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Genotypic Divergence for Maturity and Panicle Associated Traits in $F_{5:6}$ Rice Lines

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Abstract

This study was conducted to assess genetic variability for maturity and panicle components in rice. A set of 22 F5:6 lines along with their 13 parents genotypes were assessed in randomize complete block design (RCBD) with three replications grown at Agricultural Research Station, Baffa Mansehra during 2023 growing season. The data were recorded on seven morphological traits. Highly significant variations ($P \leq 0.05$) were also detected across parental lines and F6 progenies for all traits. 'Swatai 2014' showed the maximum heading (80 days) among the parents, and 'Dilrosh' the shortest maturity period (101 days). Fakhre Malakand had maximum number of primary branches per panicle (12), while it was Swat 2 for maximum secondary branches per panicle (30.1). Among the F_6 lines, ARS-185 and ARS-201 took least days to heading (89 days) while ARS-201 took least days to mature (121 days). ARS-245 had the greatest value for number of primary branches per panicle (11.7) whereas line ARS-155 had the maximum value for number of secondary branches per panicle (28.3). Days to maturity (0.92) had the highest heritability estimates followed by days to heading (0.86) and culm length (0.81). Flag leaf area (24.36%), culm length (25.86%) and secondary branches per panicle (18.46%) exhibited high genetic advance as percent of mean. The better performance of ARS-201, ARS-245, and ARS-155 on maturity and panicle attributes indicated a useful trait that implied on utilization in multi-location yield trials.

Keywords: Genetic variability, Heritability, Rice (Oryza sativa), Panicle traits, Maturity duration.

INTRODUCTION

Rice is the second most important cereal crop in the world and is a major source of energy for more than half of the world population (Hossain *et al.,* 2015). It is cultivated worldwide on 162.71 million hectares, and the production is 741.47 million tons (Rahaman & Shehab, 2019). China leads the world in rice production with about 141.2 million tons, followed by India with about 104 million tons. Indonesia ranks third with about 38.3 million tons, Bangladesh with about 35.7 million tons, and the Philippines with 12.4 million tons. More than 90% of the world's rice is both produced and consumed in Asia (Karim *et al.,* 2007). Rice kernel has 75-80% starch, 12% moisture and 7% protein contents (Oko *et al.,* 2012). Among the natural resources are magnesium, calcium, phosphorus, with copper, iron, zinc and manganese present in trace amounts. Niacin, thiamine and riboflavin are found in rice (Razzaq *et al.,* 2020) (Oko *et al.,* 2012).

One of the main crops that Pakistan grows and exports is rice. It is grown over an area of 2.75 million hectares with the producing of 6.8 million tons (Bhatti & Jabbar, 2024). It is grown on 1.13 million/hectares and average output is 3.23 million/tons Punjab. In Khyber Pakhtunkhwa (KP) the area of rice cultivation is 0.07 million hectares and a production of 0.15 million tons of rice crop is produced (Qureshi *et al.,* 2021). Heritability is the degree by which a trait is potentially transmitted to future generations (Asante *et al.,* 2019). Genetic contribution refers to the portion of observable

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trait variation that can be attributed to genetic differences between individuals compared to environmental effects. It quantifies how genetic factors (especially additive genetic variance) determine the overall phenotypic variation (Bisne *et al.,* 2009). Generally, genetic contribution is divided into two forms: narrow sense heritability and broad sense heritability (Bitew, 2016). Broad sense heritability is the proportion of the total variance between strains that can be genetically attributed, while narrow sense heritability is the proportion of the total variance due to genetic variance between strains (Abebe *et al.,* 2017). Heritability may serve as an indicator of selection success in segregating generations following a cross (Chakraborty & Chakraborty, 2010). The genetic advance signifies the increase that is expected in a character in response to a selection pressure (Dharwal *et al.,* 2017). It gives an idea of expected improvement due to selection for high-generating genotypes (Fentie *et al.,* 2014). Heritability and genetic advance are important selection parameters, which aid in forecasting the gain from selection (Lingaiah *et al.,* 2015).

Rising population and change in climatic conditions have made it hard to suffice the demand for rice (Fathelrahman *et al.,* 2015). The most important area of focus in rice breeding programs in the world include increasing crop yields per hectare and promoting varieties with shorter maturation periods (Siddika *et al.,* 2024). Therefore, the objectives of this study are: To discover possible F5:6 lines for Maturity then panicle related traits to be suited for rice breeding programs. For heritability and genetic advance in F5:6 lines in rice.

MATERIALS AND METHODS

The study was conducted at the Agricultural Research Station Baffa Mansehra during the 2023 rice growing season. In this study, 22 F6 lines were developed from 12 hybrid combinations and 13 parent combinations (Table 1). The next generation seeds were collected and individual plant screening was carried out in the F2 generation and subsequent generations. The five best growing plants in each hybrid combination were selected from the F5 generation, and the F6 seeds were planted in a four-row plot with one replicate, and each row was 3 meters long. The seedbed was prepared during the second week of May and transplanting into the main field was completed by the first week of June. The trials were put following randomized complete block design (RCBD) with three replications to ensure statistical reliability. Apart from this spacing between plants and rows were maintained respectively at 15 cm and 30 cm. Crop management practices were included irrigation, fertilization, and control of pest according to standard agronomic guidelines. For data collection, ten randomly chosen plants and observation were taken upon the following parameter, Days to heading, flag leaf area (cm), culm length (cm), days to maturity, primary and secondary branches panicle^{-1}.

Table 1: The genetic material used in this study

Parental genotypes	F6 lines
Swat 1	AUP-141
Swatai 2014	AUP-142
Swat 2	AUP-155
JP5	AUP-161
Dilrosh	AUP-165
Fakhre Malakand	AUP-173
TN-1	AUP-175
Shadab-31	AUP-181
IR-8	AUP-185
DR-82	AUP-194
DR-83	AUP-201
Dokri-Basmati	AUP-213
Sugdesi	AUP-215
	AUP-222
	AUP-223
	AUP-231
	AUP-242
	AUP-243
	AUP-245
	AUP-252
	AUP-254
	AUP-255

Statistical Analysis:

The data were analysed using analysis of variance (ANOVA) method as described by Singh and Chaudhary (1985) in parents and F6s (Table 1). Means was compared using Least Significant Difference (LSD) test.

Table 2: The analysis of variance model

Sov	**Df**	**SS**	**MS**	**F-Calculated**
Replications	r-1	RSS	M1	M1/M6
Genotypes	g-1	GSS	M2	M2/M6
Parents	p-1	PSS	M3	M3/M6
F_6 Populations	F_6-1	FSS	M4	M4/M6
P vs F_6 populations	2-1	P vs FSS	M5	M5/M6
Error	(r-1)(g-1)	ESS	M6	-
Total	rg-1	TSS	-	-

Heritability

Genetic and environmental variances for each trait were calculated from the expected mean squares as under

$$\mathrm{Vg} = \frac{(\mathrm{GMS} - \mathrm{EMS})}{\mathrm{r}}$$

$$\mathrm{Ve} = \mathrm{EMS}$$

$$\mathrm{Vp} = \mathrm{Vg} + \mathrm{Ve}$$

$$h^2{}_{\mathrm{BS}} = \frac{\mathrm{Vg}}{\mathrm{Vp}}$$

Where

Vg = Genetic variance
Ve = Environmental variance
Vp = phenotypic variance
GMS = Genotype mean squares
EMS = Error mean squares
r = number of replications
$h^2{}_{\mathrm{BS}}$ = Broad sense heritability

Genetic Advance

Genetic advance was computed using the formula of Panse and Sukhatme (1965):

$$GA = k.\sqrt{\sigma^2\mathrm{P}}.h^2$$

Where

K = 1.76 for 10% selection intensity
h^2 = Heritability coefficient
$\sqrt{\sigma^2\mathrm{P}}$ = Phenotypic standard deviation
GA = Genetic advance

RESULTS AND DISCUSSION

Days to 50% heading

Early heading is prominent in rice crops to attain maturity early so that farmers can increase the cropping intensity (Ganapati *et al.,* 2014). This may prolong the growth duration of grains, thus securing higher grain weight and ultimately grain yield. Numerous biotic and abiotic stressors can be tolerated by plants (Gangashetty *et al.,* 2013). Analysis of variance (ANOVA) tested within the scope of (Table 3) reveals that the variance among parents and F6 lines and then F6 lines with their parents was all highly significant ($P \leq 0.01$). Among the parents, mean data regarding days to heading ranged from 81 to 115 days while among F_6 lines days to heading ranged from 89 to 101 days. According to Table 4, ARS-141 had the longest heading period (101 days), whereas ARS-185 and ARS-201 exhibited the shortest (89 days). The reported variations in the number of days before heading among rice genotypes are consistent with the results of (Hasan *et al.,* 2011), who examined the various physical characteristics of 24 rice hybrids and discovered variations in the number of days before heading.

A moderate 10% genetic advancement and a high heritability of 0.86 resulted from genetic variation of 33.42 exceeding environmental variance of 5.47 (Table 8). According to (Singh *et al.,* 2011) found high h2 (0.88) and genetic advancement (16.12%) for days to heading across 81 rice genotypes.

Days to maturity

Currently, the main aim of plant breeding programs worldwide is the production of early maturing varieties (Dinesh *et al.,* 2023). The ANOVA on maturity traits showed significant differences ($P \leq 0.01$) between the parents, between parental lines and F_6 for all maturity traits and among the F_6 lines (see Table 3). The average maturity period of parental hybrids was 103-142 days, and the average maturity period of F6 lines was 121-134 days. In terms of the longest maturity period, ARS-245 performed the worst (134 days), while ARS-201 was the opposite (121 days). The maturity period of the tested genotypes was significantly different ($P \leq 0.01$), confirming the outcomes of (Seyoum *et al.,* 2012). According to (Seyoum *et al.,* 2012) also reported significant differences in maturity period among 14 rice genotypes ($P \leq 0.01$).

The variance components obtained for days to maturity, calculated separately by genotypic mean basis, demonstrated that among the genotypes studied, genotypic variance (84.35) was higher than environmental variance (6.95), indicating that the trait is essentially controlled by genetic factors. High heritability (0.92) combined with genetic advance of 12.54% also indicated the magnitude of genetic advance (Table 8). Similar findings were observed by (SANGHERA *et al.,* 2013), who reported a high heritability (0.94) and significant genetic response for days to maturity in 14 red rice ecotypes, which confirm the potential of this characteristic as selectable.

Flag leaf area (cm)

Flag leaf area appropriately designates more than 70% of vegetative matter, which subsequently contributes to seed development and, hence, grain yield potential; thus, flag leaf area tremendously enhances yield potential of grains (Dinesh *et al.,* 2023). This statement is made because variations between the parents and F6 lines were not significant (P>0.05) and other variations separating the parents and lines were regarded as highly significant (P≤0.01) as depicted in Table 3. The mean values recorded from the parents with respect to flag leaf areas ranged from 26.2 to 55.4 cm². And that of the F6 lines is found to range from 17.8 to 53.7 cm². The largest flag leaf area was exhibited by ARS-252 (53.7 cm²), followed by ARS-155 (17.8 cm²) that exhibited the least flag leaf area (Table 4). This corroborates with (Ahmad *et al.,* 2010), where significant differences in flag leaf area were observed amongst 16 rice genotypes. In the present study, the genotypic variation was greater (48.33) than environmental variation (35.62). The results showed a genetic advance, expressed as a percentage of the mean (24.36%), as well as moderate broad sense heritability of 0.58 for the trait being investigated (Table 8). The moderate heritability and genetic advance observed in the current study is in agreement with those reported by (Fathelrahman *et al.,* 2015) also reported moderate genetic advance and heritability (0.46) for flag leaf area in their evaluation of 18 rice genotypes.

Culm length (cm)

Among traits for resistance to lodging and harvest index, culm length is a most important character. Mean squares for culm length showed highly significant (P≤0.01) differences among parents and F6 lines, while parents vs. F6 lines showed non-significant differences (Table 3). The mean data on culm length among the parents ranged from 70.5 to 129.8 cm, while the mean value of culm length among the F6 lines was between 70.9 and 128 cm. Of these, ARS-231 produced the shortest height (70.9 cm) while ARS-213 showed the greatest height (128 cm) (Table 4). The present study corroborates findings from Shinde et al. (2015) and Rai et al. (2014). In the 40 rice genotypes sampled by Shinde et al. (2015), significant differences existed in culm length. Rai et al. (2014) identified highly significant differences in culm length among the 40 rice genotypes that they had studied. The genotypic variance (261.31) exceeded more than twice the environmental variance (60.50) with high heritability (0.81) and fairly high genetic advance (25.86%) (Table 8). According to (Akhtar *et al.,* 2011), higher heritability and genetic advance for culm length is also consistent with findings of their study of eight fine-grain rice lines for various morphological characters and significant differences for culm length recorded among genotypes **.**

Panicle length (cm)

The most important attribute of rice yield is panicle length, which in most direct terms determines how much grain a panicle can carry, thereby its ability to bring in a higher grain yield. Differences in panicle length between the parental, F6 lines and the combinations of the parents and F6 lines were highly significant, P≤0.01 (Table 3). The panicle length of the parents ranged from 22.4 to 31.0 cm. Average panicle length of the F6 lines ranged from 22.5 to 29.8 cm. According to Table 4, ARS-222 produced the shortest panicle (22.5 cm), while ARS-142 produced the longest one (29.8 cm). Further,(Bhadru *et al.,* 2012) studied 68 hybrids, 17 parents, and 4 controls from two different agro climatic zones and reported very significant differences in panicle length. However, genetic variability was higher (4.02) as compared to variability attributed to environment (2.14). The high heritability value (0.65) and genetic advance (10.80%) were computed for the trait (Table 8). High heritability and genetic advance of panicle length This finding is supported by (Bidhan Roy, 2010), evaluated 50 rice varieties including four indigenous, 18 high-yielding released varieties and 28 advanced breeding lines and observed high heritability (0.74) and genetic advance (12.16%) on genotypes for panicle length.

Primary branches panicle^{-1}

The number of main branches in the first panicle is a particular trait which affects yield. Parents and the F6 generation lines had significant differences in the number of main branches in the first panicle (P≤0.05). Extremely significant differences were noted in this particular trait between parents and the F6 generation lines (P≤0.01) (Table 3). The average numbers of main branches in the first panicle differed between parents from 8.3-10.8.the average of the F6 generation lines range from 9 to 12. ARS-213 had the least number of main branches in the first panicle, which was 9.0, while ARS-245 had the most number of main branches in the first panicle (Table 5). (Karim *et al.,* 2007) also confirmed that there were significant differences in the number of main branches in the first panicle among 41 aromatic rice genotypes.

For the main branch of panicle 1, the genetic variation was 0.62 and the environmental variation was 1.00. The genetic improvement rate was 8.54%, so the heritability was low (0.38) (Table 8). According to (Karim *et al.,* 2007) also found that the genetic improvement and heritability of the main branch of panicle 1 were very small in 41 aromatic rice varieties.

Secondary branches panicle-^{1}

Based on the findings in Table 3, variance analysis of the number of secondary branches in the first panicle revealed no significant difference between the parents and the F6 generation (P>0.05), while the difference between the parents and the F6 generation was highly significant (P≤0.01). Values of average numbers of secondary branches in the first panicle of parents were in the range of 13.8 to 29.1, whereas for the F6 generation, they ranged between 12.9 and 28.3. ARS-155 had the most secondary branches in the first panicle

(28.3), while ARS-194 had the least secondary branches in the first panicle (12.9) (Table 5). According to (Singh *et al.,* 2017) evaluated 14 cold-resistant local red rice ecotypes and reached the same conclusion.

Since the observed genetic variance was 12.73 and the environmental variance was 18.79, the heritability was moderate (0.40). The genetic gain for this trait was 18.46% (Table 8). According to (Hossain *et al.,* 2015), secondary branching in panicle 1 had a higher heritability (0.97), which may be due to the different genetic material and environment used in the two studies.

Table 3: Mean squares for various traits of rice genotypes at ARS BAFFA MANSEHRA 2023

Traits	**Replications (df=2)**	**Genotypes (df=34)**	**Parents (df=12)**	**F_6 lines (df=21)**	**P vs. F_6 (df=1)**	**Error (df=68)**
Days to 50% heading	0.41	105.7**	202.4**	58.4**	226.5**	5.47
Flag leaf area	163.1	180.6**	222.9**	164.4**	14.14	35.6
Culm length	17.0	844.4**	989.1**	800.2**	37.6	60.5
Panicle length	2.98	14.2**	17.6**	12.1**	18.9**	2.14
Days to maturity	13.4	260.0**	317.5**	37.4**	4243**	6.95
Primary branches panicle^{-1}	2.66	2.85**	2.35*	1.92*	28.4**	1.00
Secondary branches panicle^{-1}	16.1	57.0**	60.9**	57.4**	1.41	18.8

**, * Significant at 1% and 5% level of probability, respectively

Table 4: Means for days to heading, flag leaf area, culm length and panicle length of rice genotypes in ARS BAFFA MANSEHRA

Genotypes	**Days to heading**	**Flag leaf area (cm^2)**	**Culm length (cm)**	**Panicle length (cm)**
Parents				
1. Swat 1	93	32.5	70.5	24.8
2. Swatai 2014	81	27.9	104.3	29.1
3. Swat 2	88	29.6	77.7	27.3
4. JP5	91	43.5	99.4	27.1
5. Dilrosh	83	44.9	108.5	26.7
6. Fakhr Malakand	94	34.4	112.8	27.4
7. TN-1	91	37.1	115.1	30.0
8. Shadab-31	94	55.4	129.8	31.0
9. IR-8	96	38.1	84.2	24.1
10. DR-82	96	43.9	113.6	25.6
11. DR-83	115	49.2	99.4	28.8
12. Dokri-Basmati	89	26.2	73.0	22.4
13. Sugdesi	93	39.1	90.5	26.4
Parental Means	**92.4**	**38.6**	**98.4**	**27.0**
LSD $_{(0.05)}$ Parents	**4.2**	**10.6**	**13.8**	**2.6**
F_6 Population				
ARS-141	101	36.8	95.0	27.5
ARS-142	98	37.3	91.1	29.8
ARS-155	93	17.8	71.5	24.1
ARS-161	99	34.6	86.7	27.3
ARS-165	99	35.4	97.9	29.3
ARS-173	94	35.5	105.2	29.1
ARS-175	95	34.6	104.6	26.4
ARS-181	90	39.1	81.6	24.5
ARS-185	89	45.1	90.2	27.0
ARS-194	93	30.5	92.4	23.4
ARS-201	89	42.6	113.2	23.5
ARS-213	99	41.3	128.0	26.4
ARS-215	96	42.7	119.2	26.1
ARS-222	90	31.7	107.4	22.5
ARS-223	91	38.9	114.9	24.5
ARS-231	98	34.5	70.9	25.0
ARS-242	99	30.7	75.0	25.5
ARS-243	99	36.6	92.6	27.2
ARS-245	100	38.1	103.9	28.2

Genotypes	Days to heading	Flag leaf area (cm^2)	Culm length (cm)	Panicle length (cm)
ARS-252	95	53.7	117.5	25.9
ARS-254	95	45.7	115.6	24.1
ARS-255	96	49.4	116.6	26.2
F_6 Population Means	95.4	37.8	99.6	26.1
LSD $_{(0.05)}$ F_6 Population	4.0	10.1	13.2	2.5
Genotypes Mean	94.3	38.1	99.1	26.4
LSD $_{(0.05)}$ Genotypes	3.8	9.7	12.7	2.4

Table 5: Means for days to maturity, primary branches panicle^{-1}, secondary branches panicle^{-1} and spikelets panicle^{-1} of rice genotypes at ARS BAFFA MANSEHRA during 2023

Genotypes	Days to Maturity	Primary branches panicle^{-1}	Secondary branches panicle^{-1}
Parents			
1. Swat 1	117	10.8	24.9
2. Swatai 2014	104	9.2	21.2
3. Swat 2	106	10.8	21.2
4. JP5	108	10.4	26.0
5. Dilrosh	103	9.4	20.9
6. Fakhre Malakand	120	9.6	27.5
7. TN-1	120	9.3	19.2
8. Shadab-31	119	9.6	13.8
9. IR-8	116	8.4	29.1
10. DR-82	121	8.5	16.5
11. DR-83	142	8.3	17.1
12. Dokri-Basmati	112	8.8	24.5
13. Sugdesi	117	8.4	21.0
Parental Means	**115.6**	**9.3**	**21.8**
LSD $_{(0.05)}$ Parents	**4.7**	**1.8**	**7.7**
F_6 Population			
ARS-141	131	10.5	22.2
ARS-142	132	10.9	24.5
ARS-155	126	11.2	28.3
ARS-161	132	11.5	27.9
ARS-165	133	11.5	24.5
ARS-173	128	10.6	21.1
ARS-175	129	10.4	23.3
ARS-181	125	9.4	23.0
ARS-185	125	10.9	26.7
ARS-194	125	10.3	12.9
ARS-201	121	9.8	14.1
ARS-213	133	9.0	14.8
ARS-215	126	10.8	23.9
ARS-222	125	9.4	16.1
ARS-223	126	9.6	22.2
ARS-231	132	11.6	18.0
ARS-242	132	9.9	23.0
ARS-243	133	10.4	22.9
ARS-245	134	11.7	21.3
ARS-252	129	9.4	23.9
ARS-254	128	10.3	16.0
ARS-255	128	10.1	23.1
F_6 Population Means	**128.7**	**10.4**	**21.5**
LSD $_{(0.05)}$ F_6 Population	**4.5**	**1.7**	**7.4**
Genotypes Mean	**123.9**	**10.0**	**21.6**
LSD $_{(0.05)}$ Genotypes	**4.3**	**1.6**	**7.1**

Table 8: Variance components, heritability (h2) and genetic advance as percent of mean (GA) of morphological traits of rice genotypes at ARS Baffa Mansehra during 2023

Traits	Ve	Vg	Vp	h^2	GA (%)
Days to 50% heading	5.47	33.42	38.90	0.86	10.00
Flag leaf area	35.62	48.33	83.95	0.58	24.36
Culm length	60.50	261.31	321.82	0.81	25.86
Panicle length	2.14	4.02	6.16	0.65	10.80
Days to maturity	6.95	84.35	91.30	0.92	12.54
Primary branches panicle^{-1}	1.00	0.62	1.61	0.38	8.54
Secondary branches panicle^{-1}	18.79	12.73	31.52	0.40	18.46

Ve = environmental variance, Vg = genetic variance and Vp = phenotypic variance

CONCLUSIONS AND SUGGESTIONS FOR POLICY RECOMMENDATION

High estimates of genetic variation for yield and yield-related traits were observed in parental lines and F_6 progeny, suggesting the possibility of selection and improvement

Among the F_6 lines, ARS-185 and ARS-285 were panicle to head, whereas ARS-201 displayed the least number of days to flowering. ARS-245 exhibited maximum no of primary branches per panicle while ARS-155 was superior in no of secondary branches per panicle.

Days to flowering, heading date, and culm length exhibited high broad-sense heritability, indicating the presence of genetic factors. Moreover, secondary branches per panicle, flag leaf area and culm length also had high genetic advance as percent of mean values implying that selection would be effective for these characters.

Based on their excellent performance for major agronomic traits, ARS-201, ARS-245 and ARS-155 were identified as promising and we suggested these three lines to be included in multi-location yield trials to confirm their stability and adaptability in different environments.

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