Biological Forum – An International Journal **13(2): 386-392(2021)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Diversity Analysis of Grain Attributes in Restorer Lines of Rice (*Oryzae sativa*)

***S. Tiwari*[1*]*, G.K. Koutu*[2] *and N. Pathak*[3]**
[1]*Ph.D. Student, Department of Plant Breeding and Genetics,*
Jawahar Lal Nehru Krishi Vishwavidhyalay, Jabalpur, (Madhya Pradesh), India.
[2]*Dean of Waraseoni, College of Agriculture, Waraseoni, (Madhya Pradesh), India.*
[3]*Senior Research Fellow, Department of Plant Breeding and Genetics, College of Agriculture,*
Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur – 482004, (Madhya Pradesh), India.

(Corresponding author: S. Tiwari)*
(Received 02 March 2021, Accepted 14 June, 2021)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: The investigation in diversity of ninety restorer concluded. As, grain is the prior economic part of any crop, thus variability analysis, based on 18 grain morphological and quantitative traits has provided the significance to this research. Grain diversity study faced a major challenge in collection of diverse genotype in single platform; the problem got sorted through the contribution made by Seed Breeding Farm, JNKVV, Jabalpur, (M.P.). The huge diversion is articulated for the traits -grain length and width, decorticated grain length and grain width, thousand grain weight (g) and decorticated grain shape. ANP 526 depicted the unique morphology along with highest mean yield 39.8g, the specific anthocyanin colouration could signify morphological marker trait during breeding programme. The genetic parameter of variability revealed that thousand grain weight having high mean (23.19), high heritability (97.2) and high genetic advance as percentage of mean (53.21) among all traits and the value of above trait is highest for genotype R 710. The complete evaluation of diverse genotypes was done through the use of varied statistical parameter and therefore the restorer found better under this experiment could possibility be utilise as parent in future breeding programme.

Keywords: Diversity, Hybridization Genetic parameter, DUS guidelines, Grain morphology and Marker trait

INTRODUCTION

The semi-aquatic annual grass called Rice originated in the tropics where every year monsoon flooded the flat and low lying lands. There are only two food crop grows with their roots under the water, Rice and Taro. The crop not only covered wetlands, deep water but varied irrigated, rain-fed, upland, lowland areas along with several adverse conditions also became the ground for paddy production. This heterogeneous adaptability of rice in a wide range of growing condition makes it an asset for breeding operations. From ancient times, since 1985, rice was the major source of food energy for a huge proportion of the population. The continuous increase in population density from that time enhances the need to stretch the arc of rice production within the given area. The flexibility of the crop in fluctuating environmental conditions and its significant contribution to human nutrition lead to numerous innovative varietal improvement. Initially, the focus was on higher yield but further upcoming problems shifted the sight towards disease, insect-pest resistance, multiple resistance and quality improvement. Recently, the cynosure transfer to Genetic Evaluation and Utilization, which mainly target breeding for tolerance and physio-chemical factors. The diverse germplasms are an excellent source of developing such varieties for crop improvement. Thus, for fulfilling this purpose both qualitative and quantitative agro-morphological traits have been commonly and traditionally used to estimate relationships between genotypes (Goodman, 1972).

The grain is the major economic part of paddy and its appearance contributes to consumer acceptance. Grain characters as studied by Kato and Matsunaga (1990) have a direct effect on the marketability or commercial success of improved rice cultivars. The antixenosis mechanism of resistance may be closely linked with structural grain morphology such as spikelet & lemma-palea anthocyanin colour, lemma-palea pubescence, style, etc. The grain may display antibiosis, wherein the behaviours of the insect are affected, normally resulting in reduced feeding and oviposition. Therefore, grain characters of rice are considered as a significant trait for varietal acceptance and rejection by farmers (Sinha *et al.,* 2015) as well as one of the important agro-morphic characters for breeding for resistance. Such types of research are performed earlier also but here the assessment in restorer helps us to get the better genotype. Examining patterns of phenotypic variation has become an integral component of many management plans concerning endangered plant species (Khadivi, 2018). For broadening gene pool of rice, hybridization of the diverse parent is the key component for any hybridization programme.

MATERIAL AND METHODS

Under rice improvement project, the experiment was conducted over 90 genotypes plotted in Randomized complete block design (RCBD) with three replications and four rows each during *Kharif season* 2018 at Seed Breeding Farm, Department of Plant Breeding and Genetics, college of agriculture, Jabalpur (M.P.). As per DUS guidelines, from each replication randomly five representative plants were selected to mark the observations and evaluation of yield and yield contributing economic traits. The analysis of variance estimated through model given by Cochran and Cox (1950). Heritability for the present study was calculated in a broad sense by adopting the formula as suggested by Hanson *et al.,* (1956). The expected genetic advance was calculated by the method suggested by Johnson *et al.,* (1955).

RESULT AND DISCUSSION

The rice restorer lines indulging sufficient variability and diversity revealed some significant phenotypic distinctness. The grain morphological diversity is depicted in Table 1 with the frequencies of genotype contributes to different traits. Mostly genotypes exhibited straw colour lemma palea colour, white stigma colour, straw colour sterile lemma, yellow-white panicle colour with medium awn length and yellow spikelet colour of lemma. These are the traits preferred since ancient times as similar preponderance of traits were found during studies of researchers (Nair 2011; Parikh *et al.*, 2012; Tiwari 2013).

The directional selection for yield narrowed the genetic base; therefore this investigation manifested some genotypes with unique morphological marker traits. ANP 526 with a highest mean yield of 39.8g in table 04 report distinct morphology with purple spot or furrow on straw, purple colour stigma, purple sterile lemma, panicle purple colour of awn and long bold decorticated shape.

Table 1: Frequency distribution of morphological characters in fertility restorer lines.

Sr. No.	Character	Class	Frequency
1.	**Lemma and Palea colour**	Straw	82
		Gold and gold furrow on straw background	02
		Brown spots on straw	00
		Brown furrow on straw	00
		Brown	04
		Reddish to light purple	00
		Purple spot/ furrow on straw	02
		Purple	00
		Black	00
2.	**Spikelet: Density of pubescence of lemma**	Absent	00
		Weak	51
		Medium	39
		Strong	00
		Very strong	00
3.	**Lemma: Anthocyanin colouration of the keel**	Absent / very weak	88
		Weak	01
		Medium	00
		Strong	01
		Very strong	00
4.	**Lemma: Anthocyanin colouration of the area below the apex**	Absent	88
		Weak	00
		Medium	01
		Strong	00
		Very strong	01
5.	**Lemma: Anthocyanin colouration of the apex**	Absent	87
		Weak	00
		Medium	02
		Strong	00
		Very strong	01
6.	**Spikelet: Colour of stigma**	White	86
		Light green	00
		Yellow	00
		Light purple	00
		Purple	04
7.	**Sterile lemma**	Straw	89
		Gold	00
		Red	00
		Purple	01
8.	**Panicle: Awns**	Absent	56
		Present	34

Continue…

Sr. No.	Character	Class	Frequency
9.	**Panicle: Colour of awns**	Yellow white	30
		Yellow-brown	00
		Brown	02
		Reddish-brown	00
		Light red	00
		Red	00
		Light purple	00
		Purple	02
		Black	00
10.	**Panicle: Length of longest awn**	Very short	00
		Short	02
		Medium	32
		Long	00
		Very long	00
11.	**Panicle: Distribution of awn**	Tip only	13
		Upper half only	21
		Whole length	01
12.	**Spikelet: Colour of the tip of the lemma**	White	00
		Yellow	85
		Brown	5
		Red	00
		Purple	00
		Black	00
13.	**Thousand-grain weight**	Low (15-20)	18
		Medium (21-25)	31
		High (26-30)	21
		Very high (>30)	11
14.	**Grain length**	Very short (<6.0 mm)	01
		Short (6.1-8.5 mm)	45
		Medium(8.6-10.5 mm)	41
		Long (10.6-12.5 mm)	03
		Very long (>12.5 mm)	00
15.	**Grain width**	Very narrow (<2.0 mm)	04
		Narrow (2.1-2.5 mm)	43
		Medium (2.6-3.0 mm)	37
		Broad (3.1-3.5 mm)	05
		Very broad (>3.5 mm)	01
16.	**Decorticated grain length**	Short	9
		medium	64
		Long	17
17.	**Decorticated grain width**	Narrow (<2.0 mm)	19
		Medium (2.0-2.5 mm)	67
		Broad (>2.5 mm)	4
18.	**Decorticated grain shape**	Short slender	01
		Short bold	02
		Medium slender	06
		Long bold	30
		Long slender	34
		Extra-long slender	16

Table 2: Genetic parameter of the variability of grain variability traits.

Sr. No.	Traits	Mean	Range		h^2 (bs) %	Genetic advance As % of the mean
			Min	Max		
1.	Thousand grain weight	23.19	5.46	37.56	97.2	53.51
2.	Grain length	8.63	4.23	11.50	96.6	25.12
3.	Grain width	2.65	2.00	5.50	79.9	29.64
4.	Decorticated grain length	6.77	5.00	9.00	96.4	23.95
5.	Decorticated grain width	2.16	1.70	3.00	83.8	21.89
6.	Length/ breath ratio	3.18	2.15	5.00	88.9	32.86
7.	Grain yield per plant	21.56	9.24	39.84	63.1	36.63

The diversity traits gold and gold furrow in the straw background, purple colour stigma, purple sterile lemma were represented by genotypes Mahamaya, ANP 526, RPHR 619, NPT 14-12; brown awn colour, brown colour of the tip of the lemma, very high thousand-grain weight displayed by R 710; very long grain length by ANP 553 and very broad grain width by RPHR 619. The corresponding verdict unveiled by researchers. (Komala *et al.,* 2017).

The genetic parameters such as mean, range, heritability and genetic advance concluded variation in traits. As per Table 2 and 3 order of traits with the highest heritability and maximum percentage of divergence are thousand-grain weight > grain length > decorticated grain length > length/width ratio. The trait followed the same trend for genetic advance as a percentage of mean report preponderance of additive gene action and further good scope of improvement through selection. This finding aligned with Islam *et al.,* (2016) for thousand seed weight and length/breadth ratio; Longjam and Singh (2019) and Nadeem *et al.,* (2020) for thousand seed weight; Asfaliza *et al.,* (2012) and Kurmanchali *et al.,* (2019) for length breadth ratio and grain length. Grain yield with complexity indulges reported minimum heritability, thus can't be considered as a sole criterion for selection. The 11 genotypes exhibited highest thousand-grain weight according to phenotypic diversity reported average mean grain yield per plant almost 21 to 26g except PS 2 (with ThGWt>30; Gy/Pl 27g) depicted in Table 3. Information provided herein comprehensively explored the occurrence of genotypic variations which can be used for the development of candidate varieties responding to breeder, farmer, and consumer preference.

Table 3: Depicting genotypes with mean attributes.

GENOTYPES	ThSWt	GL	GW	DGL	DGW	L/B	GY/Pl
MAHAMAYA	31.23	8.13	3.00	6.80	2.20	3.10	21.04
R 548	26.47	8.40	3.00	6.50	2.50	2.60	22.60
R 650	24.30	8.72	2.60	6.00	2.00	3.00	25.35
R 704	33.23	8.70	3.20	6.03	2.50	2.42	22.67
ABHYA	28.80	9.10	2.80	5.50	2.00	2.75	20.33
R 321	21.50	9.00	2.50	6.27	2.03	3.12	20.01
R 294	15.33	8.90	2.83	6.80	2.03	3.36	17.55
R 712	22.20	7.50	3.00	6.93	2.50	2.77	15.44
R 710	37.57	9.40	3.30	7.00	2.90	2.41	21.67
R 304	25.43	8.30	3.10	6.70	2.30	2.92	19.15
JR 503	23.33	7.80	2.80	6.00	2.00	3.00	22.76
SUGHANDA 3	20.53	11.10	2.47	9.00	1.80	5.01	15.04
NPT 10	26.30	8.00	3.00	6.47	3.00	2.16	21.32
NPT 13-01	26.37	7.80	3.03	6.33	2.30	2.76	12.74
NPT 15	23.33	8.50	3.03	6.80	2.20	3.09	20.00
NPT 29	29.47	8.00	3.00	6.00	2.20	2.73	16.19
NPT 35-01	23.27	7.00	3.00	6.00	2.50	2.40	19.20
NPT 37	25.43	8.00	2.80	5.47	2.43	2.26	16.60
NPT 65	28.17	8.20	2.90	6.00	2.20	2.73	24.00
NPT 70	27.50	8.50	2.70	6.00	2.30	2.61	23.00
NPT (S) 8-1	24.33	9.00	3.00	8.00	2.20	3.64	12.13
SPS 71 * NPT 80	13.37	9.40	2.47	6.50	2.20	2.96	20.35
NP 72	14.17	7.00	2.27	6.50	1.80	3.62	20.67
NP 1024	17.73	8.00	2.47	6.30	1.80	3.51	22.33
NP 8421	18.33	8.10	3.07	6.00	2.00	3.01	22.80
PSP 456	16.43	8.03	3.07	6.30	1.90	3.32	23.00
NPT 31	16.00	8.70	2.63	7.00	1.80	3.90	16.33
LAXMI 144	15.57	8.50	2.23	5.50	1.70	3.24	15.33
IR 09 N 261	24.33	11.43	2.40	9.00	1.90	4.75	22.41
IR 79854-38-2-4	19.97	10.33	2.50	7.50	1.93	3.90	15.45
IR 79854-48-2-1	26.30	8.47	3.00	7.03	1.93	3.67	24.67
AD 02207	13.57	6.80	2.00	5.00	1.70	2.95	17.32
JR-1004	32.37	9.70	2.47	7.00	2.20	3.19	22.28
JR-1009	25.43	10.20	2.40	7.70	1.90	4.06	28.15
JR-1103	24.13	8.00	2.47	6.50	2.20	2.96	26.33
JR-1103-1	26.43	9.00	2.60	7.20	2.40	3.00	26.33
JR-1204	26.20	8.70	2.60	6.70	2.40	2.79	26.33
JR-1301	17.37	7.70	2.30	6.20	2.80	2.22	13.06
JR-1306	18.10	7.80	2.00	6.20	1.90	3.27	26.67
JR-1309	28.10	9.97	2.53	6.50	2.20	2.96	19.35
JR-1312	24.83	8.90	2.40	6.90	2.30	3.00	23.38
JR-1327	24.33	8.10	3.00	6.80	2.40	2.84	20.20
JR-1326	26.43	8.40	3.00	7.30	2.00	3.66	9.71

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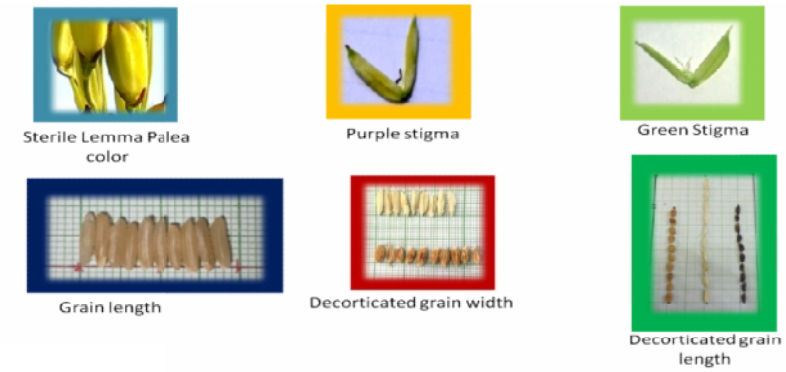
GENOTYPES	ThSWt	GL	GW	DGL	DGW	L/B	GY/Pl
JR-4319-1	18.80	7.60	2.60	5.70	2.00	2.86	23.48
JR-4322-2	13.83	7.40	2.70	5.60	2.50	2.24	24.45
RP 5911-52-13-3-2-2-1	6.50	8.60	2.30	6.40	2.20	2.91	9.24
CR 2829-PLN-32	22.33	8.30	2.40	6.00	2.00	3.00	13.18
CANP 318	17.40	8.30	2.33	7.20	1.97	3.67	14.80
ANP 526	26.20	8.80	2.53	6.50	2.50	2.60	39.85
ANP 553	28.50	11.50	2.70	8.50	1.80	4.74	22.63
NPT 32	17.53	8.50	2.40	6.60	2.00	3.30	10.22
JR 1302	31.60	9.40	2.80	6.73	2.20	3.06	26.67
IR 838614-673-13	25.43	10.00	2.50	7.30	2.10	3.48	25.67
JR 1322	21.33	8.80	2.47	7.00	2.00	3.50	20.26
NPT 89* IR64	23.47	7.67	2.43	6.80	2.00	3.43	17.91
NPT 89*IR36	22.13	8.30	2.40	7.40	2.00	3.72	23.50
NPT 14-12	24.70	9.00	2.50	7.00	2.00	3.51	19.69
NPT 40-018* Pusa Basmati	25.40	8.20	2.00	7.80	2.00	3.90	26.81
JR 81	28.33	9.80	2.40	7.50	2.20	3.41	26.33
NPT 3803	18.53	7.60	2.50	6.20	2.30	2.70	25.46
NPT 3804	22.63	8.13	2.50	7.00	1.90	3.69	21.21
NPT-3805	23.63	9.07	2.50	6.80	2.20	3.10	28.67
NPT-3806	22.60	10.00	2.20	8.20	1.90	4.32	24.67
NPT-3810	9.30	7.40	2.50	5.50	2.00	2.75	11.23
NPT 3817	22.57	7.20	2.89	6.20	2.20	2.82	23.36
NPT 3820	32.33	10.30	2.40	7.60	2.50	3.04	23.33
NPT-3821	27.47	8.33	3.00	6.20	2.30	2.70	26.33
JR-1001	16.37	8.00	2.20	5.70	2.20	2.60	21.64
JR-1008	26.13	9.30	2.70	7.20	2.00	3.61	27.33
JR-1014	24.27	9.40	3.60	7.20	2.20	3.27	29.67
JR-1018	18.30	7.30	2.30	6.20	2.10	2.95	25.33
JR-1019	23.30	9.03	2.30	7.00	2.40	2.92	23.67
JR-1021	25.40	9.40	2.40	7.00	2.00	3.51	14.41
JR-1023-1	27.47	10.00	3.20	7.30	2.40	3.05	28.33
JR-1054-4	31.50	9.60	2.97	8.00	2.40	3.34	26.33
JR-1062-1	29.27	9.40	2.87	8.00	2.60	3.08	26.49
JR-1064-1	18.00	8.20	2.70	6.07	2.20	2.76	20.67
JR-1101-6	30.50	8.60	2.77	6.30	2.30	2.74	24.67
JR-1124-4	30.53	10.30	2.30	7.10	1.90	3.74	26.33
PS 2	30.43	4.23	2.30	8.70	2.70	3.22	27.00
CBSN 168	9.50	8.00	2.00	6.40	2.00	3.21	24.76
RT CNP 28	5.47	9.00	2.80	6.70	2.00	3.36	10.47
PRR 801	27.63	9.50	2.70	6.50	2.40	2.71	25.00
PRR 805	28.37	8.60	2.50	7.60	2.40	3.17	18.97
PRR 828	25.40	8.93	2.40	6.77	2.20	3.08	23.67
PRR 831	23.30	10.30	2.20	8.00	2.00	4.01	19.64
PRR 78	31.63	8.47	2.20	8.00	1.97	4.07	26.33
RPHR 1005	13.50	7.40	2.40	5.70	1.93	2.96	19.19
RPHR 619	20.33	7.60	5.50	6.80	2.20	3.10	24.33
RPHR 2	24.50	9.00	2.40	7.50	2.00	3.75	26.67


Sterile Lemma Palea color

Purple stigma

Green Stigma

Grain length

Decorticated grain width

Decorticated grain length

Fig. 1. Grain Morphological Diversity.

Fig. 2. Image of area of work depicting the assessment of panicle morphology.

Grain length and shape are the highly heritable, polygenic trait and are independent of each other and the same was found in our research. The Ramiah committee (1964) suggested five categories of rice grain on basis of length and width, among which in India slender and long slender grains are mostly preferred traits for quality rice (Singh, 2001). Fifty out of ninety varieties were long (34) and extra-long (16) slender (> 6mm length &> 3mm width) as per phenotypic diversity with highest values in genotypes SUGHANDA 3, IR 09 N 261, ANP 553. Although grain yield and quality showed negative correlation as per many studies the genotypes articulating slender grain shape and high mean yielding varieties are JR-1009, NPT-3805, JR-1008 and JR-1014.

CONCLUSION

The grain being a key contributor of economic yield in rice needed to be evaluated stringently. Therefore, the research orientation is towards extracting the core character responsible for variability and yield. In this experiment, the thousand grain weight was found to have high heritability and high genetic advance. The choice of such trait majorly in paddy would help to differentiate among superior restorer, especially during three line hybrid production programme. Also, on assessment of all genotypes, R 710 has shown highest value of genetic parameter of variability and mean yield, has maximum potential of developing superior recombinant and release of improved hybrids in hybridization breeding programme.

FUTURE SCOPE

The current research would form baseline information for further evaluation and exploitation of restorer line and many among them could be used as an elite parent. As, we all know, generally in paddy the two line system of hybrid seed production is predominate, thus the R line diversification and characterization on basis of grain traits would help us to unveiled the diverse superior genotypes. Also, these restorers could be validate for specific gene through molecular characterization.

Acknowledgement: The authors want to show gratitude toward the College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India for providing the space and funds for conduction of the research work. Also, the support and help provided by the organization had made the performance of work smooth.

Conflict of Interest: Nil.

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How to cite this article: Tiwari, S., Koutu, G. K. and Pathak, N. (2021). Diversity Analysis of Grain Attributes in Restorer Lines of Rice (*Oryzae sativa*). *Biological Forum – An International Journal, 13*(2): 386-392.