# Field Screening of Mungbean Genotypes and the Role of Total Soluble Sugars and Phenols against Powdery Mildew Resistance

Nidhi Pathak<sup>1</sup>\*, MN Singh<sup>2</sup>, MK Mishra<sup>1</sup>, DK Singh<sup>2</sup>, Yash Pal<sup>2</sup>, SY Dhurai<sup>2</sup> and Rishi Pathak<sup>3</sup>

<sup>1</sup> College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Tikamgarh-472001, Madhya Pradesh, India <sup>2</sup> Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221002, Uttar Pradesh, India

<sup>3</sup> College of Agricultural Engineering, Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur-482004, Madhya Pradesh, India

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Powdery mildew of mungbean caused by *Erysiphe polygoni* DC may cause yield loss up to 20-40%. Mungbean (51) genotypes were screened in three consecutive seasons under natural epiphytotic conditions. Out of 51 genotypes, TM-96-2 exhibited highly resistance, nine as resistance, five as moderately resistance, 16 as susceptible and 20 as highly susceptible reactions for powdery mildew. On the basis of field screening, two resistant and 10 susceptible genotypes were selected for the study of relationship between induced resistance mechanism with total soluble sugars and phenol contents in plants. The resistant genotypes contained high level of phenols than the susceptible genotypes.

#### Key Words: Mungbean, Powdery mildew, Total phenols, Total soluble sugars

### Introduction

Mungbean [*Vigna radiata* (L.) Wilckzek], 2n = 2x = 22is one of the important pulse crops in India. In north India, it is grown in summer and rainy seasons and in southern India; it is grown in winter season. Mungbean is susceptible to various diseases like yellow mosaic virus, powdery mildew, Cercospora leaf spot and Rhizoctonia blight etc. among which powdery mildew is very serious. Powdery mildew of mungbean is caused by Erysiphe polygoni DC and causes yield loss up to 20-40% (Khare et al., 1998). It is considered as disease of South East Asia (Park and Yang 1978), being more prevalent in southern and central India. A wide range of chemicals are being used to control the disease but these chemicals are not effective under heavy infection and produce health hazards. Development of resistant variety is a cheap, viable and environment friendly approach to overcome this problem. Anatomical and biochemical features of the host are involved in disease resistance mechanism. Phenols are secondary metabolites of plants involved in several biological process of plant such as pigmentation, growth, reproduction and resistance to pathogens. At the time of disease infection, rate of production of phenols are more in resistant genotypes as

compared to susceptible one (Dakshayani *et al.*, 2005). After the infection of pathogen into the host tissue a rapid accumulation of phenols at the infection site, restricts or reduce the growth of the pathogen (Matern and Kneusal, 1988). Sugars as signalling molecules in plants (Rolland *et al.*, 2006) play an important role in defence mechanism of the host plant against diseases. Low levels of total and reducing sugars were observed in groundnut genotypes resistant to tikka disease when compared to the susceptible ones (Sindhan and Jaglan, 1987). Thus, total phenol and sugar status of mungbean plant could be correlated with host resistance.

The present experiment was aimed to identify the genotypes resistant to powdery mildew and compare changes in total soluble sugars and phenols in selected resistant and susceptible genotypes.

### **Materials and Methods**

## Field Screening of Powdery Mildew

A total of 51 diverse genotypes of mungbean obtained from AICRP on Pulses of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India which is located in the South-Eastern part of Varanasi city at 25' 18" N latitude, 83' 03" E longitude and at

<sup>\*</sup>Author for Correspondence: E-mail: nidhijnkvv@gmail.com

Grade	Disease severity (%)	Reaction	Symptom description		
0	Nil	Free/highly resistant (HR)	No infection		
1	0.1-5	Resistant (R)	Infection in traces only		
2	5.1-25	Moderately resistant (MR)	Roughly one in every four leaves showing fine coating of powdery growth on upper surface of leaves		
3	25.1-50	Moderately susceptible (MS)	Nearly 50% of the leaves infected, stem infection slight, plant size normal		
4	50.1-75	Susceptible (S)	Nearly 75% of the foliage including stem appears to be covered with white powdery coating, plant slightly stunted		
5	>75	Highly susceptible (HS)	Entire plant including pods and floral parts are infected, leaves turn pale green to yellow and start drying up, the affected plants are conspicuous because of stunted growth		

 Table 1. Methodology for scoring mungbean genotypes for powdery mildew

altitude of 75.7 meters above the mean sea level were screened against powdery mildew disease. The field screening trials were laid in randomised complete block design with three replications in three consecutive late kharif (rainy) seasons of 2009, 2010 and 2011 and date of sowing was 20<sup>th</sup> September every year. Each plot consisted of two rows of 2m length with 40 cm and 10 cm row to row and plant to plant spacing, respectively. Standard agronomic practices recommended for the mungbean crop were followed (Park and Yang, 1978). To ensure sufficient source of inoculum and uniform spread of disease, one row of HUM 26 (highly susceptible to powdery mildew) was planted as infector row after every two rows of the test entries. Further, two infector rows were also raised around the experimental plots to maintain the sufficient load of inoculum. The entire experimental material in the trial were also inoculated twice *i.e.*, 32 days after sowing and 42 days after sowing by spraying the spore suspension  $(3.5 \times 10^6 \text{ conidia/ml})$  of *E. polygoni* (Reddy et al., 1987) obtained from the infected crop of mungbean of another field. Observation of powdery mildew severity was recorded 55 days after sowing on 10 randomly selected plants from each genotype in each replication. Disease severity (%) in the plant was recorded on the basis of the visual observation of the per cent leaf area infected. The reaction of genotypes against powdery mildew was categorized by using 0-5 scale given by Reddy et al. 1987 (Table1). Each plot of a genotype was scored separately and genotypes were classified according to mean grade. Three years grade of the genotypes were pooled. The cumulative scores (0=HR, 0.1-1=R, 1.1-2=MR, 2.1-3=MS, 3.1-4=S, 4.1-5=HS) were calculated and genotypes classified accordingly.

Finally, on the basis of field screening genotypes in three consecutive seasons, two powdery mildew resistant genotypes *viz.*, ML-713 and TM -96-2 and 10 susceptible genotypes *viz.*, HUM-7, HUM-8, HUM-9, HUM-12, HUM-26, PUSA-0672, PUSA-0871, ML-515, ML-5 and IPM-02-17 were selected.

## **Biochemical Studies**

Total soluble sugars and phenols were estimated in two powdery mildew resistant (ML-713, TM -96-2) and three susceptible (HUM-7, HUM-8, HUM-9) and seven highly susceptible (HUM-12, HUM-26, PUSA-0672, PUSA-0871, ML-515, ML-5 and IPM-02-17) genotypes.

The amount of total soluble sugars was estimated by Phenol sulphuric acid reagent method (Dubois *et al.*, 1951) and the total phenols were measured by Folin Ciocalteu reagent method (McDonald *et al.*, 2001). Five plants from each of the genotypes were tested twice, in three replications before infection (30 DAS) and after infection (55 DAS) because the severity of disease was high during this period.

### **Results and Discussion**

## Field Screening of Powdery Mildew

Among the 51 genotypes, one genotype TM 96-2 exhibited highly resistance, nine genotypes as resistance, five genotypes as moderately resistance, 16 genotypes as susceptible and 20 genotypes as highly susceptible reaction. None of the genotypes were moderately susceptible to powdery mildew (Table 2).

# Level of Biochemical Constituents in Relation to Powdery Mildew Resistance

In the present investigation total soluble sugars were lowest in resistant genotypes ML-713 and TM-96-2 while, maximum in highly susceptible genotype ML-5 before and after infection (Table 3). After infection, total

Disease reaction	No. of genotypes	Name of genotypes	Score range
Highly resistant	1	TM-96-2	0.0
Resistant 9		COGG-912, DBG-1030, DBG-1045, DPM-90-1, IPM-02-3, ML-713, ML-717, TARM-1, TARM-18	
Moderately resistant	5	BDYR-1, MH-521, IPM- 02-19, TM-2000-1, UPM-98-1	1.3-2.0
Moderately susceptible	0	_	
Susceptible	16	HUM-2, HUM-8, HUM-9, HUM-7, PUSA-9531, ML-1296, ML-1294, ML-1465, PUSA RATNA, PDM-54, VRMGG-1, PDM-11, K-851, RMG-991, UPM-98-1, V. <i>Trilogata</i>	3.3-4.0
Highly susceptible	20	AKM-9904, HUM-1, HUM-6, HUM-12, HUM-15, HUM-16, HUM-26, IPM- 02-17, ML-515, ML-1451, MH-318, ML-5, PS-16, PUSA-105, Pusa-0672, Pusa-0871, PUSA VISHAL, SML-668, T-44, T-9	4.3-5.0

Table 3. Biochemical studies of powdery mildew disease before and after infection in resistant and susceptible genotypes

Genotypes	Total soluble sugar	(mg/g dry weight)	Reduction (%)	Total phenols (mg/g fresh weight)		Reduction (%)
	Before infection	After infection		Before infection	After infection	
HUM- 7	9.81	8.41	14.24	11.67	9.65	17.28
HUM-8	9.79	8.95	8.65	11.19	9.35	16.44
HUM-9	9.65	8.86	8.19	11.73	9.08	22.57
HUM- 12	9.82	8.56	12.83	11.74	9.29	20.87
HUM- 26	9.65	7.83	18.80	11.22	9.22	17.80
IPM- 02-17	9.65	8.31	13.92	11.64	9.48	18.56
ML- 515	10.58	8.46	20.07	10.85	8.46	22.08
ML- 5	11.31	9.04	20.12	10.73	8.15	24.01
ML- 713	8.49	7.75	8.71	13.17	9.87	25.04
PUSA- 0672	10.29	8.91	13.41	11.28	9.40	16.66
PUSA- 0871	9.83	8.88	9.60	10.64	8.62	19.01
TM-96-2	8.42	7.55	10.30	14.27	10.39	27.19
SEm_±	0.20	0.35		0.28	0.25	
CD (P=0.05)	0.56	1.01		0.81	0.72	

soluble sugars decreased in all genotypes, particularly in highly susceptible genotype ML-5. These results supported by the finding of Gawande and Patil (2004). The findings indicated that the pathogen uses more sugars for establishment in the host and also decreases photosynthesis (data not shown) in susceptible genotypes as compared to resistant genotypes as the large area of leaves was covered by the pathogen. Total phenols were maximum in resistant genotype TM-96-2 followed by ML-713, whereas, minimum in susceptible genotype PUSA- 0871 before infection. The levels of total phenols content decreased after infection in all the genotypes. Similar findings were observed by Sharma *et al.* (1982) and Guleria *et al.* (1998). After infection, total phenols content was maximum in resistant genotypes TM-96-2 and ML-713 whereas, minimum in susceptible genotype ML-5. It was also observed that reduction of total phenols content was more in resistant genotypes due to higher activities of polyphenol oxidase enzymes in resistant genotypes than in susceptible ones (Gawande and Patil, 2006). Different studies showed that phenolics compounds are involved in natural resistance mechanism of plants.

Therefore, it may be concluded that total soluble sugars and total phenols and their accumulation pattern decide the degree of resistance to powdery mildew in mungbean. These biochemical parameters can be used for screening of mungbean genotypes for powdery mildew resistance.

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