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## Development and characterization of backcross inbred line population for yield attributing and grain quality traits in rice (*Oryza sativa* L.)

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### Abstract

Marker assisted backcross breeding strategy was applied to develop and characterize a backcross inbred line (BIL) population for yield attributing and quality traits in rice (*Oryza sativa* L.). Significant variability was found for number of effective tillers, panicle length, amylose content, protein content, grain width, thousand grain weight, grain length, days to 50% flowering, days to maturity and plant height. Therefore, the BIL population developed could serve as an important genomic resources for identification of QTLs for agronomically important traits, their introgression into other genetic backgrounds as well as identification of novel breeding lines.

**Keywords:** Marker, backcross inbred line, yield, quality, rice

### Introduction

Rice (*Oryza sativa* L.), belonging to the family Gramineae or Poaceae, is one of the most important food crops. More than 90 percent of rice is produced and consumed in Asia, India and China being the lead producers. As the global population is rapidly increasing, the world population is expected to reach nine billion till the middle of this century, therefore, the grain yield of rice needs to be increased by 70 percent, in order to feed the increasing global population (Zeng *et al.*, 2017) <sup>[1]</sup>. India produced 124.37 million tonnes of milled rice from about 43.7 million ha of land area in the year 2020-21 (Anonymous, 2022) <sup>[2]</sup>. To achieve the targeted levels of production, rice grain yield needs to be increased for food security. Rice grain quality improvement has also become very crucial for most of the breeding programmes around the world through improvement in associated grain nutritional quality (GQ) traits. Mapping of quantitative trait loci (QTLs) for grain quality traits in rice is a forward genetic approach in marker-assisted selection and also for gene discovery (Balakrishnan *et al.*, 2020) <sup>[3]</sup>. Backcross inbred line (BIL) population is preferable among various mapping populations because it represents a useful genetic resource for QTL detection of complex agronomic traits in plants; and can also identify naturally occurring favourable alleles in the wild species. Backcross inbred lines (BILs) represent chromosomal segments of donor parent introgressed into the recipient parent, with maximum recurrent parent genome coverage, thereby, providing a base to create a novel germplasm for breeding programmes (Jeuken *et al.*, 2004) <sup>[4]</sup>. The population has also been used for introgression of genes to improve quantitative traits in exotic germplasm (Li *et al.*, 2020) <sup>[5]</sup>. In the present study, the backcross inbred line (BIL) population in rice has been characterized for the yield attributing and quality traits.

### Materials and Methods

#### A) Plant material

Backcross inbred population (K343\*<sup>3</sup>/RML22 X K343\*<sup>3</sup>/DHMAS) X K343 comprising of 146 lines was developed at School of Biotechnology, SKUAST-Jammu, Jammu and Kashmir (India) in the genetic background of rice variety K 343 (recurrent parent) by repetitive crossing and backcrossing with the donor parents DHMAS and RML 22 using marker-assisted backcross breeding strategy. The population had blast resistance genes *Pi54* and *Pi9* introgressed, respectively from DHMAS and RML22 varieties.

#### B) Plot design and data recording

The plant material was grown in the nursery for 21 days and then transplanted in the Experimental Field at a spacing of 20 x15 cm in augmented design II with four blocks and

three parents repeated as checks in each block. A total of 5 plants were randomly chosen from each line to record the data. The observations were recorded based on plant height, days to 50 percent flowering, panicle length, effective tillers per plant, number of days to maturity, grain length, grain width and thousand grain weight. The protein content was estimated using Kjeldhal method (McKenzie and Wallace., 1954) [6] and amylose content by iodine assay index method (Hall and Johnson, 1966) [7].

### C) Data analysis

The means values obtained from the data were used for statistical analysis using R software. The analysis of variance was then performed as per Gomez and Gomez (1976) [8].

### Results and Discussion

Genetic variability is an important pre-requisite in developing superior recombinants as it helps in selection of parents showing wider variability for different characters (Nayak *et al.*, 2004) [8]. In the present study, highly significant variation was recorded in the population for all the traits viz. plant height, days to 50 percent flowering, days to maturity, effective tillers per plant, panicle length, grain length, grain width, thousand grain weight, protein content and amylose content (Table 1 and Table 2). Kiran (2020) [10] also found significant variability between the parents, K343, DHMAS and RML22 and the BC<sub>2</sub>F<sub>1</sub> population for yield attributing, and quality traits in rice (*Oryza sativa* L.).

Plant height was found to have a wide variability for the 146 genotypes of BIL population with range of 120 cm -132.6 cm and mean value of 128.24 cm. Plant height in majority of genotypes was recorded between 129.8 cm to 131.2 cm as shown in Fig. 1. A wide range (88.92 -93.72) was observed for days to 50 percent flowering with mean value of 89.85, and maximum genotypes in the population had 89.88 to 90.84 days to 50 percent flowering. Days to maturity ranged from 125.6 -135.6 with mean value of 130.21, and majority of genotypes took 131.2 to 131.6 days to reach maturity (Fig. 1). Among 146 genotypes, 65 genotypes had panicle length of 21.2 cm to 22.5 cm, while the population had minimum and maximum value of 19.9 cm and 23.8 cm and mean value of 21.05 cm. The effective tillers per plant in the population ranged from 8 to 12.5, with mean value of 10.14 (Fig. 1).

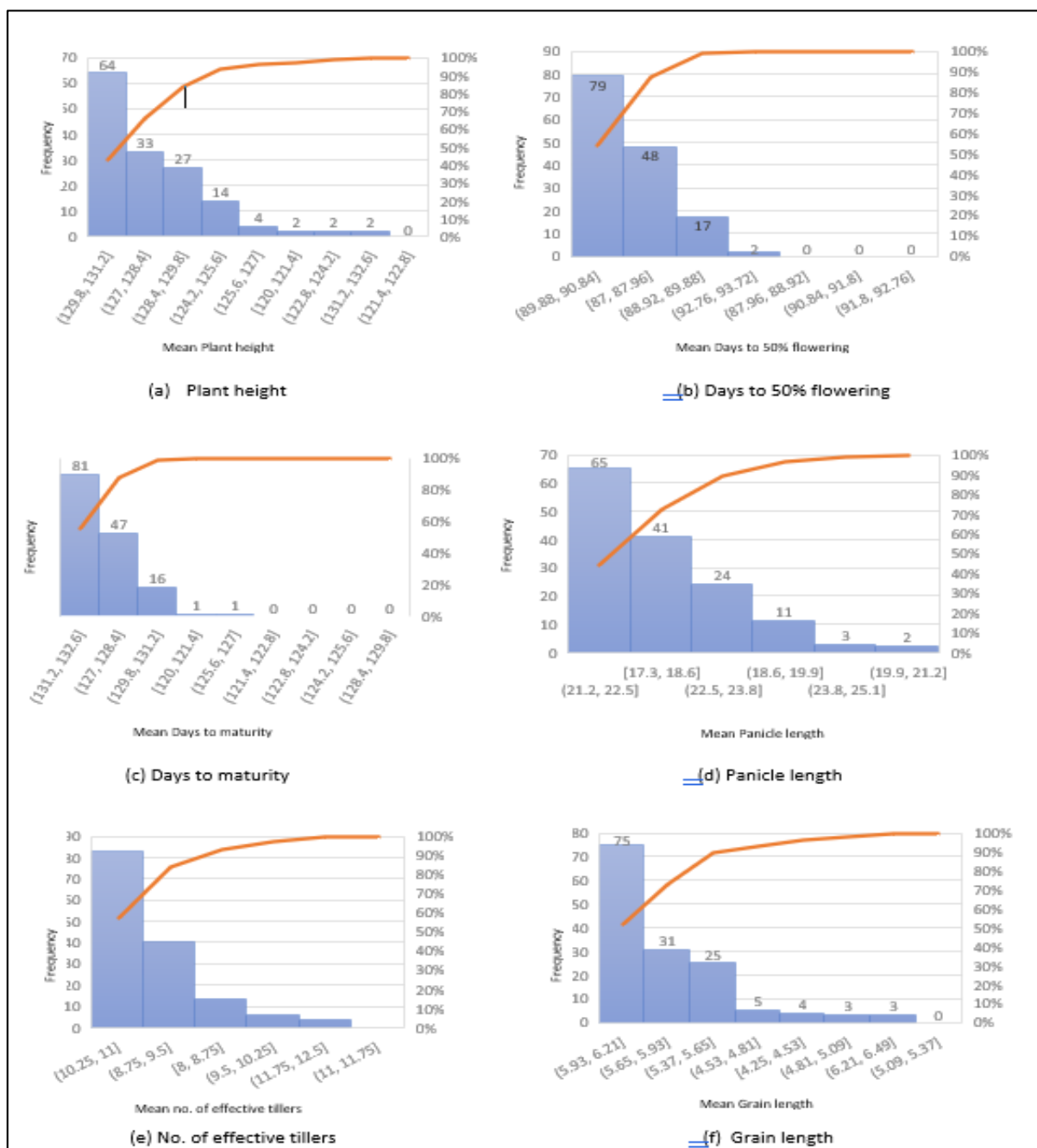
These results were similar to findings of Bhat *et al.* (2022) [10] who explained significant variability in the mapping population derived from K343 and DHMAS for grain yield and its attributing traits. Shashidhara *et al.* (2017) [12] explained that the mean values of all the genotypes showed significant variability for all the studied traits. Pachauri *et al.* (2017) [13] also reported wide variability with high range (5-26) and mean of 8.20 for effective tillers per plant, and high range (86-130) for days to maturity for 124 rice germplasm accessions. Similarly, a wide variability was also recorded by Mishra *et al.* (2016) [14] in their study. Rice grain was classified as extra-long (>7.5mm), long (6.6mm-7.5mm), medium (5.6 mm-6.5mm), and short (<5.6mm) (Bisne *et al.*, 2006) [15]. The 146 genotypes of BIL population had grain length ranging from 4.25 mm (short) to 6.49 mm (medium) with mean value of 5.84 mm, however, majority of genotypes covered medium grain length from 5.93 mm to 6.21 mm (Fig. 2). The grain width of genotypes of BIL population ranged from 1.92 mm to 2.48 mm, with mean value of 2.44 mm, while the thousand grain weight of the population was recorded from 25.10 g to 28.85 g, with mean value of 26.81 g. Johar *et al.* (2021) [16] also found significant differences for grain yield and its attributing traits in their study. The findings were also matched the results reported by Hangloo (2018) [17] who showed significant differences in the populations derived from crosses between K343 and DHMAS as well as K343 and RML22. The amylose content, and protein content are the main attributes for grain quality of the rice (Bruno *et al.*, 2017) [18]. In the present study, protein content of majority of genotypes ranged from 7.02 percent to 7.65 percent, while the population had maximum and minimum value of 5.21 percent and 7.65 percent with mean value of 6.86 percent. The amylose content of milled rice was classified into waxy (1-2 percent), very low (5-12 percent), low (12-20 percent), intermediate (20-25 percent) and high (more than 25 percent). The amylose content of the genotypes was considered very low ranging from 9 percent to 11.64 percent, while the amylose content in maximum genotypes was recorded from 10.98 percent to 11.64 percent with mean value of 10.82 percent (Fig. 2). The maximum and minimum values of grain quality traits had been found similar with the findings of Kiran (2020) [10].

**Table 1:** Analysis of variance of genotypes for BIL population (BC<sub>3</sub>F<sub>2</sub>-convergent population) for yield attributing and grain quality traits

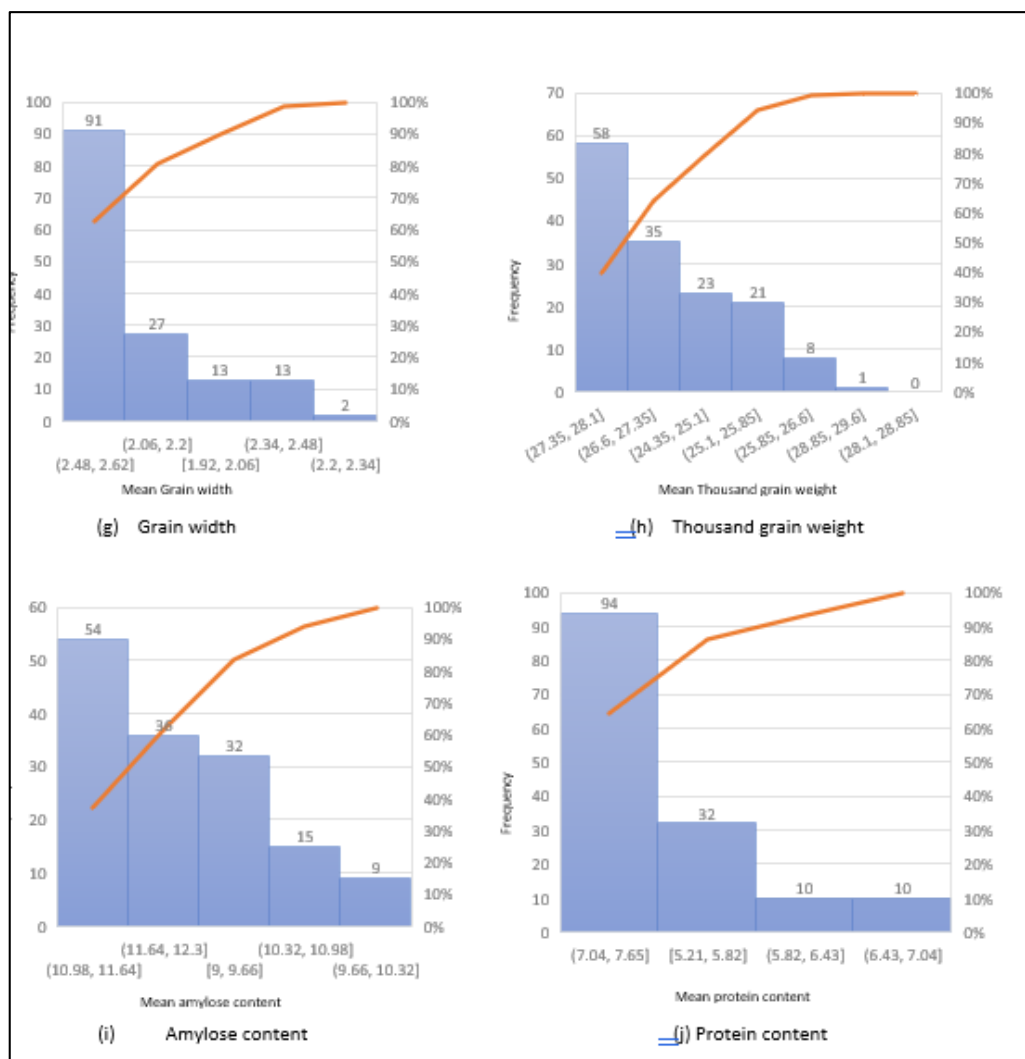
Source	Degree of freedom	Plant height (cm)	Days to 50% flowering	Days to maturity	Panicle length (cm)	No. of effective tillers	Grain length (mm)	Grain width (mm)	1000 grain weight	Protein content (%)	Amylose content (%)
Block (ignoring Treatments)	3	2.22 **	2.73 **	7.42 **	7.09 **	1 **	0.1 **	0.08 **	2.3 **	2.63 **	5.49 **
Treatment (eliminating Blocks)	148	6.47 **	4.79 **	6.11 **	4.93 **	1.65 **	0.06 **	0.03 **	1.26 **	0.87 **	1.15 **
Treatment: Check	2	72.33 **	81.33 **	16 **	16.33 **	17.33 **	1.32 **	0.38 **	13.79 **	6.25 **	2.33 **
Treatment: Test and Test vs. Check	146	5.57 **	3.74 **	5.98 **	4.77 **	1.43 **	0.05 **	0.03 **	1.09 **	0.79 **	1.13 **
Residuals	6	0.007	0.02	0.07	0.001	0.004	0.002	0.008	0.004	0.002	0.006

**Table 2:** Descriptive statistics of 149 genotypes of BIL population (BC<sub>3</sub>F<sub>2</sub>-convergent population) of rice (*Oryza sativa* L.)

Trait	Mean	Std. Error	CD (1%)	CV (%)
Plant height	128.24	0.24	0.11	2.33
Days to maturity	130.21	0.19	0.34	1.82
Days to 50% flowering	89.85	0.24	0.18	3.31
Panicle length	21.05	0.18	0.04	10.54
Number of effective tillers	10.14	0.10	0.08	11.83
Grain length	5.84	0.03	0.05	6.67
Grain width	2.44	0.02	0.11	10.24
Thousand grain weight	26.81	0.12	0.08	5.52
Protein content	6.86	0.09	0.05	11.73
Amylose content	10.82	0.09	0.10	11.18



**Fig 1:** Graph representing mean values of yield attributing traits of BIL (population) of rice



**Fig 2:** Graph representing mean values of yield attributing and quality traits of BIL population of rice.

## Conclusion

The BIL population developed would serve as an important genomic resource for identification of QTLs for agronomically important traits and their introgression into other genetic backgrounds. A thorough characterization of BIL population may lead to the identification of novel breeding lines.

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