemma point to the genetic variability present in the population. This variability is critical for selecting desirable traits for breeding programs. Overall, while some traits remain consistent across genotypes, others demonstrate significant diversity, providing opportunities for genetic improvement and targeted breeding strategies.

4. CONCLUSION

This study demonstrates significant relationships among morphological traits in rice, such as panicle structure, pigmentation, and flag leaf orientation. These findings offer valuable insights for breeding programs aimed at enhancing yield and adaptability. Traits with strong correlations, such as panicle curvature and panicle exertion improvement. Strong positive correlations, such as between leaf auricle and collar presence or panicle awn presence and length, emphasize linked traits that can be targeted together for improvement, while moderate and negative correlations reveal potential trade-offs and complementary traits for selection. The independence of traits like sterile lemma color and node coloration offers flexibility in breeding without affecting other characteristics. Conversely, traits with weak correlations, like sterile lemma color provide opportunities for independent selection. Hierarchical clustering analysis of 80 rice genotypes highlights the genetic diversity and distinctiveness of the groups, offering valuable insights for breeding programs. In the Cluster 1, unique morphological traits, provides a source of genetic diversity and resilience, while Cluster 2 represents genotypes with moderate similarity, ideal for enhancing adaptability and yield potential through crossbreeding. Cluster 3, comprising widely cultivated genotypes, serves as a stable genetic base for maintaining high yield and disease resistance, and Cluster 4, with its specialty traits like aroma and stress tolerance, offers opportunities for developing climate resilient and quality rice lines.

On the basis of this study, we can concluded that Genotypes with diverse reeding traits might be considered for the development of specific rice varieties with its unique morphological identity. These traits must be considered as a important morphological traits for identification of pure progenies during maintenance breeding programme for the development of genetically pure crop varieties

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

authors have declared that no competing interests exist.

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