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Genetic variability studies for yield and yield attributes in F₂ populations of interspecific crosses of mungbean (*Vigna radiate* (L.) Wilczek) and rice bean (*Vigna umbellata* Thunb.)

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Abstract

The natural variability available in green gram including seed yield is very limited because of its high self fertilization behavior. In order to widen the genetic base in mungbean, interspecific hybridization with closely related species is one of the means to enhance genetic variability. In the present study, interspecific hybridization between *Vigna radiata* (mungbean) and *Vigna umbellata* (rice bean) was effected under green house condition during *Kharif*-2017. The F₂ populations derived from these interspecific crosses (KKM-3 × KBR-1 and KKM-3 × RBL-6) were evaluated for yield and yield attributing traits. The genetic variability parameters *viz.*, PCV, GCV, heritability and genetic advance as *per cent* over mean were computed for ten yield attributing traits including seed yield. Significant variability existed for all the traits studied. In both the populations studied, days to 50 % flowering, days to maturity and 100 seed weight showed moderate to low PCV and GCV whereas days to 50 % flowering and days to maturity exhibited high heritability coupled with moderate to low genetic advance. The trait 100 seed weight exhibited high heritability coupled with high genetic advance. Plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod and seed yield per plant recorded high PCV, high GCV and high broad sense heritability coupled with high genetic advance.

Keywords: Interspecific hybridization, mungbean, rice bean, genetic variability and heritability

Introduction

Pulse crops are important group of food legumes which are grown in different countries of the world. They are important as a source of vegetable protein in human diet used as seeds, as feed for animals and as a component in sustainable agriculture. They fix atmospheric nitrogen in the soil and enriches the soil with N₂. Majority of the pulses can be grown in the marginal lands with low level of inputs. Since Asian diets are predominantly cereal based, the pulse protein and cereal protein complement each other and these result in much better protein utilization than the individual proteins. Pulses may surmount the rising issue of protein malnutrition which is a noteworthy nutrition problem in Asia which rigorously affects the children. Early maturity, rapid growth and easy digestibility without flatulence additionally include their incentive in different cropping systems. Pulses are grown worldwide in an area of 70.59 million hectares with a production of 61.50 million tonnes annually (Indiastat.com, 2013). In India, 29.81 million hectares area has been occupied by pulses with an annual production of 25.41 million tonnes and an average productivity level of 853 kg per hectare as compared to global productivity of 871 kg per hectare (Indiastat.com, 2018) [21]. For domestic consumption, India still depends on imports from foreign countries.

The major pulses grown in India are chickpea, pigeon pea, mungbean, blackgram, peas and lentil which contribute to the major pulse production in India. Other minor pulses which are grown in different agro-climatic regions and belongs to *Vigna* species are cowpea, horsegram, mothbean and ricebean. Among the major pulses, mungbean is one of the important pulse crops belonging to the order *Leguminosae* and family *Papilionoideae* and is botanically recognized as *Vigna radiata* (L.) Wilczek and commonly known by different names as green gram, green bean, moong, mash bean, golden gram and green soy which is also an excellent source of easily digestible protein with low flatulence which complements the staple rice diet in Asia. Mungbean seeds contain about 24 *per cent* protein which comparatively rich in lysine, the amino acid which is deficient in cereal grains. In India, mungbean is grown in an area of

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4.2 million hectares with 2.02 million tones of annual production and 477 kg/ha of productivity (Indiastat.com, 2018)^[21]. Green gram is also one of the pulses being imported in India to meet domestic requirement of pulses. Low productivity of mungbean may be due to low genetic variability available in this crop because of pollination behaviour which is highly self pollinated. In order to achieve the genetic improvement, it is very much needed to broaden the genetic base in this crop. One of the strategies to broaden the genetic base is through interspecific hybridization amongst the related species. Considering the cross compatibility for hybridization with green gram ricebean may be considered more ideal related species to take up interspecific hybridization to broaden the genetic base and for further crop improvement. In addition to cross compatibility of ricebean (*Vigna umbellata*) possess good agronomically superior traits like Mungbean Yellow Mosaic Virus (MYMV), bacterial leaf spot and bruchid resistance. Assessment of genetic variability in the derived interspecific cross populations is the prestep for selection for seed yield and yield related traits. This may also help to develop suitable plant type with genetically introgressed traits through interspecific hybridization. As the economic characters such as seed yield in mungbean are polygenetically controlled, it is necessary to partition the observed overall phenotypic variability into heritable (genetic) and non-heritable (environment) components with the help of genetic coefficient of variation and heritability. Possible genetic gain that can be made by going for selection can be done by estimating expected genetic advance. It is also very much necessary to give importance to the yield attributing characters which are relatively more heritable. Hence, the breeding material generated during the process of interspecific hybridization was used to assess the genetic variability available in the segregating population. This may aid in effective selection of genotypes with better seed yield combined with resistance to pests and diseases. Keeping these aspects in view, genetic variability studies for yield and yield attributes in F_2 populations of interspecific crosses of mungbean (*Vigna radiata* (L.) Wilczek) and rice bean (*Vigna umbellata* Thunb.) was carried out in the present study.

Material and methods

Interspecific hybridization was done by crossing between two *Vigna* species viz., *Vigna radiata* (mungbean) and *Vigna umbellata* (rice bean) which was carried out during under green house condition during *Kharif-2017* at field unit of AICRN on Potential Crops Scheme, Main Research Station, University of Agricultural Sciences, Hebbal, Bangalore. The hybridization included a green gram variety KKM-3 which is agronomically superior and well adopted variety but susceptible to MYMV which was used as female parent. Two rice bean lines KBR-1 and RBL-6 which are highly resistant to MYMV were used as male parents. F_2 seeds harvested from individual F_1 plants of respective inter specific crosses were collected separately. The F_2 evaluation was conducted without replications. The sowing was done with a spacing of 30 cm between rows and 10 cm between plants with row length of 4 meters. Each F_2 was raised with minimum of 250-300 plant population. At the time of harvest, observations were recorded on all the plants including their parents for all the ten yield and yield attributing characters such as Days to 50 % Flowering, Days to maturity, Plant height (cm), Number of branches per plant, Number of clusters per plant, Pods per

plant, Pod length (cm), Seeds per pod, 100-seed weight (g) and Seed yield per plant (g). The total variance of observations for a character in F_2 was considered as its phenotypic variance. The environmental variance for each character was estimated from the mean variance of the non-segregating parental populations from the data generated from replicated evaluation of parents. The genetic variability parameters viz., PCV, GCV, heritability and genetic advance as *per cent* over mean were computed for all the yield and yield related traits Ms excel using the appropriate formulas. Phenotypic and genotypic components of variance were computed as per the formula given by Lush (1940)^[10]. Genotypic variance and phenotypic variance was used to estimate respective co-variances (GCV and PCV) following the formula suggested by Burton and De Vane (1953)^[3]. The broad sense heritability (h^2_{bs}) was estimated by following the procedure as given by Weber and Moorthy (1952)^[21]. The predicted genetic advance was estimated according to the formula given by Johnson *et al.* (1955)^[7].

Results

The results on mean, range and genetic variability parameters obtained in Table. 1 for the population KKM-3 \times KBR-1 and Table. 2 for the population in F_2 population KKM-3 \times RBL-6. The results showed that the F_2 population of the cross KKM-3 \times KBR-1 exhibited wide and significant variation for the traits under study. Days to 50 % flowering ranged from 28 to 44 with a mean of 35.60, days to maturity ranged from 60 to 73 with a mean of 66.26, plant height ranged from 9.1 to 23.50 cm with a mean of 15.63 cm, number of branches per plant ranged from 2 to 9 with a mean of 4.47, number of clusters per plant ranged from 2.4 to 11.97 with a mean of 5.61, number of pods per plant ranged from 5.6 to 27.89 with a mean of 13.65, pod length ranged from 3.96 to 14.62 cm with a mean of 9.56 cm, number of seeds per pod ranged from 3 to 16 with a mean of 9.79. The 100 seed weight ranged from 1.31 to 3.91 g with a mean of 2.75 g and seed yield per plant ranged from 3.22 to 66.38 g with a mean of 20.12 g. Highest PCV was recorded for seed yield per plant (50.66) followed by number of branches per plant (37.97), number of pods per plant (37.92), number of clusters per plant (37.89), number of seeds per pod (26.18), pod length (22.88) and plant height (22.41). It was moderate for 100 seed weight (17.72), where as it was low for days to 50% flowering (9.69) and days to maturity (5.01). The GCV was highest for seed yield per plant (44.41) followed by number of clusters per plant (31.17), number of pods per plant (31.14), number of branches per plant (29.85), number of seeds per pod (24.53), pod length (21.66) and plant height (21.39). It was moderate for 100 seed weight (15.1). Lowest GCV was observed for days to 50 % flowering (9.17) and days to maturity (4.4). The heritability estimate was highest for plant height (91.09) followed by number of seeds per pod (87.83), days to 50 % flowering (89.64), pod length (89.59), days to maturity (77.28), seed yield per plant (76.85), 100 seed weight (72.61), number of clusters per plant (67.67), number of pods per plant (67.42) and number of branches per plant (61.78). The genetic advance as *per cent* mean was found to be highest for the traits such as seed yield per plant (80.21), number of clusters per plant (52.82), number of pods per plant (52.67), number of branches per plant (48.33), number of seeds per pod (47.36), pod length (42.23), plant height (42.05) and 100 seed weight (26.5). It was observed to be moderate for days to 50 % flowering (17.89) and low for days to maturity (7.97).

The cross KKM-3 × RBL-6 showed significant variation for all the ten quantitative traits studied. From the table 2 it can be seen that days to 50 % flowering ranged from 30 to 50 with a mean of 36.44, days to maturity ranged from 59 to 79 with a mean of 66.64, plant height ranged from 9.5 to 25 cm with a mean of 15.17 cm, number of branches per plant ranged from 2 to 8 with a mean of 4.62, number of clusters per plant ranged from 2.28 to 10.4 with a mean of 5.81, number of pods per plant ranged from 5.4 to 26.1 with a mean of 14.18, pod length ranged from 4.82 to 15.95 cm with a mean of 10.29 cm, number of seeds per pod ranged from 4 to 17 with a mean of 10.7, 100 seed weight ranged from 1.56 to 4.01 g with a mean of 2.69 g and seed yield per plant ranged from 4.33 to 74.67 g with a mean of 23.17 g. Highest PCV was recorded for seed yield per plant (49.88) followed by number of branches per plant (40.58), number of pods per plant (35.39), number of clusters per plant (34.38), number of seeds per pod (23.51), plant height (23.38) and pod length (20.94). It was moderate for 100 seed weight (18.15) and as it was low for days to 50% flowering (9.14) and days to

maturity (5.57). The GCV was highest for seed yield per plant (44.33) followed by number of branches per plant (33.85), number of pods per plant (30.77), number of clusters per plant (26.66), plant height (22.38) and number of seeds per pod (21.84). It moderate for pod length (18.92) and 100 seed weight (15.17). Lowest GCV was observed for days to 50 % flowering (8.2) and days to maturity (5.13). The heritability estimate was highest for plant height (91.62) followed by number of seeds per pod (86.3), days to maturity (84.75), pod length (81.62), days to 50 % flowering (80.49), seed yield per plant (78.98), number of pods per plant (75.57), 100 seed weight (69.85), number of branches per plant (69.61) and number of clusters per plant (60.13). The genetic advance as *per cent* mean was found to be highest for the traits such as seed yield per plant (81.16), number of branches per plant (58.18), number of pods per plant (55.1), plant height (44.12), number of clusters per plant (42.58), number of seeds per pod (41.79), pod length (35.21) and 100 seed weight (26.12). It was moderate and low for days to 50 % flowering (15.16) and days to maturity (9.72) respectively.

Table 1: Mean, range and genetic variability parameters for yield and yield attributing characters in F₂ population of interspecific cross KKM-3×KBR-1

SI. No.	Characters	Mean ±S.E.m	Range		PCV (%)	GCV (%)	h ² bs (%)	GAM
			Lowest	Highest				
1	Days to 50 % flowering	35.60±0.28	28	44	9.69	9.17	89.64	17.89
2	Days to maturity	66.26±0.27	60	73	5.01	4.4	77.28	7.97
3	Plant height (cm)	15.63±0.28	9.1	23.5	22.41	21.39	91.09	42.05
4	Number of branches per plant	4.47±0.14	2	9	37.97	29.85	61.78	48.33
5	Number of clusters per plant	5.61±0.17	2.4	11.97	37.89	31.17	67.67	52.82
6	Number of pods per plant	13.65±0.42	5.6	27.89	37.92	31.14	67.42	52.67
7	Pod length (cm)	9.56±0.18	3.96	14.62	22.88	21.66	89.59	42.23
8	Number of seeds per pod	9.79±0.21	3	16	26.18	24.53	87.83	47.36
9	100 seed weight (g)	2.75±0.04	1.31	3.91	17.72	15.1	72.61	26.5
10	Seed yield per plant (g)	4.36±0.08	1.35	5.12	46.12	40.08	71.48	75.01

Table 2: Mean, range and genetic variability parameters for yield and yield attributing characters in F₂ population of interspecific cross KKM-3×RBL-6

SI. No.	Characters	Mean ±S.E.m	Range		PCV (%)	GCV (%)	h ² bs (%)	GAM
			Lowest	Highest				
1	Days to 50 % flowering	36.44±0.26	30	50	9.14	8.2	80.49	15.16
2	Days to maturity	66.64±0.29	59	79	5.57	5.13	84.75	9.72
3	Plant height (cm)	15.17±0.28	9.5	25	23.38	22.38	91.62	44.12
4	Number of branches per plant	4.62±0.12	2	8	40.58	33.85	69.61	58.18
5	Number of clusters per plant	5.81±0.16	2.28	10.4	34.38	26.66	60.13	42.58
6	Number of pods per plant	14.18±0.39	5.4	26.1	35.39	30.77	75.57	55.1
7	Pod length (cm)	10.29±0.17	4.82	15.95	20.94	18.92	81.62	35.21
8	Number of seeds per pod	10.7±0.20	4	17	23.51	21.84	86.3	41.79
9	100 seed weight (g)	2.69±0.04	1.56	4.01	18.15	15.17	69.85	26.12
10	Seed yield per plant (g)	4.23±0.09	1.48	6.15	44.23	36.20	74.44	78.45

Discussion

Broadening of the genetic base through any means is needed when there is limited genetic variability which is essential for crop improvement (Patel *et al.*, 1998). It is important for polygenically controlled traits like seed yield. Simple biparental hybridization is usually followed for incorporation of the genes of interest through recombination, selection and stabilization. In crop like mungbean where the genetic variability is limited interspecific hybridization is one of the means for incorporation of genes of our interest. Once the hybridization is done, further steps of identification of recombinants, selection and stabilization for the gene of interest is done. At the same time the genetic variability created in the segregating material may be estimated in order

to apply the selection criteria for different polygenic traits including seed yield. In this context a preliminary estimation of the mean, range and genetic parameters in the segregation population is essential.

The results obtained on genetic in the two F₂ population of interspecific crosses revealed that days to 50 % flowering, days to maturity and 100 seed weight exhibited moderate to low values of PCV and GCV in both the F₂ populations of interspecific crosses indicating low variability for these traits. The phenotypic variation for these traits showed that relatively higher influence of environment on these characters. The results of the present study are in agreement with the earlier reports of Robinson *et al.* (1951)^[15]; Grafius (1959)^[4]; Tiwari *et al.* (1996)^[19]; Singh *et al.* (2009)^[18];

Basavaraja (2015)^[2]; Mohan (2016)^[11] and Simranjeet *et al.* (2017)^[17]. Further with respect to Days to 50 % flowering and days to maturity high heritability coupled with moderate to low genetic advance were noticed in both the F₂ populations of interspecific crosses which indicated the less influence of environment but prevalence of non additive gene action for which simple selection will be less effective. 100 seed weight exhibited high heritability coupled with high genetic advance in both the populations indicating the less influence of environment and prevalence of additive gene action, simple phenotypic selection can be done to improve this trait. Similar findings were earlier reported by Ilihamuddin *et al.* (1989)^[5]; Tiwari *et al.* (1996)^[19]; Arulbalachandran *et al.* (2010)^[1]; Basavaraja (2015)^[2]; Mohan (2016)^[11] and Simranjeet *et al.* (2017)^[17].

Plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod and seed yield per plant recorded high PCV and GCV in two F₂ populations of interspecific crosses suggesting the substantial variability in these characters and these traits are mainly under genetic control which is less influenced by the environment. These results are in agreement with the earlier reports of Ramanna and Singh (1987)^[13]; Singh *et al.* (2009)^[18]; Rahim *et al.* (2010)^[12]; Basavaraja (2015)^[2]; Mohan (2016)^[11] and Simranjeet *et al.* (2017)^[17]. All these traits exhibited high broad sense heritability coupled with high genetic advance indicating the prevalence of additive gene action in the inheritance of these traits and hence amenable for simple selection. Similar kind of results have been reported earlier by Sharma and Rathnaswamy *et al.* (1986);^[14] Lee and Lee (1987)^[9]; Tiwari *et al.* (1996)^[19]; Sharma (1999)^[16]; Singh *et al.* (2009)^[18]; Kamleshwar *et al.* (2013)^[8]; Basavaraja (2015)^[2]; Mohan (2016)^[11] and Simranje *et al.* (2017)^[17].

The present study revealed that limited genetic variability for characters such as day to 50 % flowering and days to maturity where as higher variability for Plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod and seed yield per plant which may give an idea of the direction and intensity of selection to be practiced to achieve desired recombination of traits of interest followed by the stabilization of the evaluated material.

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