Biological Forum – An International Journal **13(4): 1033-1040(2021)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Characterization of Advanced Breeding (BC_3F_5) Lines of Basmati Rice (*Oryza sativa* L.) under North-Western Himalayan conditions

Prerna Johar[1*], R.K. Salgotra[1], Manish Kr Sharma[2], Sushil Sharma[3], Tuhina Dey[4], Moni Gupta[5] and Tanveer Kour Raina[1]

[1]School of Biotechnology, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Chatha, Jammu-180009, (J&K), India.

[2]Division of Statistics & Computer Science, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Chatha, Jammu-180009, (J&K), India.

[3]Division of Agricultural Engineering, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Chatha, Jammu-180009, (J&K), India.

[4]Division of Plant Breeding and Genetics, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Chatha, Jammu-180009, (J&K), India.

[5]Division of Biochemistry, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Chatha, Jammu-180009, (J&K), India.

(Corresponding author: Prerna Johar)*
(Received 25 September 2021, Accepted 20 November, 2021)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Genetic diversity is the basis for improvement of crop plants. The study of morphological traits is considered an effective tool for the preliminary assessment of genetic diversity together with the crop improvement programme. The diversity of plant genetic resources provides an opportunity to plant breeders for the advancement of novel and improved cultivars with desirable traits. The contemporary investigation was initiated at the research farm of SKUAST-Jammu, during wet season 2020 for the characterization of BC_3F_5 population comprising the advanced breeding lines of basmati rice, developed from diverse parents. Twenty nine advanced breeding genotypes of basmati rice were laid out in a randomized block design (RBD) along with three replications. The experimentation was accomplished by applying Tukey's test. The analysis of variance (ANOVA) exhibited statistically significant differences ($p<0.01$), indicating the presence of genetic variability amongst the population, which can be assured to be beneficial for researchers and breeders to identify promising basmati lines for release as a variety or utilization as genetic stocks for use in basmati breeding programmes. The results illustrated narrow differences between PCV and GCV for all the traits, revealing little environmental effect on their expression. A high value of heritability together with high genetic advance (%) was ascertained in the number of grains per panicle and plant height, demonstrating the role of additive gene action in the phenotypic expression. The assessment of such parameters aids the breeders in a better understanding of the existing variability that will ease genotypic selection for crop improvement.

Keywords: Advanced breeding lines, genetic diversity, genotypes, genes.

INTRODUCTION

Basmati rice is well known as the 'Queen of Rice and Pearl of Rice' (Sharma *et al.,* 2014). It is considered the healthiest rice one can eat and is regarded as appropriate for everyday consumption. With the augmentation of diverse food demands and living standards of global populations, there is an urgent need to intensify grain yield along with desirable nutritional quality (Peng *et al.,* 2000). Milling recovery; grain size, shape and appearance; cooking and eating qualities are the various factors that influence the grain quality of rice (Ashfaq *et al.,* 2015). Basmati rice has gained widespread acceptance in the international market due to its superior qualities, which include a strong aroma (Mehta *et al.,* 2019), long slender grains with a kernel length of 6.6mm or more and high kernel elongation after cooking (Srivastava and Jaiswal, 2013). This aromatic rice (Mondal *et al.,* 2021) has been substantially stretched and conventionally grown in the domains of the north and north-western parts of the Indian sub-continent for many centuries (Salgotra *et al.,* 2017). The exquisite top quality of Basmati rice is generated on either rim of the Indus valley in India. The

major areas of Basmati production in India include Jammu & Kashmir, Himachal Pradesh, Punjab, Haryana, Delhi, Uttarakhand and Western Uttar Pradesh (Singh *et al.,* 2018). The crop is grown under sub-tropical conditions in the Jammu division during the Kharif season, when the temperature is higher (30-35°C) at the time of sowing and slowly declines as it reaches the stage of maturity. It is generally grown in the R.S. Pura belt of Jammu and in some areas of Samba and Kathua districts. The major variety grown in Jammu and Kashmir is Ranbir Basmati, which accounts for 69% of the share of basmati acreages in the Jammu and Kashmir region (NCML, 2019). To secure food certainty in the rice-dominating countries of the sphere, those territories will have to initiate 60% additional rice along with enhanced refinement so as to meet the consumer's demand close to 2025 (Thakur *et al.,* 2014). This supplementary rice will have to be processed on less land with less water (Anbumani *et al.,* 2020), less labour and fewer chemicals. The job becomes more laborious when rice quality selection constantly encounters extra scrutiny (Pragnya *et al.,* 2018). So to mitigate a section of constraints related to rice production, researchers felt the need to investigate genetic variation in rice, which is a pre-requisite for any breeding program, as the advancement of an efficient breeding experiment relies upon the essence of its genetic diversity and trait- association.

Agro-morphological summarization of diverse germplasm forms the basis for imparting information for diverse plant breeding programmes (Sinha and Mishra, 2013). Various breeders identify and tag desirable traits within a plant's genome and subsequently manipulate the germplasm to design the parental material from which novel hybrid lines can be developed. These advanced breeding lines with diverse genetic backgrounds are thus regarded as advantageous because they contain a vast treasure of genetic elements that may be required in future crop advancement programmes (de Oliveira *et al.,* 2020). In the present span of overpopulation, ex-situ preservation is an advanced approach to maintain these lines as minor and indigent farmers who are the crucial supervisors of traditional rice varieties are more implicated in large-scale production (Shi *et al.,* 2020) than their genetic diversification. The valuation of genetic variance is salient in rice breeding, taking into account the selection and conservation outlook (Rawte and Saxena, 2018). Therefore, assessment and characterization of authentic advanced breeding lines of rice is necessary due to the rising needs for varietal enhancement (Moukoumbi *et al.,* 2011). Hence, the contemporary investigation was undertaken to characterize 29 advanced breeding genotypes of basmati rice obtained from the North-Western Himalayan regions for the purpose of providing breeders with new genetic stock to formulate effective breeding programmes for basmati rice.

MATERIALS AND METHODS

A. Plot design

A field experiment was conducted during the Kharif season 2020 at the Research Farm of the School of Biotechnology, Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Chatha, Jammu & Kashmir, India. This experimental field is located at an elevation of 332m above the mean sea level along with 32°39′N latitude and 74°58′E longitude, in addition to an annual rainfall of 1000mm, thereby defining sub-tropical conditions. The soil surface of the investigational field was clay loam in appearance and the content of organic carbon was not more than 0.50%. The temperature of the region varied from 30°C - 41°C during the course of distinct growth phases of rice, starting from the broadcasting of seeds in a nursery in mid-May to maturity stages at the end of October.

B. Plant material and data recording

The preliminary material encompassing BC_3F_5 population of 29 advanced breeding lines developed from diverse genetic backgrounds (Table 1) of basmati rice was planted during Kharif 2020 at Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Jammu & Kashmir, India to regulate an assessment. The crosses were also attempted during offseason under greenhouse conditions. The nursery was transplanted after 21 days with mature seedlings with a spacing of 20 × 15cm. The trial was laid out in a randomized block design (RBD) with three replications. A random selection of five plants was executed from each entry in every replication to record the data. The observations were recorded based on plant height, number of days to 50% flowering, panicle length, effective tillers per plant, number of days to maturity, sterility percentage, grain yield and its attributes, such as number of grains per panicle, 1000 grain weight (Ndour *et al.,* 2016).

C. Data analysis

The mean values of the data acquired were utilized for performing statistical analysis. The recorded morpho-physiological data was subjected to analysis of variance (ANOVA) (Gomez and Gomez, 1976) and the mean values were separated using Tukey's test for evaluating magnitude of genetic modifications. The estimation of genetic relationship among contrasting genotypes of rice was executed using IBM SPSS Statistics tool.

RESULTS AND DISCUSSION

A. Genetic variability

Genetic diversity is the pre-requisite for any crop improvement programme as it helps in the development of superior recombinants through the selection of parents having wider variability for different characters (Nayak *et al*., 2004). In the aforementioned research, the BC_3F_5 population, comprised of 29 advanced breeding lines of basmati rice was considered for

evaluation. The biometrical measurements were recorded to study definite morphological attributes (Dahiru, 2018). A significant amount of variation was observed for all the nine traits viz. days to 50% flowering, days to maturity, plant height, number of effective tillers per plant, panicle length, number of grains per panicle, sterility percentage, 1000 grain weight and grain yield per plant (Table 2). The revelations made under this study clearly demonstrated the existence of a plenteous amount of variation in the advanced breeding lines of basmati rice. Similarly, a distinguishable volume of variation was observed in the study conducted by Mishra *et al.* (2016).

The various components of genetic variability involving phenotypic and genotypic coefficient of variation (PCV and GCV), broad sense heritability (h^2_{bs}) and genetic advance (GA) were calculated (Table 2) for all the traits. The values registered for genotypic variance were less than those for phenotypic variance (Bhat *et al.,* 2018). The higher PCV and GCV values were observed for sterility percentage (50.61 and 49.39) and effective tillers per plant (49.59 and 49.21), whereas lower values were estimated for days to maturity (3.10 and 3.06) and days to 50% flowering (3.49 and 3.42) (Table 2). The results showed narrow differences (Table 2) between PCV and GCV values for all the nine morpho-physiological traits, thereby signifying limited environmental influence on the expression of traits. All the traits displayed a high degree of heritability i.e., 89.10% in 1000 grain weight to 99.71% in plant height (Table 2), which further indicated the relative ease of the selection process. The values of genetic advance (%) extended from 5.63% in 1000 grain weight to 68.96% in the number of grains per panicle (Table 2). A high degree of heritability coupled with high genetic advance (%) was ascertained in the number of grains per panicle along with plant height (Table 2), which specified the role of additive gene action in the phenotypic expression. In addition, these traits could also be predetermined as reliable indices by the breeders for carrying out selection processes. However, those traits that showed a high degree of heritability with lower values of genetic advance (%), suggested that their expression is under the control of non-additive gene action and that the phenotypic selection of such traits might not prove to be effective. Similar findings were reported by Shivani *et al.* (2000). Furthermore, the analysis of variance evidently revealed highly significant treatment differences for all traits which further suggested the existence of inherent genetic differences among the genotypes.

B. Tukey's test analysis

In reference to the exploration of discrete attributes in the contemporary study, the mean values evaluated in advanced breeding lines of basmati rice recorded a highly significant dataset. The dataset that incorporated the number of days to 50% flowering was arranged into ten homogeneous subsets. The values for number of days to 50% flowering were recorded subsequent to transplanting, up to the time 50% of the plants had at least a single open flower (Islam *et al.,* 2016). The data demonstrated that the low-yielding varieties such as Genotype 13, Genotype 14 (Table 1) took longer time (Table 3) to attain 50% flowering, together with delineated statistical significance against other examined genotypes. Out of all the 29 advanced breeding lines of basmati rice, most of the genotypes took maximum time (100-109 days) to achieve 50% flowering and were found to be statistically at par with each other (Table 3). The graphical data (Fig. 1a) showed that all the examined breeding lines occupied the medium category (91-110 days) to attain 50% flowering. No genotype was found to show very early or late flowering. The dataset illustrated a minimal amount of variation among the advanced breeding lines of basmati rice. The least number of days (96.067 days) (Table 3) required to obtain 50% flowering was reported in Genotype 29 (Table 1), whereas the maximum number of days (109.733 days) (Table 3) required to obtain 50% flowering was witnessed in Genotype 14 (Table 1). In a similar manner, the number of days required to maturity was enumerated by making a record of the number of days from seeding to ripening of more than 80% of the grains on the panicle (Chang and Bardenas, 1965). According to the data, the cultivars with the lowest yield attributes matured the slowest (140.067 days) (Table 3) of all the genotypes tested later. It was also seen that a few genotypes with shorter panicle length matured earlier (123.87 days) (Table 3). All the 29 advanced breeding lines that were investigated in the field occupied the medium range of attaining maturity, which stretched between 121-140 days and no genotype was seen to acquire late maturity i.e., more than 160 days (Table 3). The graphical representation (Fig. 1 b) evidently illustrated little or nearly negligible amount of variation.

The mean plant height was assessed from the tagged principal tillers of each hill (Dahiru, 2018). Among all the explored genotypes, Basmati 370 was marked with the highest plant height of 189.467cm, followed by Basmati 123 with a plant height of 179.80cm (Table 3). Additionally, Pusa 1509 accounted for the lowest plant height of 89.133cm (Table 3). It was noted that Basmati 370 and Ranbir Basmati were statistically at par with each other (Table 3). The crossed genotypes i.e. Genotype 17, Genotype 18 and Genotype 20 (Table 1) that were taken into consideration were reported with a range of maximum mean heights (Table 3) extending from 150-160cm. Out of all the 20 homogeneous subsets, clear statistical differences were observed in the mean heights of parental genotypes and crosses, as nearly all the crossed genotypes (i.e. Genotype 13-Genotype 29) (Table 1) were recorded at a height below 160cm (Table 3). Additionally, the bar charts (Fig. 1c) denoted highly significant data along with the considerable amount of variation that occurred when discrete sets of group means were compared.

Table 1: List of various rice genotypes used in the study.

Sr. No.	Genotype	Parentage
1.	Genotype 1	Jammu Basmati 123
2.	Genotype 2	Basmati 370
3.	Genotype 3	Jammu Basmati 138
4.	Genotype 4	Ranbir Basmati
5.	Genotype 5	Basmati 564
6.	Genotype 6	Pusa 1612
7.	Genotype 7	Pusa 1509
8.	Genotype 8	Punjab Basmati 3
9.	Genotype 9	Pusa 1121
10.	Genotype 10	CST-7-1/IRGC11010//AVT-1BT-2410
11.	Genotype 11	CST-7-1/IRGC11010//Pusa 44
12.	Genotype 12	CSR-36/IRGC25966//AVT-1BT-2410
13.	Genotype 13	Ranbir Basmati/CST-7-1/IRGC11010//AVT-1BT-2410
14.	Genotype 14	Ranbir Basmati/CSR-36/IRGC25966//AVT-1BT-2410
15.	Genotype 15	Ranbir Basmati/CST-7-1/IRGC11010//Pusa 44
16.	Genotype 16	Ranbir Basmati/Punjab Basmati 3
17.	Genotype 17	Jammu Basmati 123/Pusa 1612
18.	Genotype 18	Jammu Basmati/ Punjab Basmati 3
19.	Genotype 19	Basmati 564/Pusa 1509
20.	Genotype 20	Basmati 564/Pusa 1612
21.	Genotype 21	Basmati 564/Pusa 1121
22.	Genotype 22	Basmati 370/Pusa 1121
23.	Genotype 23	Basmati 370/Pusa 1509
24.	Genotype 24	Ranbir Basmati/Pusa 1612
25.	Genotype 25	Jammu Basmati 123/Pusa 1121
26.	Genotype 26	Jammu Basmati 123/Pusa 1509
27.	Genotype 27	Basmati 370/Pusa 1612
28.	Genotype 28	Jammu Basmati 138/Pusa 1612
29.	Genotype 29	Ranbir Basmati/Pusa 1509

The number of effective tillers per plant helps in determining the number of panicles in a plant which forms an essential feature of grain yield (Sholikhah *et al.,* 2019). Proportionately, yield efficiency of rice may be defined by its tillering ability, nevertheless, rice with numerous tillers could depict higher divergence in circulating assimilates as well as nutrients amongst tillers, which could eventually lead to alterations in grain maturity and yield (Feng *et al.,* 2017). The highest number of tillers was recorded in parental genotype Jammu Basmati 138 (Table 3). The graphical illustration (Fig. 1d) clearly indicated that all the crossed genotypes (Genotype 13- Genotype 29) (Table 1) encompassed lower amount of tillers per plant which varied from 10-20 in number (Table 3). Jammu Basmati 123 and Ranbir Basmati which supported preeminent number of tillers were found to be statistically at par with each other (Table 3) and illustrated high level of significance from rest of the tested genotypes.

The linear measure of the rice panicle is influenced by the quantity of grains it retains and accordingly the yield of rice is determined. Among the distinct examined genotypes, the recorded data for panicle length demonstrated that eight parental genotypes exhibited shorter panicle lengths (below 30cm) and virtually all the crossed genotypes represented longer lengths of more than 30cm (Table 3). Only a single parental genotype i.e. Punjab Basmati 3 portrayed the shortest panicle length of 25cm and Jammu Basmati 138 displayed the highest panicle length of 37.267cm (Table 3). The graphical model (Fig. 1e) which displayed the mean panicle lengths of advanced breeding genotypes of basmati rice, clearly exhibited rigorous variation along with an extremely significant amount of dataset. Several yield attributes including the number of panicles (Kumar *et al.,* 2016) per given area and proportion of filled grains per panicle had a significant impact on crop plant yield. Usually, the number of grains per panicle is set during panicle differentiation, nearly a week after the occurrence of green ring stage. Typically, 60-70 panicles/ft^2 are required to achieve favorable results. The number of grains per panicle is determined by the kind of variety and stand density. Predominantly, the majority of the varieties generate 70-100 grains per panicle; the greater the density of plant, the lower the number of grains per panicle. The interpretations from the field trials reported that a particular genotype that resulted from a cross between Basmati 370 and Pusa 1121 contained the paramount number of grains per panicle, which recorded a mean value of 200.067 grains (Table 3). The other crossed genotypes (Genotype 20, Genotype 21) (Table 1) were seen to procure closer to the maximum obtained mean value as they accumulated 163.933 and 157.467 quantities of grains per panicle (Table 3). As illustrated in the graph (Fig. 1f), out of all the 29 evaluated advanced breeding lines, four parental genotypes, specifically, Jammu Basmati 123, Basmati 370, Jammu Basmati 138 and Ranbir Basmati, fixed in the same subset, proved to be highly significant in

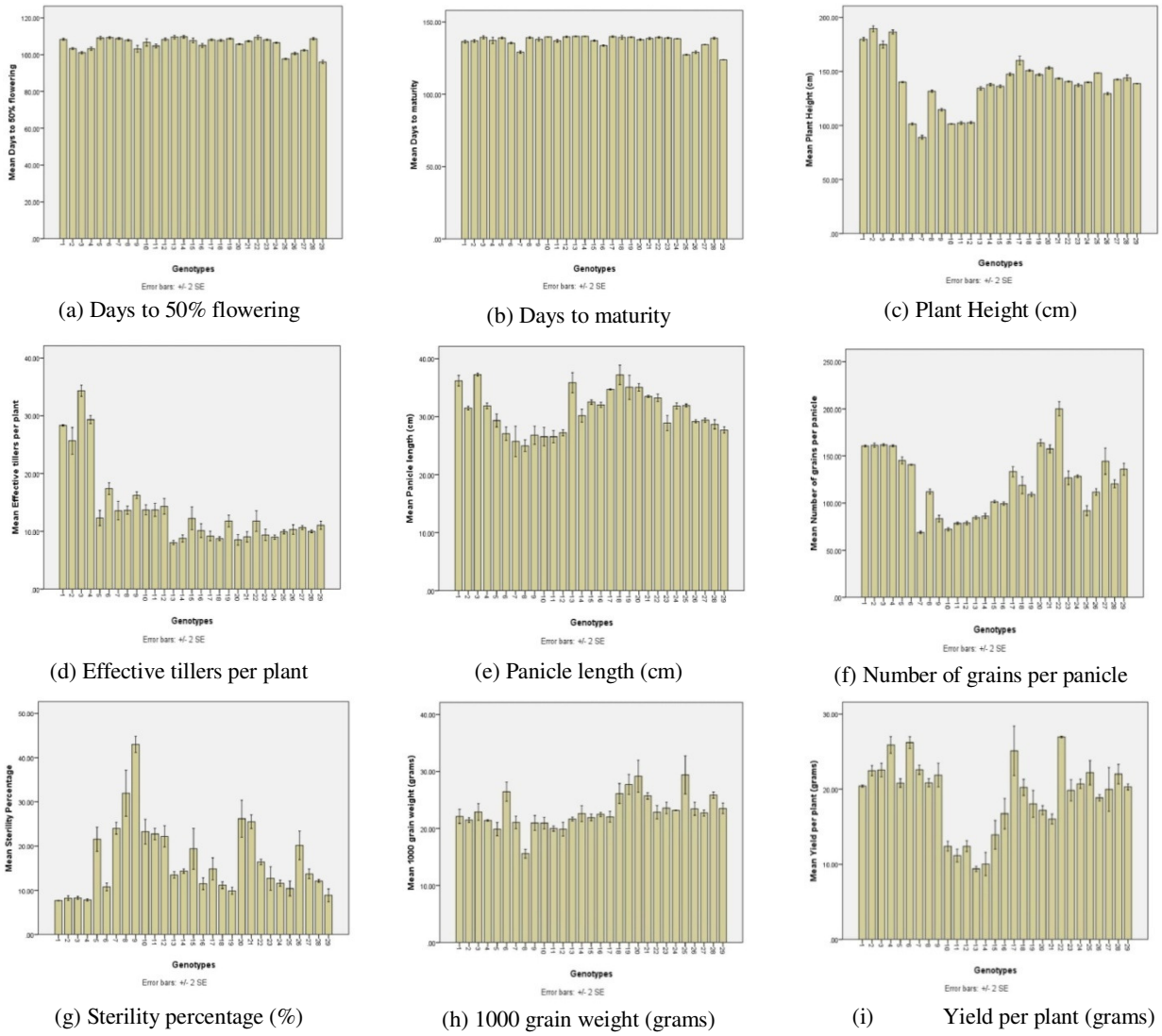
relation to other genotypes. The parental genotype (Pusa 1509) with the lowest plant height (89.133cm) also accounted for the lowest (69) number of grains per panicle on an average (Table 3). All the leftover genotypes occupied the medium range of 90-150 grains per panicle (Table 3).

Empty grains could also arise as a result of cold temperature during pollen formation. Other factors that might have minimized the proportion of filled grains include nutrient supply (excess of nitrogen); army of worms feeding on developing grains; growing environmental conditions or the genotype (Salgotra, *et al.,* 2012; Karki *et al.,* 2018). The field examination revealed that the parental genotype Pusa 1121 which accounted for a menial amount of grains per panicle was reported with the highest sterility percentage, whereas Jammu Basmati 123 reckoned with a substantial quantity of grains per panicle was marked with the lowest percentage of sterility (Table 3).

Table 2: Analysis of variance for nine morpho-physiological traits.

Traits Genetic Parameters	Days to 50% flowering	Days to maturity	Plant Height (cm)	Effective tillers per plant	Panicle length (cm)	Number of grains per panicle	Sterility percentage (%)	1000 grain weight (grams)	Yield per plant (grams)
Mean sum of square	39.906**	52.944**	1881.724**	141.017**	39.956**	3472.003**	206.985**	26.296**	69.208**
GCV (%)	3.42	3.06	17.94	49.21	11.67	27.82	49.39	12.62	24.80
PCV (%)	3.49	3.10	17.97	49.59	11.99	27.99	50.61	13.37	25.38
h^2 (%)	96.03	97.51	99.71	98.49	94.75	98.77	95.26	89.10	95.48
GA (%)	7.32	8.47	51.13	13.87	7.20	68.96	16.52	5.63	9.55

**Significant at ≤ 0.01 level



(a) Days to 50% flowering (b) Days to maturity (c) Plant Height (cm)

(d) Effective tillers per plant (e) Panicle length (cm) (f) Number of grains per panicle

(g) Sterility percentage (%) (h) 1000 grain weight (grams) (i) Yield per plant (grams)

Fig. 1. Bar charts representing mean values pertaining to various agronomic traits in advanced breeding lines of basmati rice.

Table 3: Tukey's Post-Hoc Test depicting differences of means among the nine morphophysiological traits.

Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Effective tillers per plant	Panicle length (cm)	Number of grains per panicle	Sterility percentage (%)	1000 grain weight (g)	Yield per plant (g)
Genotype 1	108.333^{ghij}	136.40^{fg}	179.800^{s}	28.333^{j}	36.200^{lm}	160.533^{l}	7.677^{a}	22.14^{bc}	20.420^{ghi}
Genotype 2	103.333^{cd}	136.867^{fgh}	189.467^{t}	25.667^{i}	31.467^{ghi}	161.400^{l}	8.220^{ab}	21.487^{bc}	22.467^{ij}
Genotype 3	101.67^{b}	139.333^{klm}	174.867^{r}	34.333^{k}	37.267^{m}	161.800^{l}	8.283^{ab}	22.903^{bcd}	22.560^{ij}
Genotype 4	103.267^{cd}	137.20^{fghij}	186.467^{t}	29.333^{j}	31.867^{hi}	160.733^{l}	7.837^{a}	21.407^{bc}	25.907^{k}
Genotype 5	109.067^{ij}	138.933^{ijklm}	140.133^{hij}	12.333^{def}	29.333^{efg}	145.200^{k}	21.557^{hi}	19.890^{b}	20.827^{ghi}
Genotype 6	109.267^{ij}	135.467^{ef}	101.467^{b}	17.400^{h}	27.067^{abcde}	140.600^{jk}	10.77^{abcd}	26.463^{g}	26.213^{k}
Genotype 7	108.80^{hij}	129.133^{c}	89.133^{a}	13.600^{ef}	25.733^{ab}	69.000^{a}	24.030^{hi}	21.067^{bc}	22.587^{ij}
Genotype 8	107.867^{ghij}	139.133^{jklm}	131.733^{de}	13.667^{ef}	25.000^{a}	112.200^{fg}	31.923^{j}	15.593^{a}	20.867^{ghi}
Genotype 9	103.133^{cd}	138.00^{ghijkl}	114.567^{c}	16.267^{gh}	26.800^{abcd}	83.467^{bc}	42.990^{k}	20.967^{bc}	21.880^{hi}
Genotype 10	106.667^{efgh}	139.667^{klm}	101.467^{b}	13.733^{ef}	26.567^{abc}	72.200^{a}	23.270^{hi}	20.953^{bc}	12.413^{bc}
Genotype 11	104.733^{de}	136.933^{fgh}	102.333^{b}	13.733^{ef}	26.567^{abc}	78.600^{ab}	22.733^{hi}	20.00^{b}	11.167^{abc}
Genotype 12	108.333^{ghij}	139.733^{klm}	102.733^{b}	14.333^{fg}	27.233^{abcde}	78.800^{ab}	22.183^{hi}	19.880^{b}	12.413^{bc}
Genotype 13	109.533^{ij}	140.067^{m}	134.400^{ef}	8.067^{a}	35.867^{lm}	84.667^{bc}	13.477^{bcde}	21.667^{bc}	9.393^{a}
Genotype 14	109.733^{j}	140.067^{m}	137.900^{fgh}	8.800^{ab}	30.180^{fgh}	86.267^{bc}	14.340^{cde}	22.60^{bc}	10.033^{ab}
Genotype 15	107.667^{fghij}	137.00^{fghi}	136.267^{fg}	12.267^{def}	32.520^{hij}	101.533^{de}	19.380^{fgh}	21.933^{bc}	13.920^{cd}
Genotype 16	105.00^{de}	133.667^{d}	147.400^{mn}	10.133^{abcd}	32.053^{hi}	99.467^{de}	11.493^{abcde}	22.467^{bc}	16.740^{e}
Genotype 17	108.133^{ghij}	139.867^{lm}	160.200^{q}	9.200^{ab}	34.720^{jkl}	133.333^{ij}	14.837^{def}	22.067^{bc}	25.113^{jk}
Genotype 18	107.80^{ghij}	139.333^{klm}	150.933^{op}	8.733^{ab}	37.220^{m}	119.000^{fgh}	11.173^{abcde}	26.133^{fg}	20.240^{ghi}
Genotype 19	108.733^{hij}	139.467^{klm}	146.933^{lmn}	11.800^{cde}	35.073^{klm}	109.200^{ef}	9.867^{abcd}	27.733^{gh}	18.053^{efg}
Genotype 20	105.667^{ef}	137.733^{ghijk}	153.267^{p}	8.533^{ab}	35.053^{klm}	163.933^{l}	26.187^{i}	29.20^{h}	17.213^{ef}
Genotype 21	107.333^{fghi}	138.60^{hijklm}	143.533^{jkl}	9.067^{ab}	33.493^{ijk}	157.467^{l}	25.510^{i}	25.733^{defg}	16.027^{de}
Genotype 22	109.40^{ij}	139.333^{klm}	140.600^{hijk}	11.800^{cde}	33.247^{ijk}	200.067^{m}	16.400^{efg}	22.867^{bcd}	26.973^{k}
Genotype 23	108.133^{ghij}	138.933^{ijklm}	137.367^{fgh}	9.400^{abc}	28.913^{cdef}	126.733^{hi}	12.687^{abcde}	23.600^{cdef}	19.853^{fghi}
Genotype 24	106.467^{efg}	138.34^{hijklm}	139.967^{ghij}	9.000^{ab}	31.853^{hi}	128.467^{hi}	11.59^{abcde}	23.20^{cde}	20.720^{ghi}
Genotype 25	97.667^{a}	127.267^{b}	148.487^{no}	9.933^{abcd}	31.953^{hi}	91.933^{cd}	10.407^{abcd}	29.400^{h}	22.207^{i}
Genotype 26	100.60^{b}	129.067^{c}	129.467^{d}	10.333^{abcd}	29.207^{defg}	111.733^{fg}	20.163^{gh}	23.467^{cdef}	18.860^{efgh}
Genotype 27	102.40^{bc}	134.333^{de}	142.533^{ijk}	10.667^{bcd}	29.400^{efg}	144.333^{k}	13.727^{bcde}	22.733^{bc}	19.967^{fghi}
Genotype 28	108.667^{hij}	138.73^{hijklm}	144.120^{klm}	10.00^{abcd}	28.680^{cdef}	120.467^{gh}	12.110^{abcde}	25.867^{efg}	22.020^{i}
Genotype 29	96.067^{a}	123.867^{a}	138.940^{ghi}	11.067^{bcd}	27.713^{bcde}	136.000^{ijk}	8.843^{abc}	23.533^{cdef}	20.313^{ghi}
SEM (±)	0.425	0.386	0.780	0.486	0.491	2.186	1.061	0.586	0.599
F-value$_{0.05}$	73.618^{**}	118.554^{**}	1031.306^{**}	198.699^{**}	55.208^{**}	242.226^{**}	61.331^{**}	25.534^{**}	64.400^{**}

** Significant at 1% level by Tukey test

Mean values followed by the same letters in the superscript are not significantly different by Tukey's test (N=3)

**Significant at ≤ 0.01 level, *Significant at ≤ 0.05 level, Not significant (NS) at > 0.05

As visualized through graphical illustration (Fig. 1g), nearly all the crossed genotypes outlined the lower proportions of sterility (below 20%), which consequently revealed significant amount of variation amongst the diverse genotypes. Test weight is considered one of the major yield computing attributes of rice. It is utilized as a supplemental criterion for varietal characterization. Various factors that influenced the yield of a crop included soil fertility, availability of water, climate, diseases/pests; plant, water and soil nutrient management (Vishwakarma, 2015). In this study, all the evaluated genotypes were seen to be stretched from a span of medium to high grain weight (Table 3). Among the assessed advanced breeding genotypes of rice, the maximum 1000 grain weight was noted in Genotype 25 (Table 1) (29.4g) (Table 3) and Genotype 21 (Table 1) (29.2g) (Table 3). Out of all the explored genotypes, eleven of them, (Genotype 1, Genotype 2, Genotype 4, Genotype 7, Genotype 9, Genotype 10, Genotype 13, Genotype 14, Genotype 15, Genotype 16, and Genotype 17) (Table 1) disclosed a test weight of 20-22g within eight subsets, which thereby depicted statistical similarity with each other (Table 3). The graphical representation (Fig.1h) apparently showed that all the genotypes illustrated their test weight ranging from 20-30g and none of them attained extremely high or low 1000 grain weight (Table 3). The advanced breeding line (Genotype 22) (Table 1) which compassed the highest number of grains per panicle depicted the maximal (26.973g) (Table 3) amount of yield per plant and exhibited a clear correlation between the number of grains per panicle and yield of a plant. The lowest (9.393g) (Table 3) paddy yield was acclaimed in Genotype 13 (Table 1). Among the parental genotypes of basmati rice, the greater yield performance was detected in three genotypes, namely, Basmati 370 (22.467g), Jammu Basmati 138 (22.56g) and Pusa 1509 (22.587g) and these genotypes were ascertained to be statistically at par with each other (Table 3). Furthermore, the two genotypes (Genotype 17 and Genotype 22) (Table 1) which were upraised towards higher grain yield showed significant results with respect to the contrasting ones. The graphical representation (Fig. 1i) evidently portrayed variation amidst distinct advanced breeding lines of basmati rice and clearly illustrated few genotypes which possessed the mean grain yield below 20g. Moreover, as documented in Singh *et al.* (2017);

Bordoloi *et al.* (2021) the data pertained to grain yield also differed significantly in different varieties of basmati rice.

CONCLUSION

The universal reliability on basmati rice in virtue of its special characteristics has led to the expansion of multitudinous genotypes with huge genetic and morphological diversification. Therefore, since modern breeding has consequently deduced advanced breeding genotypes of basmati rice due to extensive selection, the tested genotypes in the present study exhibited highly significant results, revealing a substantial amount of genetic variability in the basmati advanced breeding genotypes. High values of heritability together with genetic advance (%) were determined for the number of grains per panicle and plant height, demonstrating their effectiveness for continuous selection.

Phenotypic evaluation of the breeding population is a salient feature to distinguish vigorous lines for incorporation into *future* breeding programs. Hence, the identification of extremely diversified genotypes can provide a relevant framework to breeders for substantially broadening the potency of selections in various plant breeding programs. In the future, the potential genotypes can be released as varieties or be used as genetic stock for use in basmati breeding programmes.

Acknowledgement. We would like to thank the School of Biotechnology of Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Chatha, Jammu & Kashmir in providing financial assistance along with the other facilities for successful execution of this work.

Conflict of Interest. None.

REFERENCES

Anbumani, S., Selvakumar, S. and Thirukumaran, K. (2020). Mechanized transplanting in system of rice intensification and its evaluation. *International Journal of Chemical Studies, 8*(2): 2301–2305.

Ashfaq, M., Haider, M. S., Saleem, I., Ali, M., Ali, A. & Chohan, S. A. (2015). Basmati–Rice a Class Apart (A review). *Journal Rice Research, 03*(04).

Bordoloi, D., Sarma, D., Barua, N. S. & Das, B. K. (2021). Morphological, Biochemical and Molecular Characterization of Indigenous Aromatic Rice of Assam. *Research Square,* pp. 1–19.

Bhat, R., Singh, A.K., Salgotra, R.K., Sharma, M., Bagati, S., Hangloo, S., Bhat, M. I. J., Sharma, S. K. and Mushtaq, M. (2018). Statistical description, genetic variability, heritability and genetic advance assessment for various agronomical traits in F_2 population of rice (*Oryza sativa* L.). *Journal of Pharmacognosy & Phytochemistry, 7*(3): 985-992.

Chang, T. & Bardenas, E. A. (1965). The Morphology and Varietal Characteristics of The Rice Plant. *Technical Bulletin 4, IRRI, PHL*, 40.

Dahiru, T. M. (2018). Comparative Analysis on the Cropping System of Rice Intensification and Traditional Method of Rice Production in Mubi North, Adamawa State, Nigeria. *International Journal of Innovative Agriculture & Biology Research, 1*: 8–12.

de Oliveira, G. P., Lobo, F., de, A. and Rodríguez Ortíz, C. E. (2020). Genetic and morphological characterization of traditional rice and bean varieties from the pantanal of Mato Grosso, Brazil. *Bioscience Journal, 36*(6): 1975–1983.

Feng, X., Wang, C., Nan, J., Zhang, X., Wang, R., Jiang, G., Yuan, Q. and Lin, S. (2017). Updating the elite rice variety Kongyu 131 by improving the Gn1a locus. *Rice, 10*(1): 1–11.

Gomez, A. & Gomez, A. (2018). Statistical Procedures for Agricultural Research. *An International Rice Research Institute Book,* 6.

Islam, M. Z., Khalequzzaman, M., Bashar, M. K., Ivy, N. A., Haque, M. M. and Mian, M. A. K. (2016). Variability Assessment of Aromatic and Fine Rice Germplasm in Bangladesh based on Quantitative Traits. *The Scientific World Journal,* pp. 1-14.

Karki, S., Poudel, N. S., Bhusal, G., Simkhada, S., Regmi, B. R., Adhikari, B. & Poudel, S. (2018). Growth parameter and yield attributes of rice (*Oryza sativa*) as influenced by different combination of nitrogen sources. *World Journal of Agricultural Research, 6*(2): 58–64.

Kumar, R., Kumawat, N., Kumar, S., Kumar, R., Kumar, M., Sah, R. P., Kumar, U. & Kumar, A. (2016). Direct seeded rice: research strategies and opportunities for water and weed management. *Journal on Rice, 53*(4).

Mehta, D. S., Dhillon, B. S. & Dhillon, S. S. (2019). Performance of Basmati Rice (*Oryza sativa* L.) under Different Transplanting Dates and Plant Spacings in South West Punjab. *International Journal of Current Microbiology & Applied Sciences, 8*(07): 2016–2020.

Mishra, A., Kumar, P., Sengar, R. S., Kumar, P., Singh, R., Chaudhary, R., Kumar, A. & Fatima, P. (2016). Assessment of diversity by using morphological, biochemical and molecular approaches of selected basmati rice (*Oryza sativa* L.) varieties. *Journal of Applied & Natural Science, 8*(1): 69–76.

Mondal, D., Kantamraju, P., Jha, S., Sundarrao, G. S., Bhowmik, A., Chakdar, H., Mandal, S., Sahana, N., Roy, B., Bhattacharya, P. M., Chowdhury, A. K. & Choudhury, A. (2021). Evaluation of indigenous aromatic rice cultivars from sub-Himalayan Terai region of India for nutritional attributes and blast resistance. *Scientific Reports, 11*(1): 1–25.

Moukoumbi, Y., Sié, M., Vodouhe, R., N'dri, B., Toulou, B., Ogunbayo, S. & Ahanchede, A. (2011). Assessing phenotypic diversity of interspecific rice varieties using agro-morphological characterization. *Journal of Plant Breeding & Crop Science, 3*(5): 74–86.

Nayak, A.R., Chaudhury, D. & Reddy, J. N. (2004). Genetic divergence in scented rice. *Oryza, 41*: 79-82.

Ndour, D., Diouf, D., Bimpong, I. K., Sow, A., Kanfany, G. & Manneh, B. (2016). Agro-morphological evaluation of rice (*Oryza sativa* L.) for seasonal adaptation in the Sahelian environment. *Agronomy, 6*(1).

NCML, Gurugram, (2019), Basmati Crop Survey Report. *Basmati Export Development Foundation, APEDA, New Delhi*, *1*.

Peng, S., Laza, R. C., Visperas, R. M., Sanico, A. L., Cassman, K. G. and Khush, G. S. (2000). Grain yield of rice cultivars and lines developed in the Philippines since 1966. *Crop Science, 40*(2): 307–314.

Pragnya, K., Radha Krishna, K. V. Subba Rao, L. V. and Suneetha, K. (2018). Studies on Morphological Characterization in Soft Rice (*Oryza sativa* L.) Genotypes. *International Journal of Current Microbiology & Applied Science, 7*(5): 1348–1374.

Rawte, S. & Saxena, R. R. (2018). Morphological Characterization of Selected Rice (*Oryza sativa* L.) from Core Germplasm Group of Chhattisgarh Using DUS Descriptors. *International Journal of Current Microbiology & Applied Science, 7*(10): 350–357.

Salgotra, R. K. Bhat, J. A. Gupta, B. B. and Sharma, S. (2017). Characterization of Indian basmati rice (*Oryza sativa* L.) germplasm collected from NW Himalayas using agro-morphometric markers. *Research Journal of Biotechnology, 12*(8): 44–55.

Salgotra, R. K., Gupta, B. B. and Ahmed, M. I. (2012). Characterization of thermo-sensitive genic male sterility (TGMS) rice genotypes (*Oryza sativa* L.) at different altitudes. *Australian Journal of Crop Science, 6*(6):957-962.

Salgotra, R. K., Gupta, B. B., Sood, M. & Raina, M. (2018). Morphological and grain quality analysis of basmati rice (*Oryza sativa* L.) under different systems in north-west plains of Himalayas. *Electronic Journal of Plant Breeding, 9*(3): 1146–1156.

Sharma, R., Gangwar, K. R., Vivek, Y. & Kumar, R. (2014). Response of Basmati Rice (*Oryza Sativa*) Cultivars To Graded Nitrogen Levels Under Transplanted Condition. *Impact Journals, 2*(9): 33–38.

Shi, Z., Chang, T. G., Chen, F., Zhao, H., Song, Q., Wang, M., Wang, Y., Zhou, Z., Wang, C., Zhou, S. C., Wang, B., Chen, G. and Zhu, X. G. (2020). Morphological and physiological factors contributing to early vigor in the elite rice cultivar 9, 311. *Scientific Reports, 10*(1): 1–15.

Shivani, D., and Sreerama, R. N. (2000). Variability and heritability and genetic Advance for morphological and physiological in certain rice hybrids. *Oryza, 37*(3): 231-233.

Sholikhah, U., Parjanto Handoyo, T. and Yunus, A. (2019). Morphological characters of several black and aromatic rice (*Oryza sativa* L.) in Indonesia. *AIP Conference Proceedings*.

Singh, M., Yadav, D. B., Kumar, N., Kakraliya, S. K. and Khedwal, R. S. (2017). Performance of Different Basmati Rice on Phenology, Growth and Quality under Different Nitrogen Scheduling as Dry DSR Sown Condition in IGP. *International Journal of Current Microbiology & Applied Sciences, 6*(3): 73–80.

Singh, V., Singh, A. K., Mohapatra, T. S.G. K. and Ellur, R. K. (2018). Pusa Basmati 1121 – a rice variety with exceptional kernel elongation and volume expansion after cooking. *Rice, 11*: 19, 1-10.

Sinha, A. K. and Mishra, P. K. (2013). Agro-morphological characterization and morphology based genetic diversity analysis of landraces of rice variety (*Oryza sativa* L.) of Bankura district of West Bengal. *International Journal of Current Research, 5*(10): 2764–2769.

Srisvastava, A. K. and Jaiswal, H. K. (2013). Grain Characteristics and Cooking Quality of Indigenous Aromatic and Non-Aromatic Genotypes of Rice (*Oryza sativa* L.). *International Journal of Scientific Research and Reviews, 2* (1): 36–41.

Thakur, A. K., Singh, R. and Kumar, A. (2014). The Science behind the System of Rice Intensification (SRI). *Research Bulletin 69, Directorate of Water Management (ICAR),* 58.

Vishwakarma, A. (2015). Effect of date of transplanting and age of seedling on growth, yield and quality of rice (*Oryza sativa* L.) hybrids under system of rice intensification. *Banaras Hindu University, Varanasi*, *125004* (341385).

How to cite this article: Johar, P.; Salgotra, R. K.; Sharma, M. K.; Sharma, S.; Dey, T.; Gupta, M. and Raina, T. K. (2021). Characterization of Advanced Breeding (BC_3F_5) Lines of Basmati Rice (*Oryza sativa* L.) Under North-Western Himalayan Conditions. *Biological Forum – An International Journal*, *13*(4): 1033-1040.