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AGRO-MORPHOLOGICAL CHARACTERIZATION AND GENETIC VARIABILITY OF GERMPLASM ACCESSIONS OF RICE (*ORYZA SATIVA* L.)

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ABSTRACT

Agro- morphological characterization was studied in 52 germplasm accessions of rice (*Oryza sativa* L.) for 40 agro-morphological, 10 quantitative traits result of which revealed that characters showing huge diversity on the basis of DUS descriptors. Analysis of variance indicates that mean sum square due to the genotypes were found highly significant for most of the traits. High values of GCV and PCV was found for the traits number of unfilled grains. High heritability was observed for all the traits except panicle length and harvest index. High heritability coupled with high genetic advance as per cent of mean was observed for most of the traits except panicle length

***Keywords*:** Characterization, morphological traits, germplasm, rice.

Introduction

Rice (*Oryza sativa* L.) is an important food grain crop in India and a member of the Poaceae family with chromosome number 2n=24. There are two cultivated species *Oryza sativa* and *Oryza glaberrima*. *Oryza sativa* (2n=24 AA) is the most widely grown species, while *Oryza glaberrima* (2n=24 AA) is only widely planted in West Africa (Kanwar *et al.,* 2017). This ranks first among the three major cereals, followed by wheat and maize. It is one of the oldest cultivated sources of nutrients to flourish under a wide range of environments and it has 22 wild species in the *Oryza* genus. Rice (*Oryza sativa* L.) is the world's most significant cereal crop, providing a primary source of food for more than half of the world's population. It may be cultivated in a variety of environments, including upland, lowland, and rain-fed. It is one among India's most important crops. Moreover, half of the world's population eats rice as their primary carbohydrate source. Moreover, it is a nutrient-rich cereal crop that provides 20% of the calories and 15% of the protein consumed by the world's population. Minerals and fibres are also present. Collection and classification of existing germplasm is critical not only for using appropriate attribute-based donors in breeding programmes, but also for protecting the distinctive rice in the modern day.

Materials and Methods

The experiment study comprised of 52 germplasm accessions of rice (*Oryza sativa* L.) i.e 48 germplasm accessions received from NBPGR (National Bureau of Plant Genetic Resources), New Delhi including 4 checks namely Danteshwari, C.G. Devbhog, Swarna and IGKVR1 (Rajeshwari). The experimental material was grown in *Kharif* in Completely Randomized Completely Block Design (RCBD) with 2 replications. 21 days old seedlings of each genotype were transplanted manually in 2 rows of 2m length maintaining a spacing of 20cm between rows and 15 cm between plants in each row. Observations were recorded on 5 random plants from each genotype per replication for 10 quantitative traits and means values of these were used for statistical analysis.

Results and Discussions

Agro-morphological characterization for the characteristics Leaf: auricle, Leaf: collar, Leaf: ligule and Leaf: shape of legule form, there was no variation among the accessions. Similar findings have been reported by Sarawgi *et al.*, 2013 and presence of secondary branching. There have been moderate differences in character genotypes: Leaf: anthocyanin colouration, Leaf sheath: anthocyanin colouration, Leaf: anthocyanin colouration of auricles, Leaf: anthocyanin colouration of collar, Leaf: width of blade, Stem: anthocyanin colouration of nodes and Stem: anthocyanin colouration of internodes (Umarani *et al.,* 2017). Coleoptile: colour, flag leaf: attitude of blade ((early observation), Panicle: awns and Panicle: secondary branching.

The following characteristics show a high variation in experimental material:- "Basal leaf: sheath colour (Umarani *et al.,* 2017), Leaf: intensity of anthocyanin colouration, Leaf: pubescence of blade surface, culm: attitude and Time of heading (Umarani *et al.,* 2017), Spikelet: density pubescence of lemma, Spikelet: colour of stigma, Flag leaf: attitude of blade, Leaf: distribution of anthocyanin colouration, Leaf: length of blade, Stem: thickness (Umarani *et al.,* 2017), Lemma: anthocyanin colouration of keel, Lemma: anthocyanin colouration of area below apex, Lemma: anthocyanin colouration of apex, Spikelet: colour of tip lemma, Lemma &Palea: colour, Panicle: colour of awns, Panicle: length of longest awns, Panicle: distribution of awns, Panicle : presence of secondary branching, Panicle : attitude of branches, Panicle: exertion and Leaf: senescence.''

As a result, certain features were monomorphic, bimorphic, trimorphic, and tetramorphic, showing a broad variety of variations. It was reported that the results followed a similar pattern, Sajid *et al.* (2015), Pauchauri *et al.* (2017), Pragnya *et al.* (2018) and Rawte and Saxena (2018).

Certain of the accessions identified to be unique and showing some distinctive features in the present experiment material are given below in Table: 1

Table 1: List of unique accession based on morphological characters

S.No.	Accession	Characters
1.	**EC-887409**	Uniform purple- Basal leaf sheath colour Light purple-Spikelet colour of stigma Uniform- Leaf distribution of anthocyanin colouration Strong- Lemma anthocyanin colouration of keel Very late- Time of heading Present- Stem anthocyanin colouration of node
2.	**EC-921297**	Uniform purple- Basal leaf sheath colour Uniform- Leaf distribution of anthocyanin colouration
3.	**IC-452735**	Very strong – Leaf sheath intensity of anthocyanin colouration Very strong- Spikelet density pubescence of lemma
4.	**EC-933088**	Very late-Time of heading
5.	**IC-452286**	Very strong- Spikelet density pubescence of lemma
6.	**EC-882755**	Medium- Lemma anthocyanin colouration of keel
7.	**IC-466881**	Strong- Lemma anthocyanin colouration of keel
8.	**EC-882612**	Medium- Lemma anthocyanin colouration of area below apex
9.	**EC-882615**	Medium- Lemma anthocyanin colouration of area below apex
10.	**EC-921328**	Light purple- Spikelet colour of stigma
11.	**EC-882589**	Present- Stem anthocyanin colouration of node
12.	**EC-921413**	Brown- Spikelet colour of tip lemma
13.	**EC-933135**	Brown- Spikelet colour of tip lemma
14.	**EC-882541**	Light purple- Panicle colour of awns
15.	**IC-516155**	Purple- Panicle colour of awns
16.	**EC-933095**	Long- Panicle length of awns Whole length- Panicle distribution of awns
17.	**EC-882504**	Upper half only- Panicle distribution of awns
18.	**Ec-882634**	Upper half only- Panicle distribution of awns

Analysis of Variance

The mean sum of the squares of the genotypes appears to be highly significant for all characters, according to the analysis of variance of 10 quantitative traits shown in table 2. Plant height, days to 50% flowering, effective tillers per plant, panicle length, number of filled grains per panicle, number of unfilled grains per panicle length, biological yield, harvest index, and grain yield per plant all showed significant variability between genotypes for these traits, and selection could help to moderate genotypic improvement.

Table 2: Analysis of variance for 10 quantitative traits in 52 accessions

S. No.	Traits	Mean sum of square (MSS)		
		Replication	Genotype	Error
		d.f.(1)	d.f.(51)	d.f.(51)
1.	Plant height (cm)	5.38	1609.23^{**}	61.39
2.	Days to 50% flowering	3.85	284.00^{**}	6.51
3.	Effective tillers per plant	1.79	6.03^{**}	0.70
4.	Panicle length (cm)	3.63	11.62^{**}	5.70
5.	Number of filled grains per panicle	72.63	1721.59^{**}	181.28
6.	Number of unfilled grains per panicle	0.91	406.37^{**}	29.16
7.	Biological yield (g)	3.76	205.44^{**}	18.58
8.	100 seed weight (g)	0.09	0.33^{**}	0.04
9.	Harvest index (%)	20.07	206.08^{**}	56.89
10.	Grain yield per plant (g)	6.26	40.62^{**}	4.19

** Significant at 1 % levels respectively.

Genetic Parameters

Results for 10 quantitative characters and 16 quality characters evaluated with respect to 52 rice accessions for various genetic variability parameters such as mean, range, genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV), broad sense heritability (Hb), genetic advance (GA), and genetic advance as percent of mean (GA percent of mean).

Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV)

Table 3 shows the genetic parameters of variation derived for various quantitative characteristics. Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) are statistical measures that quantify the amount of variability present in a population for a specific trait. GCV reflects the genetic variability, while PCV encompasses both genetic and environmental effects on the trait. In almost all of the traits evaluated in the experiment, the phenotypic coefficient of variation (PCV) was greater in magnitude than the genotypic coefficient of variation (GCV). This indicates that the apparent variance is attributable not just to genes but also to the environment's little effect.

The phenotypic coefficient of variation (PCV) showed has a higher magnitude for, number of unfilled grains per panicle (42.60), number of effective tillers per plant (26.84), harvest index % (26.54), grain yield per plant (25.65), plant height (24.41), biological yield (23.93), number of filled grain per panicle (22.51) and moderate PCV was recorded 100 seed weight (18.47), Days to 50 % flowering (12.64) and panicle length (11.65).

The presence of a higher genotypic coefficient of variation (GCV) suggests that the population has a considerable of genetic diversity. The phenotypic coefficient of variation was higher than the GCV in the present research, but the difference was modest, indicating that environmental impacts on trait expression were low. Similar findings have been reported by Sarawgi *et al.* (1994), Ganesan *et al.* (1995), Sharma and dubey (1997), Debchaudhary and Das (1998) and Sadhukan and Chattopadhyay (2000).

In this study, the high magnitude of GCV obtained for the number of unfilled grains per panicle corresponds with the findings of Padmaja *et al.*, (2008) and Prasad *et al.* (2009).

Table 3: Estimation of genetic parameters for quantitative traits

S. No	Traits	Mean	Range		PCV (%)	GCV (%)	h^2 bs (%)	GA	GAM
			Min	Max					
1.	Days to 50 % flowering	95.97	81.00	133.50	12.64	12.36	95.66	23.91	24.91
2.	Plant height (cm)	118.40	80.07	185.91	24.41	23.49	92.65	55.17	46.59
3.	Number of effective tillers per panicles	6.80	3.50	13.73	26.84	23.83	78.83	2.96	43.59
4.	Panicle length (cm)	25.22	20.63	29.02	11.65	6.73	33.34	2.02	8.00
5.	Number of filled grains per panicle	137.02	76.20	202.08	22.51	20.25	80.94	51.43	37.53
6.	Number of unfilled grains per panicle	34.64	14.40	82.20	42.60	39.64	86.60	26.32	76.00
7.	Biological yield (g)	43.87	27.88	73.93	23.93	21.56	81.17	17.55	40.01
8.	100 seed weight (g)	2.46	1.28	3.67	18.47	16.61	80.84	0.75	30.77
9.	Harvest index (%)	43.37	18.11	64.54	26.54	19.96	56.59	13.42	30.94
10.	Grain yield per plant (g)	18.47	9.66	31.77	25.62	23.09	81.23	7.92	42.88

Estimates of Heritability and Genetic advance as percent of mean

In a broad sense, all of the variables under investigation had higher estimates of heritability (>60 percent, as stated by Johnson *et al.*, 1995). The heritability values for each of the 10 variables ranged from 33.34 % for panicle length to 95.66% for days to 50 % flowering. The greatest heritability was found in the days to 50% flowering, (95.66 %) followed by plant height (92.65%), number of unfilled grains per panicle (86.60%), grain yield per plant (81.23%), biological yield (81.17%), number of filled grains per panicle (80.94%), 100 seed weight (80.84%) and number of effective tillers per plant (78.83%).

High estimates of genetic advance as a percentage of the mean were observed for number of unfilled grains per panicle (76.00), plant height (46.59), number of effective tillers per plant (43.59), grain yield per plant (42.88), biological yield (40.01), number of filled grains per plant (37.53), harvest index (30.94), 100 seed weight (30.77), days to 50 % flowering (24.91). No characters of modest genetic advance as a percentage.

High heritability coupled with high genetic advance as a percentage of mean was recorded for all quantitative traits and rest of the traits panicle length exhibited low. It's indicating the control of expressions by higher additive gene action and selection for this trait would be useful for selection criteria for further crop improvement.

In the current study, high genetic advance as a percentage of mean was reported for the traits number of unfilled grains per panicle, 100 seed weight, grain yield per plant and number of filled grains per panicle, which is consistent with the similar findings were reported by Chandra and Pradhan (2003), Singh (1994), Rao and Shrivastava (1994). Number of filled grains per panicle, number of unfilled grains per panicle, biological yield, 100 seed weight and grain yield per plant showed high heritability coupled with high genetic advance. Similar findings were observed by Nandekar *et al.* (2022).

Conclusions

The germplasm accessions *viz.,* EC-887409,), EC-921297, IC-452735, EC-933088, IC-452286, EC-882755, IC-466881, EC-882612, EC-882615, EC-921328, EC-882589, EC-921413, EC-933135, EC-882541, IC-516155, EC-933095 and EC-882504 were found to be unique which can be utilized as reference variety for DUS testing. Analysis of variance indicated the mean sum of squares due to genotypic were highly significant for all of the quantitative characters. Higher GCV and PCV was recorded for Number of unfilled grains per panicle, Number of effective tillers per plant, Harvest index %, Grain yield per plant, Plant height, biological yield, Number of filled grain per panicle. High heritability coupled with high genetic advance as a percentage of mean was recorded for all quantitative traits except panicle length.

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