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Estimation of Genetic Variability for Powdery Mildew Resistance and Yield Related Traits in $F_{2:4}$ Population in Mungbean [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

Powdery mildew is one of the serious diseases of mungbean [*Vigna radiata* (L.) Wilczek] caused by *Erysiphe polygoni* D.C. It can reduce yield of mungbean by 20 to 40 %. In this study, 101 $F_{2:4}$ families derived from the cross DGGV-2 × TARM-1 were evaluated for their response to powdery mildew under field conditions, for various yield and yield related traits and analyzed for different genetic parameters. High phenotypic coefficient of variation and genotypic coefficient of variation were observed for the characters *viz.*, seed yield, number of seeds per plant and per cent disease index. Moderate values of PCV and GCV were observed for number of pods per plant and number of seeds per pod. High heritability in broad sense of 87.35 per cent and high genetic advance over mean of 43.53 was observed for per cent disease index. Heritability in broad sense and genetic advance as per cent over mean were high for mean seed yield, number of seeds per plant, number of pods per plant and number of seeds per pod. Correlation study showed that per cent disease index (powdery mildew disease) was negatively correlated with yield and yield contributing traits.

Keywords

Erysiphe polygoni, Heritability, Mungbean, Percent disease index, Powdery mildew

Introduction

The Mungbean is esteemed among the entire pulse species because it is an excellent source of easily digestible protein with low flatulence. It is a good source of amino acids like aspartic acid, glutamic acid and fairly good source of some essential amino acids like isoleucine, leucine, lysine and phenylalanine (Lambrides and Godwin 2007). Short crop duration (60-75 days), low input requirement and high global demand make mungbean an ideal rotation crop for small land holding farmers.

The important foliar diseases which affect the production of mungbean are mungbean yellow mosaic virus (MYMV), powdery mildew and cercospora leaf spot of which powdery mildew caused by *Erysiphe polygoni* (an obligate parasite) may reduce yield of mungbean by 20 to 40 % (Fernandez and Shamugasundaram, 1987) and 100 % when it occurs at the seedling stage (Reddy *et al.*, 1994). Severe infection of powdery mildew occurs in cool-dry months. Powdery mass growth on the surface of the leaf adversely affects the photosynthetic activity of the plant which in turn reduces yield as well as its market price thus causing enormous economic loss to farmers. Disease can be controlled by use of fungicides but it increases production cost and has negative effect on environment and human health. Therefore, the most effective way to control powdery mildew is the development and use of resistant varieties for which genetic variability is the pre-requisite. Therefore in this study an attempt was made to study various genetic parameters in the segregating population derived from the cross involving parents differing for powdery mildew response.

Materials and Methods

The material for present study included 101 $F_{2:4}$ families derived from the cross DGGV-2 × TARM-1. DGGV-2 is a high yielding and popular mungbean variety released during 2012 from University of Agricultural Sciences (UAS), Dharwad, but it is highly susceptible to powdery mildew. TARM-1 was powdery mildew resistant released by Bhabha Atomic Research Centre (BARC) in 1995**.** However on screening 130 genotypes, during *kharif* and *rabi* season of 2016 at Main Agricultural Research Station (MARS), UAS, Dharwad TARM-1 showed moderate resistance to disease (Pooja, 2017). Since no other mungbean genotypes included in the study showed resistance to powdery mildew, TARM-1 was used as a resistance source to develop segregating population. For powdery mildew evaluation 101 $F_{2:4}$ families were sown in augmented design, during *rabi* season of 2017, at IABT Garden of Main Agricultural Research Station, UAS, Dharwad. In order to assess the disease incidence, double row of spreader variety *viz*., DGGV-2 was sown nearby and around the plot as an infector row. In addition, susceptible line DGGV-2 and resistant line TARM-1 were also sown as checks after every eight progeny rows for comparison. To create disease pressure artificial inoculation was done. Individual $F_{2:4}$ plants were scored for powdery mildew response under good disease pressure from the first incidence of the disease up to maturity (five weeks) using the scoring system described by Mayee and Datar, per cent disease index was calculated. Observations for various traits such as number of pods per plant, number of seeds per pod, number of seeds per plant and seed yield were recorded on five randomly selected plants in each family for quantitative characters. Estimation of phenotypic and genotypic coefficients of variation (GCV and PCV), heritability (h^2_{bs}), phenotypic correlation and genetic advance as percent over mean (GAM) were carried out for all the traits.

Results and Discussion

The percent disease index among 101 families ranged from 4.47 to 34.32 and among which sixty five families showed moderately resistant reaction to the disease, thirty one families were rated as moderately susceptible and five families were susceptible to the disease. None of the plants showed immune, resistant and highly susceptible response to the disease.

Percent disease index of DGGV-2 was 55.64 % and grouped as highly susceptible whereas TARM-1 showed a PDI of 3.42 % and categorized as moderately resistant. Normal frequency distribution was observed for all the traits studied. Number of pods per plant in 101 families ranged from 4 to 23 with the mean of 10.27, number of seeds per pod ranged from 1 to 7.8 with the mean of 5.67, number of seeds per plant ranged from 18 to 214 with the mean of 67.94 and seed yield ranged from 0.68 to 5.99 with the mean of 3.00 (Table 1).

Table.1 The genetic parameters estimated for yield and yield contributing traits in $F_{2:4}$ population

Trait	Range			%		h^2_{bs}	GA	GAM	CV (%)	C.D. @ 5%
	Mean	Min	Max	PCV	GCV					
Number of pods per plant	10.27	4	23	17.52	16.57	91.53	5.14	32.43	19.33	2.57
Number of seeds per pod	5.67	1	7.8	14.63	13.41	80.29	1.56	24.84	17.58	1.52
Number of seeds per plant	67.94	18	214	26.42	24.98	89.64	32.74	49.28	21.63	14.71
Seed yield (g)	3.00	0.68	5.99	28.63	26.5	83.98	1.48	48.52	22.53	0.87
Per cent disease index	10.92	4.47	34.32	24.19	22.61	87.35	14.1	43.53	21.28	5.09

Min: Minimum; Max: Maximum; PCV= Phenotypic co-efficient of variation; GCV= Genotypic co-efficient of variation; h^2bs= heritability (broad sense); GA= Genetic advance; GAM= Genetic advance over Mean and CV= Coefficient of variation.

Table.2 Correlation analysis for yield and yield contributing traits in $F_{2:4}$ population

Trait	Number of pods per plant	Number of seeds per pod	Number of seeds per plant	Seed yield	Per cent disease index
Number of pods per plant	1.00	0.081	0.892^{**}	0.785^{**}	-0.243^{**}
Number of seeds per pod		1.00	0.340^{**}	0.295^{**}	-0.089
Number of seeds per plant			1.00	0.914^{**}	-0.324^{**}
Seed yield				1.00	-0.155^{**}
Per cent disease index					1.00

** Significance level at 1 % and * Significance level at 5 %

Phenotypic coefficients of variation were higher than genotypic coefficients of variation for all the traits under study (Table 1) indicating the variability was not only due to genotype but also due to influence of environment on these traits. Relatively high magnitude of both PCV and GCV was recorded for the characters *viz*., seed yield, number of seeds per plant and per cent disease index. This indicates improvement is possible through selection for these traits. Number of pods per plant and number of seeds per pod were having moderate GCV and PCV values in the $F_{2:4}$ population. These results are in accordance with the results of Konda *et al.*, (2009), Singh *et al.*, (2009) and Basamma (2011).

In this study high broad sense heritability of 87.35 per cent and high genetic advance over mean of 43.53 was observed for per cent disease index (Table 1). The result indicated that resistance to powdery mildew in TARM-1 is principally governed by genetic factor(s). Similar result was reported by Kasettranan *et al.*, (2009) in recombinant inbred lines (RILs) and Chankaew *et al.*, (2013) in $F_{2:4}$ population for powdery mildew resistance. Heritability in broad sense and genetic advance as per cent over mean were high for mean seed yield, number of seeds per plant, number of pods per plant and number of seeds per pod indicating that these traits were controlled by additive genes indicating the availability of sufficient heritable variation that could be made use in the selection programme and can be easily transferred to successive generations. Similarly Konda *et al.*, (2009), Singh *et al.*, (2009), Arulbalachandran *et al.*, (2010), Rahim *et al.*, (2011) and Perera *et al.*, (2017) reported high heritability in broad sense and genetic advance as per cent over mean for these traits.

The yield is a complex trait and it depends on many other traits. To get desirable yield, certain yield contributing traits should be improved and some yield limiting factors (diseases, pests *etc.*) has to be fixed. In the present study, per cent disease index (powdery mildew disease) was negatively correlated with yield and yield contributing traits. Significant negative correlation was observed between per cent disease index and mean seed yield (-0.155). This is because the mycelium of *Erysiphe polygoni* covers the upper surface of the leaves which affects the photosynthetic efficiency leading to significant reduction in the yield. Significant positive correlation was observed between mean seed yield and number of seeds per plant (0.914), number of pods per plant (0.785) (Table 2). These results are in accordance with the findings of Chen *et al.*, (2013), Gupta *et al.*, (2013), Alam *et al.*, (2014), Nair *et al.*, (2017) and Perera *et al.*, (2017).

In conclusion, the $F_{2:4}$ families showed considerable genetic variability for powdery mildew resistance with several other useful agronomic traits. The study reveals that per cent disease index, number of seeds per plant, number of pods per plant, number of seeds per pod and mean seed yield provide promising selection criteria, as they possess high values of heritability and genetic advance. Therefore, emphasis should be placed on these characteristics for formulating reliable selection indices for the development of promising powdery mildew resistant mungbean varieties.

References

Alam, A. M., Somta, P. and Srinives, P., 2014, Identification and confirmation of quantitative trait loci controlling resistance to mungbean yellow mosaic disease in mungbean [*Vigna radiata* (L.) Wilczek]. *Mol. Breed.*, 34: 1497-1506.

Arulbalachandran, D., Mullainathan, L.,

Velu, S. and Thilagavathi, C., 2010, Genetic variability, heritability and genetic advance of quantitative traits in black gram by effects of mutation in field trail. *Afr. J. Biotechnol*., 9(19): 2731-2735.

Basamma, 2011, Conventional and molecular approaches in breeding for high yield and disease resistance in urdbean [*Vigna mungo* (L.) Hepper]. *Ph. D. Thesis*, Univ. Agric. Sci., Dharwad, Karnataka (India).

Chankaew, S., Somta, P., Isemura, T., Tomooka, N., kaga, A., Vaughan, D. A. and Srinives, P., 2013, Quantitative trait locus mapping reveals conservation of major and minor loci powdery mildew resistance in four sources of resistance in mungbean (*Vigna radiata* L. Wilczek). *Mol. Breed*., 32: 121-130.

Chen, H. M., Ku, H. M., Schafleitner, R., Bains, T. S., Kuo, C. G., Liu, C. A. and Nair, R. M., 2013, The major quantitative trait locus for mungbean yellow mosaic India virus resistance is tightly linked in repulsion phase to the major bruchid resistance locus in a cross between mungbean [*Vigna radiata* (L.) Wilczek] and its wild relative *Vigna radiata* ssp. *sublobata*. *Euphytica*, 192(2): 205-216.

Fernandez, G. C. J. and Shanmugasundaram, S., 1987, The AVRDC mungbean improvement programme: The past, present and future. In: *Proc. Second Int. Symp*. Asian Vegetable Research and Development Center, Shanhua, Taiwan, pp. 58–70.

Gupta, S. K., Gupta, D. S., Anjum, T. K., Pratap, A. and Kumar, J., 2013, Inheritance and molecular tagging of MYMV resistance gene in blackgram [*Vigna mungo* (L.) Hepper]. *Euphytica*, 193: 27-37.

Kasettranan, W., Somta, P. and Srinives, P., 2009, Genetics of the resistance to powdery mildew disease in mungbean [*Vigna radiata* (L.) Wilczek]. *J. Crop Sci. Biotechnol*., 12 (1): 37-42.

Konda, C. R., Salimath, P. M. and Mishra, M. N., 2009, Correlation and path coefficient analysis in blackgram [*Vigna mungo* (L.) Hepper]. *Legume Res*., 32(1): 59-61.

Lambrides, C. J. and Godwin, I. D., 2007, Mungbeans. School of Land and Food Sciences, Plant Improvement Group, The Univ. of Queensland, St Lucia (Australia), p. 4072.

Mayee, C. D. and Datar, V. V., 1986, Phytopathometry Tech. Bull. No. 1-3. M. A. U., Parbhani (India), p. 146.

Nair, R. M., Gotz, M., Winter, S., Giri, R. R., Boddepalli, V. N., Sirari, A., Bains, T. S., Taggar, G. K., Dikshit, H. K., Aski, M. and Boopathi, M., 2017, Identification of mungbean lines with tolerance or resistance to yellow mosaic in fields in India where different begomovirus species and different *Bemisia tabaci* cryptic species predominate. *European J. Plant Pathol.*, 149(2): 349-365.

Perera, U. I. P., Chandika, K. K. J. and Ratnasekara, D., 2017, Genetic variation, character association and evaluation of mungbean genotypes for agronomic and yield components. *J. Natn. Sci*., 45(4): 347-353.

Pooja, S. K., 2017, Generation of mapping population and identification of molecular markers associated with powdery mildew in mungbean (*Vigna radiata* L.). *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci., Dharwad, Karnataka (India).

Rahim, M. A., Mia, A. A., Mahmud, F., Zeba, N. and Afrin, K. S., 2011, Genetic variability, character association and genetic divergence in mungbean (*Vigna radiata* L. Wilczek). *Plant Omics J.*, 3(1): 1-6.

Reddy, K. S., Pawar, S. E. and Bhatia, C. R., 1994, Inheritance of powdery mildew (*Erysiphe polygoni* D. C.) resistance in mungbean [*Vigna radiata* (L.) Wilczek]. *Theor. Appl. Genet*., 88: 945-948.

Singh, T., Sharma, A. and Ahmed, F. A., 2009, Impact of environment on heritability and genetic gain for yield and its component traits in mungbean. *Legume Res*., 32(1): 55-58.