Original Research Article

Variability and Heritability Analysis for Yield and Grain Quality Attributes in F_2 Intervarietal Populations of Rice

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A B S T R A C T

Distribution pattern of segregants and heritability estimates in paddy (*Oryza sativa* L.) crop for 12 quantitative traits in two F_2 populations derived from the cross AD 16019 x ADT43 and AD16019 x WGL 14377 was studied at TRRI, Aduthurai during 2016-18. Platykurtic symmetrical curve for the traits with positive skewness was registered for the traits 1000 grain weight and single plant yield. The traits have also manifested high heritability estimates with low or medium genetic advance as percent of gain. Number of filled grain, grain length and Alkali spreading value were observed to have positive skewness in distribution and platykurtic kurtosis in both the F_2 population. Days to flowering, number of filled grains/panicle, grain length, L/B ratio and gelatinization temperature are found to be are positively skewed with mostly platykurtic distribution. Hence intense selection at early cycle will improve the traits flowering, filled grains per panicle and grain length and biparental mating can be adopted to obtain extreme genotypes. For the traits 1000 grain weight and single plant yield selection may be done at later stages of segregating generation for more genetic gain. The breeding strategy would be development of hybrids (heterosis) or biparental mating to create more variability and selection.

Introduction

Rice being a major cereal provides 23 per cent of global per capita energy and 16 per cent of protein to the human population (Shashidhara *et al.,* 2017). In the recent days, the expanding utility of rice crop for different by products and a shift in the consumer preference for grain cooking quality makes the rice breeders to look into the quality aspects to have a better consumer acceptance along with increase in yield, which determines the profit margin of rice growers (Devi *et al.,* 2016).

Breeding for a genotype with all desirable traits for the complex grain yield and quality traits always warrants existence of a wide genetic heritable variability in the positive trend. Selection at early generation always requires an insight about the nature of gene actions/interaction governing the traits which determines the yield increase and grain quality improvement. The skewness and kurtosis statistical analysis provides the information about nature of gene action (Fisher *et al.,* 1932) and number of genes controlling the trait (Robson, 1956). Hence, to understand the

nature of variability, gene action, number of genes controlling the yield attributes and grain physical characters in rice, the present study was conducted with two F_2 populations.

Materials and Methods

The material for the present experiment comprised of F_2 population of two crosses of rice *viz.*, AD 16019 x ADT 43 and AD 16019 x WGL 14377 and their parents. The ovule parent AD 16019 is a bold grain culture matures in 98-100 days and shows endurance to mild drought. The male parents namely ADT 43 and WGL 14377 are known for good cooking/grain quality and yield.The field trial was conducted at Tamil Nadu Rice Research Institute, Aduthurai during rabi 2017-18. Twenty eight days old seedlings were space planted by adopting a spacing of 20 x 15 cm with a single plant in a hill. Each F_2 was raised with minimum of 1000 plants and individual plant observations were recorded from 300 randomly tagged plants. Data on single plant yield and yield attributes were recorded at appropriate crop growth stages. For grain length and breadth measurements, ten kernels were randomly selected and dehulled. Length or breadth of these kernels was measured in millimeter with the help of graph paper. The value were averaged and recorded in millimeter. The L/B ratio was arrived and the grain shape was classified by adopting Standard Evaluation System (IRRI, 1996). The Gel consistency (GC) was analysed based on the method described by Campang *et al.,* (1973) and Alkali Spreading Value based on method developed by Little (1958).

The statistical analysis was done in using 'SPSS' software program. The mean, range and frequency distribution for biometrical traits in F_2 were computed with respect to parents and progenies (Panse and sukhtame, 1961). The GCV and PCV values were computed by the formula suggested by Burton

and De Vane (1953). The estimates of PCV and GCV were categorized as low when it is less than 10 % and high if the estimate is more than 20% and medium if the estimate is 10-20 % (Sivasubramanian and Madhavamenon, 1973). Skewness and kurtosis were estimated as per Snedecor and Cochran (1974). Three types of kurtosis are recognized based on the kurtosis value which depends on distribution curve Robson (1956). If kurtosis value is 3 with a normal curve, it is referred as mesokurtic, > 3 with a Leaping curve denoted as leptokurtic and if kurtosis value is < 3 with a Flat curve and is referred as platykurtic. Similarly, the lack of symmetry *i.e.,* skewness was recognized based on the co-efficient of skewness values which range from -3 to +3. The type of distribution based on the skewness values are if skewness value is zero which is called Symmetrical distribution and skewness value is negative or positive, accordingly negatively skewed distribution or positively skewed distribution.

Results and Discussion

The F2 populations derived from AD 16019 x ADT 43 and AD 16019 x WGL 1477 had shown wide range of variability in all the yield attributes except days to flowering and grain dimensions viz., Grain length and breadth. Similar findings were reported by Islam *et al.,* (2015). Variability in general for most of the traits existed more in the cross AD 16019 x ADT 43 than AD 16019 x WGL 1477. This suggested possibility of improvement of the highly variable characters created by segregation and recombination, whereas, it may not be equally effective for a character, namely grain length and breadth which exhibited narrow range of variability.

In AD 16019 x ADT 43 population the flowering ranged from 77 to 109 days with a mean of 87 days which is five and 22 days longer than the parents ADT 43 and AD

16019 respectively thus making amenable for selection of different duration group (Table 1). The distribution is leptokurtic and positively skewed suggesting the involvement of relatively few number of non-additive genes with complimentary interaction and majority of them having increasing effects as the right tail of the curve is fattier than left tail. In this population, the estimate of coefficient of variation (5.71) is low with high heritability (60.6) and the genetic advance as per cent of mean is also low (2.88). High values of heritability with low genetic advance ascertained the non-additive effects in controlling the trait. This result was similar with the findings of Srujana *et al.,* (2017), Devi *et al.,* (2017) and Patel *et al.,* (2018). In the cross AD 16019 x WGL 14377, the range is comparatively minimum of 78 - 98 days with a mean of 86 days, such narrow range of variability for days to flowering was earlier reported by Kahani and Hittalmani (2015) and may be due parents with similar maturity period. In this population the kurtosis is with negative values and positively skewed indicating the absence of gene interactions between additive genes which exerts normal cumulative effects. The PCV and GCV is low and exhibited low heritability in the population AD 16019 x WGL 14377. Hence the scope for getting very early or longer duration genotypes than the parents by selection is very low from this population. This was earlier reported by Kahani and Hittalmani (2015).

Plant height has showed negative skewness in both the population with a mean of 88.56 cm in AD 16019 x WGL 14377 and 83.30 cm in AD 16019 x ADT 43. Most of the segregants are well within the mean and tends to be more towards the female parent. Dwarf segregants may be efficiently selected for non-lodging plant type from both the population. The character plant height has showed high amount of variability with high heritability

and low genetic advance in the F_2 population of AD 16019 x WGL 14377 (Table 3) whereas the variability for the plant height in AD 16019 x ADT 43 is medium and low genetic advance coupled with high heritability (Table 2). This result was in accordance with Patel *et al.,* (2018). The existence of high variability for plant height in WGL 14377 based population may be due to tallness exhibited by WGL 14377 (100.2 cm) (Table 1) compared to height of ADT 43 (87.8 cm) and AD 16019 (86.2cm). The estimate of high heritability coupled with low genetic advance for plant height suggested the non-additive gene action and high heritability is due to the favourable influence of the environment. Simple selection to improve the trait "plant height" at early segregating generation may not be successful.

For the trait panicle length, negative skewness with leptokurtosis distribution was evidenced in both the population indicates the low phenotypic variability for the cross. Similar findings were recorded by Govindharaj *et al.,* (2017). Negative skewness and leptokurtic distribution for the traits indicated that these evolved from duplicate gene action of few major genes, which helps to conserve the individual plants from deleterious alleles arising from existing variability (Roy, 2000). The estimate of heritability is medium and the genetic advance as per cent gain is low in both the population for the trait panicle length. This shows that both additive and non-additive interaction is involved and that can be used for rice improvement programme but their expression can be influenced very much by the environment. This was earlier reported by Srujana *et al.,* (2017).

The distribution for the characters, number of productive tillers/plant and grain breadth are negatively skewed in the F_2 population of AD 16019 x ADT 43 which explains that the characters has governed by epistatic interaction and in particular additive x additive

gene actions may be the underlying interaction for the distribution of the above said traits. The progenies for the trait "L/B ratio" had distributed in leptokurtic with negative skewness. Similar findings were reported by Kiran *et al.,* (2013) which explains that these traits are controlled by fewer dominant genes with majority of them having decreasing effects and duplicate type of interaction. Selection in the early segregating generations may not give desirable recombination. Hence mild selection is effective for the improvement of the traits plant height and L/B ratio.

The trait gel consistency had shown the distribution of negative skewness with symmetrical kurtosis in the population derived from AD 16019 x ADT 43 whereas platykurtic distribution was found in AD 16019 x WGL 14377 population with negative skewness indicating that more small alleles may be involved with less interaction effect and hence most of the genotypes are congregated near the mean and some

segregants exhibited low gel consistency (hard gel). The selection of genotypes for soft gel cannot be done as segregants at the positive side (soft gel) are limited.

Number of filled grain, grain length and Alkali spreading value were observed to have positive skewness in distribution and platykurtic kurtosis in both the F_2 population. Similar findings were reported by Kiran *et.al.* (2013) and Raghavendra and Hittalmani (2015). Positive skewness for number of filled grain and grain length is advantageous which facilitates for the selection of more segregants with panicles possessing dense grain arrangement and medium to long grain type. Platykurtic kurtosis with positive skewness explains that large number of segregating genes are involved in the expression of these traits with majority of them having decreasing effect and dominance based complimentary type of interactions may be present. Intense selection can be done for the above said traits in the early generation itself for rapid gain.

Table.1 Mean value of parents

Character	ADT 43	AD 16019	WGL 14377
Days to flowering	82	65	67
Plant height (cm)	87.76	85.2	100.22
Panicle length (cm)	25.8	22.12	28.58
No. of productive tillers/plant	14	9	13
No. of grains/panicle	114	111	153
1000 grain weight (g)	15.33	20.56	16.93
Single plant yield(g)	27.24	22.16	24.68
Grain length (mm)	5.90	6.19	6.46
Grain breadth (mm)	1.92	1.96	2.02
Grain L/B ratio	3.10	3.15	3.20
Gel consistency	77	97.5	91
Alkali spreading value	2.47	2.19	6.10

Table.2 Estimation of genetic variability parameters for twelve quantitative and quality characters in F_2 generation of AD 16019 X ADT 43

| Character	Range	Mean	PCV	GCV	Skewness	Kurtosis	(h^2)	GA	GAM
DF	77-109	86.88	7.34	5.71	1.700	3.391	60.6	2.50	2.88
PH (cm)	46 - 110	83.39	13.44	12.69	-1.986	12.162	89.1	3.34	4.25
PL (cm)	14.2 - 29.5	22.69	12.44	6.98	-0.003	-0.837	31.5	0.99	4.37
NPT	4 - 16	10.59	27.32	17.99	-0.360	-0.133	43.4	1.32	12.45
NGP	41 - 248	124.97	28.95	27.77	0.777	0.371	92.0	6.06	4.85
TGW (g)	6.7 - 28.6	16.37	29.89	24.82	0.231	-0.840	68.9	2.35	14.32
SPY (g)	9.5 - 29.6	18.14	25.38	20.32	0.202	-0.775	64.1	12.09	12.09
GL (mm)	4.2 - 6.6	5.19	9.96	7.24	0.868	-0.198	52.8	0.15	12.48
GB (mm)	1.1 - 2.2	1.78	8.62	2.29	-0.336	1.962	7.1	0.06	3.15
L/B ratio	2.3 - 4.5	2.92	9.84	7.26	1.490	5.118	54.4	0.49	16.89
GC	25 - 127	100.36	22.88	17.56	-0.943	-0.072	58.9	4.65	4.64
ASV	1 - 7	3.32	50.15	50.02	0.635	-0.490	99.5	0.71	21.48

GCV - Genotypic Coefficient of Variance, PCV - Phenotypic Coefficient of Variance, (h^2) - Heritability, GA - Genetic advance, GAM - Genetic advance as per cent mean, DF - Days to flowering, PH - Plant height, PL - Panicle length, NPT - Number of productive tillers per plant, NGP – Number of grains/panicle, TGW - 1000 grain weight, L – Grain length, B – Grain breadth, L/B – Grain length and breadth ratio, GC – Gel consistency, ASV – Alkali spreading value, SPY - Single plant yield.

Table.3 Estimation of genetic variability parameters for twelve quantitative and quality characters in F_2 generation of AD 16019 X WGL 14377.

Character	Range	Mean	PCV	GCV	Skewness	Kurtosis	(h^2)	GA	GAM
DF	78 – 98	85.65	3.90	1.23	0.198	-0.301	10.0	0.37	0.43
PH (cm)	59 – 100.2	88.54	59.54	58.53	-0.289	0.338	96.6	3.96	6.88
PL (cm)	14.5 – 30.1	22.67	12.13	9.26	0.832	1.393	58.6	1.61	7.08
NPT	3 - 26	10.73	35.42	12.72	-0.115	-0.228	12.9	0.50	4.66
NGP	24 - 234	116.92	33.64	20.29	0.550	0.089	36.4	4.14	3.59
TGW (g)	10.6 - 32	19.48	20.45	17.79	-0.090	-0.176	75.7	2.19	11.22
SPY (g)	9.6 - 32	20.50	18.49	18.07	-0.147	-0.217	95.5	1.76	8.60
GL (mm)	5.7 - 7	6.408	4.29	1.85	0.085	-0.417	18.7	0.19	2.99
GB (mm)	1.7- 2.6	2.03	9.25	8.47	0.382	-0.257	83.9	0.47	23.38
L/B ratio	2.6 – 3.95	3.17	70.78	68.90	0.211	-0.616	100	0.52	10.30
GC	15-150	96.03	24.78	22.12	-0.635	0.665	79.1	5.38	5.60
ASV	1 - 7	3.88	46.88	46.7	0.264	-1.032	99.3	0.80	20.73

GCV - Genotypic Coefficient of Variance, PCV - Phenotypic Coefficient of Variance, (h^2) - Heritability, GA - Genetic advance, GAM - Genetic advance as per cent mean, DF - Days to flowering, PH - Plant height, PL - Panicle length, NPT - Number of productive tillers per plant, NGP – Number of grains/panicle, TGW - 1000 grain weight, L – Grain length, B – Grain breadth, L/B – Grain length and breadth ratio, GC – Gel consistency, ASV – Alkali spreading value, SPY - Single plant yield.

Frequency curves for yield and quality traits of the cross AD 16016 x ADT 43
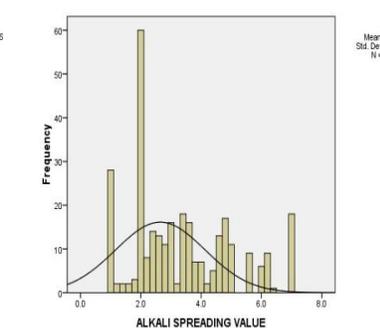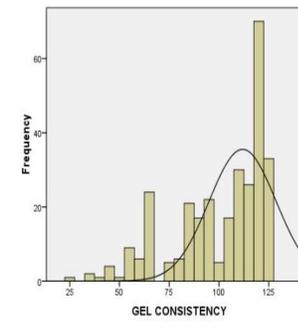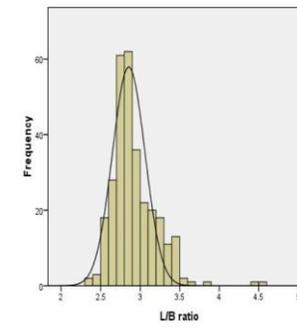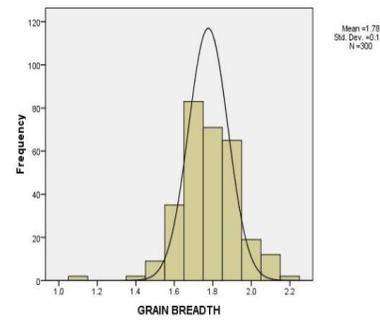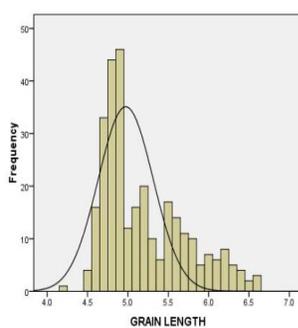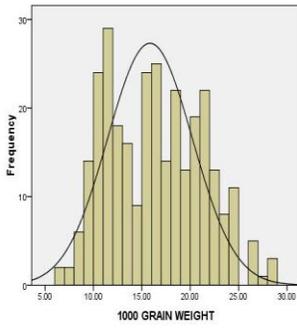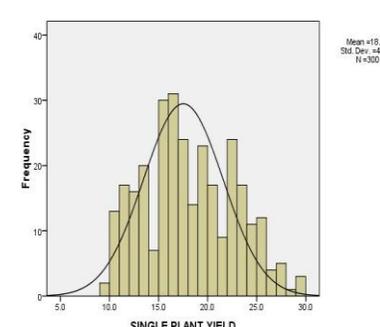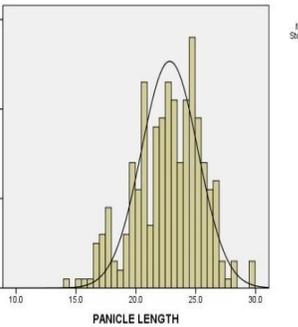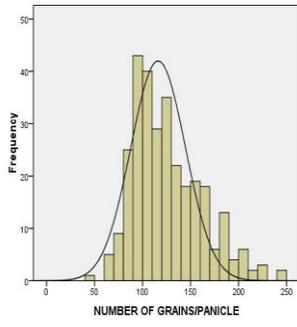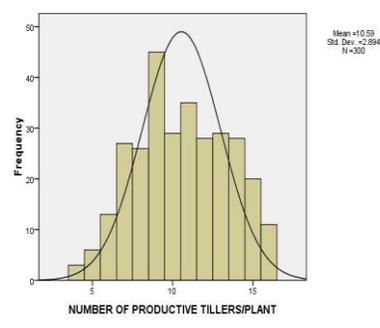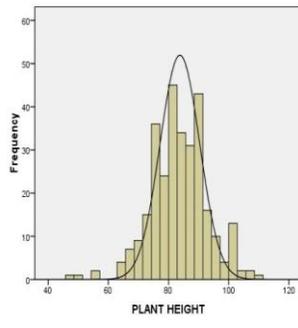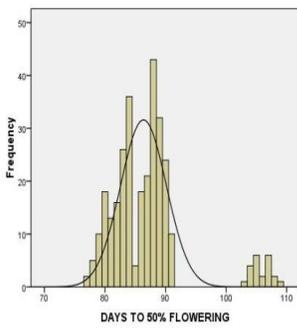
Frequency curves for yield and quality traits of the cross AD 16019 X WGL 14377
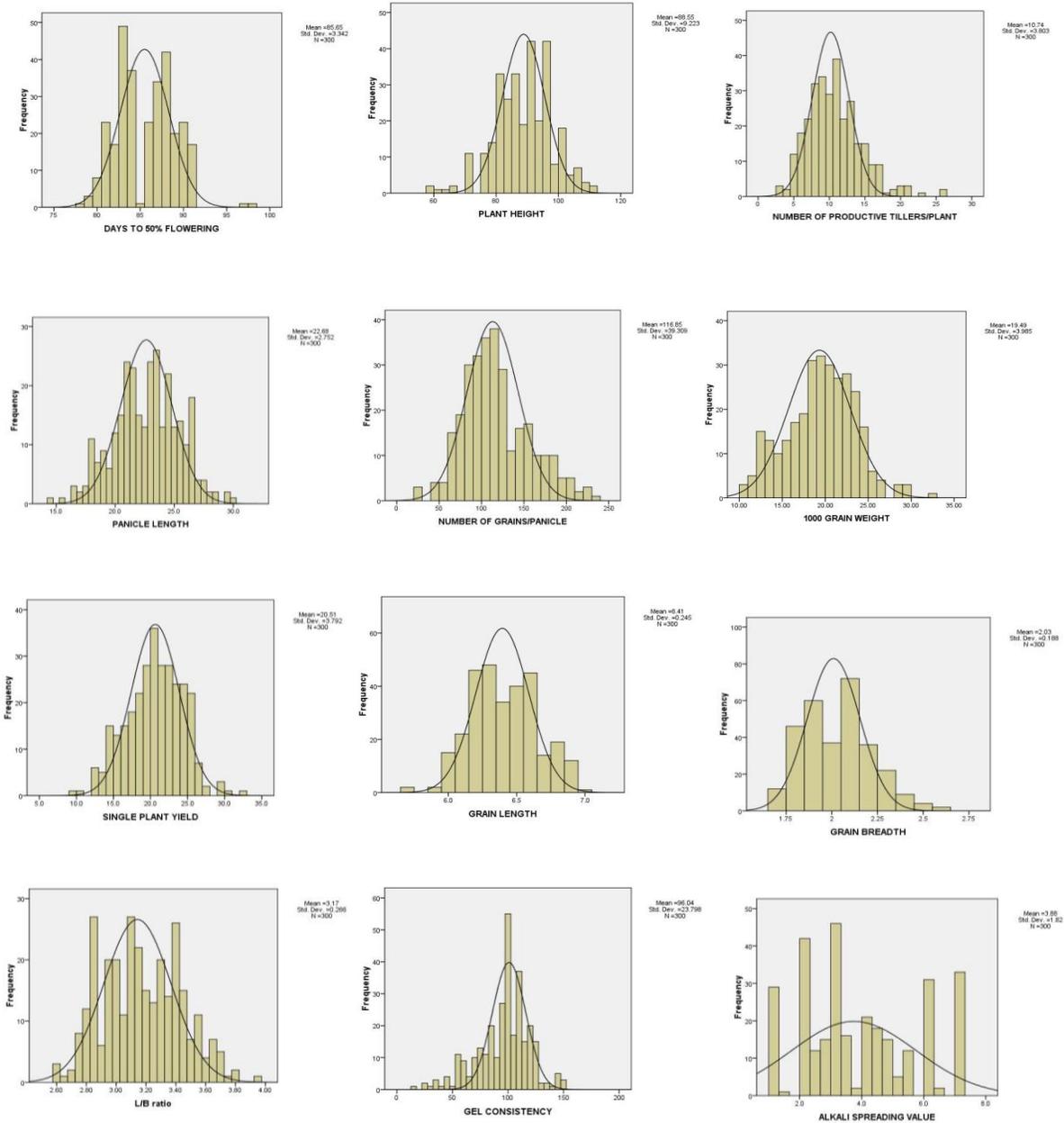
The traits 1000 grain weight, single plant yield and grain breadth shows mixed response in both the populations. In AD 16019 x ADT 43 cross, the traits 1000 grain weight and single plant yield are positively skewed which is in accordance with the reports of Raghavendra and Hittalmani (2015), indicating that more number of progenies have exhibited grain yield higher than the parents and the shift in the mean is towards the positive side which is advantageous for selection for higher yield. In the AD 16019 x WGL 14377 derived F_2 population, both the traits namely single plant yield and 1000 grain weight showed negative skewness.

In the present study, the GCV in both the F_2 population was found to be high for number

of grains per panicle and alkali spreading value and moderate variability range was found in number of productive tillers per plant (Table 5 and 6). This was similar with the report of Srujana *et al.,* (2017) for number of grains/panicle and Dhanawani *et al.,* (2013). Low amount of variability is exhibited by grain length, grain breadth and L/B ratio in both the population. This was in accordance with the findings of Nandeshwar *et al.,* (2010). The characters 1000 grain weight, single plant yield and gel consistency manifested high amount of coefficient of variability in the population AD 16019 x ADT 43 and medium in AD 16109 x WGL 14377. High variability for the traits 1000 grain weight and single plant yield was also found in the study of Bornare *et al.,* (2014) and moderate variability was reported by Gokulakrishnan *et al.,* (2014). Such comparatively high variability in the population of AD 16019 x ADT 43 than the other cross combination may be attributed by larger *per se* value difference between the parents. (Table 2)

The characters 1000 grain weight and single plant yield has showed high heritability and low genetic advance in both the population. It suggested non additive gene action for the expression of these characters High heritability values may be due to favourable influence of environment rather than genotype and as such simple selection based on these characters may not be rewarding. This was earlier reported by Srujana *et al.,* (2017). Low heritability was recorded in the traits number of grains per panicle, grain length and grain breadth. These characters are highly influenced by the environment and hence direct selection will be ineffective. This was in accordance with Balat *et al.,* (2018). The trait alkali spreading value and grain breadth exhibited high heritability coupled with high / medium genetic advance. Simple selection will improve the trait as it is controlled by

additive gene interaction with less environmental influence. This was in accordance with Gokulakrishnan *et al.,* (2014).

Thus in this study, based on the distribution of progenies in the F_2 generation for different traits, it is observed that the traits days to flowering, number of filled grains/panicle, grain length, L/B ratio and gelatinization temperature are governed by many dominant genes either with decreasing or increasing effect depending upon the shift in the range mean either in the positive or negative direction. The distribution pattern that most of the segregants are congregated near the mean values. Hence intense selection at early cycle for these traits will improve the traits. Biparental mating can be adopted to obtain extreme genotypes.

The characters plant height and gel consistency trait have duplicate type of interaction (additive x additive) more genes. The breeding strategy need to be adopted is the mild selection for the trait and at early breeding cycles.

Good amount of variability for the characters, number of grains per panicle, 1000 grain weight, single plant yield and alkali spreading value provides a platform to exercise better selection pressure. However these characters have manifested high heritability estimates with low or medium genetic advance as percent of gain, which implies the preponderance of non- additive gene action in governing these traits. Since these characters are influenced by environmental effects and selection may not be useful. The frequency estimates showed a, platykurtic symmetrical curve with positive skewness for 1000 grain weight and single plant yield, which depicts the involvement of large number of dominant genes having complete ambi-directional epistasis. Intense selection may be done at

later stages of segregating generation for more genetic gain or can be improved through biparental mating. The breeding strategy would be development of hybrids (heterosis) or biparental mating to create more variability and selection.

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