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Unveiling Morphological Variability in Rice (*Oryza sativa* L.) Restorer Lines for Trait Optimization through DUS Characterization and Diversity Analysis

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Abstract

The experiment was conducted during the *kharif* season (July to November, 2020) at the Seed Breeding Farm, Rice Improvement Project, Department of Plant Breeding & Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India to investigate the morphological variability in rice (*Oryza sativa* L.) restorer lines. A total of eighty restorer lines were evaluated and morphologically characterized in accordance with the Distinctness, Uniformity, and Stability (DUS) guidelines. Additionally, the Shannon-Weaver diversity index was calculated for all the observed traits, providing insights into the genetic diversity present within the lines studied. The results indicated significant variability and diversity in traits such as color of stigma, sterile lemma color, density of pubescence of lemma, distribution of awns, and attitude of flag leaf blade (both early and late stages). This variation will be instrumental in selecting specific genotypes for protection, conservation, and further breeding programs. Conversely, minimal variability was observed in traits such as color of tip of lemma, anthocyanin coloration of the keel, panicle exertion, anthocyanin coloration of internodes, anthocyanin coloration of the apex, and leaf auricles. Traits consistently present across all the genotypes such as leaf collar, leaf ligule, split shape of ligule, white ligule color, drooping curvature of the panicle main axis, presence of secondary branching of panicle, and semi-erect panicle branches were determined to be monomorphic, indicating uniformity among all genotypes for these characteristics.

Keywords: Restorer lines, DUS guidelines, morphological characterization

1. Introduction

Asia consumes 90% of the world's rice (Alshiekheid et al., 2023), and it is expected to continue being a staple food in the region for the foreseeable future (Futakuchi et al., 2021; Mohidem et al., 2022).

Cultivated rice is a self-pollinating, diploid monocot of the Poaceae family, with a 430 Mb genome and 24 chromosomes. Its caryopsis is primarily composed of starchy endosperm (Shakri et al., 2021). It is rich in essential nutrients like calcium, iron, zinc, potassium, phosphorus, sodium, and various vitamins and minerals important for human health (Zafar and Xu, 2023; Fukagawa and Ziska, 2019). The genus *Oryza* includes two main cultivated species, *Oryza sativa* and *Oryza glaberrima*, and around 20 wild species (Mohapatra and Sahu., 2021; Hamzelou et al., 2020). In 2022–2023, global rice production reached 514 mt, with India contributing 135.75 mt (Anonymous, 2024). Projections estimate the global population will reach 9.7 billion by 2050, requiring over a 70% increase in food production to meet demand (Yang et al., 2024; Kang and Cho, 2022).

To meet the growing global demand, increasing rice production by focusing on hybrid varieties is crucial (Zhou et al., 2022). This strategy helps to reduce the yield gap, rather than relying on low-yielding cultivars (Ouyang et al., 2022; Rout et al., 2020). In India, the widespread adoption of hybrid rice offers a viable solution to food security challenges (Pranathi et al., 2016). The three-line system, or cytoplasmic genetic male sterility (CMS) system, is a proven method for producing hybrid rice seeds. It involves three distinct lines: the CMS line (A), the maintainer line (B), and the restorer line (R) (Azad et al., 2022; ElShamey et al., 2022). Identifying robust fertility restorer lines is essential for developing high-yielding rice hybrids (Sruthi et al., 2024) Lines that effectively restore

fertility are crucial for hybrid rice seed production (Vinay et al., 2023). There is an urgent need to search for and characterize these key lines to ensure high fertility when hybridized with cytoplasmic male sterile lines.

Morphological characterization refers to the phenotypic assessment of visual qualitative traits. Discriminating genotypes based on appearance quantifies diversity, which is crucial in evolutionary biology. Understanding genetic diversity is key to effectively utilize genetic resources within and among varieties. Assessing plant phenotypes necessitates evaluation across various environments and developmental stages (Hannah et al. 2020). The PPV & FR Act of 2001 was established to protect the interests of breeders, researchers, and farmers by focusing on the DUS (Distinctiveness, Uniformity, and Stability) characteristics of plant varieties (Prasanna et al., 2024; Akshay et al., 2022). These DUS traits are essential for identifying unique varieties (Veeraghattapu et al., 2024) and are a prerequisite for implementing the PPV & FR Act (Gayathri et al., 2023; Singh et al., 2023). Various morphological characteristics were observed at different growth stages following the procedures outlined in the DUS test guideline of the PPV & FR Act, 2001. The percentage frequencies of phenotypic classes for each character were calculated, and the Shannon-Weaver diversity index (H) was computed from these frequencies to evaluate overall phenotypic diversity. This index is widely used to measure phenotypic diversity in discrete characters (Dickman, 1968). Higher value indicates higher diversity and vice versa (Anand et al., 2024).

2. Materials and Methods

The experiment involved 80 restorer lines (Table 1) grown in

Table 1: List of 80 rice restorer lines used in the study programme

Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype
1.	Mahamaya	28.	Laxmi-144	55.	JNPT-81
2.	R-548	29.	IR09N26	56.	JNPT-782
3.	R-650	30.	IR-79854-38-2-4	57.	NPT14-12
4.	R-704	31.	IR-79854-48-2-1	58.	JNPT767
5.	Abhya	32.	AD02207	59.	JR-81
6.	R-321	33.	PAU-3832-79-4-3-1	60.	NPT-3803
7.	R-296	34.	RP5219-9-6-7-3-2-1-1	61.	NPT-3804
8.	R-712	35.	MTU1153	62.	NPT-3805
9.	R-710	36.	UPR2628-9-1-1	63.	NPT-3806
10.	R-304	37.	MTU11320-41-2-1	64.	NPT-3810
11.	JR -503	38.	P-3123	65.	NPT-3817
12.	Sugandha-3	39.	MC-13	66.	NPT-3820
13.	NPT-10	40.	TRC2013-2	67.	NPT-3821
14.	NPT-13-01	41.	VNR-212	68.	E-TP-1001
15.	NPT-15	42.	CR3424-2-2-5	69.	E-TP-1008
16.	NPT-29	43.	HRI-183	70.	E-TP-1014
17.	NPT-35-01	44.	NP-9165	71.	E-TP-1018
18.	NPT-37	45.	CR3703-11-1	72.	E-TP-1019
19.	NPT-65	46.	RP5911-52-13-3-2-2-1	73.	E-TP-1021
20.	NPT-70	47.	CR2829-PLN-32	74.	E-TP-1023
21.	NPT(S) 81	48.	CANP-318	75.	E-TP-1054
22.	JNPT809	49.	ANP-526	76.	E-TP-1062
23.	NP-72	50.	ANP-553	77.	E-TP-1064
24.	NP-1024	51.	Johar	78.	IME-1101
25.	NP-8421	52.	PR35766-B-24-3-18	79.	E-TP-1124
26.	PSP-456	53.	IR838614-678-8	80.	1E-TP-2
27.	Gemini	54.	HRT-181		

a Randomized Complete Block Design with three replications. Twenty-one-day-old seedlings were transplanted, with each genotype planted in three rows of five-meter length, spaced 15×20 cm^2 with one seedling per hill. Gaps were filled within a week to ensure uniform plant population. Fertilizer was applied at 100 kg N, 60 kg P_2O_5, and 40 kg K_2O per hectare, with P_2O_5, K_2O, and half of the nitrogen applied as a basal dose. The remaining nitrogen was split into two applications during active growth and grain filling. Standard agronomic practices were followed for crop growth.

Morphological observations were conducted according to the National DUS guidelines for rice, developed by ICAR-IIRR, Hyderabad, and approved by PPVFR, New Delhi. For evaluating yield and related traits, data were collected from five randomly selected competitive plants per line in each replication. The mean of the main, average, and smallest panicles from these plants was used to record panicle traits. The traits that were analyzed included leaf auricles, anthocyanin coloration of auricles, leaf collar, anthocyanin coloration of collar, leaf ligule, shape of ligule, color of ligule, attitude of flag leaf blade (early and late observation), density of pubescence of lemma, anthocyanin coloration of keel, anthocyanin coloration of area below apex, anthocyanin coloration of apex, color of stigma, anthocyanin coloration of nodes, intensity of anthocyanin coloration of nodes, anthocyanin coloration of internodes, curvature of main axis of panicle, color of tip of lemma, lemma and palea color, panicle awns, color of awns, length of longest awns, distribution of awns, presence of secondary branching of panicle, intensity of secondary branching, attitude of panicle branches, panicle exertion, sterile lemma color.

The Shannon-Weaver diversity index, (H), as outlined by Hutchenson (1970), is expressed as follows:

$$H = \sum_{i=1}^{n} Pi \log ePi$$

Here, Pi represents the proportion of individuals in the i^{th} category of an n class character, where n denotes the number of phenotypic categories for a specific trait. The H values were utilized to assess the diversity of individual traits.

3. Results and Discussion

3.1. Morphological characterization

Phenotypic characterization following DUS (Distinctness, Uniformity, and Stability) guidelines, along with frequency distribution analysis of specific descriptors, revealed significant variation among genotypes across different descriptor categories (Table 2). Traits showing zero variability, thus monomorphic diversity, included presence of leaf collar, absence of anthocyanin coloration of collar, presence of leaf ligule, split shape of ligule, white ligule color, absence of anthocyanin coloration of node, drooping panicle curvature of main axis, and presence of secondary branching of panicle. These results align with Priyanga et al. (2020) for leaf collar,

Table 2: Frequency distribution mentioning diversity index of phenotypic characters in fertility restorer lines

Sl. No.	Character	Class	Note/ Score	Number of genotypes	Percentage (%)	SWDI
1.	Leaf auricles	Absent	1	79	98.75	0.07
		Present	9	1	1.25	
2.	Anthocyanin coloration of auricles	Colorless	1	69	86.25	0.40
		Light purple	2	0	0	
		Purple	3	11	13.75	
3.	Leaf collar	Absent	1	0	0	0.00
		Present	9	80	100	
4.	Anthocyanin coloration of collar	Absent	1	80	100	0.00
		Present	9	0	0	
5.	Leaf ligule	Absent	1	0	0	0.00
		Present	9	80	100	
6.	Shape of ligule	Truncate	1	0	0	0.00
		Acute	2	0	0	
		Split	3	80	100	
7.	Color of ligule	White	1	80	100	0.00
		Light purple	2	0	0	
		Purple	3	0	0	

Table 2: Continue...

Sl. No.	Character	Class	Note/ Score	Number of genotypes	Percentage (%)	SWDI
8.	Attitude of flag leaf blade (early observation)	Erect	1	56	70	0.61
		Semi erect	3	24	30	
		Horizontal	5	0	0	
		Drooping	7	0	0	
9.	Density of pubescence of lemma	Absent	1	0	0	0.65
		Weak	3	22	27.5	
		Medium	5	57	71.25	
		Strong	7	1	1.25	
		Very strong	9	0	0	
10.	Anthocyanin coloration of keel	Absent	1	78	97.5	0.12
		Weak	3	0	0	
		Medium	5	2	2.5	
		Strong	7	0	0	
		Very strong	9	0	0	
11.	Anthocyanin coloration of area below apex	Absent	1	78	97.5	0.13
		Weak	3	0	0	
		Medium	5	1	1.25	
		Strong	7	1	1.25	
		Very strong	9	0	0	
12.	Anthocyanin coloration of apex	Absent	1	79	98.75	0.07
		Weak	3	0	0	
		Medium	5	1	1.25	
		Strong	7	0	0	
		Very strong	9	0	0	
13.	Color of stigma	White	1	24	30	0.87
		Light green	2	0	0	
		Yellow	3	0	0	
		Light purple	4	49	61.25	
		Purple	5	7	8.75	
14.	Anthocyanin coloration of nodes	Absent	1	80	100	0.00
		Present	9	0	0	
15.	Anthocyanin coloration of internodes	Absent	1	79	98.75	0.07
		Present	9	1	1.25	
16.	Attitude of flag leaf blade (late observation)	Erect	1	18	22.5	0.53
		Semi erect	3	62	77.5	
		Horizontal	5	0	0	
		Deflexed	7	0	0	
17.	Curvature of main axis of panicle	Straight	1	0	0	0.00
		Semi straight	3	0	0	
		Deflexed	5	0	0	

Table 2: Continue...

Sl. No.	Character	Class	Note/ Score	Number of genotypes	Percentage (%)	SWDI
		Drooping	7	80	100	
18.	Color of tip of lemma	White	1	0	0	0.13
		Yellowish	2	78	97.5	
		Brown	3	1	1.25	
		Red	4	0	0	
		Purple	5	1	1.25	
		Black	6	0	0	
19.	Lemma and palea color	Straw	1	77	96.25	0.18
		Gold and gold furrows on straw background	2	2	2.5	
		Brown spots on straw	3	0	0	
		Brown furrows on straw	4	0	0	
		Brown (tawny)	5	0	0	
		Reddish to light purple	6	1	1.25	
		Purple spots/furrows on straw	7	0	0	
		Purple	8	0	0	
		Black	9	0	0	
20.	Panicle awns	Absent	1	67	83.75	0.44
		Present	9	13	16.25	
21.	Color of awns	Yellowish white	1	12	15	0.49
		Yellowish brown	2	0	0	
		Brown	3	0	0	
		Reddish brown	4	0	0	
		Light red	5	0	0	
		Red	6	0	0	
		Light purple	7	0	0	
		Purple	8	1	1.25	
		Black	9	0	0	
		None	-	67	83.75	
22.	Length of longest awns	Very short	1	1	1.25	0.49
		Short	3	0	0	
		Medium	5	12	15	
		Long	7	0	0	
		Very long	9	0	0	
		None	-	67	83.75	
23.	Distribution of awns	Tip only	1	3	3.75	0.62
		Upper half only	3	5	6.25	
		Whole length	5	5	6.25	
		None	-	67	83.75	
24.	Presence of secondary branching of panicle	Absent	1	0	0	0.00

Table 2: Continue...

Sl. No.	Character	Class	Note/ Score	Number of genotypes	Percentage (%)	SWDI
		Present	9	80	100	
25.	Intensity of secondary branching of panicle	Weak	1	19	23.75	0.55
		Strong	2	61	76.25	
		Clustered	3	0	0	
26.	Attitude of panicle branches	Erect	1	0	0	0.00
		Erect to Semi erect	3	0	0	
		Semi erect	5	80	100	
		Semi erect to Spreading	7	0	0	
		Spreading	9	0	0	
27.	Panicle exertion	Partly exerted	3	1	1.25	0.07
		Mostly exerted	5	79	98.75	
		Well exerted	7	0	0	
28.	Sterile Lemma color	Straw	1	54	67.5	0.68
		Gold	2	25	31.25	
		Red	3	0	0	
		Purple	4	1	1.25	

anthocyanin coloration of collar and node; Manjunatha et al. (2018) for presence of secondary branching of panicle; Deepika et al. (2023) for leaf ligule and split shape of ligule; and Gayathri et al. (2023) for white ligule color and drooping panicle curvature of main axis.

Auricles were present at the base of the leaf blade in 79 rice genotypes, with a frequency of 98.75%. Purple auricles were observed in 13.75% of genotypes, while 86.25% had colorless auricles. For density of pubescence of lemma, no extreme phenotypes like absent or very strong pubescence were observed; 27.5% of genotypes exhibited weak pubescence, 71.25% medium, and 1.25% strong. Anthocyanin coloration of the keel was absent in 97.5% of genotypes, with only 2.5% showing keel anthocyanin coloration. The 97.5% of genotypes had no anthocyanin coloration in the area below the apex of the lemma, with 1.25% displaying medium or strong coloration.

The apex was devoid of coloration in 98.75% of genotypes, with medium purple coloration observed in only one genotype (1.25%). The stigma, the apex part of the pistil, showed light purple coloration in 61.25% of individuals, while 30% had a white stigmatic surface, and 8.75% exhibited purple stigma coloration. Anthocyanin coloration in internodes was noted in a single genotype (1.25%), with the remaining 98.75% showing no coloration. Erectness was reported in 18 restorers (22.5%), and 62 genotypes (77.5%) had a semi-erect attitude of the blade, with none displaying horizontal or deflexed traits. Panicle curvature, influenced by parameters such as the number of grains, filled grains, and stem strength, helps in the characterization of genotypes. The investigation revealed that all rice restorers exhibited drooping curvature (100%). Yellowish coloration of the tip of the lemma was observed in 97.5% (78) of genotypes, with one genotype each showing brown and purple coloration. The lemma, which forms the outer covering of the rice grain, was straw-colored in 96.25% of genotypes, with 2.5% displaying gold and gold furrows on a straw background, and 1.25% showing reddish to light purple coloration. Awns were absent in 83.75% of genotypes, while 16.25% had awns. Among the 13 genotypes with awns, 12 (15%) displayed yellowish-white coloration, and 1 (1.25%) had purple awns, with the remaining 67 (83.75%) restorers being awnless.

In this investigation, 15% of genotypes had medium-length awns, while only 1.25% had very short awns. Awn distribution varied across genotypes, with 6.25% showing distribution along the entire panicle length or only the upper half, and 3.75% displaying awns only at the tip. Secondary branching of panicle was predominantly strong in 76.25% of genotypes, with 23.75% showing weak branching, and no genotypes exhibited clustered branching. Panicles were mostly exerted in 98.75% of genotypes, with partial exertion observed in 1.25%, and none were well-exerted. Sterile lemma color was predominantly straw (67.5%), followed by gold (31.25%) and purple (1.25%). Table 3 representing characterization of rice restorer lines according to DUS guidelines. The similar kind of morphological classification was performed previously by Parikh et al. (2012), Roy et al. (2014), Qayyum et al. (2019), Kujur et al. (2019), Priyanga et al. (2020), Komala et al. (2017), Sajid et al. (2015), Manjunatha et al. (2018), Deepika et al. (2023), Gayathri et al. (2023).

3.2. Diversity analysis for morphological traits

The Shannon- Weaver diversity index estimated for 29 morphological traits (Table 3, Figure 1) ranged from 0 to 0.87. the highest diversity index was estimated by trait color of stigma (0.87) followed by, sterile lemma color (0.68), density of pubescence of lemma (0.65), distribution of awns (0.62), attitude of flag leaf blade(early) (0.61), secondary branching of panicle (0.55), attitude of flag leaf blade (late) (0.53), length of longest awns (0.49), color of awns (0.49), panicle awns (0.44), anthocyanin coloration of auricles (0.4), lemma and palea color (0.18), color of tip of lemma (0.13), anthocyanin coloration of keel (0.12), panicle exertion, anthocyanin coloration of internodes, anthocyanin coloration of apex and leaf auricles (0.07).

Traits that have zero diversity index were leaf collar, anthocyanin coloration of collar, leaf ligule, shape of ligule, color of ligule, anthocyanin coloration of nodes, intensity of anthocyanin coloration of nodes, curvature of main axis of panicle, presence of secondary branching of panicle, attitude of panicle branches. Similar analysis was performed by Rabara et al. (2014) to determine phenotypic diversity in rice genotypes.

Table 3: Characterization of rice restorer lines according to DUS guidelines

Sl. No.	Genotypes	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	Aa	Ab
1.	Mahamaya	9	3	9	1	9	3	1	1	3	1	1	1	5	1	1	3	7	3	1	9	1	1	3	9	2	5	5	2
2.	R-548	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	2
3.	R-650	9	3	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	9	-	-	-	9	2	5	5	2
4.	R-704	9	1	9	1	9	3	1	1	3	1	1	1	5	1	1	3	7	2	1	1	-	-	-	9	2	5	5	2
5.	Abhya	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	1	5	5	1
6.	R-321	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	2
7.	R-296	9	1	9	1	9	3	1	1	1	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	1	5	5	2
8.	R-712	9	1	9	1	9	3	1	3	1	1	1	1	4	1	1	3	7	2	1	9	1	5	1	9	2	5	5	1
9.	R-710	9	1	9	1	9	3	1	3	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	1	5	5	2
10.	R-304	9	1	9	1	9	3	1	3	3	1	1	1	4	1	1	3	7	2	1	9	1	5	5	9	2	5	5	2
11.	JR -503	9	3	9	1	9	3	1	3	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	2
12.	Sugandha-3	9	1	9	1	9	3	1	3	1	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	2
13.	NPT-10	1	1	9	1	9	3	1	3	3	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	2	5	5	2
14.	NPT-13-01	9	1	9	1	9	3	1	3	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	3	2
15.	NPT-15	9	1	9	1	9	3	1	3	1	1	1	1	1	1	1	3	7	2	2	1	-	-	-	9	2	5	5	2
16.	NPT-29	9	1	9	1	9	3	1	3	1	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	2	5	5	2
17.	NPT-35-01	9	1	9	1	9	3	1	3	1	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	1	5	5	2
18.	NPT-37	9	1	9	1	9	3	1	3	1	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
19.	NPT-65	9	1	9	1	9	3	1	3	1	1	1	1	1	1	1	3	7	2	1	9	1	5	3	9	2	5	5	2
20.	NPT-70	9	1	9	1	9	3	1	3	1	1	1	1	4	1	1	3	7	2	1	9	1	5	3	9	2	5	5	1
21.	NPT(S) 81	9	3	9	1	9	3	1	3	3	1	1	1	4	1	1	3	7	2	1	9	1	5	5	9	2	5	5	1
22.	SPS71×NPT80 (JNPT809)	9	1	9	1	9	3	1	3	3	1	1	1	1	1	1	3	7	2	1	9	1	5	5	9	2	5	5	1
23.	NP-72	9	1	9	1	9	3	1	3	1	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
24.	NP-1024	9	1	9	1	9	3	1	3	3	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
25.	NP-8421	9	1	9	1	9	3	1	3	3	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
26.	PSP-456	9	1	9	1	9	3	1	3	1	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
27.	Gemini (NPT-31)	9	1	9	1	9	3	1	3	1	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
28.	Laxmi-144	9	1	9	1	9	3	1	3	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1

Table 3: Continue...

Sl. No.	Genotypes	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	Aa	Ab
29.	IR09N26	9	1	9	1	9	3	1	3	3	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
30.	IR-79854-38-2-4	9	1	9	1	9	3	1	3	1	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	1	5	5	1
31.	IR-79854-48-2-1	9	1	9	1	9	3	1	3	1	1	1	1	5	1	1	3	7	2	1	1	-	-	-	9	1	5	5	1
32.	AD02207	9	1	9	1	9	3	1	1	1	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	2
33.	AVT2E-TP-1004 (PAU-3832-79-4-31)	9	1	9	1	9	3	1	1	3	1	1	1	5	1	1	3	7	2	1	1	-	-	-	9	1	5	5	1
34.	AVT2E-TP-1009 (RP5219-9-6-7-3-2-1-1)	9	1	9	1	9	3	1	1	1	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	1	5	5	1
35.	AVT-1E-TP1101 (MTU1153)	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
36.	AVT-1E-TP-1103 (UPR2628-9-1-1)	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	2
37.	AVT-2E-TP1240 (MTU11320-41-2-1	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	2
38.	AVT-1E-TP1301 (P-3123)	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	1	5	5	2
39.	AVT-1E-TP-1306 (MC-13)	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
40.	AVT-1E-TP1309-(TRC2013-2)	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	2	1	-	-	-	9	2	5	5	1
41.	AVT-1E-TP1312- (VNR-212)	9	1	9	1	9	3	1	1	3	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
42.	AVT-1E-TP-1327 (CR3424-2-2-5)	9	3	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	1	5	5	2
43.	AVT-1E-TP-1326 (HRI-183)	9	1	9	1	9	3	1	1	1	1	1	1	4	1	1	1	7	2	1	1	-	-	-	9	1	5	5	1
44.	IVT-Bio-fort4319 (NP-9165)	9	1	9	1	9	3	1	1	3	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
45.	IVT-Bio-fort4322 (CR3703-11-1)	9	1	9	1	9	3	1	1	3	1	1	1	5	1	1	1	7	2	1	1	-	-	-	9	2	5	5	1

Table 3: Continue...

Sl. No.	Genotypes	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	Aa	Ab
46.	IVT-Bio-fort-4323 (RP5911-52-13-3-2-2-1)	9	1	9	1	9	3	1	1	1	1	1	1	1	1	1	1	7	2	1	1	-	-	-	9	2	5	5	1
47.	IVT-Bio-fort4338 (CR2829-PLN-32)	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
48.	CANP-318	9	1	9	1	9	3	1	1	3	5	5	1	1	1	1	3	7	5	1	1	-	-	-	9	2	5	5	2
49.	ANP-526	9	1	9	1	9	3	1	1	5	5	7	5	5	1	1	1	7	2	7	9	8	5	1	9	1	5	5	4
50.	ANP-553	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	9	1	5	3	9	1	5	5	2
51.	Johar (NPT32)	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
52.	AVT1E-TP1302 (PR35766-B-24-3-18)	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	1	7	2	1	1	-	-	-	9	1	5	5	2
53.	AVT1E-TP1304 (IR838614-678-B)	9	3	9	1	9	3	1	1	1	1	1	1	4	1	1	1	7	2	1	1	-	-	-	9	2	5	5	2
54.	AVT1E-TP-1322 (HRT-181)	9	1	9	1	9	3	1	1	3	1	1	1	1	1	1	1	7	2	1	1	-	-	-	9	2	5	5	1
55.	NPT89×IR64 (JNPT-782)	9	1	9	1	9	3	1	1	1	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
56.	NPT89×IR-36 (JNPT-782)	9	1	9	1	9	3	1	1	3	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
57.	NPT14-12	9	1	9	1	9	3	1	1	3	1	1	1	5	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
58.	NPT40-01×Pusa basmati (JNPT767)	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
59.	JR-81	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
60.	IVT-NPT-3803)	9	1	9	1	9	3	1	1	3	1	1	1	1	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
61.	IVT-NPT-3804	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	9	1	5	5	9	2	5	5	1
62.	IVT-NPT-3805	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
63.	IVT-NPT-3806	9	3	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
64.	IVT-NPT-3810	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	1	7	2	1	1	-	-	-	9	2	5	5	1
65.	IVT-NPT-3816	9	1	9	1	9	3	1	1	3	1	1	1	1	1	1	1	7	2	1	1	-	-	-	9	2	5	5	1
66.	IVT-NPT-3820	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
67.	IVT-NPT-3821	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	1	7	2	1	1	-	-	-	9	1	5	5	1
68.	IVT-E-TP-1001	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	1	5	5	1
69.	IVT-E-TP-1008	9	3	9	1	9	3	1	1	1	1	1	1	1	1	1	1	7	2	1	1	-	-	-	9	2	5	5	1
70.	IVT-E-TP-1014	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	1	7	2	1	1	-	-	-	9	2	5	5	1
71.	IVT-E-TP-1018	9	1	9	1	9	3	1	1	1	1	1	1	4	1	1	1	7	2	1	1	-	-	-	9	2	5	5	1
72.	IVT-E-TP-1019	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	1	7	2	1	1	-	-	-	9	1	5	5	1
73.	IVT-E-TP-1021	9	3	9	1	9	3	1	1	3	1	1	1	4	1	1	1	7	2	1	1	-	-	-	9	1	5	5	1

Table 3: Continue...

Sl. No.	Genotypes	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	Aa	Ab
74.	IVT-E-TP-1023	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	1	7	2	1	9	1	5	3	9	2	5	5	1
75.	IVT-E-TP-1054	9	1	9	1	9	3	1	1	3	1	1	1	1	1	1	3	7	2	1	9	1	5	1	9	2	5	5	1
76.	IVT-E-TP-1062	9	1	9	1	9	3	1	1	1	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1
77.	IVT-E-TP-1064	9	3	9	1	9	3	1	1	3	1	1	1	1	1	1	1	7	2	1	1	-	-	-	9	2	5	5	1
78.	AVT-2-IME-1101	9	1	9	1	9	3	1	1	3	1	1	1	1	1	1	1	7	2	1	1	-	-	-	9	2	5	5	1
79.	AVT-1E-TP-1124	9	3	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	1	5	5	1
80.	PS-1E-TP-2	9	1	9	1	9	3	1	1	3	1	1	1	4	1	1	3	7	2	1	1	-	-	-	9	2	5	5	1

A: Leaf auricles; B: Anthocyanin coloration of auricles; C: Leaf collar; D: Anthocyanin coloration of collar; E: Leaf ligule; F: Shape of ligule; G: Color of ligule; H: Attitude of flag leaf blade (early observation); I: Density of pubescence of lemma; J: Anthocyanin coloration of keel; K: Anthocyanin coloration of area below apex; L: Anthocyanin coloration of apex; M: Color of stigma: N: Anthocyanin coloration of nodes; O: Anthocyanin coloration of internodes; P: Attitude of flag leaf blade (late observation; Q: Curvature of main axis of panicle; R: Color of tip of lemma; S: Lemma and palea color; T: Panicle awns; U: Color of awns; V: Length of longest awns; W: Distribution of awns; X: Presence of secondary branching of panicle; Y: Intensity of secondary branching of panicle; Z: Attitude of panicle branches; Aa: Panicle exertion; Ab: Sterile Lemma color.

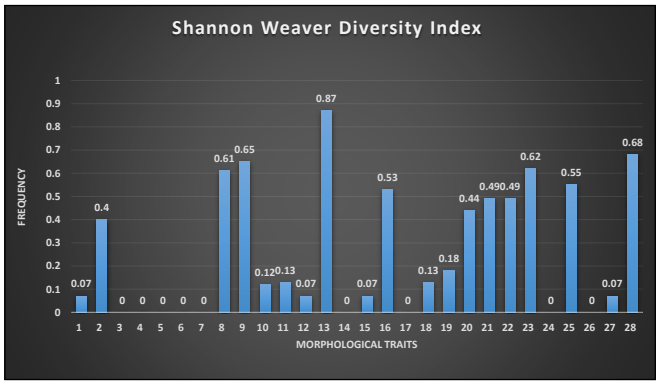

Figure 1: Shannon Weaver Diversity Index for different traits

4. Conclusion

This study revealed significant diversity among genotypes for traits anthocyanin color of stigma, sterile lemma color, pubescence density of lemma, awn distribution, and attitude of flag leaf blade (early and late). Awns enhanced seed adaptation to environmental stresses while flag leaves were crucial for photo-assimilate synthesis and translocation, affecting grain yield. Unique traits, such as anthocyanin coloration of keel, apex, internodes, and lemma, were observed in a few genotypes.

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