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RESEARCH ARTICLE

Evaluation of Common Bean (*Phaseolus vulgaris* L.) Germplasm for Agro-Morphological and Yield Traits and Resistance to Bean Common Mosaic Virus (BCMV) in Western Himalayan Kashmir

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Kashmir Himalayas abounds in bean genetic resources with adaptive capacity and better quality. In the present study 110 common bean germplasm accessions were evaluated between 2019-2021 for yield traits as well as for BCMV resistance. BCMV is the most common and most destructive disease of beans and can cause a yield loss as high as 100%. Substantial variability was recorded in the material as depicted by broad range and high GCV, PCV and heritability and significant mean squares in ANOVA. Five accessions recorded stable resistance to BCMV while as 11 accessions were moderately resistant. Several genotypes were identified as novel sources of traits in respect of plant architecture, pod and seed traits as well as overall yielding ability. Promising genotypes identified for BCMV resistance as well as other traits of economic importance can be used as stable donors for improving common bean yield and BCMV resistance for sustainable bean farming in the region.

Key Words: BCMV, Common bean, Genetic resources, Resistance, Western Himalayas

Introduction

Common bean (*Phaseolus vulgaris* L.) also called as French bean or Rajmash is an important summer season legume and is an indispensable component of subsistence farming, thus involving low input marginal farmers. There is increasing evidence coming up about the livelihood and health benefits of this crop making it very popular among the farmers due to its quality, nutritional balance and higher biological efficiency. It is an important source of carbohydrate (61.4 %), proteins (17.5-28.5%) and minerals (3.2-5.0%), as well as vitamin C and pro-vitamin A. Besides it contains substantial amount of dietary fiber and minerals like Iron, Potassium, Phosphorus, Magnesium, Copper etc. In India, it is mainly cultivated by the small and marginal hill farmers of Western Himalayan states of Himachal Pradesh, Jammu & Kashmir and Uttarakhand over an area of about 26.75 thousand hectares (Anonymous, 2020). The UT of Jammu and Kashmir (33°17′-37° 20′ N latitude, 73°25′-80°30′ E longitude) harbours great variation in the in common bean genetic resources primarily in the form of traditional landraces and farmers varieties. There is a need to undertake in-depth characterization of the available genetic diversity of common bean to identify trait specific sources that can be used to develop varieties for yield, quality and resilience.

The productivity of common bean is constrained by various intrinsic (pertaining to biology and metabolism) and extrinsic (pertaining to management, climate change, diseases, pest and abiotic stresses) factors. Legumes are invariably low yielding on account of protein energy compensation and energy shifts towards nitrogen fixation. It is also implicated by various biotic and abiotic factors such as diseases, pests, drought, heat and cold stress. Bean Common Mosaic Virus (BCMV) severely affects common bean yield to the extent of complete crop failures and as such demand immediate breeding attention for development of resistant varieties. Collins *et al.* (2019) reported that BCMV is the most common and most destructive and can cause a yield loss as high as 100%. BCMV has been a global bean constraint and is reported from all bean growing areas and has persisted on account of its seed transmission and as such occurs in mild or severe form depending upon the cultivar and environmental conditions.

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BCMV known as Bean Virus-1 or Phaseolus Virus-1 is found in almost all common bean growing areas of the world largely due to its seed-borne nature (Drijfhout 1978; Mckem *et al*., 1992). In India, the occurrence of BCMV was reported for the first time by Yaraguntaiah and Nariani (1963). BCMV infects five major families including *Leguminoceae, Amaranthaceae, Chenopodiaceae, Solanaceae* and *Tetragoniaceae* (Bos and Gibbs, 1995). BCMV causes a variety of symptom pattern and severity depending upon strain, host variety, temperature, management conditions and population of transmitting vectors. There is an urgent need to identify common bean varieties that combine productivity with resilience. The varieties released thus far have not exhibited enough resilience against BCMV and as such there is an urgent need to screen the available common bean germplasm and identify lines that can be promoted as varieties or used as parents in breeding programmes aimed at achieving sustainable BCMV resistance. The conventional field and greenhouse based screening protocols can be combined with molecular tools to identify QTLs/ genes governing BCMV resistance.

In Western Himalayan states of J&K, Himachal Pradesh and Uttarakhand BCMV occurs in mild or severe forms. The major races identified have been NL1, NL1n, NL7 and NL7n (Kapil *et al.,* 2011; Hamid *et al.,* 2016). The varieties released thus far both at state level as well as under AICRP MULLaRP have not exhibited enough resilience against BCMV. Rigorous filed and greenhouse screening coupled with molecular tools can help identify QTLs/ genes governing BCMV resistance. The present study was aimed at characterizing a core set of common bean representing diverse market classes for phenological and yield traits, besides screening the set against BCMV resistance response across multiple environments under field and greenhouse conditions.

Materials and Methods

Plant material: The Plant material used for the present study comprised of a set of 110 diverse genotypes of common bean including 5 checks (Shalimar Rajmash-1, Shalimar Rajmash-2, Shalimar French Bean-1, Arka Anoop, Arka Sharath (Fig. 1). The planting material was from diverse sources representing a variety of growth habits, use categories and seed and pod variants, comprising both local landraces and exotic genotypes. It represented major market classes such as small seeded red, large kidney red, yellow, white navy, white great northern beans, black beans and chocolate beans. Among the checks Shalimar Rajmash-1, Shalimar Rajmash-2 and Shalimar French Bean-1 are varieties released by SKUAST-K, Arka Anoop and Arka Sharath are varieties released by IIHR-Bangalore.

Experimental site: The experimental plant material was planted at four environments between 2019-2021, including four different locations of Kashmir (Fig. 2), besides under greenhouse conditions. The environments were:

Environment-1 (E4 2020 and E5 2021): Research field of Division of Genetics and Plant Breeding FoA Wadura (34^{o} 17′ N and 74^{o} 33′ E at an altitude of 1594 masl). The soil of the experimental site at Wadura is a typical inceptisol with clay loam texture.

Environment-2 (E1 2019): Dryland Agricultural Research Station, Rangreth (33^{o} 98’ N and 74^{o} 79’ E at an altitude of 1640 masl). The soil is an inceptisol with silty clay texture

Environment-3 (E2 2020): KVK Ganderbal, Shuhama. The site is located at an altitude of 1588 masl (34^{o} 12’ N and 74^{o} 46’E). The soil is an alfisol with clay loam soil.

Environment-4 (E3 2020): Farmer’s field at Saloora. The site is located at an altitude of 1619 masl (34^{o} 12’ N and 74^{o} 46’E) with clay loam soil.

Environment-5 (E6 2020): Greenhouse FoA Wadura. The soil mix was derived from the research field of the Faculty with addition of sand and vermicompost to ensure better growth.

Experimental design: The experiment was set up in an augmented block design (Federer, 1956).The design comprised of five (5) blocks, each containing twenty one (21) test genotypes and five (5) checks. Thus in each block there were 26 entries. The checks in each block were randomly allocated for estimation of error as well as standard errors of comparison.

Data recording on agronomic traits: In order to study the magnitude of variability for yield and its contributing traits among 110 lines, data was recorded for 10 agro-morphological traits at Research field of Division of Genetics and Plant Breeding FoA Wadura. The traits were days to flowering, days to maturity, plant height, number of pods per plant, pod length, seeds per pod, seed length, seed breadth, 100-seed weight and seed yield per plant.

Field and greenhouse screening of genotypes for BCMV

resistance: For screening BCMV resistance response, common bean genotypes were screened against bean common mosaic virus at 3 weekly stages beginning from 25 days after emergence stage. Screening was done in the open field trials at three locations *viz*., FoA Wadura, KVK Ganderbal, and Farmer's field at Saloora and scored as per scale developed by Horsfall and Barrat (1945) and Drijfout (1978) and the genotypes were grouped into various response classes by scale developed by CIAT (Mills and Silbernagel, 1992).

Under greenhouse screening, the leaves at trifoliate stage were inoculated by sap method as proposed by Kelly *et al.* (1995) by extracting the sap from plants showing BCMV symptoms by macerating symptomatic leaves with a mortar and pestle in cold phosphate buffer, pH 7.0 for stabilizing the inoculum. The primary leaves were inoculated using conventional leaf rub method following abrasion. The inoculum was maintained on ice until the inoculation process was completed. The plants were monitored for 15 days and evaluated for symptomatic variation using the 1-9 scale given by Mills and Silbernagel (1992). 1-2 Resistant; 3-4 moderately resistant; 5-6 moderately susceptible; 7 Susceptible; 8-9 Highly susceptible.

The leaves were critically observed for the established symptoms of BCMV such as mosaic, stunting, curling, discoloration and chlorosis. The observed results were further validated by leaf observations against sunlight as well as under microscope to identify chlorotic patches. The per cent disease incidence (PDI) of BCMV was estimated for each accessions based on data obtained from each seasons at two locations and the final mean of PDI was calculated based on average PDI mean of five seasons and across the location. The per cent disease incidences of BCMV for each accession were computed by using the formula given below.

Statistical analysis: The mean data from first experiment was analyzed for estimation of basic statistics and analysis of variance (ANOVA) for assessing variation according to the expected value of mean square as described by Federer (1956) and Federer and Searle (1976). The analysis of augmented design was carried out by SPAD (Statiscal package for augmented design) platform developed by IASRI (Rathore *et al*., 2004). The genetic variability components estimated were phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), broad sense heritability (h^2), expected genetic advance (GA) and expected genetic advance as percent of mean (GAM) (Burton and Devane, 1953). Phenotypic and genotypic coefficients of variation (PCV and GCV) for each trait were computed as PCV = $\{\sqrt{\sigma^2 P}/\text{ mean}\} \text{ x } 100$, GCV = $\{\sqrt{\sigma^2 G}/\text{ mean}\} \text{ x } 100$ as per (Burton 1952). Heritability was estimated as $h^2 = \{\sigma^2 G/\sigma^2 P\} \text{ x } 100$ as per method of Lush (1940) and further classified into low, medium and high (Robinson 1966). Genetic advance as percent of mean was estimated as GA= $k \text{ x } h^2 \text{ x } \sigma P$ as per Johnson *et al.* (1955). The standard value of k at 5 % selection intensity is taken as 2.06. Homogeneity of variance was tested before statistical analysis on the adjusted pooled means as per procedure of Levene (1960). Principal components (PC) were computed to determine the patterns of variation and the genetic relationship existing between accessions in the collection using XLSTAT Version 2021.4 (Addinsoft Inc.).

Results and Discussion

Variability for agro-morphological traits

Plant height: Plant height ranged widely as the genotypes characterized comprised both determinate bush and indeterminate pole types (Table 1). The mean plant height was 68.13cm with the minimum and maximum values of 36.70 cm and 213.00 cm respectively. Genotypes such as WB-923, Arka Komal WB-352, KDFB-38, WB-1441 were having smaller plant height (< 40 cm), whereas genotypes WB-1282, WB-222, GL-1, WB-451 were taller in height (>150 cm).

Days to flowering and maturity: Among phenological traits, the mean value recorded for days to flowering (Table 1) was 43.62 days with lowest value recorded for genotypes WB-662, WB-1319, WB-1249, WB-651 (37 days) followed by WB-662, WB-1644, N-2, N-4, WB-185, WB-923 (38 days) whereas the genotypes WB-1518, WB-1455, WB-901, WB-206, Arka Komal, WB-252, WB-1282, WB-451, WB-1189, WB-222 were late in flowering (53 days). Days to maturity also had a broad range with a few genotypes such as WB-222, GL-1 and GL-2 as late maturing. The mean value recorded was 81.03 days with lowest value recorded for WB-1319, WB-651, WB-923 (68 days) followed by WB-662, WB-1634, N-1, N-4, WB-185, WB-923, SFB-1 (73 days) whereas the genotypes GL-1, GL-2, WB-222 matured in 99 days.

Similar results in common bean have been reported under Himalayan conditions in earlier studies of Rana *et al.* (2015), Iram Saba *et al.* (2017), Rani Shama (2019) and Sofi *et al.* (2020). The lower variation range in

Table 1. Variability parameters for 10 quantitative traits in common bean

Trait	Mean	Min	Max	PCV	GCV	Heritability	Genetic advance (% of mean)
DF	43.62	36.00	58.00	10.82	10.05	0.86	19.17
DM	81.03	68.00	99.00	13.88	13.06	0.88	25.16
PH (cm)	68.13	36.70	213.00	25.12	23.18	0.89	46.06
NPP	14.40	4.80	47.66	24.46	24.76	0.92	46.36
PL (cm)	11.26	9.10	17.33	9.08	7.91	0.83	15.52
SPP	4.63	3.00	7.34	17.67	15.75	0.77	28.03
SL (mm)	12.60	7.83	17.42	8.56	7.18	0.75	13.23
SB (mm)	7.38	4.57	9.74	7.27	5.09	0.67	10.03
100SW (g)	33.55	15.75	55.72	14.76	14.39	0.98	29.80
SYPP (g)	22.27	19.56	89.54	21.15	19.77	0.79	34.42

DF=days to flowering, DM=days to maturity, PH= plant height, NPP= number of pods/plant, PL= pod length, SPP= seeds per pod, SL= seed length, SB= seed breadth, 100SW= 100-seed weight, SYPP=seed yield per plant

Table 2. Analysis of augmented design for morphological, maturity and yield traits in 110 genotypes of common bean

Trait	df	DF	DM	PH	NPP	PL	SPP	SL	SB	100SW	SYPP
Block	4	9.63**	12.11	53.12**	52.08**	3.81*	0.36*	0.02	0.01	5.46 *	27.74
Among Genotypes	109	22.30**	126.54**	16016.91**	86.11**	9.08 **	0.67**	0.04**	0.03**	177.63**	111.18**
Among Test entries	104	60.27**	466.72**	260.11**	79.29**	8.76**	8.50**	0.04**	0.05**	209.09**	142.85**
Among Checks	4	24.15**	10.95**	16422.51**	373.38**	5.26**	0.61**	0.06**	0.01**	236.60**	57.58**
Test entries v/s checks	1	87.12**	10.23	54451.13**	278.65**	98.23**	0.82**	0.06**	0.01**	119.51**	75.44**
Error	16	3.09	14.56	17.26	6.80	1.49	0.15	0.02	0.02	2.05	23.30

DF=days to flowering, DM=days to maturity, PH= plant height, NPP= number of pods/plant, PL= pod length, SPP= seeds per pod, SL= seed length, SB= seed breadth, 100SW= 100-seed weight, SYPP=seed yield per plant

Fig. 1. Diversity in common bean germplasm under evaluation

maturity traits is due to the fact that farmer's preference for short duration varieties has driven selection for early maturity. However the indeterminate types are more preferable under maize based intercropping systems and are invariably late in maturity. The estimates of PCV, GCV, heritability and genetic advance (% of mean) were higher for plant height followed by days to maturity and days to flowering. The heritability estimates were 0.89, 0.88 and 0.86 respectively for these traits.

Pod traits: The mean value recorded for number of pods per plant was 14.40 with highest value recorded in WB-864 (47.66) followed by WB-371 (40.30), WB-1634 (33.10) and WB-341 (29.20) whereas the lowest value was recorded for KDFB-38 (4.80). Similarly, the mean value recorded for pod length was 11.26 cm with highest pod length recorded for WB-195 (17.33) followed by N-7 (15.10 cm), WB-970 (13.90 cm), WB-923 and WB-966 (13.40 cm each) whereas the lowest value was recorded for WB-651 (9.10 cm) and KDFB-38 (9.10 cm). The mean value recorded for seeds per pod was 4.63with highest value recorded for WB-371 (7.34) followed by N-1 (6.12) and WB-1634 (5.26) whereas the lowest value was recorded for WB-6 and N-5 (3.00). The estimates of PCV, GCV and genetic advance (% of mean) were higher for number of pods per plant followed by seeds per pod and pod length. The heritability estimates were 0.92, 0.77 and 0.83 respectively for these traits (Table 1). Similar results have been reported for pod traits under Kashmir conditions by Sofi *et al.* (2014), Iram Saba *et al.* (2017), Rani Shama (2019), Asmat Ara (2019) and Sofi *et al.* (2020). Since common bean pods are a favorite vegetable in Kashmir and as such, pod traits also assume importance in varietal development (Sofi *et al.,* 2020).

Seed traits: Mean value recorded for seed length was 12.60 mm with highest value recorded for WB-1441 (17.42 mm) followed by WB-832 (17.32 mm) and WB-966 (17.10 mm) whereas the lowest value was recorded for WB-435 (9.08 mm). The seed breadth was also substantially variable, with mean value of 7.38 mm. The highest value for seed breadth was recorded for WB-1249 (9.47 mm) followed by WB-966 (8.97 mm) and WB-970 (8.91 mm) whereas the lowest value was recorded for WB-603 (4.72 mm). For 100-seed weight, the mean value recorded was 33.55 g with highest value recorded for WB-6 (55.72 g) followed by WB-967 (55.00 g) and WB-966 (54.60 g) whereas the lowest value was recorded for GL-3 (14.76 g) . Seed yield per plant was also highly variable with broad range. The mean value recorded was 22.27 g with highest value recorded for N-1 (89.54 g) followed by N-4 (79.14.00g) and WB-1634 (68.27 g) whereas the lowest value was recorded for KDFB-38 (19.56 g). The estimates of PCV, GCV and genetic advance (% of mean) were higher for seed yield per plant and low for seed length and seed breadth (Table 1). The heritability estimates for these traits were 0.98 (100-seed weight) followed by seed yield per plant (0.79), seed length (0.75) and seed breadth (0.67). Similar results have been reported for seed traits under Kashmir conditions by Sofi *et al.* (2014), Iram Saba *et al.* (2017), Choudhary *et al.,* 2018, Asmat Ara (2019). Sofi *et al.* (2020) also reported high heritability estimates for seed traits ranging from 76.69 % for seeds per pod to as high as 98.36 % for 100-seed weight. The smaller difference between the GCV and the PCV, with GCV invariably smaller than PCV indicates that the observed variation and expression of traits is mainly due to genetic factors while larger difference in case of traits like seed length and seed breadth indicate the greater role of the environment. Higher heritability for most of the traits indicated that these traits may be governed by additive genes and use of simple selection methods may bring significant improvement.

In the present study 105 test entries along with 5 checks were evaluated in an augmented block design for agro-morphological and yield traits. The analysis of variance revealed that the net block effect (after eliminating treatment effect) was non-significant for days to maturity, seed length, seed breadth and seed yield per plant. The mean square due to genotype effect (after eliminating block effect), test entries as well as checks was significant for all the 10 traits studied. The test genotype effect was significant for days to flowering, days to maturity, days to mid pod fill, and days to pod fill and non-significant for days to pod set (Table 2). The mean square due to test vs. check comparison was significant for all the traits except days to maturity. The substantial variability in the material as indicated by significant mean sum of squares for genotypes, test entries as well as checks can be effectively utilized for development of varieties in various use category classes (such as dry, snap and shelled) based on maturity, pod and seed characters. Substantial variability in common bean germplasm comprising both local landraces and material from national and international gene banks has been reported in Western Himalayan conditions by

Fig. 2. Representative range of BCMV symptoms recorded in the field

Rana *et al.* (2015), Iram Saba *et al.* (2017), Choudhary *et al.* (2018), Rani Shama (2019) and Sofi *et al.* (2020). Pod and seed traits have also been reported to be highly heritable traits (Nienhuis and Singh, 1988, Sofi *et al.,* 2014, Langat *et al.,* 2019) and as such there is ample scope for improvement using appropriate selection strategies in target environments.

Identification of novel trait sources for plant architecture, maturity and yield components: Despite the fact that major focus of present study was on assessment of variability for phenological and yield traits and screening bean germplasm for BCMV resistance, nevertheless, an attempt was made to identify novel trait sources for phenological and yield traits. Out of the 110 germplasm lines that were evaluated across locations, many novel trait specific genotypes were identified (Supplementary Fig. 2) based on early maturity (WB-923, WB-662, WB-956, SFB-1, N-4, WB-1319, N-2 and WB-1455), pod length (N-7, WB-970, WB-195, WB-956), number of pods per plant (WB-864, WB-371, WB-1634), seeds per pod (WB-371, WB-901, WB-451, N-7, WB-258, WB-1282), 100-seed weight (WB-6, WB-257, WB-216, WB-967, WB-1439, N-7, WB-1492), pod shattering resistance (WB-216,WB-1129, WB-1006, WB-46 and WB-206), stay green (WB-216), erect plant type (N-1). There is an urgent need to identify common bean genotypes with novel trait combinations that improve their fitness in farming systems as well as combine productivity with resilience and quality. This requires in-depth characterization of natural variation in available genetic diversity for productivity and water stress adaptive traits. Already a large number of accessions are collected and conserved in gene banks that need to be characterized in depth. In national gene bank (NBPGR), a total of 172 accessions of bean germplasm from Jammu and Kashmir are conserved. (Source: pgrportal.nbpgr.ernet.in).

The trait-specific germplasm is highly imperative for genetic enhancement of crop varieties for various traits. In the present study various unique germplasm for specific traits Identified hold a great promise in improving common bean crop in the region. More importantly, the BCMV resistant genotypes that were identified in the present study could be used as stable sources of resistance as the genotypes have exhibited resistance response under diverse screening environments. The early maturing genotypes which mature within 70-75 DAS could play an important role in sustaining dry bean production as the early maturity will be an important motivation for farmers to bring more area under bean cultivation. Some of the highly productive pole type lines could be utilized for maize-bean intercropping that is prevalent in Western Himalayan region. Overall a few genotypes had combined advantage of higher yield and BCMV resistance including N-1, WB-1634, and WB-1129.

Symptom spectrum of BCMV under field conditions: Bean common mosaic virus causes a variety of symptom pattern and severity depending upon strain, host variety, temperature and management conditions as well as population of transmitting vectors. In the present study, a variety of diverse symptoms ranging from complete death of the plant to varied degree of mosaic, leaf discoloration, leaf chlorosis, yellowing, leaf crinkling, puckering were observed (Fig. 2).

Vectors recorded under field conditions: BCMV is laterally transmitted through viruleferous aphids (Hampton, 1975; Morales and Castaño, 1987). Various viruliferous aphids such as bean aphid (*Aphis fabeae*), Pea aphid (*Acyrthosiphon pisum*) and green peach aphid (*Myzus persiceae*) can transmit BCMV and increase infection upto 100% (Galvez and Morales, 1989). However, the aphids transmit the virus in a non-persistent manner. In the present study two aphid species were recorded under field conditions at FOA Wadura that might have a possible role in horizontal transmission of BCMV that needs to be investigated further. However, green peach aphid (*Myzus persiceae*) was not recorded under field conditions.

Mean reaction pattern of common bean genotypes to BCMV across four screening environments: Pooled across environments (filed as well as green house) the phenotypic screening of 110 common bean genotypes against BCMV resistance (Supplementary Table 1) revealed that out of 110 genotypes screened, only five genotypes (less than 5%) genotypes namely WB-1129, WB-216, WB-206, N-10 and WB-45 were resistant, 11 genotypes (10%) namely N1, WB-1691, WB-916, WB-765, WB-1131, WB-1680, WB-1256, Arka Anup, WB-1710, WB-1634, WB-373 were moderately resistant, 62 genotypes (56%) were moderately susceptible, 29 genotypes (26%) were susceptible and three genotypes (less than 3%) genotypes namely N-2, SR-1 and WB-1698 were highly susceptible with BCMV score of >8 (Supplementary Table 1 and Table 4).

Earlier various studies have been undertaken in western Himalayan conditions for screening common bean reaction to BCMV. In Himachal Pradesh, Sharma *et al.* (2006) evaluated ninety four common bean accessions comprising of landraces, exotic collections and recommended cultivars against three strain groups (I, IV, VI) of BCMV and reported two exotic varieties TopCrop and Amanda highly resistant to all the three strain groups. Sharma *et al.* (2008) screened a larger core set of 397 common bean accessions of diverse origin revealing the presence of effective sources of resistance against bean common mosaic potyvirus strains prevalent in Himachal Pradesh; 21accessions *viz*., KR 7, KR 225, KR 295, KRC 4, KRC7, KRC 11, KRC 12, KRC 13, KRC 16, KRC 22, Amanda, Black Turtle Soup, Contender, Hans, Great Northern UI 123, Improved Tender Green 40031, Jubila, Kentucky wonder, Monroe, Premier and Sanilac were found resistant to NL-1n and NL-7n strains. In Western Himalayan Kashmir, local and exotic common bean genotypes have also been screened earlier BCMV resistance based on field and greenhouse evaluations. Wani *et al.* (2017) and Rani Shama (2019) revealed various resistant lines (WB-399, WB-640, WB-359, WB-375, WB-494, WB-933, WB-939 and also WB-335) were found phenotypically resistant. The result was later ascertained by molecular analysis by using different microsatellite markers. Rani Shama (2019) had also identified genotypes WB-206, WB-1129, WB-642 and Arka Komal) as resistant. The present study has thus validated the resistance response of various genotypes such as WB-1129, WB-206, WB-642 and Arka Komal as well as the susceptible response of genotypes SR-1, KDFB-37, WB-1187, WB-1644, WB-662, WB-1446, WB-435, and WB-482 reported earlier.

Conclusion

In the UT of J&K, a large diversity of beans largely in form of landraces is grown. These landraces have evolved under natural and farmer-driven selection process and are locally very well adapted. In terms of varietal output, three varieties namely Shalimar Rajmash-1 and Shalimar Rajmash-2 (dry beans) and Shalimar French Bean-1 (Snap) have been released by

Table 4. Status of reaction of 110 common bean genotypes against BCMV in filed screening

Reaction type	Genotypes	Number of genotypes
Resistant	WB-206, WB-1129, WB-216, N-10, WB-45	5
Moderately Resistant	N-1, WB-1691, WB-916, WB-765, WB-1131, WB-1680, WB-1256, Arka Anup, WB-1710, WB-1634, WB-373	11
Moderately susceptible	WB-6, WB-22, WB-92, WB-112, WB-185, WB-191, WB-195, WB-218, WB-371, WB-401, WB-418, WB-429, WB-451, WB-630, WB-634, WB-642, WB-643, WB-650, WB-651, WB-665, WB-716, WB-832, WB-846, WB-901, WB-955, WB-957, WB-967, WB-1006, WB-1136, WB-1137, WB-1184, WB-1185, WB-1255, WB-1274, WB-1282, WB-1310, WB-1318, WB-1436, WB-1441, WB-1446, WB-1492, WB-1496, WB-1518, WB-1554, WB-1560, WB-1574, WB-1587, WB-1643, WB-1677, WB-1678, WB-1682, N-11, N-5, N-7, N8, GLY-1, KDR-98, DARS-10, DARS-38, SR-2, SFB-1, Arka Sharat	62
Susceptible	WB-46, WB-83, WB-115, WB-333, WB-352, WB-487, WB-489, WB-565, WB-662, WB-869, WB-923, WB-956, WB-1171, WB-1182, WB-1249, WB-1319, WB-1435, WB-1437, WB-1455, WB-1485, WB-1644, N-4, GLP-1, KDFB-81, KDFD-3, KDR-63, KDR-97, DARS-10-1, DARS-43	29
Highly susceptible	N-2, SR-1 and WB-1698	3

SKUAST-Kashmir and two varieties are in pipeline. In the present study, an attempt was made to characterize a set of 110 genotypes revealing substantial variability in agro-morphological and yield traits indicating usefulness of the material for further selection. A number of genotypes with novel traits related to plant architecture, pod and seed traits have been identified. Moreover, a number of stable sources of resistance to BCMV were identified that can be used in a planned hybridization programme to combine productivity with resilience. Out of the present material several desirable lines have been already submitted to ICAR and IC numbers received that will ensure conservation and utilization of these valuable genetic resources in future rajmash breeding programmes in the country. Moreover, a large number of crosses have been developed based on this study that are at different stages and are being currently evaluated for identification of desirable segregants.

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Supplementary Table 1. Screening score of 110 common bean genotypes for resistance to BCMV across six screening environments

Genotype	2019 (E1)	2020 (E2)	2020 (E3)	2020 (E4)	2021 (E5)	2020 (E6)	Mean Score
WB-6	5.3	6.1	5.4	4.7	4.2	5.5	5.20
WB-22	6.3	4.5	7.0	6.5	4.7	7.0	6.00
WB-45	2.5	1.3	2.0	1.8	3.7	5.0	2.72
WB-46	7.9	8.0	7.3	7.2	3.5	9.0	7.15
WB-83	7.1	7.9	6.3	6.0	8.0	8.0	7.22
WB-92	7.3	7.0	7.8	7.3	4.8	7.0	6.87
WB-112	5.6	5.0	5.0	5.3	5.4	7.0	5.55
WB-115	7.3	7.6	7.5	7.0	8.3	7.0	7.45
WB-185	5.6	6.4	5.7	5.5	4.7	5.0	5.48
WB-191	5.0	4.7	5.0	5.3	8.3	5.0	5.55
WB-195	6.3	7.0	6.3	6.0	5.5	6.0	6.18
WB-206	1.8	0.5	2.0	1.7	2.0	2.0	1.67
WB-216	1.6	0.5	1.5	1.3	2.8	2.0	1.62
WB-218	5.2	5.0	4.7	5.0	6.2	6.0	5.35
WB-333	6.7	7.0	6.7	6.0	9.0	7.0	7.07
WB-352	6.8	6.5	7.5	7.3	8.8	6.0	7.15
WB-371	5.9	6.6	6.8	7.0	4.7	3.0	5.67
WB-373	4.8	4.0	5.0	5.3	5.8	5.0	4.98
WB-401	6.0	7.0	6.5	5.7	6.5	5.0	6.12
WB-418	6.5	6.6	6.0	6.5	5.8	7.0	6.40
WB-429	6.3	6.0	7.5	6.7	5.8	5.0	6.22
WB-451	6.3	6.6	6.7	6.0	5.3	6.0	6.15
WB-487	7.5	7.4	8	7.7	5.7	7.0	7.22
WB-489	7.5	7.6	7.5	8.0	4.5	7.0	7.02
WB-565	6.8	7.6	6.5	6.0	8.8	7.0	7.12
WB-630	6.2	6.6	6.3	5.8	6.1	6.0	6.17
WB-634	5.9	6.6	5.7	5.5	4.7	6.0	5.73
WB-642	6.7	6.0	6.7	7.0	6.2	7.0	6.60
WB-643	6.3	6.4	6.3	6.5	7.3	6.0	6.47
WB-650	6.8	7.0	6.7	6.3	6.5	7.0	6.72
WB-651	6.4	7.8	6.0	5.7	8.1	6.0	6.67
WB-662	7.6	7.4	7.7	7.2	6.2	8.0	7.35
WB-665	6.7	7.6	6.0	6.0	4.7	7.0	6.33
WB-716	7.0	7.5	6.7	6.7	6.8	7.0	6.95
WB-765	4.3	4.0	5.0	5.0	4.2	5.0	4.58
WB-832	6.4	6.1	6.3	6.0	1.0	7.0	5.47
WB-846	5.8	5.7	6.7	5.7	8.0	6.0	6.32
WB-869	8.0	8.0	8.0	7.0	7.8	9.0	7.97
WB-901	6.0	6.3	5.7	6.0	6.0	6.0	6.00
WB-916	4.2	5.3	4.7	5.0	4.2	4.0	4.57
WB-923	8.0	7.8	7.5	7.7	5.9	9.0	7.65
WB-955	6.7	7.0	7.0	6.7	5.7	6.0	6.52
WB-956	6.8	7.4	6.0	6.0	8.7	8.0	7.15
WB-957	7.1	7.5	6.5	6.5	5.0	8.0	6.77
WB-967	6.5	8.0	5.5	4.7	5.0	8.0	6.28
WB-1006	5.3	6.5	6.0	3.5	6.3	5.0	5.43
WB-1129	1.3	1.4	1.7	1.0	1.0	1.0	1.23

Genotype	2019 (E1)	2020 (E2)	2020 (E3)	2020 (E4)	2021 (E5)	2020 (E6)	Mean Score
WB-1131	4.6	6.6	4.5	3.2	5.8	4.0	4.78
WB-1136	4.7	6.0	4.8	4.0	7.5	4.0	5.17
WB-1137	5.5	6.0	5.3	4.8	7.0	6.0	5.77
WB-1171	7.3	7.7	6.0	7.0	6.7	8.0	7.12
WB-1182	7.2	7.8	7.0	7.0	8.7	7.0	7.45
WB-1184	6.4	7.4	5.8	5.5	5.5	7.0	6.27
WB-1185	6.4	7.6	6.5	5.5	7.0	6.0	6.50
WB-1249	7.1	7.8	6.5	6.3	8.0	8.0	7.28
WB-1255	6.9	6.5	7.0	7.0	7.2	7.0	6.93
WB-1256	5.3	4.0	5.0	5.0	5.2	5.0	4.92
WB-1274	6.6	7.0	6.3	6.0	5.8	7.0	6.45
WB-1282	6.5	6.1	7.0	7.0	5.8	6.0	6.40
WB-1310	6.6	7.0	6.3	6.0	8.2	7.0	6.85
WB-1318	6.3	7.0	6.0	6.0	6.1	6.0	6.23
WB-1319	7.4	7.9	6.8	7.0	7.0	8.0	7.35
WB-1435	7.4	7.0	7.0	8.0	7.3	8.0	7.45
WB-1436	6.0	6.0	6.0	6.0	7.0	6.0	6.17
WB-1437	7.0	7.0	6.5	6.3	7.3	8.0	7.02
WB-1441	6.9	8.0	7.0	5.7	6.2	7.0	6.80
WB-1446	6.5	7.1	6.7	5.3	7.8	7.0	6.73
WB-1455	7.1	7.8	6.3	6.5	7.3	8.0	7.17
WB-1485	7.1	7.5	6.5	6.3	7.3	8.0	7.12
WB-1492	6.2	7.3	6.5	6.0	6.8	5.0	6.30
WB-1496	5.1	5.0	5.3	6.3	7.0	4.0	5.45
WB-1518	6.1	6.5	5.7	5.3	4.7	7.0	5.88
WB-1554	6.6	7.0	6.3	6.0	6.4	7.0	6.55
WB-1560	6.6	7.6	6.0	5.7	7.4	7.0	6.72
WB-1574	6.2	7.4	5.7	5.7	7.3	6.0	6.38
WB-1587	5.6	5.5	6.7	4.7	7.3	6.0	5.97
WB-1634	5.1	6.3	4.8	4.3	4.3	5.0	4.97
WB-1643	5.7	6.1	5.7	4.0	4.0	7.0	5.42
WB-1644	6.9	8.0	6.7	5.0	7.8	8.0	7.07
WB-1677	6.0	5.8	5.7	5.5	4.5	7.0	5.75
WB-1678	6.5	6.6	6.0	6.4	8.5	7.0	6.83
WB-1680	4.6	4.3	4.3	5.0	5.8	5.0	4.83
WB-1682	6.3	6.5	6.0	5.7	5.3	7.0	6.13
WB-1691	4.7	4	5.0	4.7	2.7	5.0	4.35
WB-1698	8.0	8.0	7.3	7.7	9.0	9.0	8.17
WB-1710	4.9	4.7	5.0	5.0	5.0	5.0	4.93
N1	3.2	3.1	4.2	2.6	2.8	3.6	3.25
N10	2.1	2.7	1.8	3.0	1.0	3.0	2.27
N11	6.3	4.5	6.3	5.8	5.5	6.5	5.82
N2	7.6	8.1	7.8	7.7	8.8	8.2	8.03
N-4	7.0	7.9	6.7	6.5	8.8	7.0	7.32
N5	6.2	5.3	5.8	6.2	6.0	6.7	6.03
N7	4.7	5.6	5.2	6.1	6.0	6.1	5.62
N8	5.4	6.1	6.4	5.4	6.6	5.8	5.95

Genotype	2019 (E1)	2020 (E2)	2020 (E3)	2020 (E4)	2021 (E5)	2020 (E6)	Mean Score
GLY-1	7.1	7.4	7.0	7.0	5.7	7.0	6.87
GLP-1	8.5	6.9	7.6	8.1	8.4	8.4	7.98
KDFB-81	7.6	7.0	7.8	7.5	7.9	8.0	7.63
KDFD-3	7.6	7.9	7.7	7.7	7.4	7.0	7.55
KDR-63	7.2	7.0	8.0	7.7	9.0	6.0	7.48
KDR-97	6.9	7.0	6.7	7.0	7.5	7.0	7.02
KDR-98	6.9	7.5	6.0	6.0	6.0	8.0	6.73
DARS-10	6.7	7.8	5.8	6.3	6.8	7.0	6.73
DARS-10-1	7.4	7.5	7.7	7.5	6.9	7.0	7.33
DARS-38	6.8	6.8	6.0	6.3	7.1	8.0	6.83
DARS-43	7.2	7.6	6.7	6.3	7.3	8.0	7.18
SR-1	7.9	8.0	7.5	7.2	9.0	9.0	8.10
SR-2	6.3	7.0	6.0	5.2	7.3	7.0	6.47
SFB-1	5.4	6.3	5.0	4.3	6.1	6.0	5.52
Arka Anup	5.4	6.3	5.0	4.5	2.3	6.0	4.92
Arka Sharat	4.4	5.7	5.6	5.7	5.7	6.4	5.58

$$PDI\ (\%) = \frac{\text{Total number of infected plants per plots}}{\text{Total number of plants per plots}} \times 100$$

Supplementary Fig. 1. View of field experiments across locations and years

WB-216 (BCMV resistant)

N-1 (Erect plant type)

WB-1129 (BCMV resistant)

WB-216 (Stay green)

WB-1129 (High pod number)

WB-1634 (High pod number)

WB-1129 (Shattering resistant)

WB-662 (Early flowering)

WB-371 (High seed number)

Supplementary Fig. 2. Promising genotypes with better trait expression