



E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2019; 8(3): 3642-3644
Received: 19-03-2019
Accepted: 21-04-2019

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Inheritance of powdery mildew resistance in mung bean. [*Vigna radiata* (L.) R. Wilczek]

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Abstract

In a study of inheritance of powdery mildew resistance, two parents, their reciprocal crosses, F₂, B₁ and B₂ of both crosses were screened against powdery mildew. There were no significant difference between the F₁ of Kopergaon x BPMR-145 and its reciprocal cross for powdery mildew susceptibility, indicating that the resistance is governed by recessive gene and also absence of maternal inheritance for powdery mildew resistance. The F₂ data of both crosses i.e. Kopergaon x BPMR-145 and BPMR-145 x Kopergaon was good fitted in 3:1 (susceptible: moderately resistant) ratio which indicated the involvement of single recessive gene which confirmed from backcrosses data. The moderately resistant plants identified for powdery mildew in F₂ should be utilized for development of powdery mildew resistant variety in mung bean. There is need to develop complete resistant donor to powdery mildew disease.

Keywords: Inheritance, mung bean, powdery mildew, Chi-square

Introduction

Mung bean [*Vigna radiata* (L.) R. Wilczek] 2n=2x=22 is the most important pulse crop in India after chickpea and pigeon pea. A pulse, best known as "poor man's meat" and mung bean (green gram) is one of them. Seed proteins of mung bean are easily digestible proteins and it does not produce flatulence or heaviness. It is also good source of vitamin B. Its sprouts contain Vitamin C as well as E.

It is originated from Indian sub continent (Decandolle, 1886) [2]. At national level total area of 38.32 lakh hectare with the production of 16.03 lakh tones. The national average productivity is 418 kg/ha. In Maharashtra, it is the important *Kharif* crop grown on an area of 3.85 lakh ha. with production of 0.72 lakh tones and having productivity of 187 kg/ha. (Anonymous, 2015 - 2016) [1]

As per *Ayurveda* mung bean is one of the best pulse among all kind of pulses or legumes, it is due to its inborn or natural qualities which is really helpful or beneficial to recover all kinds of diseases. It is sweet and little bit astringent by taste, cool in potency. It is trifling, prosaic and lucid in nature.

However, the productivity of mung bean is very low. One of the major reason for low productivity of mung bean is powdery mildew disease, which is the most prevalent fungal disease of this crop. It can be effectively controlled by incorporation of genetic resistance into susceptible species. The powdery mildew disease is caused by an Ascomycetes fungal species *Erysiphe polygoni* D.C. which belong to family of *Erysiphaceae*. Powdery mildew is an air borne disease with a worldwide distribution. The yield losses due to powdery mildew are reported to be 20% to 40% and 100% at the seedling stage (Reddy *et al.*, 1994) [9].

Genetic method is the cheapest and efficient strategy to disease management as it is most economical and environment friendly than chemical control. Therefore, study of inheritance of powdery mildew resistance is necessary for the development of resistant variety and it would form an important of systematic breeding programme of mung bean.

Considering the importance of the crop and for desired improvement in the crop, the present investigation was undertaken.

Materials and method

The present investigation was conducted at Post Graduate Farm and at Pulses Improvement Project, Mahatma Phule Krushi Vidyapeeth, Rahuri during 2014 to 2016. The experimental material for the present study comprised of two varieties *viz*; Kopergaon (susceptible to powdery mildew) and BPMR-145 (resistance to powdery mildew) obtained from Pulses Improvement Project, MPKV., Rahuri. With these two parents two crosses were effected *viz*;

Kopergaon x BPMR-145 (SxR) and BPMR-145 x Kopergaon (RxS) during summer-2015. Parts of F₁ seeds harvested from these two crosses were sown during summer-2016. Selfing of F₁'s and backcrosses were done to get F₂, B₁ and B₂ generations.

Un-replicated experiment was conducted with two parents, 2F₁'s, 2F₂'s, 2B₁'s and 2B₂'s of two crosses viz; Kopergaon x BPMR-145 and BPMR-145 x Kopergaon on 7th July, 2016 at Pulses Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri. Each parent represented by two rows and F₁, B₁ and B₂ were represented by single row, whereas F₂'s were represented by eighteen rows. Kopergaon was sown after every four test entries as a infector row to ensure high disease pressure. All treatments were sown with three meter row length and spaced at 30 cm apart with 10 cm distance between plants in a row.

Spreader row technique was used for screening against powdery mildew disease. Kopergaon was sown 15 days before the main experiment sowing i.e. on 23rd June, 2016 as a border rows. Additionally at vulnerable stages of mung bean i.e. 20 and 40 days after sowing, the spray of inoculated with an aqueous conidial suspension (about 1 x 10⁷ spores ml⁻¹) of fungus *Erysiphe polygoni* were taken on plants for uniform infection and for creation of high disease pressure. All the recommended package of practices was followed except spraying of any fungicide.

Observations were recorded for percent disease intensity (PDI). When 100 % disease was observed on infector rows (Kopergaon). The powdery mildew disease incidence was recorded on selected leaves of individual plant of parents, F₁, F₂, B₁ and B₂ generations and leaves were graded as per the 0 to 5 progressive scale (Table 1). The PDI was calculated using the formula given by Wheeler (1969)^[11].

Table 1: Rating scale for powdery mildew reaction

Scale	PDI	Reaction
0	0	Immune
1	0.1-10	Resistant
2	10.1-25	Moderately resistant
3	25.1-50	Moderately susceptible
4	50.1-75	Susceptible
5	Above 75.1	Highly susceptible

$$PDI = \frac{\text{Sum of all numerical rating}}{\text{Number of leaves observed} \times \text{Maximum rating}} \times 100$$

The goodness of fit test to Mendelian segregation ratio in the segregating populations was tested by Chi-square test (Fisher, 1930).

Results and discussion

Development of powdery mildew disease is a complex phenomenon and it depends upon the genetic potential of the genotype to resist the development of pathogen, prevalence of fungal biomass and availability of the congenial atmosphere for the development of powdery mildew disease.

The reaction of parents revealed that the parents involved in the present investigation are genetically diverse for resistance to powdery mildew disease (Table 2). The F₁ of the cross I and II showed PDI 76.15 and 78.65 per cent respectively, which indicating that the resistance is governed by recessive gene, because the F₁ of both the crosses i.e. S x R and R x S showing susceptible reaction. Similarly there was no significance difference between the F₁ of cross I (Kopergaon x BPMR-145) and it's reciprocal cross II (BPMR-145 x

Kopergaon) for powdery mildew resistance, indicating absence of maternal or cytoplasmic inheritance of powdery mildew resistance in mung bean.

Based on estimates of percent disease intensity (PDI) of two crosses the F₂ and their test crosses (B₁ & B₂) were grouped in to moderately resistant, susceptible and highly susceptible. For the sake of convenience and to draw a valid conclusion susceptible and highly susceptible classes are grouped as a susceptible, leaving the first class of moderately resistant separately (Table 3). To test the genetic ratio, the F₂ segregation in the monogenic ratio 3 susceptible: 1 moderately resistant gave best goodness of fit for both crosses viz., Kopergaon x BPMR-145 (S x R) and BPMR-145 x Kopergaon (R x S). The present study was further confirmed by F₁'s cross with their resistant parent i. e. B₂ of cross I (Kopergaon x BPMR-145) and B₁ of cross II (BPMR-145 x Kopergaon) which had good fit to the 1 moderately resistant :1 susceptible segregation ratio which indicating that single recessive gene governed the powdery mildew resistance. Similar results were reported by Kaushal and Singh (1989)^[3], Nisar and Ghafoor (2009)^[7]. Kute *et al.* (2003)^[6] reported resistance governed by three duplicate recessive genes. However, the contradictory results were reported by Khajudparn *et al.* (2007)^[4], Srivastava *et al.* (2013) and Pulate (2016)^[8]. They reported that the resistance to powdery mildew was governed by a single dominant gene. Whereas, Reddy (1994)^[9] and Kumari Basamma (2011)^[5] reported two dominant gene governed the resistance.

Conclusion

From this study, it can be concluded that single recessive gene governed the powdery mildew resistance in mung bean. The moderately resistant plants identified for powdery mildew in F₂ should be utilized for development of powdery mildew resistant variety in mung bean. There is need to develop complete resistant donar to powdery mildew disease.

Table 2: The reaction of parents and their F₁'s of two crosses against powdery mildew disease in mung bean.

Parents/ Crosses	Percent disease intensity (PDI)		Reaction
	Mean	Range	
Parents			
Kopergaon	95.20	51.35-100	Susceptible
BPMR-145	16.84	12.12-23.80	Moderately Resistant
F₁'s			
Kopergaon x BPMR-145	76.15	62.10-100	Susceptible
BPMR-145 x Kopergaon	78.65	65.23-100	Susceptible

Authors' contribution

Conceptualization of research (DGK, NSK, MRB); Designing of experiments (DGK, NSK,MRB,GPD); Contribution of experimental material (DGK, MRB, CPJ); Execution of field experiments and data collection (DGK, VYP, GPD); Analysis of data and interpretation (DGK,VYP, GPD,MDG); Preparation of manuscript (DGK, NSK).

Declaration

The authors declare no conflict of interest.

Acknowledgements

The authors gratefully acknowledge Associate Dean, Post Graduate Institute, MPKV, Rahuri Dr. M.R. Bedis and Dr.

N.S. Kute, Sr. Scientist Pulses, Pulses Improvement Project, MPKV., Rahuri for growing the crop in their respective experimental stations and providing the grain samples.

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