HERITABILITY, PCA AND SELECTION RESPONSE FOR MORPHOLOGICAL PARAMETERS IN F₃ SEGREGATING POPULATION OF RICE

Salman Ali[1], Muhammad Iqtidar khan[2], Muhammad Babar[3]*, Asia Maqbool[4], Mamonila Jahandad[5], Abdul Rauf Shaikh[6], Iqbal Nisa[7], Anum Abbas[8], Muhammad Kashif Iqbal[9], Muhammad Qasim Kamal[10], Hamna Aslam[11]*

Abstract

Practically chances of new genotypes with superior attributes in response of local hybridization in self-pollinated crops are low in comparison with cross pollinated crops. Keeping in view the little chances of improvement a set of 18 parents were crossed with the aim to evaluate both heritability and selection response in19 F₃ populations for various morphological traits at "The University of Agriculture, Peshawar" during the growing season 2022. Highly significant differences were exhibited among the genotypes for studied traits; Days to 50% heading, Days to maturity, Culm length, Flag leaf area, Primary branches panicle-1 Secondary branches panicle-1, except Panicle length. Minimum days to heading were taken by F₃ population IR-8/Sugdesi (96 days) while Dokri-Basmati/Basmati-6129 recorded minimum days to maturity (124 days). Maximum panicle length (52.9 cm) was by observed by F₃ population DR-92/Dokri-Basmati, whereas the F₃ populations Basmati-6129/Basmati-370 and Dokri-Basmati/Pakhal demonstrated superiority for both the primary branches panicle^{-1} (11 no) and the secondary branches panicle^{-1} (39 no). Maximum broad sense heritability was estimated for days to heading (0.86), days to maturity (0.88), panicle length (0.75) and primary branches panicle^{-1} (0.87) for F₃ populations Basmati6129/Basmati-370, IR-8/Sugdesi, Sada Hayat/Mathar and Sada Hayat/khushboo. The F₃ population Dokri-Basmati/Sugdesi showed maximum broad sense heritability, coupled with high genetic advance, for the traits flag leaf area (35.8%) and secondary branches panicle^{-1} (52.9%). The F₃ populations IR-8/Sugdesi, Dokri-Basmati/DR-92 and Basmati-6129/Dokri-basmati showed maximum genetic advance for the traits days to heading (9.7%), days to maturity (15.9%) and primary branches panicle^{-1} (24.5%). The F₃ population Sada Hayat/Mathar showed maximum genetic advance (22.6%) for panicle length. As the above-mentioned segregating populations displayed superiority for the most studied traits, it is suggested that, these traits can be improved further through enhanced breeding programs, in order to develop rice cultivars that will exhibit higher potential yields.

Key words: Rice, F₃ populations, Heritability, Genetic advances, segregating population

[1]Cereal Crops Research Institute, Pirsabak, Nowshera, Khyber Pakhtunkhwa, Pakistan

[2]Department of Plant Breeding and Genetics, The University of Agriculture Peshawar, Pakistan

[3]*Department of Agriculture, University of Swabi-Anbar, Khyber Pakhtunkhwa, Pakistan

[4]Institute of Botany, University of the Punjab, Lahore, Pakistan

[5]Department of Horticulture, PMAS Arid Agricultural University, Rawalpindi, Pakistan

[6]Institute of Chemistry, Shah Abdul Latif University, Khairpur Mir's, Sindh, Pakistan

[7]Department of Microbiology, Women University Swabi, Pakistan

[8]Hussain Ebrahim Jamal Research Institute of Chemistry (HEJ), International Center for Chemical and Biological Sciences, University of Karachi, Karachi, Pakistan

[9]Lucky Core Industries Pakistan Limited, Bahawalpur 63100, Pakistan

[10]Department of Horticultural Sciences, The Islamia University of Bahawalpur, Bahawalpur, Pakistan

[11]*Institute of Plant Breeding and Biotechnology, MNS University of Agriculture, Multan, Pakistan

*Corresponding Author: Muhammad Babar, Hamna Aslam

*Department of Agriculture, University of Swabi-Anbar, Khyber Pakhtunkhwa, Pakistan,

Email: babarkhanuos@gmail.com

*Institute of Plant Breeding and Biotechnology, MNS University of Agriculture, Multan, Pakistan,

Email: hamnaaaslam@gmail.com

Eur. Chem. Bull. **2024**, *13(Regular Issue 3), 63 – 73*

63

Introduction

Rice (O. sativa L.) holds the prime position among all the cereal crops, both for its nutritional value and for its overall consumption. It is considered to be an important staple food among many of the world's populations. Total worldwide rice production for 2021 was 787 million tones. China was the leading producer of rice with total production of 212.8 million tones followed by India (195.4 million tons), Bangladesh (56.9 million tons) while Pakistan ranked in 9th with total production of (13.9 million tons) (Sources, "FAOSTAT". www.fao.org. 2021). nearly 90% of the world's rice is cultivated in the Asian region. In Pakistan, it is cultivated on an area of 3.33 million hectares with a production of 9.32 million tons. The Punjab Province produced 5.77 million tones, Sindh produced 2.86 million tones, Balochistan produced 0.52 million tones and Khyber Pakhtunkhwa province produced 0.15 million tons (www.pbs.gov.pk, 2021-22). Rice plays quite an important role in Pakistan's economy by contributing, it contributes 1.9 percent of value added in agriculture and 0.4 percent in GDP. (Source: Pakistan Bureau of Statistics, 2021-22).

The amount of genetic variation in breeding materials on-hand is a prerequisite for both effective selection and gain under selection as defined the amount of increase in performance that is achieved annually through artificial selection (Xu *et al.*, 2017) Differences in a certain trait of interest observed in a given population can be split into heritable and non-heritable components. Heritability is the variation in a trait associated with genetic transmission of that trait from parents to their offspring (Smith, 1952). The heritability assessments for the traits being studied takes into account the extent of transmissibility of these traits from parents to the next generation and, thus, plays a critical role in the potential enhancement of breeding programs (Khan & Naqvi, 2011). When there is considerable degree of genetic variation among individuals of breeding material, selection is effective (Sumanth *et al.* 2017). Heritability estimates for a particular trait can be said to act as a predictive tool in expressing the dependency of the phenotypic value Genetic advance or selection response is the degree of expected genetic improvement of a given offspring population for the studied genotypes associated with the different traits resident in their parents. It is a result of the amount of genetic variation, heritability and selection intensity (Allard, 1960). It will be a great challenge to meet this demand with the current rate of genetic gain in the yield of rice as estimated by (Rahman *et al.* (2019). Heritability, together with high genetic advance or selection response, would be more effective predictors of the outcome effect in selection of better genotypes for yield, and its contributing traits (Singh *et al.*, 2011).

Genetic divergence is the statistical distance between genotypes. It is determined by using cluster analysis into different groups. Genetic distance measures based on phenotypic characters are one of the main multivariate techniques used to provide criteria for choosing parents. According to Vivekananda and Subramanian (1993) genetic divergence is an efficacious tool for an effective choice of parents for hybridization and breeding program. Genetic diversity of rice plays an important role in sustainable development and food security as it allows the cultivation of crops in the presence of various biotic and abiotic stresses (Wijayawardhana et al 2015). Principal component analysis is one of the multivariate statistical techniques PCA is a powerful tool for investigating and summarizing underling trends in complex data structures. The researchers must be utilizing available genetic resources to reconstruct the ideotype of the plant in order to meet the ever increasing requirements of the population through improvement in yield, other desirable agronomic and phenological traits as well as quality of rice. In this context, the present study was carried out to make effective selection for heritability and genetic advance for different morphological traits under study in F₃ segregating populations of rice and to identify the best-performing F₃ populations for future breeding programs.

Materials and Methods

In the present study, 18 parents and their 19 F₃ populations were grown in randomized complete block design, using three replications, in a field experiment conducted at the Plant Breeding and Genetic Research Farm, The University of Agriculture, Peshawar during zaid kharif season 2022. Parental and F₃ populations used in the study are presented in table 1. Each rice genotype was planted in a three-row plot with a row length of 3 m. Row-to-row distances of 40 cm and plant-to-plant distances of 10 cm were maintained. The nursery was raised in the first week of June, while transplantation was done in a highly-puddled field in the first week of July. Data were recorded on flag leaf area, days to heading, culm length, days to maturity, panicle length, primary branches panicle^{-1} and secondary branches panicle^{-1} using ten randomly selected plants of each genotype in each replication.

Data were analyzed using the analysis of variance (ANOVA) technique, as proposed by Singh and

Eur. Chem. Bull. **2024**, *13(Regular Issue 3), 63 – 73*

64

Chaudhary (1985). For mean comparison and separation, least significance difference tests were used. Broad sense heritability for a particular trait was computed for F_3 populations of each cross-combination using the modified version of the formula suggested by Mahmud and Kramer (1951):

$$h^2 = \frac{V_{F3} - \sqrt{V_{P1} \times V_{P2}}}{V_{F3}}$$

Where V_{F3} = Variance of F_3 population for a specific trait, V_{P1} and V_{P2} = Variances of parent 1 and parent 2 of a specific F_3 population. Genetic advance was also computed as using the following formula of Panse and Sukhatme (1965):

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

Where K = 1.76 for 10 % selection intensity, h^2 = Heritability coefficient, $\sqrt{\sigma^2 P}$ = Phenotypic standard deviation, GA = Genetic advance. Genetic advance expressed as percent of the mean was computed as
GA % = GA/ $\bar{x}$ x100 where $\bar{x}$ is mean of a particular F_3 population.

Cluster analysis: Hierarchical clustering was attempted by using paired group algorithm with Mahalanobis genetic distance (D2).The Cubic clustering criterion (CCC), pseudo F (PSF) statistic and the pseudo T2 (PST2) statistic were examined by using PROC clustering strategy to decide the numbers of clusters using SAS version 9.2

Principal Component Analysis: PCA components based on correlation matrix were calculated by following procedure of SAS version 9.2 (SAS, 2008) to examine the contribution of each character for the total variation. The PCs with Eigen values greater than one was select as proposed by Jeffers (1967). Correlations between the original traits and the respective PCs were calculated. The principal component analysis was computed using the following equation: PC1=b11(x1) + b12+b1p= (XP), Where, pc1= the subjects score on pc1 (the first component extracted), b1p=the regression coefficient (weight) for observed variable p, as used in creating principal component 1 and xp=the subjects score on observed variable P.

Table 1. List of the 18 rice parents and 19 F_3 population studied for 7 traits.

Parents	F₃ Populations
1. IR-8	1. Sada Hayat/Mathar
2. DR-92	2. Sada Hayat/Khushboo
3. Dilrosh	3. Sathar/Sada Hayat
4. TN-1	4. NIAB-IR-9/IR-8
5. Basmati-370	5. IR-8/Shadab-31
6. Sugdesi	6. IR-8/Sugdesi
7. Kashmir-Basmai (K-Basmati)	7. Basmati-6129/Basmati-370
8. Pakhal	8. Basmati-6129/Dokri-Basmati
9. NIAB-IR-9	9. Basmati-2008/K-Basmati
10. DR-83	10. Basmati-2008/TN-1
11. Basmati-6129	11. Basmati-2008/Dilrosh
12. Basmati-2008	12. Dokri-Basmati/DR-92
13. Shadab-31	13. Dokri-Basmati/Pakhal
14. Dokri-Basmati	14. Dokri-Basmati/Basmati-6129
15. Sada Hayat	15. Dokri-Basmati/DR-83
16. Khushboo-95	16. Dokri-Basmati/Sugdesi
17. Sathra	17. DR-92/DR-83
18. Mathar	18. DR-92/Dokri-Basmati
	19. IR-8/NIAB-IR-9

Results
Days-to-50% heading: Highly significant (P≤0.01) differences were observed among rice genotypes for days to 50% heading. Mean squares data for days-to-heading showed highly significant (P≤0.01) differences among the parents, F_3 populations and parents vs. F_3 contrast (Table 2). Among parents, Dilrosh exhibited the minimum days-to-heading (95 days). Among the F_3 crosses,

the value of this trait ranged from 96 to 112 days. F_3 population Dokri-Basmati/Basmati-6129 demonstrated minimum days-to-heading (96 days) while F_3 population IR-8/Sugdesi exhibited maximum days-to-heading (Table 3). Among the F_3 populations, broad sense heritability for days-to-heading ranged from 0.30 to 0.86, indicating low to high heritability (Table 4). F_3 population Basmati-6129/Bas-370 showed maximum broad sense

Eur. Chem. Bull. **2024**, *13(Regular Issue 3), 63 – 73*

65

heritability (0.86) while minimum broad sense heritability (0.30) was manifested by F$_3$ population Dokri-Basmati/Dr-83. F$_3$ population IR-8/Sugdesi manifested maximum genetic advance (9.7%) while F$_3$ population Basmati-2008/TN-1 showed minimum genetic advance (1.2%) (Table 4).

Flag leaf area: Analysis of variance showed highly significant (P≤0.01) differences among rice genotypes for parents and F$_3$ populations, while parents vs. F$_3$ populations showed significant (P<0.05) differences (Table 2). Maximum flag leaf area (51.9 cm^2) among parents was achieved by Basmati-6129. Among F$_3$ populations, mean values varied from 25.7 to 49.0 cm^2. Maximum value of 49 cm^2 was recorded for F$_3$ population Dokri-Basmati/Sugdesi, while F$_3$ population DR-92/Dokri-Basmati displayed minimum value of 25.7cm^2 for this trait (Table 3). High broad sense heritability (0.81) was observed for F$_3$ population Dokri-Basmati/Sugdesi, while minimum heritability (0.40) was recorded for F$_3$ population IR-8/NIAB-IR-9 (Table 10). High genetic advance (35.8%) was recorded for F$_3$ population Dokri-Basmati/Sugdesi, while F$_3$ population Basmati-6129/Basmati-370 displayed minimum genetic advance (11.3%) (Table 4).

Culm length: Analysis of variance for culm length showed highly significant (P≤0.01) differences among rice genotypes i.e., parents, F$_3$ populations and parents vs. F$_3$ populations (Table 2). Among parents, genotype DR-83 showed maximum culm length (115.5 cm). Among F$_3$ populations mean values for culm length ranged from 96.1 to 111.9 cm. F$_3$ population IR-8/Sugdesi produced maximum culm length of 111.9 cm while F$_3$ population Dokri-Basmati/Basmati-6129 manifested minimum culm length (96.1 cm) (Table 3). Broad sense heritability for culm length ranged from 0.34 to 0.88, indicating moderate-to-high heritability (Table 4). Among the F$_3$ populations, Dokri-Basmati/Basmati-6129 exhibited minimum broad sense heritability (0.34) while maximum broad sense heritability (0.88) was observed for F$_3$ population Basmati-6129/Basmati-370. Maximum genetic advance of 19.1% was recorded for F$_3$ population DR-92/DR-83 while minimum genetic advance (1.4%) was recorded for F$_3$ population Basmati-2008/Dilrosh (Table 4).

Days-to-maturity: Highly significant differences (P≤0.01) were observed for days-to-maturity among parents, F$_3$ populations and parents vs. F$_3$ contrast (Table 2). Minimum days-to-maturity (125) among parents were counted for genotype DR-83. Among F$_3$ populations, Dokri-Basmati/Basmati-6129 was early maturing (124 days), while F$_3$ population IR-8/Sugdesi was late

maturing (142 days) (Table 3). Broad sense heritability among F$_3$ populations varied from 0.40 to 0.88. F$_3$ population IR-8/Sugdesi exhibited maximum broad sense heritability (0.88) while minimum heritability (0.40) was recorded for F$_3$ population Dokri-Bas/Bas-6129. Maximum genetic advance (15.9%) was calculated for F3 population Dokri-Bas/DR-92, while minimum (1.2%) was recorded for F3 population Bas-2008/TN-1 (Table 4).

Panicle length: Mean square data revealed highly significant (P≤0.01) differences for F$_3$ population among the genotypes for panicle length, while non-significant (P≥0.05) variations were observed for parents and parents vs. F$_3$ contrast (Table 2). Among the parental population, maximum panicle length (30.3 cm) was observed for genotype Basmati-2008. Among F$_3$ populations, mean values for the this trait ranged from 24.6 to 52.9 cm. Maximum panicle length (52.9 cm) among F$_3$ populations was recorded for Dr-92/Dokri-Basmati, while minimum (24.6 cm) was recorded for Dokri-Basmati/Pakhal (Table 3). Broad sense heritability for panicle length ranged from 0.41 to 0.75, indicating moderate to high heritability, while genetic advance ranged from 5.9 to 22.6% (Table 10). Maximum heritability (0.75) along with higher genetic advance (22.6%) was estimated for F$_3$ population Sada Hayat/Mathar, while minimum heritability (0.41) coupled with low genetic advance (5.9%) was observed for F$_3$ population NIAB-IR-9/IR-8 (Table 4).

Primary branches panicle^{-1}: Highly significant (P≤0.01) differences among rice genotypes were revealed for Primary branches panicle-1. Parents, F$_3$ populations and parent's vs F$_3$ contrast exhibited highly significant (P≤0.01) differences for the said trait (Table 2). Among parents, maximum primary branches panicle^{-1} (13) was manifested by genotype Sada Hayat. Among F$_3$ populations, primary branches panicle^{-1} ranged from 8 to 11. F$_3$ population Basmati-6129/Basmati-370 showed maximum (11) primary branches panicle^{-1}, while F$_3$ population Basmati-2008/Dilrosh revealed minimum (8) primary branches panicle^{-1}(Table 3). Broad sense heritability values among the F$_3$ populations varied from 0.38 to 0.74. Maximum broad sense heritability for primary branches panicle^{-1} (0.74) was observed for F$_3$ population Sada Hayat/Khushboo while minimum heritability (0.38) was observed for F$_3$ population Dokri-Basmati/DR-83. Maximum selection response (24.5%) was observed for F$_3$ population Basmati-6129/Dokri-Basmati, while minimum selection response (7.9%) was estimated for Dokri-Basmati/DR-83 (Table 4).

Eur. Chem. Bull. **2024**, *13(Regular Issue 3), 63 – 73*

66

Secondary branches panicle^{-1}: Mean square table showed highly significant (P≤0.01) differences among rice genotypes for parents while F$_3$ populations showed significant (P<0.05) differences. Parent's vs F$_3$ contrast exhibited non-significant (p≥0.05) variation for this trait (Table 2). Among parents, maximum secondary branches panicle^{-1}(44) was recorded for Sada Hayat. Among F$_3$ populations, mean data for secondary branches panicle^{-1} ranged from 27 to 38. F$_3$ population Dokri-Basmati/DR-92 displayed minimum secondary branches panicle^{-1}(27) while F$_3$ population Dokri-Basmati/Pakhal showed maximum (38) secondary branches panicle^{-1} (Table 3). F$_3$ population Basmati-2008/Dilrosh showed minimum heritability (0.27) while maximum heritability (0.87) was observed for F$_3$ population Dokri-Basmati/Sugdesi. Minimum genetic advance (7.4%) was observed for F$_3$ population Dokri-Basmati/DR-83 while maximum genetic advance (52.9%) was observed for F$_3$ population Dokri-Basmati/Sugdesi (Table 4).

Table 2. Mean squares for various traits of rice genotypes evaluated at The University of Agriculture, Peshawar Pakistan.

Traits	Replications (df=2)	Genotypes (df=36)	Parents (df=17)	F$_3$ Populations (F$_2$) (df=19)	P vs. F$_3$ (df=1)	Error (df=72)
Days to 50% heading	8.2	104.2**	134.6**	69.8**	203.1**	13.8
Days to maturity	10.4	113.27**	134.5**	82.9**	295.9**	15.3
Flag leaf area	21.8	89.51**	104.5**	77.1**	55.7*	9
Panicle length	16.5	60.37	8.2	111.8**	20.1	40
Culm length	8.1	105.94**	133.4**	73.5**	221.0**	11
Primary branches panicle-1	0.02	2.59**	3.9**	1.4**	0.01	0.5
Secondary branches panicle-1	31	63.97**	104.7**	28.1*	16.1	16

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

Table 3. Mean values for various morphological traits of rice genotypes evaluated at The University of Agriculture, Peshawar, Pakistan.

Genotypes	Days to 50% heading	Culm length	Flag leaf area	Days to maturity	Panicle length	Primary branches panicle^{-1}	Secondary branches panicle^{-1}
Parents							
IR-8	108	107.3	38.7	137.6	25.7	11	35
DR-92	110	109.7	34.4	139.3	27.0	9	30
Dilrosh	95	95.0	37.3	125.2	27.5	11	37
TN-1	100	99.8	29.7	129.5	25.6	10	32
Basmati-370	115	114.6	27.3	143.9	26.1	11	33
Sugdesi	113	113.0	31.6	142.7	28.2	10	26
K-Basmati	96	95.7	30.7	125.9	28.4	8	23
Pakhal	99	98.8	32.9	128.8	28.0	10	26
NIAB-IR-9	111	111.7	28.2	141.7	25.0	11	27
DR-83	115	115.5	32.9	146.4	27.9	9	24
Basmati-6129	107	107.2	51.9	136.8	30.2	11	29
Basmati-2008	96	96.4	44.9	126.5	24.7	8	28
Shadab-31	112	111.2	36.2	142.0	28.4	9	27
Dokri-Basmati	108	107.7	33.7	138.1	28.1	10	33
Sada Hayat	103	103.3	36.5	133.3	30.3	13	44
Khushboo-95	102	102.7	38.3	132.3	26.8	11	42
Sathra	112	111.7	36.3	141.7	29.6	9	36
Mathar	108	108.2	37.0	138.0	27.0	10	34
Parental Means	106	106.1	35.5	136	27.5	10	31
LSD (0.05) Parents	106	106.1	35.5	6.9	1.9	0.9	5.9
F$_3$ Populations							
Sada Hayat/Mathar	108	107.9	31.7	137.5	27.6	10	34
Sada Hayat/Khushboo	108	108.1	36.1	137.9	26.8	10	29
Sathar/Sada Hayat	105	104.7	28.9	134.7	25.9	10	29

Eur. Chem. Bull. **2024**, *13(Regular Issue 3), 63 – 73*

67

NIAB-IR-9/IR-8	110	109.5	31.7	139.3	24.8	10	30
IR-8/Shadab-31	111	110.8	32.2	140.4	26.5	11	31
IR-8/Sugdesi	112	111.9	36.9	142.1	29.3	10	32
Basmati-6129/Basmati-370	103	103.1	30.7	132.7	27.8	11	35
Basmati-6129/Dokri-Basmati	103	102.7	29.9	132.7	28.4	10	31
Basmati-2008/K-Basmati	103	103.1	35.3	133.1	28.5	11	35
Basmati-2008/TN-1	103	102.8	40.4	132.8	26.4	10	29
Basmati-2008/Dilrosh	101	101.1	37.5	130.7	26.1	8	28
Dokri-Basmati/DR-92	100	100.0	38.2	126.5	26.6	9	28
Dokri-Basmati/Pakhal	100	100.2	33.9	128.5	24.7	10	39
Dokri-Basmati/Basmati-6129	96	96.1	31.2	124.8	26.7	9	31
Dokri-Basmati/DR-83	97	96.9	33.5	125.6	25.1	10	36
Dokri-Basmati/Sugdesi	97	97.2	49.0	127.1	29.4	10	36
DR-92/DR-83	101	97.4	31.8	129.8	27.2	10	33
DR-92/Dokri-Basmati	100	100.1	25.7	129.3	52.9	10	32
19. IR-8/NIAB-IR-9	109	108.4	32.7	138.2	27.6	11	33
F₃ Populations Means	103	103.3	34.1	132.8	28.3	10	32
LSD (0.05) F₃ populations	5.2	3.9	11.4	6.0	14.5	1.2	6.5
Genotypes Means	104.7	104.6	35.8	134.4	27.9	10.0	31.9
LSD (0.05) Genotypes	6.1	5.4	13.0	6.4	10.3	1.2	6.5

Table 4. Heritability and genetic advance as percent of mean (GA) for various morphological traits of rice genotypes at The University of Agriculture, Peshawar, Pakistan.
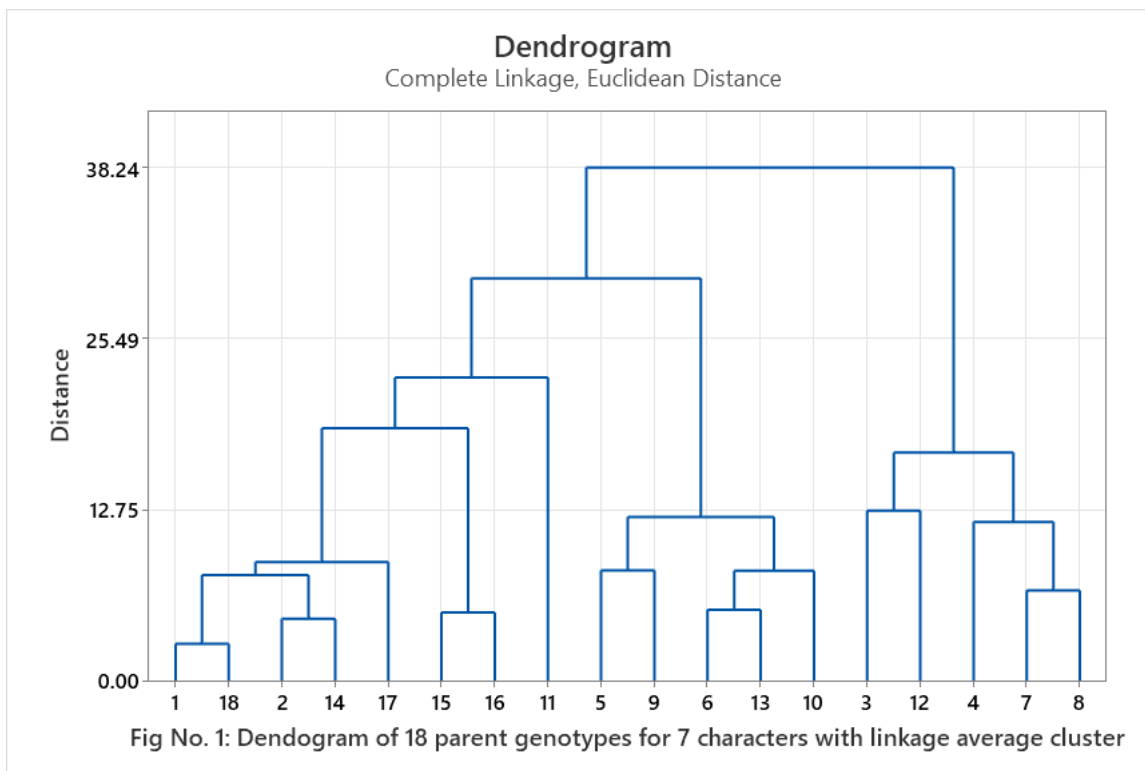
Genotypes	Days to heading		Culm length		Flag leaf area		Days to maturity		Panicle length		Primary branches panicle⁻¹		Secondary branches panicle⁻¹	
	h^2	GA	h^2	GA	h^2	GA	h^2	GA	h^2	GA	h^2	GA	h^2	GA
F₃ Populations														
Sada Hayat/Mathar	0.41	2.0	0.51	2.9	0.44	13.8	0.61	2.8	0.75	22.6	0.56	16.5	0.65	26.47
Sada Hayat/Khushboo	0.64	4.0	0.67	4.3	0.63	22.2	0.66	3.5	0.67	17.3	0.74	21.9	0.52	22.08
Sathar/Sada Hayat	0.69	5.8	0.66	5.7	0.45	11.4	0.56	4.1	0.42	8.2	0.49	11.4	0.57	19.85
NIAB-IR-9/IR-8	0.72	7.2	0.75	7.2	0.69	21.2	0.85	6.8	0.41	5.9	0.63	18.8	0.64	26.14
IR-8/Shadab-31	0.72	5.0	0.70	4.8	0.54	15.0	0.71	4.2	0.46	8.8	0.57	14.8	0.63	18.22
IR-8/Sugdesi	0.72	9.7	0.80	9.7	0.74	20.1	0.88	8.9	0.49	8.5	0.73	23.4	0.40	38.78
Basmati-6129/Basmati-370	0.86	8.8	0.88	8.9	0.50	11.3	0.68	5.6	0.72	16.1	0.57	16.7	0.46	15.25
Basmati-6129/Dokri-Basmati	0.76	7.4	0.62	6.2	0.62	16.9	0.73	5.8	0.59	14.8	0.71	24.5	0.46	23.85
Basmati2008/Kash.Basmati	0.78	5.4	0.67	4.9	0.81	30.7	0.82	4.6	0.60	12.1	0.52	11.9	0.65	24.85
Basmati-2008/TN-1	0.40	1.2	0.55	1.7	0.54	16.9	0.50	1.2	0.58	10.4	0.56	22.3	0.38	13.45
Basmati-2008/Dilrosh	0.62	2.2	0.48	1.4	0.69	27.7	0.76	2.6	0.48	8.2	0.49	12.8	0.27	7.81
Dokri-Basmati/DR-92	0.57	3.3	0.46	2.4	0.61	27.2	0.79	15.9	0.52	10.3	0.47	12.4	0.60	22.66
Dokri-Basmati/Pakhal	0.36	2.0	0.59	3.4	0.48	17.4	0.61	3.3	0.52	9.6	0.59	15.2	0.40	14.43
Dokri-Basmati/Basmati-6129	0.35	1.8	0.34	1.6	0.62	19.0	0.40	2.0	0.59	13.6	0.40	9.8	0.42	14.35
Dokri-Basmati/DR-83	0.30	1.2	0.42	1.7	0.50	20.9	0.55	2.6	0.53	7.9	0.38	7.9	0.29	7.41
Dokri-Basmati/Sugdesi	0.54	2.7	0.58	3.0	0.81	35.8	0.65	3.8	0.59	12.4	0.44	11.7	0.87	52.92
DR-92/DR-83	0.72	5.1	0.69	19.1	0.49	15.8	0.75	4.3	0.58	9.0	0.72	22.0	0.44	13.57
DR-92/Dokri-Basmati	0.76	7.7	0.79	7.7	0.63	27.0	0.79	6.4	0.52	11.8	0.51	12.3	0.53	19.79
IR-8/NIAB-IR-9	0.79	9.3	0.80	8.6	0.40	18.8	0.85	7.0	0.49	10.6	0.60	16.6	0.72	31.58

Clustering of genotypes: The eighteen rice parental genotypes were grouped into five distinct clusters using Mahalanobis (D2) analysis (Table 5 and Figure 1). The number of genotypes in each cluster has showed variation from cluster to cluster.

Cluster I comprising total of 5 genotypes (27.77 %), cluster II has 2 genotypes (11.11%), cluster III has 1 genotype (5.55%), cluster IV and cluster V has same genotypes (27.77% each), respectively.

Eur. Chem. Bull. **2024,** *13(Regular Issue 3), 63 – 73*

68

Table 5. Clustering of 18 rice Parental genotypes based on D2 statistics.

Cluster No	No of genotypes	Proportion (%)	List of genotypes
I	5	27.77	1-2-14-17-18
II	2	11.11	15-16
III	1	5.55	11
IV	5	27.77	5-6-9-10-13
V	5	27.77	3-4-7-8-12

Fig No. 1: Dendogram of 18 parent genotypes for 7 characters with linkage average cluster

Cluster mean analysis: The mean value of all the 7 traits in each cluster is presented (Table 6). Cluster I comprised of 5 genotypes that had its own unique characteristics, of late 50% heading period (109.2 days), late maturing period (138.94 days), relative high flag leaf area (36.02 cm), medium panicle length (27.48 cm) with relative moderate culm length (108.92 cm), minimum number of primary branches panicle1 (9.80 no) and moderate secondary branches panicle-1 (33.60 no). Cluster II had two genotypes with possessing of early heading period (102.50 days), relatively early maturing period (132.80 days), flag leaf area (37.40 cm), tall panicle length (28.55 cm), moderate culm length (103.00 cm) with maximum number of primary branches panicle1 (12.00 no) and highest number of secondary branches panicle-1 (33.60 no). On the other hand, cluster III had only one genotype and had moderate in maturing period (107.00 days), late maturing (136.80 days), maximum flag leaf area (51.0 cm), maximum panicle length (30.20 cm), long culm length (107.20 cm), maximum primary branches panicle1 (11.00 no) with moderate number of secondary branches panicle-1 (29.00 no). Cluster IV contained 5 genotypes, appeared maximum late heading period (113.20 days), maximum late in maturity (143.34 days), least flag leaf area (31.24 cm), moderate panicle length (27.12 cm), highest long culm length (113.20 cm), moderate primary branches panicle1 (10.00 no) with moderate number of secondary branches panicle-1 (27.40 no). Similarly, the last cluster consisted of 5 genotypes highest in early maturing (97.20 days), among early in all cluster genotypes having maturity of (127.18 days), moderate flag leaf area (35.10 cm), shortest panicle length (26.84 cm), lowest in culm length (97.14 cm), highest minimum number of primary branches panicle1 (9.40 no) and moderate number of secondary branches panicle-1 (29.20 no).

Eur. Chem. Bull. **2024,** *13(Regular Issue 3), 63 – 73*

69

Table 6: Cluster mean for 7 traits of 18 rice parental genotypes.

Traits	I	II	III	IV	V
DH	109.20	102.50	107	113.20**	97.20*
DM	138.94	132.80	136.8	143.34**	127.18*
FL	36.02	37.40	51.9**	31.24*	35.10
Pl	27.48	28.55	30.2**	27.12	26.84*
CL	108.92	103.00	107.2	113.20**	97.14*
PBP[1]	9.80	12.0**	11	10.00	9.40*
SBP[1]	33.60	43.00**	29	27.40*	29.20

"**" and "*" indicates the highest values and the lowest values, respectively. DH= Days to Heading, DM= Days to Maturity, FLA= Flag Leaf area, PL= Panicle length, CL= Culm Length, PBP[-1]= Primary Branches per panicle, SBP[-1]= Secondary Branches per panicle

Principal component analysis (PCA): Current study for principal component analysis, 7 principal components (pcs) generated, out of these, the first three principal components that revealed Eigen values greater than one were found to be significant. The remaining four PCs explained non-significant amount of variation and were not worth interpreting. The Eigen values are used to determine how many factors to retain. The principal component analysis showed in this experiment that three principal components PC-1, PC-2 and PC-3 showed more than one eigen value with the eigen values of 3.1134, 1.7786 and 1.1483, respectively, and explained about 86.30% of the total variation for all the characters with high correlation among the traits analyzed (Table 7). Therefore, variation for these three PCs was given an emphasis for further explanation. According to Guei et al. (2005) the first three principal components are often the most important in reflecting the variation patterns among accessions, and the characters associated with these, are more useful in differentiating accessions. According to characters with larges absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute

values closer to zero. Studies chosen to determine the cutoff limit for the coefficients of the proper vectors; this criterion treated coefficients greater than 0.3 as having a large enough effect to be considered important, while traits having a coefficient less than 0.3 were considered not to have important effects on the overall variation.

Moreover, in the present study, the first principal component (PC1) which accounted for 44.50% of the total morphological variability among genotypes were attributed to discriminatory traits, namely, days to heading and days to maturity (0.562 each) and culm length (0.561) suggesting that these components reflected the yield potential of each genotype through some yield component aspects and they were the ones that more differentiated the clusters. Likewise, 25.40 % of total morphological variability among the tested genotypes accounted for the second PCA originated from variation due to primary branches panicles[1] (0.641), followed by secondary branches panicles[1] (0.633) and panicle length (0.345). Similarly, the third PCA which accounted for 16.40 % of the total variation contributed from number of primary branches panicle[1] (0.330).

Table 7: Eigen values total variance, percent of variance and cumulative variance of 18 rice parents studied for 7 traits.

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
DTH	0.562*	0.058	-0.031	0.099	-0.051	-0.73	-0.367
DTM	0.562*	0.053	-0.041	0.108	-0.034	0.682*	-0.449
FLA	-0.189	0.245	-0.63*	0.721*	0.13	-0.01	-0.006
PL	0.052	0.345	-0.646*	-0.676*	-0.062	0.002	0.01
CL	0.561*	0.066	-0.026	0.117	-0.028	0.047	0.814*
PB panicle[1]	0.009	0.641*	0.33	-0.053	0.691*	-0.005	-0.016
SB panicle[1]	-0.121	0.633*	0.27	0.12	-0.705	0.011	-0.001
Eigen value	3.1134	1.7786	1.1483	0.6559	0.2991	0.0033	0.0012
percent of variance	44.50	25.40	16.40	0.094	0.043	0	0
Cumulative variance	44.50	69.90	86.30	0.957	0.999	1	1

"*" Indicating loading value greater than 0.3, DTH= Days to Heading, DM= Days to Maturity, FLA= Flag Leaf area, PL= Panicle length, CL= Culm Length, PB Panicle[-1] = Primary Branches per panicle, SB Panicle[-1] =Secondary Branches per panicle.

Eur. Chem. Bull. **2024**, *13(Regular Issue 3), 63 – 73*

70

Discussion

Early heading is an important agronomical trait in rice-breeding programs as early heading provides more time for grain formation and development, whereas late heading compresses the time available for grain filling due to a shortening of the time period between heading and harvest, resulting in low grain weight. In the present study, highly significant variations ($P \leq 0.01$) among parents, F_3 populations and parents vs. F_3 contrast were observed for days-to-heading. Demeke et al (2022) studied seventy rice genotypes and observed significant differences among studied genotypes for days-to-heading. They also reported high heritability (96.11%) with maximum genetic advance for days-to-heading. The findings of the current study are in agreement with their results, as most of the F_3 populations showed high broad sense heritability coupled with maximum genetic advance. High heritability for days to flowering with high genetic advance is the result of more genetic control on this trait. Flag leaf contributes the majority of photosynthates after rice flowering. Photosynthesis is the only source of energy for plants. Highly significant ($P \leq 0.01$) differences among parents and their F_3 populations were observed for flag leaf area. In the present study, high heritability with maximum genetic advance was also observed for most of the F_3 populations. Our results are in line with the findings of (Kumar *et al* 2023) who studied five rice population and reported significant differences among rice genotypes for the studied trait. They also reported higher heritability coupled with high genetic advance for flag leaf area, which our present results supported. High heritability for this trait provides the best opportunity for desirable selection in earlier generations.

The culm length is an important agronomical trait in cereal crops. It has an impact on lodging resistance, yield production, and biomass accumulation. (Mo et al 2020) studied culm length among rice genotypes and observed significant variation among genotypes for this trait. Our results are in conformity with their findings, as significant ($P \leq 0.01$) differences among genotypes, parents, F_3 populations and parents vs. F_3 populations were observed in the present study. Our findings show that heritability estimates for culm length were high for the majority of the F_3 populations. Ogunbayo *et al*. (2014), Khan et al (2022) also estimated high heritability, respectively, with maximum genetic advance for culm length. Highly significant differences were observed for days-to-maturity among rice genotypes in the present study. These results are compatible with the results of Iqbal *et al.*

(2018). He studied 16 rice genotypes including four parents and their respective twelve F_2 populations. Most of the F_3 populations in the present study manifested high heritability with low genetic advance for this trait. Our results are also in agreement with the findings of Chowdhury et al (2023), who also had estimated high heritability with low genetic advance for the same trait.

The length of the rice panicle determines the number of grains it can hold, and, consequently, the resulting rice yield. It is, therefore, one of the most important traits assessed in yield-related research. In our current finding highly significant ($P \leq 0.01$) differences were observed among the F_3 populations, while parents and parents vs F_3 populations showed non-significant ($P > 0.05$) variation. Shrestha *et al* (2021) also observed significant variations for panicle length among different rice genotypes. Heritability and selection response estimates for panicle length were high for most of the F_3 populations. These results suggested that this trait is under less environmental control. Khalequzzaman et al (2023) also estimated high heritability of 86% coupled with high genetic advance for the studied trait, which our current findings support.

Maximum primary branches panicle^{-1} is also one of the most important yield components, and leads to an increase in the final yield. Sanghera *et al*. (2013) also reported significant differences among 14 rice genotypes for the studied trait. Our results are in conformity with theirs, i.e., significant ($P < 0.05$) differences among genotypes for parents, F_3 populations and parents vs F_3 contrast were observed for primary branches panicle^{-1}. Low (0.38) to high (0.78) broad sense heritability estimates for this trait in our study also support the Longkho et al (2020) results. They also reported low (69.2 %) broad sense heritability values for this trait. Rahayu et al (2018) observed significant variations in F2 and F2R rice population for secondary branches panicle^{-1}. Similarly Agalya *et al*. (2024) also reported significant differences among different rice genotypes for the secondary branches panicle^{-1}. Our results are consistent with both of these studies, i.e., in the present study genotypes showed significant ($P < 0.05$) differences in F_3 populations. Ram *et al* (2020) assessed moderate heritability with maximum genetic advance for the studied trait. In our current study broad sense heritability ranged from low to high and hence selection for this trait would be effective in earlier generations.

Eur. Chem. Bull. **2024**, *13(Regular Issue 3), 63 – 73*

71

Conclusions:

Significant variation among the parents and F3 - populations was observed for all the studied traits. F3 population IR-8/Sugdesi manifested minimum days to heading while F3 population Dokri-Basmati/Basmati-6129 displayed minimum days to maturity. Maximum panicle length was observed for F3 population DR-92/Dokri-Basmati while F3 population Basmati-6129/Basmati-370 showed superiority for primary branches panicle-1. F3 population Dokri-Basmati/Basmati-6129 was early maturing while F3 population Dokri-Basmati/Pakhal showed maximum secondary branches panicle-1. Maximum broad sense heritability days to heading, days to maturity, panicle length and primary branches panicle-1 were observed for F3 populations Basmati6129/Basmati-370, IR-8/Sugdesi, Sada Hayat/Mathar and Sada Hayat/khushboo while F3 population Dokri-Basmati/Sugdesi manifested maximum heritability coupled with high genetic advance for flag leaf area and secondary branches panicle-1. F3 populations IR-8/Sugdesi, Dokri-Basmati/DR-92 and Basmati-6129/Dokri-basmati showed maximum genetic advance for days to heading, days to maturity and primary branches panicle-1. These results demonstrated that different F3 populations exhibited varied potential for the selection of the desired traits. Five diverse clusters were made for 18 rice parents' genotypes for 7 traits which showed genetic variability. Principle component analysis (PCA) of the 18 rice parents exhibited that the first three PCs having Eigen values greater than one explained 86.30% of the total variation. This suggested a strong correlation among the characters examined. PCA-1 accounted about 44.50%, PCA-2 explained 25.40% and PCA-3 for 16.40% variability was assigned for the variation, respectively. On the basis of superiority for maturity and panicle-related traits, it is recommended that the segregating F3 populations of Dokri-Basmati/Basmati-6129, IR-8/Sugdesi, Basmati-6129/Basmati-370, Sada Hayat/Mathar and Dokri-Basmati/Sugdesi be considered for future breeding programs to develop desirable inbred lines and rice cultivars.

Acknowledgment

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Conflict of Interest: The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

20. Agalya, J. S., Hari, P. P., Ramchander, S., Kumar, P., Devesena, N., Naveenkumar, R., & John, K. N. (2024). Assessment of variability parameters and diversity of panicle architectural traits associated with yield in rice (Oryza sativa L.). *Plant Science Today*, *11*(1), 109-118.

21. Allard, R.W 1960. *Principles of Plant Breeding*. Jhon Wiley and Sons Inc., New York.

22. Chowdhury, N., Islam, S., Mim, M. H., Akter, S., Naim, J., Nowicka, B., & Hossain, M. A. (2023). Characterization and genetic analysis of the selected rice mutant populations. SABRAO J. Breed. Genet, 55(1), 25-37.

23. Demeke, B., Dejene, T., & Abebe, D. (2022). Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (Oryza Sativa L.) genotypes at pawe, northwestern Ethiopia. Cogent Food & Agriculture, 9(1), 2157099.

24. Iqbal, A., Shah, S. M. A., Rahman, H., Aman, F., & Rahman, A. (2018). Genetic variability, heritability and genetic advance for morphological traits in f5: 6 rice lines. *Sarhad Journal of Agriculture*, *34*(4), 888-895.

25. Jeffers JNR, 1967, Two case studies in the application of Principal Component Analysis, Journal of the Royal Statistical Society, Series C (Applied Statistics), 16(3),225-236

26. Khalequzzaman, M., Chakrabarty, T., Islam, M. Z., Rashid, E. S. M. H., Prince, M. F. R. K., & Siddique, M. A. (2023). Deciphering Genetic Variability, Traits Association, Correlation and Path Coefficient in Selected Boro Rice (Oryza sativa L.) Landraces. *Asian Journal of Biology*, *19*(2), 33-45.

27. Khan, W. U., Shah, S. M. A., Ullah, H., Khalil, I. H., Jadoon, S. A., & Wang, D. (2022). Development of rice germplasm based on genetic variability in F 5 segregating populations. *SABRAO J. Breed. Genet*, *54*(5), 993-1003.

28. Khan, N., & Naqvi, F. N. (2011). Heritability of morphological traits in bread wheat advanced lines under irrigated and non-irrigated conditions. *Asian Journal of Agricultural Sciences*, *3*(3), 215-222.

29. Kumar, D. M., Srinivas, T., Rao, L. S., Suneetha, Y., Sundaram, R. M., Kumari, V. P.,

& Ratnam, T. V. (2023). Generation Mean Analysis for Yield and Yield Component Traits in Inter-specific Cross of Rice (Oryza sativa L.). Agricultural Science Digest. doi, 10.

30. Longkho, K., Kole, P. C., & Behera, P. P. (2020). Genetic parameter studies in F4 segregating generation of rice. *Journal of Pharmacognosy and Phytochemistry*, *9*(1), 1647-1651.

31. Mahmud, I & H.H. Kramer. 1951. Segregation of yield, height and maturity following soyabean crosses. *Agron. J*. 43: 605-606.

32. Mo, Y., Jeong, J. M., Kim, B. K., Kwon, S. W., & Jeung, J. U. (2020). Utilization of elite Korean japonica rice varieties for association mapping of heading time, culm length, and amylose and protein content. The Korean Journal of Crop Science, 65(1), 1-21.

33. Ogunbayo, S. A., Si&e, M., Ojo, D. K., Sanni, K. A., Akinwale, M. G., Toulou, B., ... & Gregorio, G. B. (2014). Genetic variation and heritability of yield and related traits in promising rice genotypes (Oryza sativa L.). *Journal of Plant Breeding and Crop Science*, *6*(11), 153-159.

34. Principal Component Analysis for Special Types of Data. In: Principal Component Analysis. Springer Series in Statistics. Springer, New York, NY. https://doi.org/10.1007/0-387-22440-8_13

35. Rahayu, S., Ghulamahdi, M., Suwarno, W. B., & Aswidinnoor, D. H. (2018). Panicle morphology of rice (Oryza sativa L.) under various application of nitrogen fertilizer. *Jurnal Agronomi Indonesia*, *46*, 145-52.

36. Rahman, M. A., Quddus, M. R., Jahan, N., Rahman, M. A., Sarker, M. R. A., Hossain, H., & Iftekharuddaula, K. M. (2019). Field rapid generation advance: An effective technique for industrial scale rice breeding program. *The Experiment*, *47*(2), 2659-2670.

37. Ram, A. A., Elsy, C. R., & Beena, C. (2023). Deciphering Variability and Genetic Parameters in Traditional Scented Rice (Oryza sativa L.) Genotypes of Kerala, India. *International Journal of Plant & Soil Science*, *35*(18), 2230-2236.

38. Sanghera, G. S., Kashyap, S. C., & Parray, G. A. (2013). Genetic variation for grain yield and related traits in temperate red rice (Oryza sativa L.) ecotypes. *Notulae Scientia Biologicae*, *5*(3), 400-406.

39. Shrestha, J., Subedi, S., Kushwaha, U. K. S., & Maharjan, B. (2021). Evaluation of rice genotypes for growth, yield and yield components. *Journal of Agriculture and Natural Resources*, *4*(2), 339-346.

40. Singh, R.K. and B.D. Chaudhary. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publisher, New Delhi, India, pp-318.

41. Singh, S. K., Singh, C. M., & Lal, G. M. (2011). Assessment of genetic variability for yield and its component characters in rice (Oryza sativa L.). *Research in Plant Biology*, *1*(4).

42. Smith, H.H., 1952. Fixing transgressive vigar in *NicotianaRustica*. Iowa State College Press, Ames, USA, pp 552. Soyabean crosses. *Agron. J*., 43: 605–606.

43. (Source: Pakistan Bureau of Statistics,2021-22)

44. (Sources, "FAOSTAT". www.fao.org. 2021).

45. Sumanth, V., Suresh, B. G., Ram, B. J., & Srujana, G. (2017). Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (Oryza sativa L.). Journal Ofrmacognosy and Phytochemistry, 6(4), 1437–1439.

46. Vivekananda, P., Subramanian, S., 1993. Genetic divergence in rainfed rice. Oryza 30, 60–62

47. Wijayawardhana, H. C. D., Herath, H. M. V. G., Weerasinghe, P. A., & Herath, H. M. D. A. K. (2015). Morphological variation in selected Sri Lankan rice (Oryza sativa L.) accessions in relation to the vegetative parameters.

48. Xu, Y., Li, P., Zou, C., Lu, Y., Xie, C., Zhang, X., ... & Olsen, M. S. (2017). Enhancing genetic gain in the era of molecular breeding. *Journal of Experimental Botany*, *68*(11), 2641-2666.

*Eur. Chem. Bull. **2024**, 13(Regular Issue 3), 63 – 73*

73