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ASSESSMENT OF VARIABILITY OF RICE (*ORYZA SATIVA* L.) IN RILs DERIVED POPULATION USING AGRO-MORPHOLOGICAL CHARACTERIZATION

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Abstract

The present study was carried out to characterize one hundred twenty one along with parents recombinant inbred lines on the basis of twelve morphological and twelve agronomical traits. Most of the morphological characters showed variation in different RILs lines. A significant amount of variation was displayed for most of the agronomical traits examined. After evaluation of one hundred twenty one RILs lines for twelve quantitative characters, on the basis of mean values, top ten accessions were identified for the yield ancillary traits. These can be used to identify phenotypic ally divergent sources for traits of interest in breeding programmes. This phenotyping is useful for identification QTLs for yield and yield attributing traits.

Key words : Agro-morphological characters, RILs, variability, rice.

Introduction

Rice (*Oryza sativa* L.) is an important food crop feeding half of the world's population. High yielding rice cultivars with good quality and improved pest resistance should help to keep pace with increased demand for rice by the rapid expansion of the world population. But, yielding varieties have replaced the traditional varieties especially in the irrigated rice ecosystem leading to reduced genetic base and thus increased genetic vulnerability. In past few decades, increase in share of high yielding varieties and shrinkage in the area of local varieties have been reported in India (Hore, 2005 and Rana *et al*., 2009) as well as in several other countries (Chaudhary *et al*., 2006 and Itani, 1993). Collection and characterization of existing germplasm is not only important for utilizing the appropriate attribute based donors in breeding programmes, but is also essential in the present era for protecting the unique rice. There is an urgent need to broaden the genetic base of the important crop by introgressing genes from diverse sources. Thus, there is a need to collect, exploit and evaluate the untapped genetic material. In this context, an attempt was made to *Japonica* x *Indica* derived F_{11}, one hundred twenty one Recombinant Inbred lines were developed. Population of Recombinant Inbred Lines can serve as a powerful tool to cover the complexity of yield related traits. They are the recombinant output from which superior stabilized segregants can be directly used as breeding lines. Considering the above facts the RILs population were characterize for different morphological and agronomic traits and to identify the variability of yield and its component traits.

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Materials and Methods

The material for the present investigations consisted of one hundred twenty one Recombinant Inbred lines along with two parents (JNPT 89 & IR 64) were planted in an Alpha lattice design with two replications during *Kharif* 2011 at Seed Breeding Farm, Department of Genetics and Plant Breeding, J.N.K.V.V., Jabalpur (M.P.), India. Twenty one days seeding of each genotype was planted in five rows of three meter length with 20 cm row spacing keeping single seedling per hill. Recommended package of practices were followed to a raise a good crop.

Observations were recorded on five randomly chosen plants of each accession for twenty four morphological and agronomical traits. The traits studied were *viz*., seed coat colour, seed length, seed width, beak shape, plant

Table 1 : Frequency distribution of morphological characters in rice genotypes.

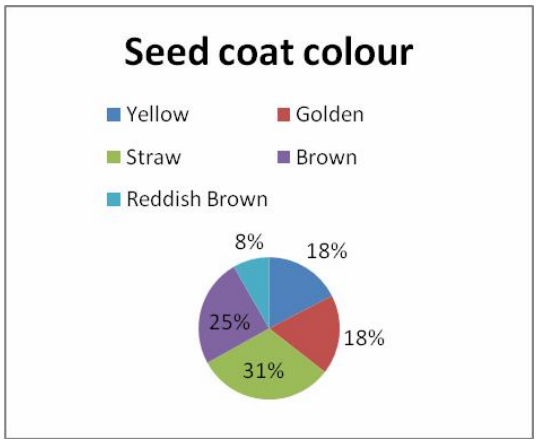
Character	Classes	Number of /frequency	Percentage of entry
1. Seed coat colour	Yellow	21	17.4
	Golden	22	18.2
	Straw	38	31.4
	Brown	30	24.8
	Reddish Brown	10	8.3
2. Seed length	Extra long	53	43.8
	Long	46	38.0
	Medium	14	11.6
	Short	8	6.6
3. Seed width	High	12	9.9
	Medium	67	55.4
	Narrow	42	34.7
	Very narrow	0	0.0
4. Beak shape	Straight	63	52.1
	Slightly curved	58	47.9
	Curved	0	0.0
5. Plant habit	Compact	42	34.7
	Open	79	65.3
	Laying/Deep watered	0	0.0
6. Leaf colour	Pale green	-	-
	Green	54	44.6
	Dark green	67	55.4
	Purple	0	
7. Leaf width	Narrow	-	-
	Medium	89	73.6
	Broad	32	26.4
8. Collar colour	Green	74	61.2
	Pale	47	57.3
	Purple	-	-
9. Ligule colour	Whitish	82	67.8
	Light purple	39	32.2
	Purple	-	-
10. Ligule length	Short	11	9.1
	Medium	40	33.1
	Long	70	57.9
11. Auricle colour	Pale green	31	25.6
	Light brown	88	72.7
	Purple	2	1.7
12. Panicle type	Compact	50	41.3
	Bunchy	71	58.7
	Semi compact	0	0.8

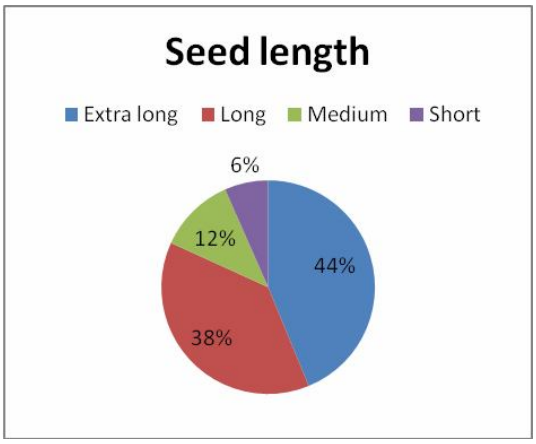
habit, leaf colour, leaf width, collar colour, ligule colour, ligule length, auricle colour and panicle type and days to fifty per cent flowering, culm height, plant height, panicle length, panicle weight per plant, total tillers per plant, number of filled grains per panicle, number of unfilled spikelets per panicle, total number of spikelets per panicle, 1000 grain weight biological yield per plant and grain yield per plant as per the guidelines by UPOV guidelines for rice (1985). The frequency distribution was computed to categorize the accession into different classes. Simple statistics (means, ranges) was calculated to have an idea of the level of variation.

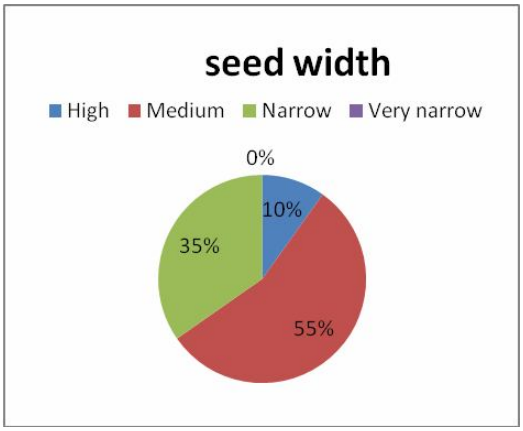
Results and Discussion

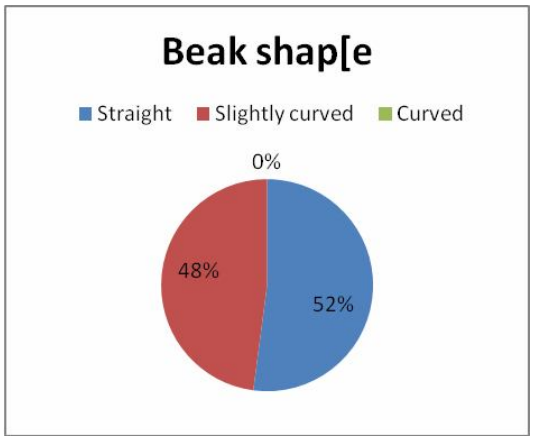
(A) Morphological characterization : Qualitative characters are important for plant description (Kurlovich, 1998) and mainly influenced by the consumers preference, socio-economic scenario and natural selection (Hien *et al*., 2007). Frequency distribution for eight qualitative traits is depicted in table 1 and its graphical representation of frequency distribution showed in figure 1. Most of the morphological characters showed variation. A majority of accessions were found to possess seed coat colour (31.4% straw), seed length (43.8% extra long), seed width (55.40% medium), beak shape (52% straight), plant habit (65.3% open type), leaf: colour (55.4% dark green), leaf: width (73.6% medium), collar colour (61.2% light green), ligule colour (67.8 % whitish), ligule length (58% long), auricle colour (72.7% light brown) and panicle type (58.7% bunchy). Similar type of work was also reported by Bisne and Sarawgi (2008) and Moukoumbi *et al.* (2011).

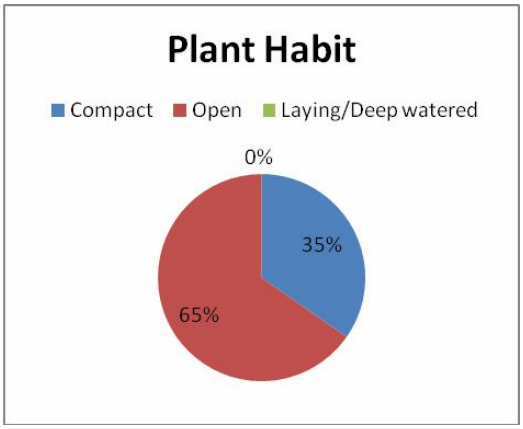
B) Agronomical characterization : Rice accessions were evaluated for agronomical traits *viz*., days to fifty per cent flowering, culm height, plant height, panicle length, panicle weight per plant, total tillers per plant, number of filled grains per panicle, number of unfilled spikelets per panicle, total number of spikelets per panicle, 1000 grain weight biological yield per plant and grain yield per plant. RILs showing transgressive

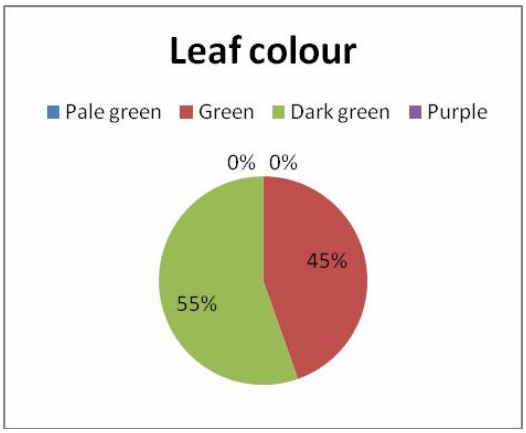

Seed coat colour
Yellow
Golden
Straw
Brown
Reddish Brown
8%
18%
18%
25%
31%

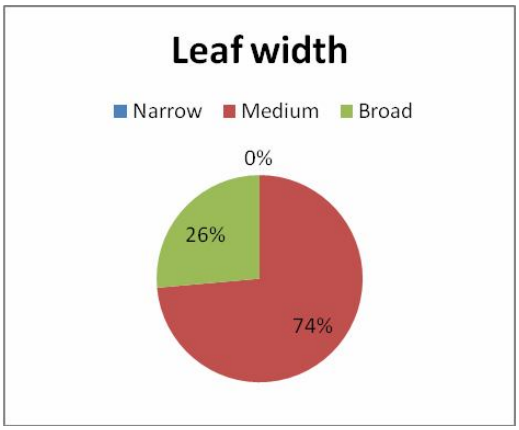

Seed length
Extra long
Long
Medium
Short
6%
12%
44%
38%

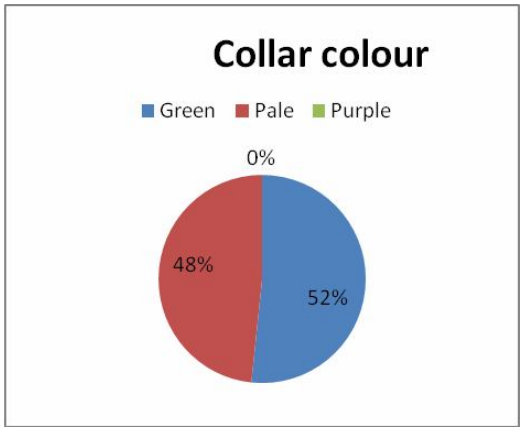

seed width
High
Medium
Narrow
Very narrow
0%
10%
35%
55%


Beak shap[e
Straight
Slightly curved
Curved
0%
48%
52%


Plant Habit
Compact
Open
Laying/Deep watered
0%
35%
65%


Leaf colour
Pale green
Green
Dark green
Purple
0%
0%
45%
55%


Leaf width
Narrow
Medium
Broad
0%
26%
74%


Collar colour
Green
Pale
Purple
0%
48%
52%

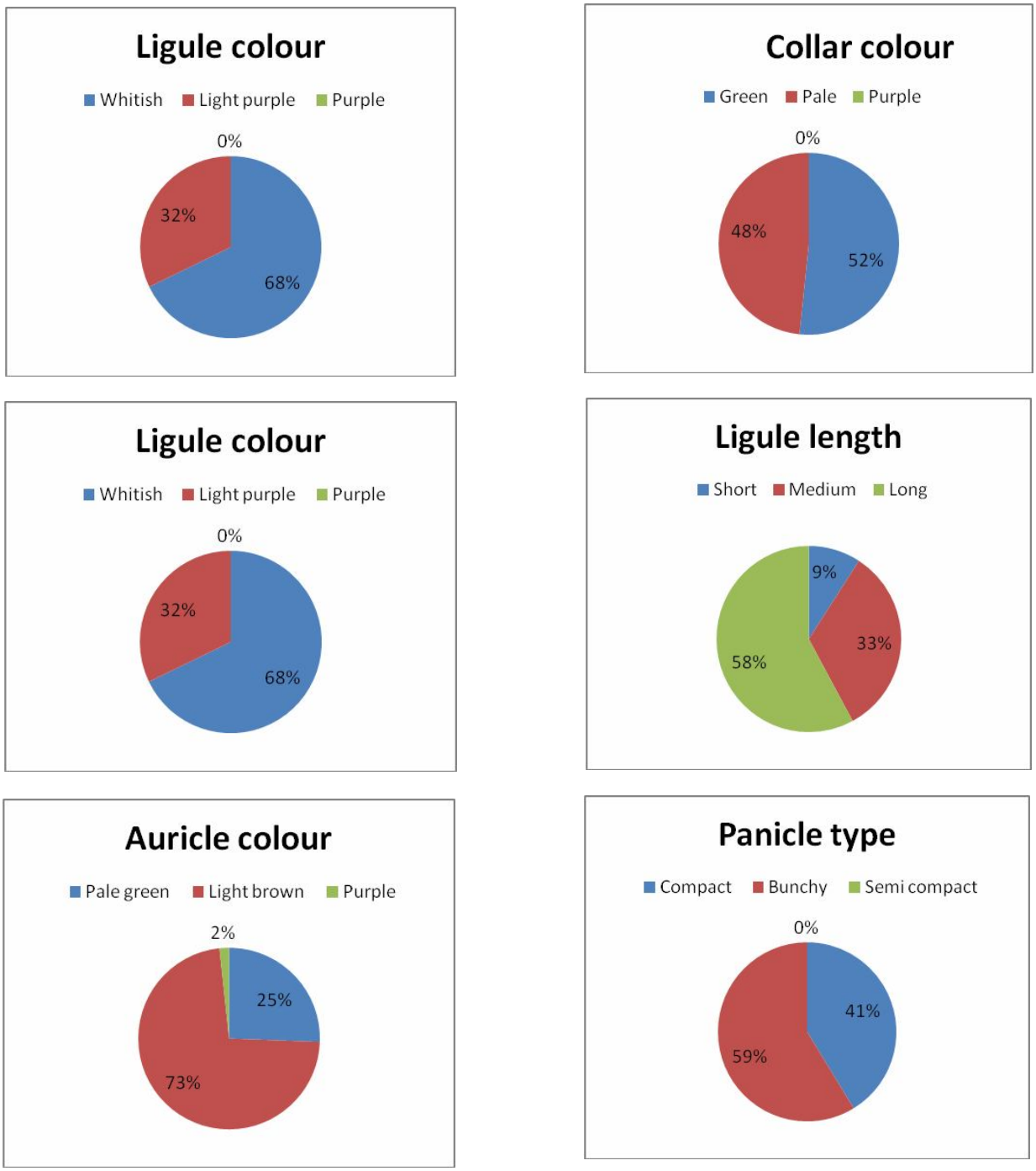


Fig. 1 : Frequency distribution of important morphological characters.

segregants for yield attributing traits and extreme (maximum and minimum) performance of RILs for different traits are shown in tables 2 and 3.

Days to 50% flowering

Days to 50% flowering varied from 70.50 to 113.50 days with a mean value of 95.05 days. RIL No. 75 and RIL No. 101 were found to be very early with days to fifty percent flowering.

Culm height

It had wide range (57.70 to 129.45 cm) of variation with a mean value of 76.09cm. The mean was the highest in the RIL19 followed by RIL 52 and lowest in the RIL 97 followed by RIL 3.

Panicle length

It had wider range from 21.20 to 29.55 cm with a mean value of 25.32 cm. The maximum panicle length

Table 2 : List of RILs showing transgressive segregants for yield and yield attributing traits.

Trait	Transgressive segregants				Parental Value	
	Highest		Lowest			
	RIL Number	Value	RIL Number	Value	JNPT 89	IR64
DTF	RIL53	113.5	RIL75	70.5	102.5	88.5
DTM	RIL53	113.5	RIL75	70.5	132.5	118.5
CH	RIL19	129.45	RIL97	57.70	74.55	64.45
PL	RIL99	29.55	RIL60	21.20	28.30	25.25
PH	RIL19	155.40	RIL97	80.80	102.85	89.70
TT	RIL14	13.25	RIL58	2.85	3.70	9.10
FSN	RIL81	280.30	RIL31	94.05	301.50	126.95
NOUS	RIL91	239.60	RIL98	6.25	93.50	8.15
TNS	RIL91	413.40	RIL101	128.61	395.00	135.10
PWPP	RIL91	49.75	RIL102	17.60	31.60	37.10
TGW	RIL84	31.70	RIL22	19.05	27.73	24.80
BYPP	RIL112	80.05	RIL18	34.45	56.85	54.55
GYPP	RIL77	47.00	RIL3	9.50	34.85	31.12

Table 3 : Extreme performing RILs for yield and yield attributing traits.

Lines	Highest	2nd Highest	Lowest	2nd Lowest
DTF	RIL53	RIL22	RIL75	RIL101
DTM	RIL53	RIL22	RIL75	RIL101
CH	RIL19	RIL52	RIL97	RIL3
PL	RIL99	RIL8	RIL60	RIL91
PH	RIL19	RIL8	RIL97	RIL74
TT	RIL14	RIL111	RIL58	RIL57
FGN	RIL81	RIL37	RIL31	RIL73
NOUS	RIL91	RIL18	RIL98	RIL78
TNS	RIL91	RIL18	RIL101	RIL102
PWPP	RIL91	RIL61	RIL102	RIL27
TGW	RIL84	RIL69	RIL22	RIL60
BYPP	RIL112	RIL79	RIL18	RIL3
GYPP	RIL77	RIL80	RIL3	RIL11

was observed in the RIL 99. Although, it contributes positively yet maximum panicle length is not the only factor responsible for higher grain yield (Abbasi *et al.*, 1995). So panicle length alone does not determine the high grain yield as traits such as grain size, grain shape, higher number of tillers per plant, longer panicles and greater numbers of grains per panicle ultimately contribute to higher grain yield (Akram *et al*., 1994).

Plant height

It had wider range varied (80.80 to 155.40 cm) of variation with a mean value of 101.49 cm. Ali *et al.* (2000) have also observed relatively greater range in plant height than the other characters. Plant height in rice is a complex character and is the end product of several genetically controlled factors called internodes (Cheema *et al*., 1987). Reduction in plant height may improve their resistance to lodging and reduce substantial yield losses associated with this trait (Abbasi *et al*., 1995).

Total tillers per plant (no.)

It also exhibited high range (2.85 to 13.25 no.) with a mean value of 6.64. It is another yield attributing trait (Abbasi *et al*., 1995). Highest number tiller per plant was observed the RIL 14 followed by RIL111 and lowest in the RIL 58 followed by RIL 57.

Filled grains per panicle (no.)

It also exhibited high range (94.05 to 301.50) with a mean value of 173.17. It is very important yield attributing trait. Highest number filled grains per panicle was observed the RIL 81 followed by RIL 37 and lowest in the RIL 31 followed by RIL 73.

Number of unfilled spikelets per panicle

It also exhibited high range (6.25 to 239.59) with a mean value of 53.70. Lowest number of unfilled spikelets per panicle was observed in the RIL 98 followed by RIL 78.

Total number of spikelets per panicle

It also exhibited high range (128.61 to 413.39) with a mean value of 227.59. Highest total number of spikelets per panicle was observed in the RIL 91 followed by RIL 18 and lowest in the RIL 101 followed by RIL 102.

Panicle weight per plant (g)

Panicle weight per plant varied from 17.60 to 49.75 g with a mean value of 28.15 g highest panicle weight per plant was exhibited in the RIL 91 followed by RIL 61 and lowest in the RIL 102 followed by RIL 27.

Test weight (g)

Test weight varied from 19.05 to 31.70 g with a mean value of 25.02 g. Highest test weight was recorded in the RIL 84 followed by RIL 69 and lowest in the RIL 22 followed by RIL 60.

Biological yield per plant (g)

Biological yield per plant varied from 34.45 to 80.05 g with a mean value of 57.67 g. The highest biological yield per plant was observed in the RIL112 followed by RIL 79 and lowest in the RIL 18 followed by RIL 33.

Grain yield per plant (g)

Grain yield per plant varied from 9.50 to 47.0 g with a mean value of 57.67 g. The highest grain yield per plant was observed in the RIL 77 followed by RIL 80 and lowest in the RIL 3 followed by RIL 11.

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