J. Mater. Environ. Sci. 3 (5) (2012) 967-982
ISSN : 2028-2508
CODEN: JMESCN

Morphological Characterization of Wide Crosses Derivative Rice (*Oryza sativa*)

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Received 15 May 2012, Revised 11 June 2012, Accepted 11 June 2012
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Abstract

The study was conducted at Experimental Field Block of Genetics Department, Hazara University Garden Campus during 2008-11. The field conditions, as well as data on various plants' parameters (i.e. for each genotype) were recorded at different stages of the plants' development. Two wild species i.e. *O. longistaminata* and *O. rufipogon*, having 62 genotypes each) and four cultivated varieties of rice of Pakistan were evaluated on the basis of various morphological traits in experimental fields, having randomize complete block design. The data of 3 cultivated rice could not be presented here due to its non availability & because of non synchronization with 2 wild sp. However there was a significant variation for all the traits studied among the selected genotypes as well as both the wild species. Both the morphological traits and the mean values showed significant variation among each other. *O. longistaminata* was found not suitable due to its late booting and flowering (occurring in November-December) which does not coincide with that of the local cultivars. Again the at that time is close to freezing point. The maturity period of the local cultivars is shorter than *O. longistaminata* . Besides other morphological traits, the weigh of 100 grains was observed to be 4.50 grams in G-58 followed by 4grams in G-5. Dendrogram of 62 genotype showed similar results among each other in all the morphological traits. The mean square values of morphological traits correlated significantly in percent sterility 328.576, percent fertility 319.121, and 100 grams of seed weight 1.11788. Inheritance of botanical traits in rice (*O. sativa x O.rufipogon* F1 and F2 showed 89cm and 83.38cm for plant height, where as the leaf length were at par (38 cm). Differences were observed among spikelets panicle of 113 and 129 while pollen sterility were also 78 and 28 respectively. The twenty selected genotypes on the basis of yield parameters were further evaluated for seed quality through measurements. All the seed traits studied also showed significant variation amongst the genotypes. The seed length and seed width showed maximum variation (88%) with respect to other seed traits. The derived information would be very useful for selecting suitable breeding program**.**

Keywords : Rice.genotype. morphology. traits .KPK. Pakistan

Introduction

Rice is one of the agronomically and nutritionally important cereal crop and is the second principle staple food after wheat in Pakistan [1]. It is grown under a wide range of agro-climatic conditions. Any crop improvement program depends on the utilization of germplasm stock available with sound authentic source. To meet the worlds rice requirements will also depends upon the developments of high yielding varieties having resistance against biotic and abiotic stresses using conventional and biotechnical approaches [2]. There is a remarkably rich diversity in cultivated rice; however, a series of biotic and abiotic stresses continue to limit its productivity[1].Morphological traits , both qualitative and quantities have been employed for estimating diversity[3] . Improvement of the rice grain yield per unit area is the only way to achieve high rice production because of the reduction in area devoted to rice production [4].Rice yield can also be increased by adopting the intensified cropping system [5-6].

Selection efficiency in rice can be enhanced by increase genetic variability for agronomic and quality traits [7].Different morphological traits play different important role for more rice production with new plant type characters associated with the plant yield [1-8]. Phonological properties of rice also associated with the yield potential of the different rice varieties for selection of the best varieties that further involved in rice breeding program[9]. Abbasi [10], reported that during polymorphic survey, out of 60 rice genotypes, 32 lines were observed with *xa5* gene which includes cultivated Pakistani Basmati varieties, i.e, Kashmir Basmati, Basmati Pak, Shahley Basmati and Basmati-C-622 showed the presence of *xa5*.gene.Thousand of rice cultivars have been evolved through selection from the cultivated material many centuries ago, which are well adapted to the local environments. Many of those rice cultivars having good quality characteristics and higher yield potential under biotic and abiotic stress environment. [11]. Study of genetic divergence among the plant materials is an important tool to the plant breeders for an efficient selection of the diverse parents for their potential use in a rice breeding program for the improvement of the rice production. Parents identified on the basis of divergence for any breeding program would be more promising [12-13]. The knowledge of the effective resistance genes and the pathogen population structure would be helpful in deploying the suitable resistance genes in different rice growing areas [14].

The appearance of rice with bran "brown" and without bran "white" is important to the consumers. Thus, components of appearance traits are one of the first criteria for rice quality that breeders consider in developing new varieties for open release and commercial production [15]. Grain shape is an important agronomic trait in cereal crops such as rice, wheat, and barley because it is directly or indirectly related to quality and quantity of grain products [16,17-18]. Factors contributing to general grain appearance are grain size, shape and color. Intensive work has been done by breeders to select for bright, clear, translucent grains with spindly shape [19-20]. Rice seed length,width are the two important quantitative traits also closely related to the exterior quality of the rice [21]. Genetic analyses of length and width of rice kernels have been reported by some of the researchers and most of the studies have shown that rice grain shape is quantitatively inherited [22-23]. It has been shown that rice grain shape is controlled by triploid endosperm genes, cytoplasmic genes, and maternal genes [24] and their genotype into environment interaction effects. The length, width and seed thickness is one of the quantitative measures of grain shape. Grain morphology i.e. color, size and shape having unique position for the breeders during the selection and evaluation process [25-26]. It is thought to relate to the largest shape variation in small grain crops. On the other hand, length width ratio is the major genetic variation of rice grain shape and highly associated with the quantitative traits parameters and can be used in the breeding program for the improvement of the rice varieties [27]. In this vary study, measured the morphological traits of two wild species and sixty two genotype of rice under field condition for the selection of best parents on yield parameter basis. The selected parents on yield basis were further evaluated on the basis of grain shape of each genotype i.e., length,width and thickness. All the genotypes used in this study were the *Bas-385 x O.rufipogon*(F_1 & F_2) . The objectives of this study were to evaluate the phenotypic diversity of rice based on morphological traits and seed parameters and identification of the morphological traits responsible for the yield difference among the rice genotype.

2. Materials and methods

During the years from 2008 to 2011 the study on morphological characterization has been observed for further evaluation and screening on the agronomic traits.

2.1.Plant material: The following two wild species were provided by International Rice Gene bank Collection (IRGC)“IRRI” *Oryza longistaminata* , *Oryza rufipogon* have been used,were obtained from PGRI/NIGAB NARC, (PARC) Islamabad . The list of wild species used a/w their accession number and source is given in the Table 1.

Four indigenous cultivars (JP-5, Fakhar Malakand , Swat-1 and Bas-385), sixty two advance lines of BC_1F_2 were also treated for experimentation but only Bas-385 synchronized with wild specie of *O. rufipogon*, their F_1 hybrids and F_2 progenies. It is observed the due to late flowering and booting of *O.longistaminata* in our local condition non of indigenous cultivars were synchronize with the said one during all the study period . Hence only morphological data of both the wild species has been obtained separately and presented in following tables. While one genotype No.53 reserved for back cross with *O.rufipogon*. The data of 3 cultivated rice i.e., JP-5, Fakhar Malakand , Swat-1 could not be available to presented ,further these var. were not synchronized with wild sp. *O.longistaminata*.

Table 1 : International Rice Gene-bank Collection(IRGC) "IRRI accession number , source of countries of wild species used in the study

Wild rice species	Accession number	Source country
O.longistaminata	1001200	Nigeria
O.rufipogon	1003308	Taiwan

2.2. Nursery: Before sowing, seeds of all genotypes were treated with fungicide @2 g/kg. The sandy clay loam soil was well prepared with Farm Yard Manure (FYM) for growing of rice nursery. The seeds of each genotype were sown separately in different blocks in equal line already tagged to distinguish between them . The nursery of young rice plants were used for transplanting after 29 days from sowing**.**

2.3. Field Practice: The nursery of all the rice genotypes was transplanted in the field using randomized complete block design (RCBD) with three replications. Thirty cm row - row & plant - plant distance was maintained for each genotype in each replication. Each block consisted on 5 lines of each genotype with 10 transplanted plants. Some of agrochemicals were used for the controlling grasshopper attack only. Some time it covered by green propylene sheets which have 80 % of shade to control the insect attack and this practice was for the few time only due to no other crop was existent at that time in the near by field.

2.4. Data Observance: Morphological traits were measured at the physiological maturity stage taking 3 plants from each genotype for mean values. Morphological data were obtained and recorded as per standard practice of rice . Plant height was measured in cm from the plant base to the tip of the highest leaf (or panicle, whichever was longer). Productive tillers of each plant were counted to determine the total number of panicles in each plant. The panicle length of the central tiller of the each plant was measured in cm. The leaf breadth and length was measured in centimeter of main tiller of each plant of the flag leaf with respect to the each genotype. Seeds per panicle of main tiller of each plant was counted separately after harvesting, Seed weight per panicle of main tiller of each plant was measured in grams after harvesting, The 100 seed weight of each genotype was measured after harvesting.

2.5. Seed traits measurements: On the basis of morphological traits 20 genotypes i.e., Basmati-385 x *O.rufipogon* , performing batter with respect to morphological traits contributing were selected for further screening and evaluation . Seed length and width of these genotypes were measured with vernier calipers. The seed length, width and thickness of these genotypes were measured with bran and without bran. The 10 seeds of each genotype were randomly selected for the seed size and shape measurement. Initially measured the seeds of each genotype with bran, and then after removing the husk manually measured the seeds of all genotypes without bran.

2.6. Seed classification: The seed size and shapes of each genotype were measured by using vernier calipers. Seed size was defined by the length in its longest dimension and was categorized as very long (>7.50 mm), long (6.61-7.50 mm), medium (5.51-6.60 mm) and short (< 5.50 mm). Seed shape was defined by the length: width (L/W) ratio and ranges from slender (3.0 or>3.0), medium (2.1-3.0), bold (2) and round (1 or < 1). Length and width ratio was calculated by the following formula:

$$\text{Seed length width ratio} = \frac{\text{Seed Length (mm)}}{\text{Seed Width (mm)}}$$

Grain appearance is largely determined by the amount of chalkiness either on the dorsal side of the grain (white belly) or in the center(white center) following scale was used for classifying endosperm chalkiness of the middle grain.[28].

Scale	% area with chalkiness
0	-
1	<10
5	10-20
9	>20

2.7. Statistical analysis: Data were analyzed by simple analysis of variance (ANOVA)[29]. Principal Component analysis was used to determine genetic variability for these traits. Genotypic means were used for the PCA with respect to each trait. Each data analysis was conducted by using SAS (Statistical Analysis System) version 9.2

3. Results and discussion

3.1. Analysis of variance (ANOVA) indicated significant at 0.05 level of significance , effects of genotypes in almost all the traits studied. The (ANOVA) of mean square values of all the morphological traits are presented in the (Table 5) below . All the genotypes showed highly significance variations for all the traits studied. Furthermore there was a significant effect of genotypic into environmental interaction on all the traits. The extent of variability for any character is very important for the improvement of crop through breeding. Significant variation in all the traits studied indicated the presence of high genetic diversity among all the genotypes of rice. In case of wild species is was quite clear that there was a lot of difference between all the characters except Culm angle, ligules hairiness ,anther color and grain shape , while days to flowering and their booting time was quite different. This may be due to the W.species characters resemble because one originated from Nigeria and other from Taiwan. *O.rufipogon* were well acclimatized in local conditions and has synchronism ability with the local cultivars specially. An very high variation was also observed among each other during its booting stage. Due to non synchronization of *O.longistaminata* dropped from the study.

Table 2 : Evaluation of two wild species of rice for morphological traits under field condition at Genetics experimental block at Hazara University Mansehra (KPK)

Wild species	*O.longistaminata*	*O.rufipogon*
Parameters	Morphological traits comparison	
Culm angle	Erect	Erect
Node color	Green	Purple
Internodes color	Green with brownish	Dark green
Basel leaf sheath color	Green	Purple
Flag leaf sheath color	Erect	Horizontal
Ligules color	Brownish off white	Purple off white
Ligules hairiness	Glabrous	Glabrous
Auricle color	Auricleness	Light green
Flowering month	Nov 3rd week	Sept. 2nd week
Synchronization with other genotype local condition	No	yes
Blooming time	1000 am	1300 after noon
Panicle type	Compact	Widely Open
Awning	Partially Awn	Fully Awn
Awn color	Very light green	Very light green
Apiculus color	Purple	Red
Stigma color	White	Purple/yellowish
Anther color	Yellow	Yellow
Lemma and palea pubescence	Golden	Grayish
Sterile glumes color	light green	Spring light green
Sterile glumes shape	Arrow shape	Arrow shape
Seed coat color	Dark Brown	Golden Brown
Grain Shape	Slender	Slender

Table 3 : Mean values of morphological traits of two wild species under local filed condition of Mansehra at Experimental field block of Hazara University (KPK)

Wild species	*O.longistaminata*	*O.rufipogon*
Parameters	Mean values comparison	
Culm length	140	115
1st internodes length	5.7	12.3
Peduncle length	55.7	34.9
No of nods	7	5
No of inter nods	6	4
Flag leaf length	30.00	25.1
Flag leaf breadth	1.34	1.22
Ligule length	26.3	16.2
Days to flowering	186	134
Panicle length	33	22
Primary branches panicle	13	11
Mean length of primary branches	9	9.4
Plant Height (feet)	9	5

3.2. Table 3 represents the mean values of all morphological measurement that were showed quite variation among each other in case of both the wild species . *O.longistaminata* were ahead of *O.rufipogon* in all the 13 traits right from culm length to plant height . It was therefore noted that *O.rufipogon* would be the most suitable w sp.for the cultivated rice lines in the environment of (Mansehra)KPK., where the hot and humid days are short as compare to the winter. However some special management are also required for F_1, F_2, F_3 etc., The mean cumulative values of table-4 indicated that maximum numbers of panicles 39 in G-9 followed by G-5 i.e.,35 recorded. While the lowest one was 6 in G-40 . Maximum primary panicles branches 14 followed by 13 recorded in G-12, whereas minimum were found 7 in G-9, G-38, G-41, and G-60. Maximum Secondary Panicle branches were of 15 & minimum of 14 recorded in G-24 & G- 25, 29,34, 57, 59 respectively. The maximum grain were noted in G-56 (121) while the lowest one was G-4 with only 44.

Table 4 : Mean cumulative values of morphological traits under local field conditions of rice 62 genotypes.

Genotypes Tage (BC_1F_2)	NP	PPB	SPB	G/P	SS/P	FS/P	PL (cm)	AL (cm)	SGL (cm)	SGW (cm)	% S	% F	100 G.Wt
1	19	10	9	117	34	83	23.00	3.5	0.59	0.21	29.0598	70.9401	2.00
2	28	9	10	83	23	60	23.50	4.00	0.61	0.20	27.7108	72.2891	2.00
3	16	14	11	67	14	53	22.00	5.60	0.60	0.21	20.8955	79.1044	1.50
4	20	9	7	96	17	79	23.50	2.80	0.70	0.20	17.7083	82.2916	2.00
5	22	8	6	67	16	51	26.00	Abs	0.58	0.23	23.8805	76.1194	4.00
6	20	9	8	56	4	52	21.00	1.50	0.55	0.22	7.14285	92.8571	3.00
7	17	9	7	88	16	72	26.00	1.50	0.60	0.20	18.1818	81.8181	1.50
8	27	10	11	99	10	89	23.50	Abs	0.65	0.23	10.1010	89.8989	2.50
9	39	7	7	83	13	70	24.50	8.00	0.60	0.22	15.6626	84.3373	2.20
10	29	11	9	136	27	109	25.30	3.00	0.52	0.28	19.8529	80.1470	2.50
11	19	9	9	98	9	89	24.00	1.00	0.69	0.23	9.18367	90.8163	2.00
12	27	13	11	136	32	104	26.00	1.40	0.58	0.22	23.5294	76.4705	2.00
13	20	9	7	95	6	89	22.20	0.30	0.59	0.23	6.31578	93.6842	2.50
14	17	11	10	113	4	109	25.50	3.00	0.60	0.21	3.53982	96.4601	2.00
15	20	10	11	95	22	73	23.50	0.40	0.60	0.23	23.1578	76.8421	2.50
16	17	8	9	78	13	65	21.00	2.20	0.70	020	16.6666	83.3333	2.00

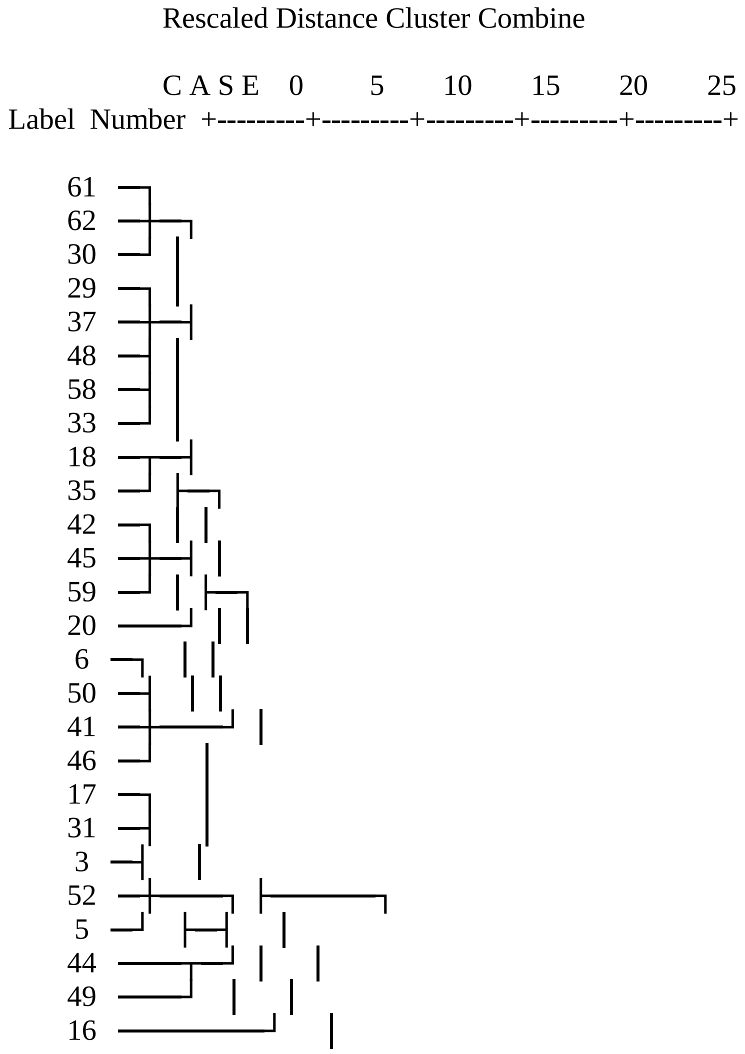
17	21	12	12	60	10	50	20.00	0.70	0.60	0.20	16.6666	86.3333	2.50
18	9	11	13	64	1	63	24.50	6.00	0.60	0.20	1.5625	98.4375	1.50
19	28	12	12	110	24	86	25.00	3.50	0.60	0.20	21.8181	78.1818	1.20
20	19	9	13	73	14	59	18.00	Abs	0.55	0.20	1.1780	80.8219	2.00
21	19	9	11	95	16	79	23.00	1.30	0.60	0.20	16.8421	83.1578	3.00
22	17	11	13	87	9	78	21.50	6.00	0.62	0.20	10.3448	89.6551	2.50
23	23	10	12	90	14	76	25.50	6.50	0.61	0.21	15.5555	84.4444	2.00
24	18	11	15	118	21	97	26.00	2.10	0.55	0.21	17.7966	82.2033	2.50
25	18	8	11	80	13	67	21.50	1.50	0.61	0.20	16.25	83.75	1.50
26	17	9	12	100	48	52	26.00	2.00	0.59	0.21	48	52	1.50
27	25	10	14	86	12	74	21.50	5.00	0.57	0.20	13.9534	86.0465	2.00
28	20	9	13	113	12	101	22.50	4.50	0.60	0.20	10.6194	89.3805	2.50
29	26	9	14	64	5	59	24.50	1.50	0.60	0.19	7.8125	92.1875	3.00
30	20	8	12	72	4	68	22.00	0.50	0.60	0.21	5.55555	94.4444	2.00
31	18	9	12	64	10	54	20.00	Abs	0.67	0.21	15.625	84.375	2.00
32	15	10	13	90	14	76	25.00	6.00	0.70	0.20	15.5555	84.4444	1.50
33	14	10	13	70	8	62	22.00	Abs	0.59	0.20	11.4285	88.5714	1.50
34	22	10	14	109	5	104	20.50	1.00	0.50	0.28	4.58715	95.4128	2.50
35	10	10	13	67	4	63	20.00	5.00	0.60	0.21	5.97014	94.0298	2.00
36	22	12	7	91	10	81	25.50	1.50	0.71	0.21	10.9890	89.0109	2.00
37	22	11	9	62	4	58	24.00	4.50	0.75	0.19	6.45161	93.5483	2.00
38	27	7	9	44	25	19	20.00	0.50	0.59	0.22	56.8181	43.1818	2.50
39	12	9	11	90	7	83	20.50	Abs	0.70	0.20	7.77777	92.2222	3.00
40	6	9	13	103	9	94	24.50	Abs	0.59	0.20	8.73786	91.2621	3.00
41	14	7	9	57	1	56	22.50	Abs	0.52	0.20	1.75438	98.2456	1.50
42	15	10	11	78	8	70	24.00	4.50	0.59	0.20	10.2564	89.7435	2.50
43	24	10	13	79	30	49	25.00	5.50	0.69	0.20	37.9746	62.0253	3.00
44	27	8	9	52	10	42	16.00	4.40	0.60	0.21	19.2307	80.7692	2.00
45	13	9	12	78	8	70	19.00	2.00	0.60	0.20	10.2564	89.7435	1.50
46	9	8	11	60	7	53	26.00	4.50	0.60	0.23	11.6666	88.3333	2.50
47	16	8	9	50	18	32	17.20	2.50	0.59	0.21	36	64	1.50
48	22	9	10	68	8	60	19.00	3.20	0.60	0.22	11.7647	88.2352	2.00
49	16	8	12	43	6	37	20.50	2.80	0.60	0.20	13.9534	86.0465	2.00
50	13	9	13	55	4	51	16.50	5.80	0.60	0.21	7.27272	92.7272	2.50
51	35	8	11	91	17	74	21.50	1.60	0.70	0.20	18.6813	81.3186	2.50
52	32	9	13	64	11	53	22.60	4.50	0.59	0.21	17.1875	82.8125	2.00
53	Reserved for back cross												
54	21	9	10	83	21	62	22.00	3.90	0.60	0.21	25.3012	74.6987	2.50
55	25	11	12	120	4	116	28.50	2.00	0.60	0.200	3.33333	96.6666	1.50
56	29	12	13	121	11	110	26.20	3.80	0.59	0.21	9.09090	90.9090	2.00
57	25	12	14	110	23	87	21.80	2.50	0.59	0.20	20.9090	79.0909	2.50
58	15	10	11	84	14	70	23.20	8.00	0.59	0.20	16.6666	83.3333	4.50
59	23	10	14	67	8	59	22.20	3.20	0.60	0.20	11.9409	88.0597	3.00
60	7	9	11	73	4	69	17.00	2.50	0.60	0.20	5.47945	94.5205	2.50
61	16	7	9	98	7	91	23.20	2.80	0.70	0.21	7.14285	92.8571	2.50
62	30	8	12	76	5	71	23.40	3.50	0.59	0.21	6.57894	93.4210	1.50
63	31	9	13	74	4	70	21.50	3.20	0.55	0.29	5.40540	94.5945	2.50

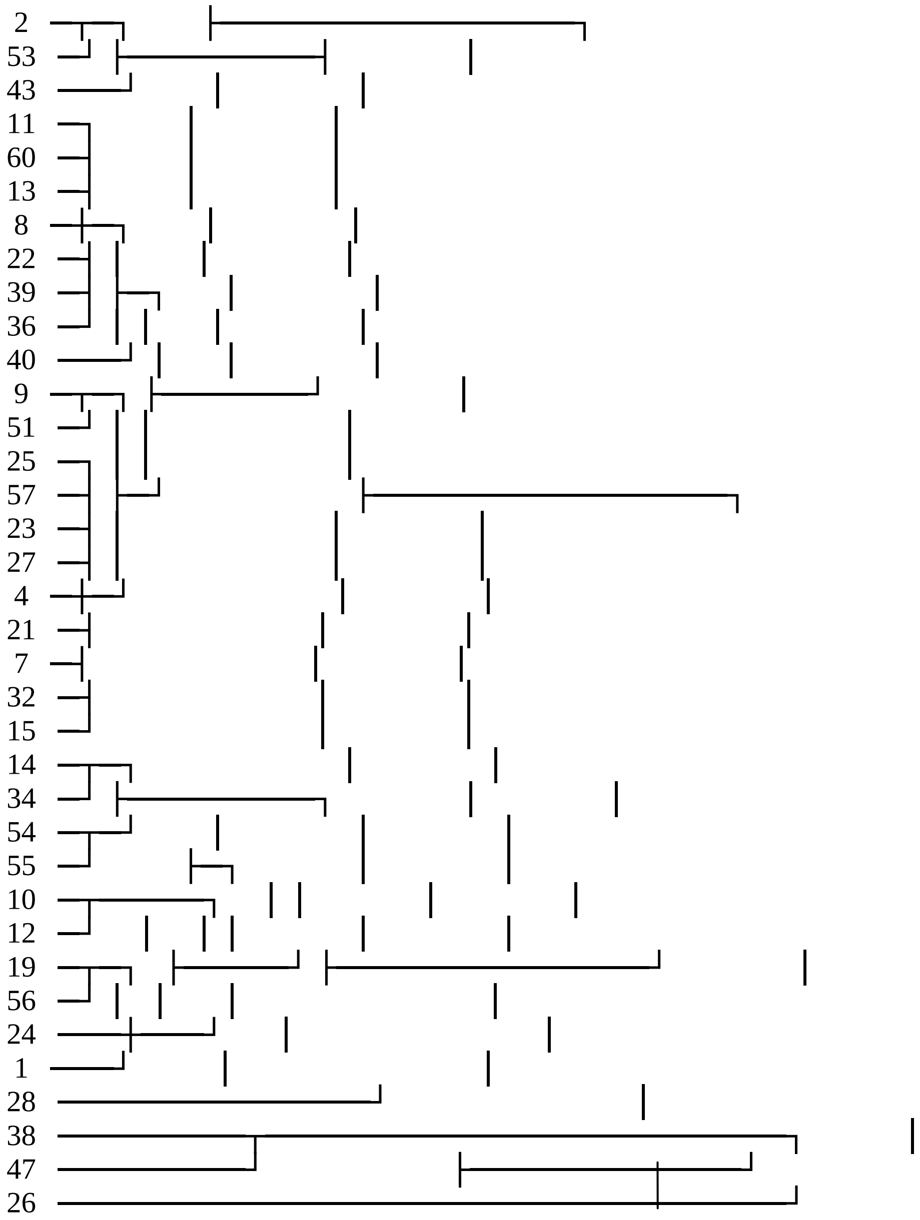
Gen= Genotype; NP= No of panicle; PPB =Primary Panicle Branches ;SPB =Secondary Panicle Branches; G/P =Grain/panicle; SS/P= Sterile seed / Panicle ;FS/P= Fertile seed / Panicle ;PL(cm)= Panicle length in cm; AL(cm)= Awn length in cm; SGL(cm)= Single Grain Length in cm; SGW(cm)= Single grain width in cm; % S=% of sterility; % F= % of fertility; 100 G.Wt=100 Grain weight in gram

3.3. Table 4 resulted regarding sterile and fertile seed panicle mean values that minimum one sterile was recorded in G-18 and maximum fertile was noted 116 in G-55 followed by 110 in G-56 this may be due large heterogeneity in each genotype among each other. There was no so much difference in between panicle length it was around 21 to 26 cm in all the genotypes. However there was a difference among each other genotype for awn length 9 genotype were found no awn length while the minimum 01 is recorded in 2 genotype i.e, G-11 and 34 respectively. Maximum AL (cm) 8 observed in G-9 and 58 respectively. Most of the genotype was found the above maximum single grain length that of above 50 cm while maximum mean values were recorded 75 in only genotype and width are more or less similar with each other i.e., 19 cm to 23 cm at the maximum. Percent sterility and fertility was quite different among each other in each genotype this may be due to heteroses in all the genotype. Perhaps some of the genotypes have bacterial blight resistance genes like Xa5 , Xa13 , this may only verify through DNA and PCR. Maximum 100 grain weight was observed 4.50 grams in G-58 followed by 4 in G-5.

The variation among the each rice genotypes based on their eigen values and their principal component as shown in the Figure 1. Those principal components having more than one eigen value that showed more variation among the rice genotypes for the selection of the diverse parents. Abbasi[14], reported the genetic divergence among the rice genotypes on the basis of their phonological traits that take part in the selection of the diverse genotypes for the further improvements of the rice varieties through breeding. Each principal component described separately for the various morphological traits of the each rice genotypes.

Figure 1: Dendrogram of BC_1F_2 population based on dissimilarity matrix of Euclidean distance for qualitative traits using Average Linkage (Between Groups)





3.4. Table 5 revealed that all the genotypes showed highly significant variations for all the traits studied at $P<0.05$. Further there was a significant effect of genotypic into environmental interaction on all the traits. The extent of variability for any character is very important for the improvement of crop through breeding. Significant variation in all the traits studied indicated the presence of high genetic diversity among all the genotypes of rice. No. of panicles ,primary panicle branches ,secondary panicle branches, grain per panicle ,sterile seed/panicle ,fertile seed /panicle ,panicle length in (cm) ,awn length (cm) ,single grain length (cm) ,single grain width (cm) ,percent sterility ,percent fertility 100 gram weight showed highest variations among the genotypes.

3.5. Table 6. Revealed that *O.rufipogon* x cultivar Bas-385 in respect to their inheritance botanical traits alone in case of both sp. and cv.was different. However F_1 and F_2 were not at par with each others the data recorded showed that 90 & 83.38, 49 & 23, 38 & 38.8, 2.9 & 2.4 , 6 & 4.5 , 19 & 21.4 and 3.4 & 88 in height mean (cm) ,culm numbers means , leaf length mean (cm),ligules length mean(cm),culm diameter mean (mm),panicle length mean(cm), awn length mean (cm) ,spikelet panicle ,pollen sterility (%) respectively.

Table 5 : Mean square values of (BC_1F_2) morphological parameters of rice under field condition at Field experimental block of Gen. Dept. of Hazara University

Source Variation	D.F	No. of Panicles	Primary panicle branches	Secondar panicle branches	Grain pe panicle	Sterile seed/panile	Fertile seed /panicle	Panicle length (cm)	Awn length cm	Single grain length (cm)	Single grain width (cm)	Percent sterility	Percent fertility	100 Gran weight
Genotypes	62	105.783**	7.6520**	84.145**	1427.98**	233.825**	1203.04**	16.4833**	34.6856**	0.00890**	2.07029**	328.576**	319.121**	1.11788*
Rep	2	12.333	6.22749	645.656	32.96	8.444	9.29	0.1454	8.7420	0.03831	2.06919	0.134	2.859	0.22178
Error	124	4.355	3.000	76.108	3.11	0.815	0.72	2.1936	5.6366	0.00321	2.07388	0.134	1.057	0.02468

Level of significance $P<0.05$= **

Table 6 : Inheritance of botanical traits in rice (*O.sativa x O.rufipogon)*

Species / Var Bas-385	Height mean (cm)	Culm No means (numbers)	Leaf length mean (cm)	Ligules length mean(cm)	Culm diameter mean (mm)	Panicle length mean (cm)	Awn length mean (cm)	Spikelet panicle	Pollen sterility (%)
O.rufipogon	90	46	30	1.4	3.8	19.6	2.8	93	2.4
O.sativa var. Bas-385	71	16	36.67	2.5	4.7	25	2.1	113	6
O.sativa x O.rufipogon F1	89	49	38	2.9	6	19	4.8	129	78
O.sativa x O.rufipogon F2	(30.6-112)* 83.38	(3-46) 23	(26-56) 38.8	(1-4) 2.4	(2.9-6.1) 4.5	(10-29) 21.4	(0-6.8) 3.4	(36-144) 88	(8.9-56) 28

3.6. Table (7(a-h) and figures: 2-9) revealed in traits /parameters studied for pollen sterility, no.of grains per panicle, no of tillers per plant, awn length, panicle length, culm diameter, ligule length, leaf length, that there were 5 group in each case while each group contain numbers of plants that contain similar range were become in the said group for the observance of each individual parameters. It was evaluated that all the parameters are not at par with each other both in groups and no of plants comprising as under ,(61 Σ=1696.5/61 μ=27.8%), (60 Σ=5267/60 μ=88), (71 Σ=1612/71μ=22), (79 Σ=270.3/79 μ=3.4cm), (66 Σ=1410.5/66 μ=21.37), (66 Σ=297/6 μ=4.5), (65 Σ=158/65 μ=2.4) (68 Σ=2636.6/68 μ=38.8) . The analysis showed a lot variation among each others in this vary data . It might be attributed that each individual has their own character which represent / resemble the genotypes for further assessment.

Table 7(a): Percent pollen sterility (*O.sativa x O.rufipogon)*

S.No	Group	Frequency	Percent pollen sterility		
1	8.9-18	17	*Bas-385*	6%	Σ=1696.5/61 μ=27.8 %
2	19-27	12	*O. rufipogon*	2.4%	
3	28-36	14	F1	78%	
4	37-45	10	Total	61	
5	46-56	2			

Figure 2: Percent pollen sterility

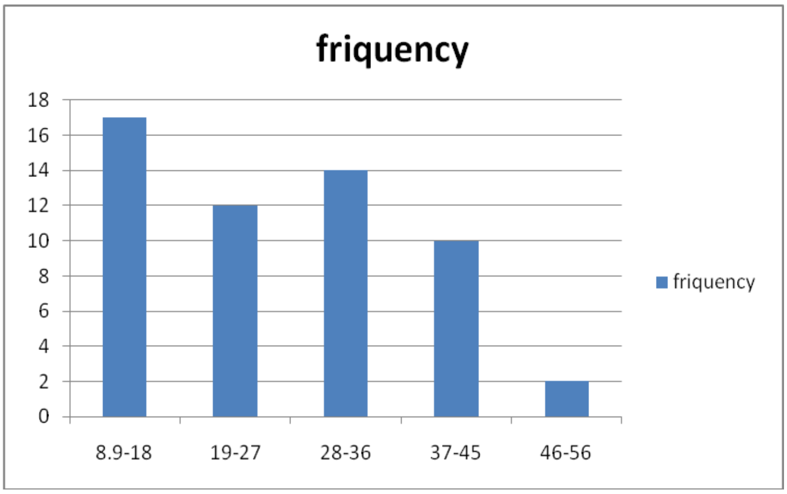


Table 7(b) : No of grains per panicle

S. No	Group	No	Total=60 Σ=5267/60 μ=88
1	36-58	9	
2	59-80	13	
3	81-102	21	
4	103-124	10	
5	125-146	7	

Figure 3 : No of grains per panicle

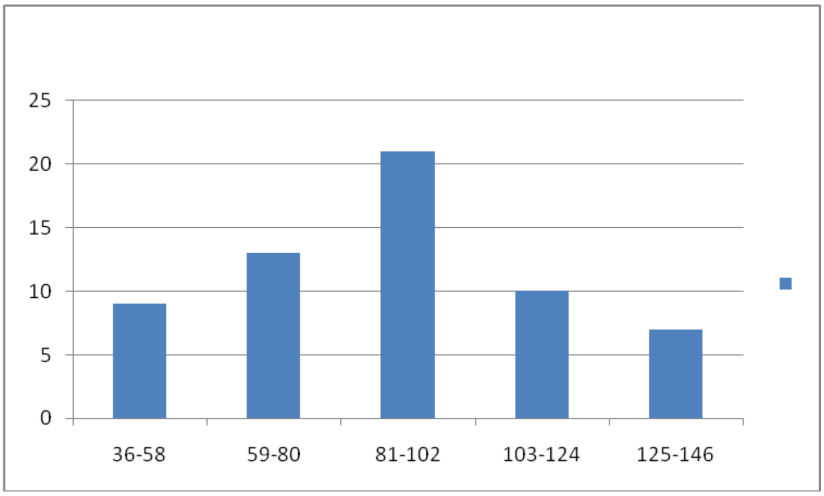


Table 7(c): No of tillers per plant

S.No	Group	No	
1	3-12	8	Total= 71 Σ=1612/71 μ=22
2	13-21	31	
3	22-30	15	
4	31-39	12	
5	40-48	4	

Figure 4: No of tillers per plants

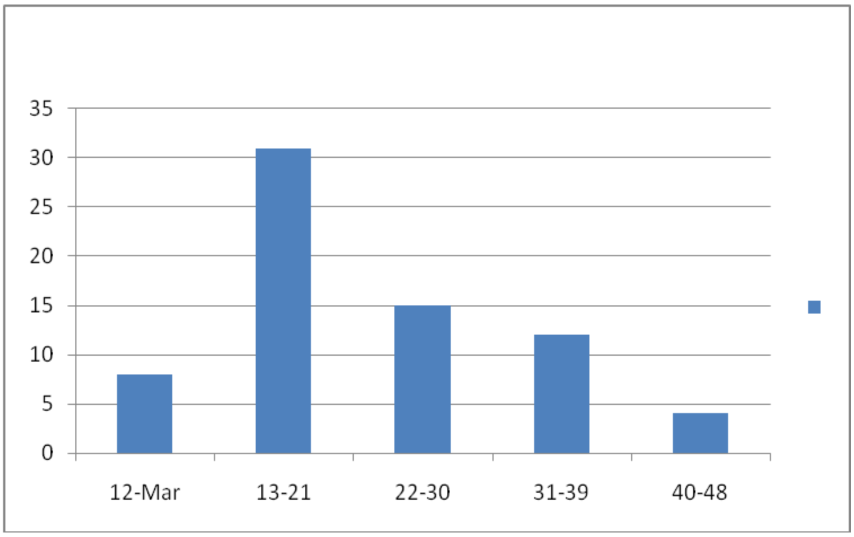


Table 7(d) : Awn length per plant

S.No	Group	No	
1	0-1.4	7	Total=79 Σ=270.3/79 μ=3.4cm
2	1.5-2.8	19	
3	2.9-4.20	21	
4	4.3-5.6	24	
5	5.7-6.8	4	

Figure 5 : Awn length /panicle

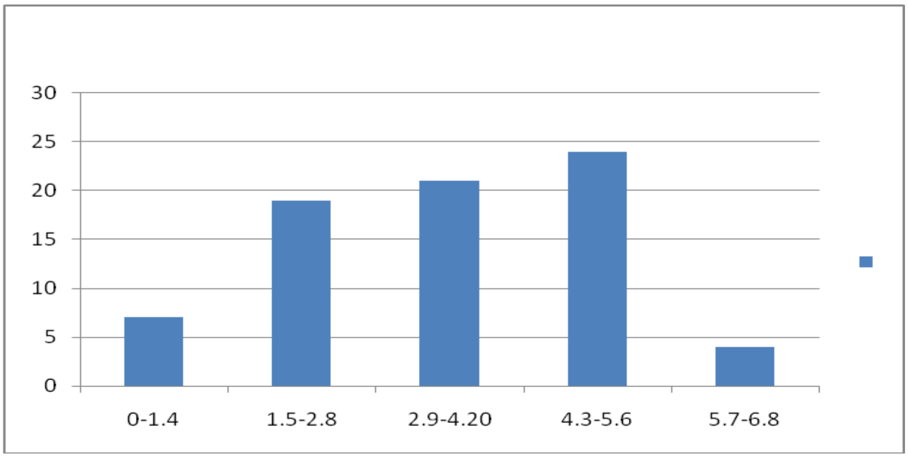


Table 7(e) : Panicle length

S.No	Group	No	Total=66 Σ=1410.5/66 μ=21.37
1	10-13.8	2	
2	13.9-17.6	5	
3	17.7-21.4	30	
4	21.5-25.2	22	
5	25.3-29	3	

Figure 6: Panicle length

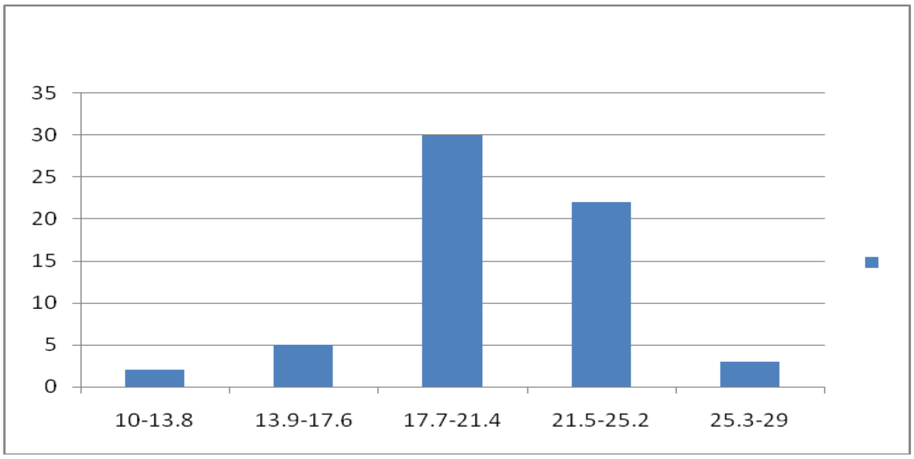


Table 7(f) : Culm diameter

S.No	Group	No	Total=66 Σ=297/6 μ=4.5
1	2.9-3.5	9	
2	3.6-4.2	18	
3	4.3-4.8	23	
4	4.9-5.5	4	
5	5.6-6.1	7	

Figure 7: Culm diameter

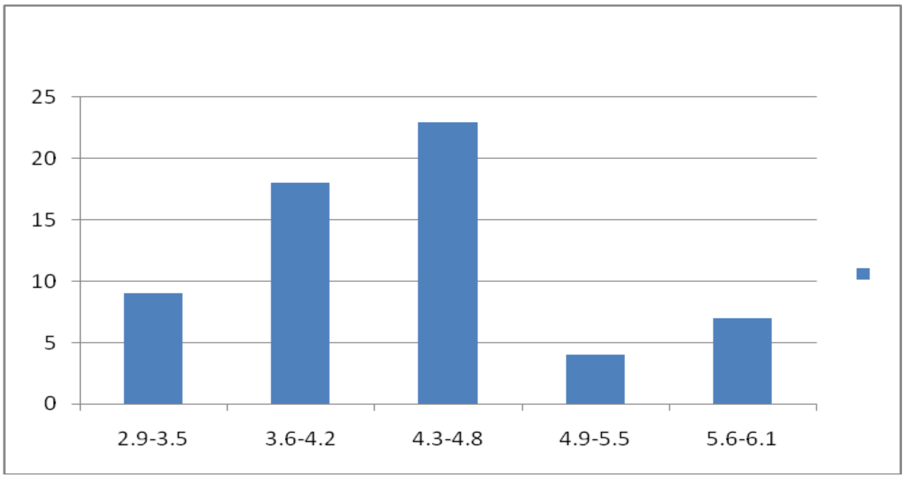


Table 7(g) : Ligules length

S.No	Group	No	Total=65 Σ=158/65 μ=2.4
1	1-1.6	9	
2	1.7-2.2	16	
3	2.3-2.8	14	
4	2.9-3.4	12	
5	3.5-4	10	

Figure 8: Ligules length:

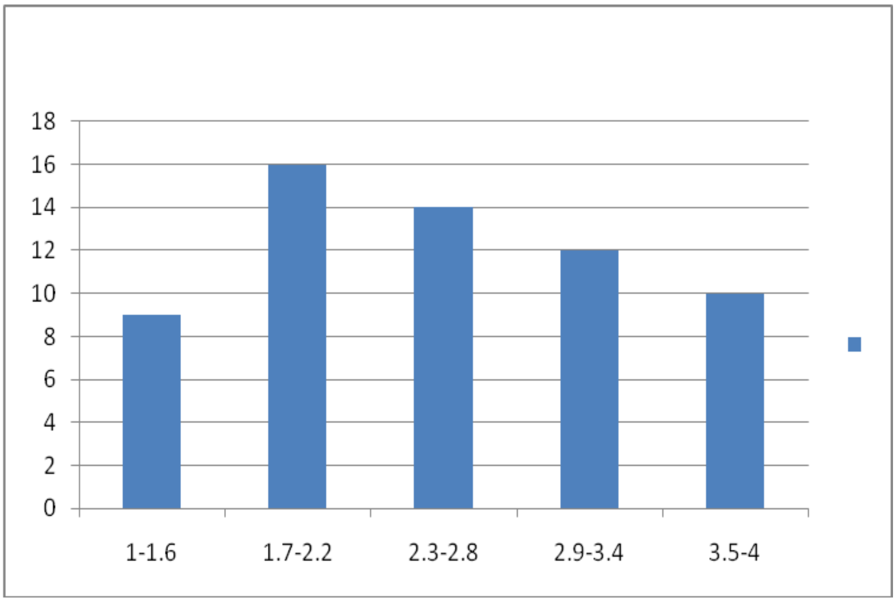


Table 7(h): Leaf length

S.No	Group	No	Total=68 Σ=2636.6/68 μ=38.8
1	26-32	8	
2	33-38	30	
3	39-44	23	
4	45-50	4	
5	51-56	2	

Figure 9: leaf length

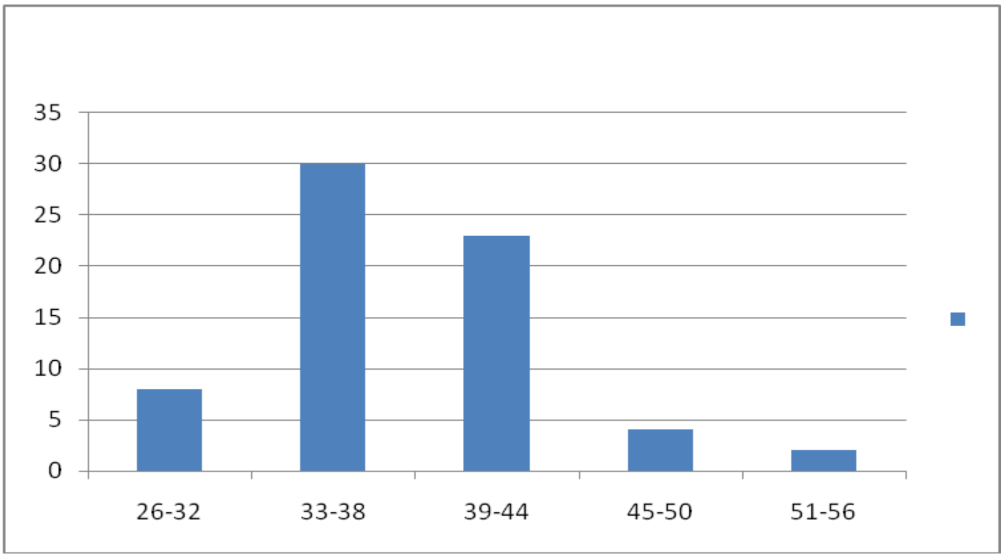


Table 8 : Mean mid and high parent heterosis values for variance quantitative traits of Bas- 385x*O.rufipogon* and their F1

Traits	*Bas-385*	*O.rufipogon*	*Bas-385 x O.rufipogon* F1	Mid parent heterosis (%)	High Parent heterosis (%)
Plant height (cm)	71	90	89	10.56	-1.1
Culm length (cm)	60	65	60	-4	-7.69
Culm diameter (mm)	4.7	3.8	6	41.18	27.66
Culm number	16	46	49	58	6.52
Panicle length (cm)	29	30	25	-15.25	-16.66
Leaf length (cm)	37	30	38	13.43	2.7
Leaf width (cm)	1	0.6	1.2	33.33	2.7
Leaf area $(cm)^2$	37	18	46	67.27	24.32
Flag leaf length (cm)	12	21.5	19	13.43	-11.63
Flag leaf width (cm)	0.8	.7	1	33.33	25
Flag leaf area $(cm)^2$	10	15	19	52	26.67
Ligule length (cm)	2.5	1.4	2.9	49	16
Auricle length (cm)	5	5.2	6	17.65	15.38
Auricle hair length (mm)	3	2.8	3.2	10.34	6.66
Panicle length (cm)	25	19.6	19	-14.8	-24
No of primary branches per Panicle	8	11	10	5.26	-9.09
No of secondary branches per panicle	9	13	13	18.18	-
No of spikelet per panicle	113	93	129	20.16	14.16
Grain length (mm)	8.2	8	8.1	-	-1.22
Sterile lemma length (mm)	2.8	2.1	2.6	6.12	-7.14
Awn length (cm)	2.1	2.8	4.8	95.92	71.43
Anther length (mm)	2	4.9	3.1	-8.8	-36.7

On the basis of these traits the genotypes, which perform better with respect yield and yield contributing traits were selected for the further genetic analysis for the improvement of the rice crop. All the quantitative traits mentioned in above tables that directly contributed to the yield of the rice genotypes were also important with respect to the yield of the plants. Phenotypic correlations among all the morphological traits presented in the Table 8. Some of the genotypes having more contribution in yield and yield related traits with respect to their great genetic potential. Phenotypic and genotypic divergence was present in all the genotypes under study with respect to their respective traits. Table 9 represented that seed traits and observed that on the basis of above morphological traits twenty genotypes were selected out of 62 genotype for the seed traits measurements. The analysis of variance & mean square values of all the seed traits were presented in the Table 9. The genotypes studied for the seed parameters with and without bran showed highly significant variation for all the seed traits. The results indicated that the genetic variation occurred among the genotypes.

Table 9: Mean square seed (length x width x thickness) of (BC_1F_2) genotypes with and without barn

Source of Variation	D. F	Seed length (mm) (with barn)	Seed width (mm) (with barn)	Seed thickness (with barn)	Seed length width ratio	Seed length (mm) (no barn)	Seed width (mm) (no barn)	Seed thickness (no barn)	Seed length width ratio (no barn)
Genotypes	19	1.15 **	0.0552**	0.0431**	0.611 **	0.7532**	0.0523 **	0.0316**	0.475**
Rep.	2	0.2503	0.00089	0.0078	0.1299	0.0419	0.0099	0.0103	0.090
Error	38	0.3320	0.0160	0.0139	0.213	0.2300	0.0070	0.0107	0.088

Level of significance P<0.01= **

3.7. The mean values of these traits (length, width, thickness & seed length width ratio) lead to the determination of seed size and shape of the each genotype . It was indicating that the shape and size variation of the seed of each genotype is explainable using those components. The seed traits with bran and without bran, some principal components having positive values and some having negative values for all the seed traits with and without bran.

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(2012) http://www.jmaterenvironsci.com/