Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

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Statistical description, genetic variability, heritability and genetic advance assessment for various agronomical traits in F₂ population of rice (*Oryza sativa* L.)

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Abstract
In the present study, F_2 segregating population was developed from the crosses between the parental lines K343 and DHMAS rice during *Kharif* 2016 and evaluated for statistical description, genetic variability components i.e. GCV & PCV, heritability (broad sense) and genetic advance of various agronomical traits. The experiment was conducted using augmented design-I, analysis of variance (ANOVA) revealed statistically significant differences ($p<0.05$) indicating the existence of genetic variability amongst the population. The mean value and range in days to maturity, duration of grain filling and spikelet fertility % age was greater than that of other traits. The values recorded for genotypic variance was less than those of the phenotypic variance. In the present study spikelet density (7.24) and yield per plant (7.02) showed the highest GCV values whereas days to maturity showed the lowest GCV value (2.61). The low GCV and PCV values, indicates that trait expression was less influenced by the environment. Heritability was estimated from medium to high ranging from 56.00 to 97.00 percent for all the traits, except duration of grain filling which showed the heritability estimate of 25 per cent only. Heritability coupled with genetic advance was also recorded for all the given traits in the population. The estimation of these parameters helps the breeder in achieving the required crop improvement by selection.

Keywords: rice (*Oryza sativa* L), anova, heritability, genetic variability, genetic advance

Introduction
Rice (*Oryza sativa* L.), having a place with family Graminae (Poaceae), genus Oryza, tribe Oryzeae and sub tribe Oryzineae and class monocotyledon is a self-pollinated, having chromosome number 2n=24 with 430 Mb genome size (Hooker 1979) [7]. The genus *Oryza* has two cultivated and twenty two wild species. The cultivated species are *Oryza sativa* (Asian rice) which is grown worldwide and the *Oryza glaberrima* (African rice) (Singh *et al.* 2015) [4], which is cultivated on limited scale in West Africa. Across the world, there are more than 40,000 different varieties of the Asian rice (*Oryza sativa*). Rice being important crop is considered a model plant because of its relatively small gnome size, vast germplasm collection, enormous repertoire of molecular genetic resources, and efficient transformation system (Paterson *et al.* 2005) [18].

Rice is one of the critical cereal crops and is vital to the lives of billions of individuals around the globe. It is the most important grain as to human sustenance and caloric intake, giving more than one fifth of the calories expended worldwide by people (Khan *et al.* 2009) [15]. Rice occupies a significant part of principle human food consumption globally (Juliano 1999) [11], it fills in as the staple sustenance of the greater part the total populace. For the year 2016 statistics demonstrate that globally rice (*Oryza sativa* L.) is consumed by roughly 650 million individuals, with the production of 740 million metric tons (i.e. 30% of world grains) utilizing 157 million hectares of land (i.e. 8% of world product arrive). To fulfil the expanding worldwide need of developing populace, a half increment in rice yield will be required by the year 2050 (Sasaki *et al.* 2017) [21], especially in developing countries of Asia and Africa, where populations have been increasing dramatically (Seck *et al.* 2012) [22].

In Indian agriculture rice has significant position among the cereals and it is tremendously diverse. During the year 2016, rice was cultivated on an area of approximately 43 million hectares with the production of 104.41 million tonnes and productivity of 2.37 tonnes ha⁻¹. It is the source of livelihood for 120-150 million rural households contributing 43 percent to the total food grain and 53 percent to the cereal production and thus holds the key for food

sufficiency in India (IRRI, 2017). Jammu and Kashmir's economy is dominatingly reliant on agribusiness and allied activities. In Jammu and Kashmir, during the year 2013-14, rice was grown over an area of 259.32 lakh hectares with production and productivity of 5760 lakh tonnes and 22.21 tonnes ha^{-1}, respectively. So as to take care of the demand of expanding populace in India and to support the independence in rice production, the current production level (94.11 million tons) needs to be expanded to 120 million tons by the year 2020 (Kaloo and Choure 2015) [14].

To alleviate a portion of the limitations to rice production by developing improved varieties researchers studied genetic variability in rice which is pre-essential for rice breeding program, since the development of an effective rice breeding program is dependent upon the existence of genetic variability and character association. Therefore, before creating any breeding program, estimation of genetic variability with the help of suitable parameters such as genotypic coefficient of variation, heritability estimates and genetic advance are totally important to begin an efficient breeding program (Abebe *et al*. 2017) [1]

In the present study phenotypic evaluation was carried out in both parents and F$_2$ population for various traits *viz.* days to 50 percent flowering, number of tillers per plant, panicle number per plant, plant height, days to maturity, duration of grain filling, panicle length, spikelet density, spikelet fertility per plant, grain length, grain width, thousand grain weight and yield per plant. The availability of genetic variability is prerequisite for crop improvement. Important quantitative characters like yield is mainly influenced by large number of genes and also greatly influenced by environmental factors. Variability is partitioned into heritable and non-heritable components with suitable genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h$^2_{bs}$) and genetic advance.

Materials and Methods
Plant material and choice of parents
The plant material used for the present study was F$_2$ population, derived from a cross between two contrasting parents' K 343 and DHMAS. K 343, a predominant non-basmati rice cultivar, developed by High Mountain Rice Research Station, Khudwani, SKUAST-K for hill and temperate ecologies of J&K, was selected as female, it is a high yielding variety and generally matures around 100 to 130 days with an average yield of approx. 5.5-6.0 t/ha. The male parent selected was DHMAS, a long grain cultivar developed by doubled haploid marker assisted selection is obtained from CSK HPKV Palampur (HP) and it is an IRRI generated material. DHMAS being tall (grows up to 160cm); lodges in heavy soils leading to a very low yield. It generally matures around 120 to 140 days.

Population development
For a self-pollinating species like rice, populations likely originate from parents that are both highly homozygous. In the present study, F$_1$ seeds were developed by crossing the parents, K 343/DHMAS. Selfing and crossing are essential in crop improvement process. In rice anthesis commences shortly after emergence of panicle. Spikelets at the tip bloom first and proceed downwards. Each spikelet remains open 30 minutes and then closes. Emasculation was carried out to make a cross pollinated crop and to prevent self-pollination i.e. removal of stamens or anthers or killing the pollen or removal of male flower without the female reproductive organ. The F$_1$ plants were raised during *Kharif 2015* along with its parents in pots (as shown in photo 1) and successful crossed plants were identified for further selection. During *Kharif 2016*, two parental lines i.e. K 343 and DHMAS, F$_1$ plants along with the F$_2$ population were sown and transplanted in an Augmented Design (unreplicated design) at Experimental Farm of School of Biotechnology, SKUAST-Jammu. The nursery was transplanted in 18 × 5 meter (length × breadth) plot area and with planting density i.e. an intra-row spacing of 20cms and inter-row spacing of 20cms were maintained to accommodate 250 F$_2$ plants, out of which 233 F$_2$ plants survived and were used for genotypic and phenotypic evaluation.

Photo 1: Pots With Parents' K 343, DHMAS and F$_1$ generated from the crossing of these parents, in the year 2015

Phenotypic observations recorded
All the plants in each row were tagged individually in the plot and phenotypic data was recorded on each F$_2$ plant as per the DUS guidelines of DRR, Hyderabad (Rani *et al.* 2006) [20] for various traits: days to flowering (DFL), tiller per plant (TPP), panicle per plant (PPP), plant height (PH), days to maturity (DMT), days to grain filling (DGF), panicle length (PL), spikelet density (SD) number of filled grain/panicle (FGN), total grain number (TGN) spikelet fertility (SFP), grain length (GL), grain width (GW), yield per plant (YPP), 1000 grain weight (TGW) and some data for characters like: panicle curvature of main axis, panicle presence of secondary

branching, panicle exertion, spikelet colour of tip of lemma was also recorded as shown in table 1 and 2.

Table 1: Descriptive statistics for various agronomic traits in the parents

Traits	Mean± SD		Range (K 343)		Range (DHMAS)		CV value	
	K 343	DHMAS	Max.	Min.	Max.	Min.	K 343	DHMAS
Days to flowering	65±0.84	86 ±3.63	67	65	89	80	1.27	4.21
Panicle no./ plant	24±0.84	20±0.84	25	23	22	20	3.46	4.02
Days to maturity	115.5±1.03	131.34±0.85	116.7	114	132	130	0.90	0.65
Duration of grain filling	98±2.17	115±4.62	100	95	120	108	2.21	3.99
Plant height(cm)	32±2.19	29±1.14	35	29	31	28	6.76	3.88
Panicle length (cm)	26.62±0.40	27.48±0.47	27	26	28.2	26.9	1.49	1.71
Spikelet density	4.15±0.22	4.72±0.28	4.42	3.85	4.91	4.26	5.19	5.94
Spikelet fertility % age	92.62±3.09	81.40±3.15	96.08	89.47	84.38	77.78	3.33	3.87
Grain length (mm)	4.50±0.12	5.26±0.09	4.67	4.32	5.32	5.1	2.77	1.75
Grain width (mm)	2.46±0.02	2.04±0.02	2.49	2.43	2.05	2.0	0.91	1.06
1000 grain weight	28.52±0.43	22.48±0.46	29	28	23	21.99	1.52	2.06
Yield /plant (g)	41.42±0.50	33.47±0.37	42	40.98	34	33	1.23	1.11

Table 2: Descriptive statistics for various agronomic traits in F_2 population

Traits	Mean± SD	Range		CD value		
		Max	Min.	Test	Check	CV value
Days to flowering	83.90 ±7.08	91.00	65.00	8.85	4.17	8.43
Panicle no./ plant	19.18± 2.62	28	15	1.44	0.68	13.66
Days to maturity	126.61± 10.78	140.90	100	3.32	1.56	8.51
Duration of grain filling	111.83± 6.94	126	94	16.301	7.68	6.20
Plant height(cm)	27.93± 2.79	36	24	8.11	3.82	9.99
Panicle length (cm)	25.65± 3.02	32.6	13.2	1.54	0.72	11.78
Spikelet density	5.07±0.83	8.18	3.61	1.03	0.48	16.42
Spikelet fertility % age	86.80± 7.82	100	56.47	12.29	5.79	9.01
Grain length (mm)	4.77 ± 0.48	7.08	3.92	0.52	0.24	10.05
Grain width (mm)	2.35 ± 0.15	2.70	1.97	0.092	0.043	6.62
1000 grain weight	25.07 ± 2.12	31.71	20.11	1.09	0.51	8.48
Yield /plant (g)	37.57 ± 5.90	50.12	29.07	0.90	0.42	15.70

Data analysis
The data collected for each character was subjected to analysis of variance (ANOVA) using augmented design, Phenotypic and Genotypic Coefficients of Variability (PCV & GCV), broad sense heritability (h^2_{bs}) and genetic advance was estimated by SPSS (version 20) software and R-software Rosmaina *et al*. 2016).

Results
Phenotyping of the F_2 population
A total number of 600 F_2 seeds were developed out of which 233 plants were obtained till maturity for further analysis. The plants of parent 1 (K343) and parent 2 (DHMAS) along with a population of 233 F_2 plants were evaluated for various morphological characters during the year 2016 as: Descriptive statistics, used to describe the basic features of the data in a study, they provide simple summaries about the sample and the measures; Table of characters, gives the scales of various agronomical traits as per DUS guidelines, 2007, and Analysis of variance (ANOVA), an analysis tool used in statistics.

Statistical Description: For the various traits under study analysis of mean values was in evaluated both the parents K343 and DHMAS and F_2 population as shown in Figure 1 and Figure 2 and values depicted in Table 1 and Table 2 respectively. The mean distributions both in parents as well as in F_2 population were highly significant.
Table of characters (Table 3) indicates that 117 F_2 individuals had semi straight and 106 had deflexed type of panicle: curvature of main axis, which resemble the characters of the parental line, where DHMAS was semi-straight and K 343 was deflexed and only a few had dropping type. Since both the parents had the presence of panicle: presence of secondary branching, as such it was present in all the F_2 population. 136 plants were seen having mostly exerted panicle exertion like DHMAS, while only 97 plants were well exerted. 135 F_2 individuals were observed with yellowish spikelet: colour of tip of lemma while 98 plants were observed with brown colour, resembling their parental line where K 343 had yellowish and DHMAS had brown colour of spikelet: Colour of tip of lemma.
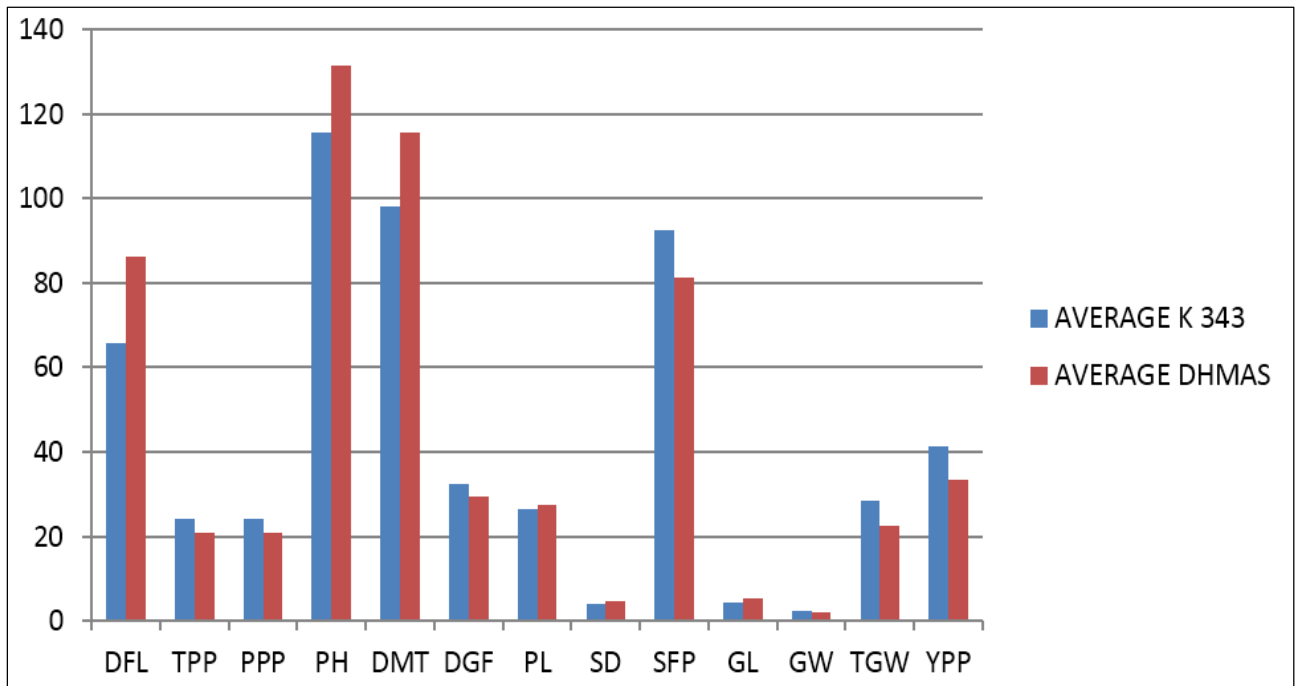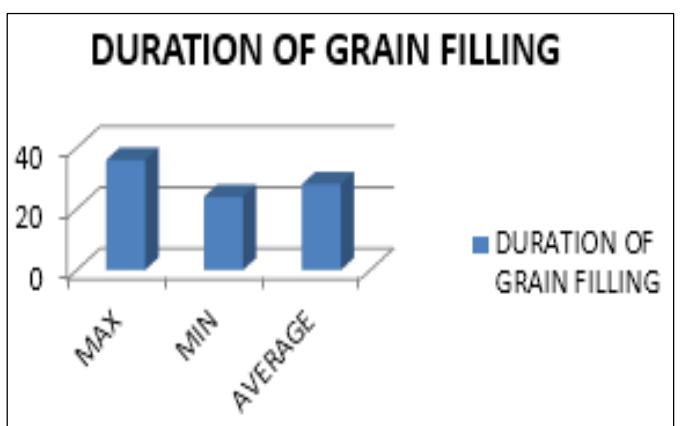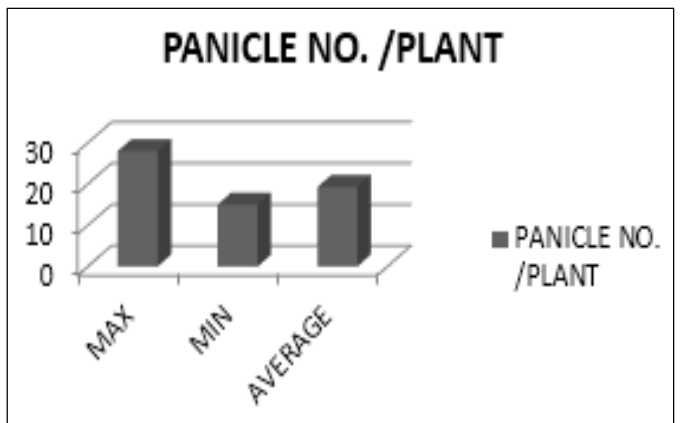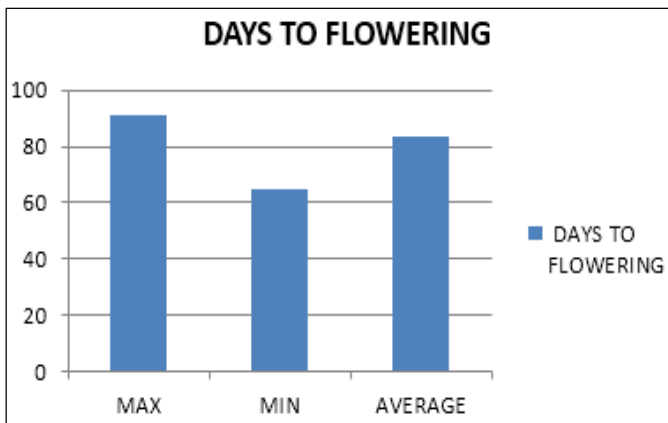
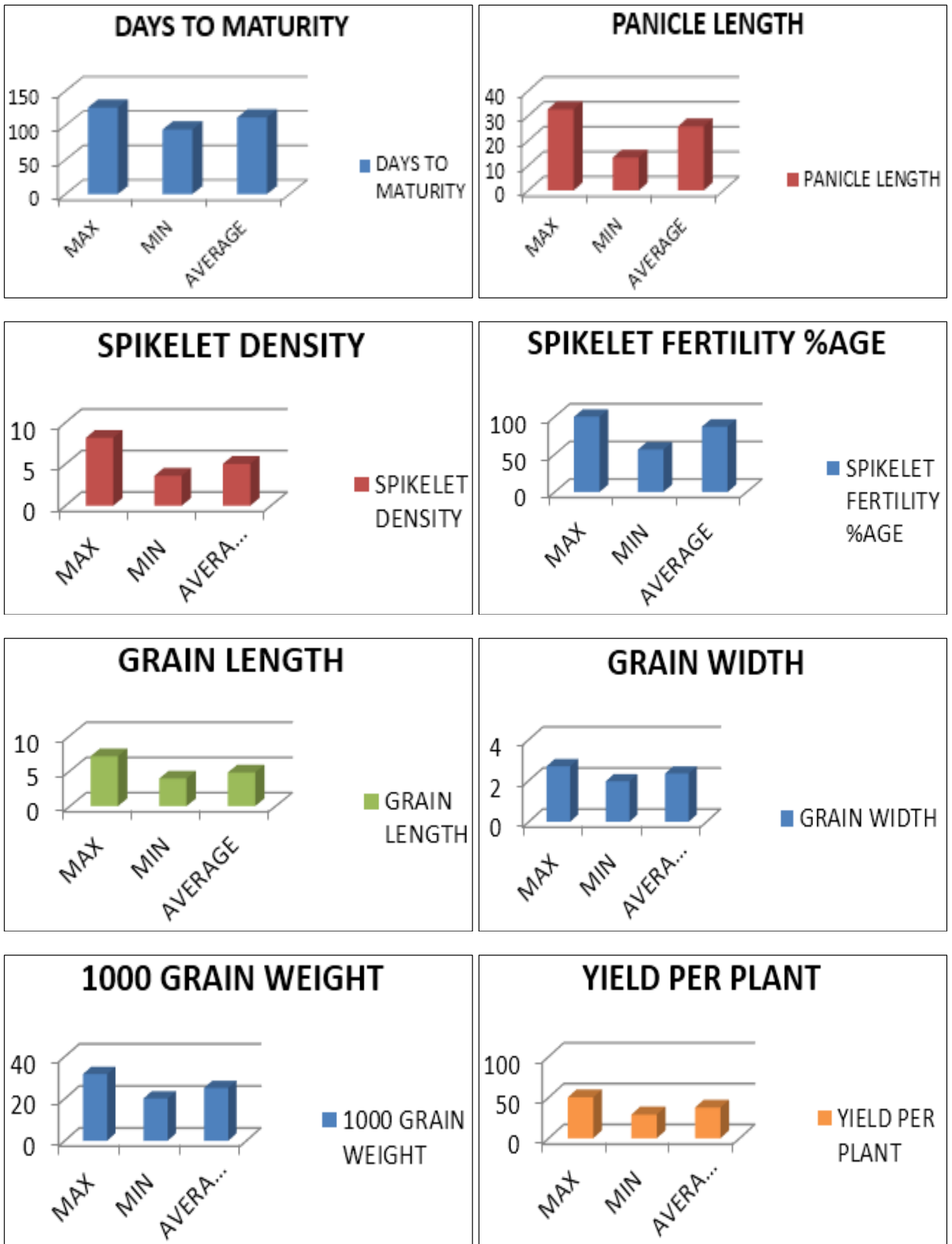**Fig 1:** Descriptive statistics for various agronomic traits in the parents

Fig 2: Descriptive statistics for various agronomic traits in the F$_2$ plants

Table 3: Tables of characters (DUS guidelines, 2007)

Characters	States	Code	Parents	F$_2$ Population
Panicle: Curvature of main axis	Straight	1	DHMAS K 343	-
	Semi straight	3		117
	Deflexed	5		106
	Dropping	7		10
Panicle: Presence of secondary branching	Absent	1	K 343/ DHMAS	-
	Present	9		233
Panicle: Exertion	Partly exertion	3	K 343/ DHMAS	-
	Well exertion	5		97
	Mostly exertion	7		136
Spikelet: Colour of tip of lemma	White	1	K 343 DHMAS	-
	Yellowish	2		135
	Brown	3		98
	Red	4		-
	Purple	5		-
	Black	6		-

Analysis of variance (ANOVA): The analysis of variance (ANOVA) for F$_2$ population as shown in Table 4, indicated that the all the traits are highly significant variation at 5percent level of significance. It reflected the existing of large variability among tested genotypes and this variability can be further utilized in the rice improvement program.

Table 4: Analysis of Variance for F$_2$ population

Source of variation	Df	DFL MSS	PPP MSS	PL MSS	DTM MSS	DGF MSS	PL MSS	SD MSS	SFP MSS	GL MSS	GW MSS	TGW MSS	YPP MSS
Among entries (e)	234 (e-1)	59.95*	7.09*	117.01*	55.56*	8.25	9.16*	0.73*	71.31*	0.24*	0.03*	5.03*	34.98*
Among checks (c)	1 (c-1)	1040.40*	28.90*	627.26*	756.90	22.50*	1.85*	0.82*	314.69*	1.44*	0.45*	91.20*	158.24
Among varieties (v)	232 (v-1)	53.60*	6.62*	115.39*	51.97*	7.90	9.19*	0.72*	70.88*	0.23*	0.02*	4.69*	34.75*
c. vs. v	1	613.33*	103.50*	98.05*	243.68*	83.82*	18.53*	3.92*	0.12	0.12*	0.11*	1.90*	0.16
Error	8 [c (b-1)]	6.95	0.70	0.90	13.00	3.05	0.19	0.06	9.73	0.01	0.00	0.20	0.20
Total	242 (N-1)												

*Significant at 5percent (level of significance)

Estimation of genetic variability components

Estimates of variance components: Genetic variability components (Table 5) like phenotypic variances (σ^2_P), genotypic variances (σ^2_G), Phenotypic Coefficients of Variation (PCV) and Genotypic Coefficients of Variation (GCV) were estimated in F$_2$ plants to determine the heritable potential of the concerned genes and in addition the effect of environment over them. The values recorded for genotypic variance was less than those of the phenotypic variance. In the present study spikelet density (7.24) and yield per plant (7.02) showed the highest GCV values; followed by number of tiller per plant (5.87), panicle number per plant (5.84) and panicle length (5.21); days to maturity showed the lowest GCV value (2.61) whereas 1000- grain weight (3.92), days to flowering (3.89), plant height (3.81), grain width (3.06), showed medium GCV values. The low estimations for GCV and PCV, indicates the less influence of environment on the trait expression.

Table 5: Genetic variability components and heritability (h$^2_{bs}$), genetic advance estimations in F$_2$ population

Traits	GCV	PCV	Heritability (h$^2_{bs}$)	Genetic advance
Days to flowering	3.89	5.01	0.6	5.21
Panicle no./plant	5.84	7.27	0.65	1.87
Days to maturity	3.81	3.88	0.96	9.74
Duration of grain filling	2.61	4.15	0.4	3.78
Plant height (cm)	3.64	7.21	0.25	1.06
Panicle length (cm)	5.21	5.48	0.9	2.62
Spikelet density	7.24	8.77	0.68	0.62
Spikelet fertility % age	4.04	5.4	0.56	5.4
Grain length (mm)	4.43	4.99	0.79	0.39
Grain width (mm)	3.06	3.2	0.91	0.14
1000 grain weight	3.92	4.31	0.83	1.84
Yield /plant (g)	7.02	7.12	0.97	5.36

Heritability and genetic advance: Heritability values are helpful in predicting the expected progress to be achieved through selection process. Broad sense heritability (h$^2_{bs}$) estimates were categorized into low (0-30 percent), moderate (30-60 percent) and High (>60 percent) as shown in table 5. Duration of grain filling showed low heritability, days to flowering, panicle no. per plant, days to maturity, spikelet fertility percentage showed moderate heritability, whereas plant height, panicle length, spikelet density, grain length, grain width, 1000- grain weight, yield per plant showed high heritability. The characters having very high heritability indicated relative small contribution of the environment factors to the phenotype and selection for such characters could be fairly easy due to high additive effect.

Genetic advance (GA) under selection referred to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at given selection intensity. Estimates of GA are shown in table 5, low genetic advance was seen in plant height (9.74) followed by Spikelet fertility percentage (5.40), yield per plant (5.36), days to flowering (5.21), days to maturity (3.78), panicle length (2.62), 1000-grain weight (1.84), no. of tillers per plant (1.89), panicle no. per plant (1.89) and spikelet density (0.62).

Discussion

In present study, phenotypic evaluation was done to the F$_2$ population obtained from the cross of the parents' K 343 and DHMAS which were sown and transplanted in experimental field using augmented design-I, similar design was also used in research done by Fahliani et al. (2010) [5]. Assessment of genetic variability available in crop species is the initial step to choose better performing lines among the divergent group

later quantifying the extent of variability created for traits of interest. The knowledge of heritability and genetic advance help the breeders to select superior plants with high heritability and genetic advance so that the plants can perform predominant for the traits of interest in subsequent generations. Further genotype and environment interaction reduces the effectiveness of early generation selection (Whan et al. 1981; Rahman et al. 1986) [27, 19]. Large environmental differences may lead to failure of parental yield to be indicative of the yield of progeny (Barman and Borah, 2012) [3].

Shashidhara et al. (2017) [23] explained that the range and mean of genotypes for all studied traits indicated wide ranges of variation which also revealed possible amount of variability among the genotypes. In present study, the range in days to maturity and duration of grain filling was greater than that of other traits. The mean value of panicle length recorded was 25.65 cm with maximum and minimum value of 32.6cm and 13.2 cm respectively. According to Bioversity International Fisher and Yates, (1963) panicle length is classified as very short (<11 cm), short (~15 cm), medium (~25 cm), long (~35 cm) and very long (>40 cm). Thus, based on this argument, the present finding showed that there is enough medium variability for panicle length among the genotypes for improving panicle architecture and grain yield due to high association of this trait. The same variability for panicle length, according to this classification was shown by (Abebe et al. 2017) [1].

The variability is the sum total of hereditary effects of concerned genes as well as environmental influence. Hence, the variability is partitioned into heritable and non-heritable components with suitable genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA). GCV and PCV estimates were classified as low (0-10percent), moderate (10-20percent) and high (>20percent) (Johnson et al. 1955), which suggests the possibility of improving this trait through selection. The narrow difference between PCV and GCV observed for most traits was an indication of low environmental influence for traits under study. GCV value for days to flowering (3.89) was similar to GCV value given in reports by Kahani and Hittalmani (2015) [12], plant height (3.81), grain weight (3.06) values were found similar to GCV value given by Kahani and Hittalmani (2016) [13], which indicated less influence of environment on the trait expression, these results are also supported by the study carried out by Bhuvaneswari et al. (2015) [4], their study also explained that the values of Phenotypic Coefficient of Variation (PCV) in the F_2 generation was higher than the Genotypic Coefficient of Variation (GCV) for the traits studied.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore high heritability helps in effective selection for a particular character. The characters studied in the present investigation expressed low to high heritability estimates ranging from 25.00 to 97.00 percent. High heritability (in broad sense) was noted for plant height (96 percent) similar to results shown by Padmaja et al. (2008) [17], Umesh et al. (2015) [26]; Bhuvaneswari et al. (2015) [4] and Shashidhara et al. (2017) [23], panicle length (90 percent), spikelet density (68 percent) similar to reports of Ogunbayo et al. (2014) [16]; Shrivastava et al. (2015) and Shashidhara et al. (2017) [23], yield per plant (97percent) similar to reports of Padmaja et al. (2008) [17], Augustina et al. (2013) [2] and Bhuvaneswari et al. (2015) [4],

100-grain weight (83 percent) similar to results shown by Padmaja et al. (2008) [17], grain length (79 percent) and grain width (91percent) similar to results of Fahliani et al. (2010) [5] and Ogunbayo et al. (2014) [16]. and moderate heritability was noted for days to flowering (60 percent), days to maturity (40percent) as given by Abebe et al. (2017) [1], number of Tiller per plant (65 percent), panicle no. per plant as reported by Ogunbayo et al. (2014) [16] and spikelet fertility percentage Umesh et al. (2015) [26], only duration to grain filling showed low heritability (25 percent) which indicates greater role of environment on the expression of the traits, thus, direct selection for these traits will be ineffective.

Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotypes. Hence, knowledge about heritability coupled with genetic advance is most useful. Thus, in the present study, medium to high heritability coupled with related genetic advance was recorded. Although Low estimates of genetic advance as percent mean was noticed for plant height (9.74) followed by spikelet fertility percentage (5.40), yield per plant (5.36), days to flowering (5.21), days to maturity (3.78) and panicle length (2.62), this indicates the characters governed by non-additive gene action and heterosis breeding will be useful. Similar results were reported by Hoque (2013) [8] for panicle number per panicle. Thus, these results indicate that the traits were simply inherited in nature and controlled by few major genes or possessed additive gene effects. Hence, making based on simple selection could be effective for improving those characters, as reported by (Abebe et al. 2017) [1].

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