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Research Article

Variability Studies in Melon (*Cucumis melo*. L) F_2 Population of Kashi Madhu X COHB38 for Powdery Mildew Disease Resistance

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Abstract
The present investigation was carried at College of Horticulture, Bengaluru. Evaluation of melon F_2 population (Kashi Madhu X COHB38) was conducted during rabi 2016 for resistance to powdery mildew disease under natural field condition. Percent Disease Index (PDI) and AUDPC (Area Under Disease Progress Curve) value was calculated to assess the reaction of F_2 (Kashi Madhu X COHB38) segregating population of melon along with the parents (COHB38 and Kashi Madhu) and F_1. Based on PDI for powdery mildew disease, 152 F_2 plants were classified into different categories. Twenty-five F_2s were resistant (0-25% PDI), 27 were moderately resistant (25.1-40% PDI), 88 were susceptible (40.1-60% PDI) and 12 F_2s were highly susceptible (>60% PDI). Among 152 F_2 plants, F_2-34 was found to be highly resistant with zero PDI and zero AUDPC value (no disease) followed by F_2- 46 and 92 with PDI of 13.89 % and 16.11 % and 46.94 and 55.00 AUDPC value, respectively. The PDI of the disease showed a continuous distribution from highly resistant to highly susceptible phenotypes, without showing any typical segregation pattern.

Keywords: Muskmelon; Powdery mildew; Percent disease index; AUDPC

Introduction
Melons (*Cucumis melo* L., 2n=2x=24) are one of the important crop in the Cucurbitaceae family and has great importance because of its commercial value and is grown mostly for its fruits. Melon cultivation is threatened due to many pests and diseases. The diseases are powdery mildew, downy mildew, cucumber green mottle mosaic viruses, fusarium wilt and gummy stem blight. Among these, powdery mildew is one of the serious foliar diseases which hinder the production and reduce the quality of fruits worldwide (McCreight, 2006). Powdery mildew is caused by two biotrophic pathogens *Podosphaera xanthii* and *Golvinomyces cicchoracearum. P. xanthii*, the most

prevalent species in India (Gupta and Sharma, 2012) requires 25-30°C for its growth and survival and thrives well in tropical and subtropical regions of the world, whereas *G. cicchoracearum* survives in temperature range of 15-25°C and majorly occurs in temperate and cooler regions of the world (Kristkova *et al.*, 2009). Cool and dry weather favours the disease. The disease is characterized by white to gray powdery growth on surface of leaves, petioles and stem. Severely infected leaves become yellow and dry, finally leads to stunting of plants. The disease severely affects the quality of the fruits (McCreight, 2006). Because of the difficulties associated for the control of this disease by chemical fungicides, farmers experienced great losses in cucurbits. Disease resistance genes from resistant source are introgressed to cultivated lines through backcrossing, pedigree and other breeding methods. The early segregating generations like F_2s provide wide variability for different traits and the inheritance pattern of characters could also be understood. F_2s also serve as mapping population to map genes and quantitative trait loci (QTL). Therefore, by considering the importance of disease resistance breeding a study on reaction of melon F_2s to powdery mildew disease was carried out under field conditions to assess the reaction of the melon genotypes to the Eastern dry zone of Karnataka.

Material and Methods

The field experiment was conducted in *rabi* 2016 at College of Horticulture, Bengaluru located at 12°58' latitude North, 77°11' longitude East and altitude of 930 meters above mean sea level and it is situated in the Eastern dry zone of Karnataka. The experimental material used for this study included F_1 of two diverse melon parents Kashi Madhu and COHB38. COHB38 was identified as resistant to powdery mildew diseases from the previous study (Sudhakara, 2014). The susceptible check Kashi Madhu is a popular high yielding variety with superior fruit quality (Pandey *et al.*, 2008) and it was provided by Indian Institute of Horticulture Research, Bengaluru. F_1 hybrids were developed by crossing Kashi Madhu and COHB38 in reciprocal crosses in *rabi* 2015. F_2 were generated through selfing (manual) of F_1 (Kashi Madhu X COHB38) plants in summer 2016. Both F_1 and F_2 were developed under shade net condition in order to avoid pollinators. The F_2s were un-replicated and parents were replicated thrice. Seedlings were raised in protrays and then transplanted to main field after 15 days of sowing. The experimental plot was irrigated through drip system. All necessary care was taken to establish a healthy melon crop. Plots were kept free from weeds by regular hand weeding and prophylactic sprays taken against pest at different intervals. Pheromone traps were installed to reduce the fruit flies damage. The experiment was conducted in open field condition with spacing of 2.5m x 0.45m. The experimental land was prepared by ploughing. Well decomposed farm yard manure at the rate of 25 tonnes per hectare was applied and other agronomic practices were undertaken as per the package of practices for horticultural crops given by University of horticultural Sciences, Bagalkot (Anon., 2013).

Result and Discussion

The percentage of powdery mildew incidence was recorded as per cent leaf area infected for all the F_2 plants, which were scored following 0 to 5 disease rating scale (Shashikumar *et al.*, 2016) (Table 1).

Table 1: 0 to 5 disease rating scale (Shashikumar et al., 2016).

Score	**Reaction**
0	No disease symptoms, free from fungal infection
1	1-10 % of leaf area covered with fungal growth
2	10.1-25 % of leaf area covered with fungal growth
3	25.1-50 % of leaf area covered with fungal growth
4	50.1-75% of leaf area covered with fungal growth
5	>75 % of total leaf area covered with fungal growth

Per cent disease index (Wheeler, 1969) was calculated by using the formula,

$$\mathrm{PDI} = \frac{\mathit{Sum\ of\ numerical\ disease\ ratings}}{\mathit{Number\ of\ leaves\ gronded\ X\ Maximum\ disease\ rating}} \times 100$$

Based on the PDI, the F_2 population was categorized into four groups (Pitchaimuthu *et al.,* 2012) shown in Table 2/

Table 2: four groups categories of F_2 population

PDI	Disease reaction
0.1 - 25	Resistant
25.1-40	Moderately resistant
40.1-60	Susceptible
>60	Highly susceptible

Area under disease progress curve (AUDPC) by Perchepied *et al.*, 2005

$$\mathrm{AUDPC} = \sum_{i}^{n} \left[\frac{x_i + x_{i+1} - 2}{2} \right](\mathrm{ti} + 1 - \mathrm{ti})$$

Where,

x_i = mean disease score of each plant at date *i*,
x_{i+1} = mean disease score of each plant at date *i* + 1
$t_{i+1} – t_i$ =number of days between scoring date *i* and scoring date *i* + 1
n = number of readings.
i = number of scorings

Result and Discussion

The F_2 segregating population (152 lines) of Kashi Madhu x COHB38 were evaluated in open field condition at College of Horticulture, Bengaluru for resistance to powdery mildew disease under natural disease condition. Percent disease index (PDI) and area under disease progress curve (AUDPC) were calculated to assess the reaction of F_2 segregating population along with the parents (Kashi Madhu and COHB38) and F_1 (Table 3). Evaluation of F_2 Population of melon for resistance to powdery mildew disease revealed that, the resistant parent COHB38 and F_1 were resistant with PDI of 15.74 % and 21.30 %, respectively. The susceptible parent Kashi Madhu was highly susceptible with 75.56 % (Table 3). Based on PDI for powdery mildew, F_2 plants were classified into different categories (Table 4). Out of 152 F_2s, 25 were resistant (0-25% PDI), 27 were moderately resistant (25.1-40% PDI), 88 were susceptible (40.1-60% PDI) and 12 F_2s were highly susceptible (>60% PDI). The distribution of 152 F_2 lines of Kashi Madhu and COHB38 for powdery mildew disease area is given in Fig.1. F_2 -34 was found to be highly resistant with zero PDI and zero AUDPC value (no disease) followed by F_2- 46 and 92 with PDI of 13.89 % and 16.11 % and 46.94 and 55.00 AUDPC value, respectively (Table 3). The disease progress curve of different categories of F_2s chosen randomly is presented in Fig. 2. The PDI of powdery mildew showed a continuous distribution from highly resistant to highly susceptible phenotypes, without showing any typical segregation pattern (Fig. 3). The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2), genetic advance (GA) and genetic advance as percent mean (GAM) for PDI of powdery mildew is presented in Table 5 and Fig. 4. The population mean for PDI of powdery mildew was found to be 44.38 % and it ranged from 0.00 (no disease) to 81.67%. The PCV and GCV were found to be high for PDI of powdery mildew with 33.96 and 24.11 percent, respectively. The heritability was 70.99 % with genetic advance as percent mean of 48.96 (Table 5 and Fig. 4). Among 152 F_2s screened, 25 were resistant and 27 were moderately resistant. The rest of the lines were susceptible. Resistant as well as susceptible lines irrespective of their fruit characters were selfed to forward the lines to next generation. Genetic control of powdery mildew resistance is generally by major dominant genes but modifier genes and recessive control are also commonly observed (McCreight, 2003 and Pitrate, 2008). There are few reports available for mapping QTLs related to powdery mildew resistance in melon and indicates the role of more than one gene (Pitrat, 1991; Perin *et al*., 2002; Pitrat, 2002; Perchepied *et al*., 2005; Fukino *et al*., 2008; Longzhou *et al*., 2008; Texiera *et al*., 2008; Wang *et al*. 2011; Yuste-Lisbona *et al*. 2011; Zhang *et al*., 2013 and Ning *et al*., 2014). Various populations like F_2 (Liou et al., 1998 and Brotman *et al*., 2000), BC_1 (Wang *et al*., 1997) and recombinant inbred lines (Fukino *et al*., 2008) were used in analysing the inheritance pattern of powdery mildew resistance. The PCV, GCV, heritability and genetic advance as percent mean values were also high for resistance to powdery mildew. Perchepied *et al*. (2005) and Shashikumar *et al*. (2010) also noticed high heritability for powdery mildew disease resistance.

Table 3: PDI and AUDPC of 152 F2 lines of Kashi Madhu × COHB38 for powdery mildew disease.

Resistant lines								
F_2. No	**PDI**	**AUDPC**	**F_2. No**	**PDI**	**AUDPC**	**F_2. No**	**PDI**	**AUDPC**
10	17.22	58.06	87	18.33	61.11	123	16.67	53.61
11	20.56	71.11	89	16.67	57.50	125	23.33	83.61
28	17.78	60.56	92	16.11	55.00	129	23.33	83.61
31	16.67	53.61	98	21.67	78.06	131	25.00	89.17
32	23.33	83.61	100	17.22	58.06	137	18.33	61.11
34	0	0	103	21.67	78.06	138	16.67	57.50
46	13.89	46.94	107	16.67	53.61	141	22.22	78.61
53	21.11	73.61	114	17.22	58.06	F1	21.30	74.44
80	17.22	58.06	115	21.67	78.06	P2	15.74	54.63
Moderately resistant lines								
F_2. No	**PDI**	**AUDPC**	**F_2. No**	**PDI**	**AUDPC**	**F_2. No**	**PDI**	**AUDPC**
1	33.89	119.44	58	35.00	124.44	90	33.33	107.22
20	32.22	111.94	71	36.11	119.72	93	40.00	125.56
21	36.11	117.78	72	31.11	97.22	99	37.78	127.22
22	27.78	90.00	73	31.11	101.11	128	31.67	99.72
25	32.78	112.50	74	40.00	139.17	132	40.00	135.28
26	35.56	123.06	75	30.56	102.50	133	36.11	119.72
27	29.44	95.56	81	35.00	124.44	136	34.44	116.11
33	33.89	111.67	84	33.33	109.17	145	36.11	121.67
35	30.00	103.89	88	40.00	139.17			

Table 3: PDI and AUDPC of 152 F2 lines of Kashi Madhu × COHB38 for powdery mildew disease **(Contd.)**

Susceptible lines								
F$_2$. No	**PDI**	**AUDPC**	**F$_2$. No**	**PDI**	**AUDPC**	**F$_2$. No**	**PDI**	**AUDPC**
2	55.56	183.89	59	53.89	168.61	110	46.67	149.72
3	52.22	176.67	60	51.11	169.72	111	51.11	165.83
4	52.78	175.28	61	49.44	156.39	112	47.78	156.67
5	55.00	183.33	62	55.56	183.89	113	51.67	168.33
6	53.33	173.89	63	50.56	165.28	116	51.67	170.28
7	58.33	198.33	66	52.22	163.06	117	51.11	167.78
8	54.44	182.78	67	50.56	161.39	119	59.44	205.28
9	46.11	158.89	68	50.56	163.33	120	54.44	188.61
12	46.67	149.72	69	53.89	178.33	121	58.33	204.17
13	50.56	165.28	70	51.67	164.44	122	55.56	189.72
14	51.67	168.33	76	51.67	168.33	124	46.67	149.72
15	51.67	168.33	77	51.67	168.33	126	50.56	165.28
16	51.67	170.28	78	51.67	170.28	127	51.67	168.33
17	51.67	170.28	79	51.11	169.72	130	51.67	168.33
18	49.44	156.39	82	49.44	156.39	134	51.67	170.28
29	55.56	183.89	83	55.56	183.89	135	51.11	169.72
30	51.11	167.78	85	51.11	167.78	139	49.44	156.39
36	40.56	137.78	86	56.67	167.50	140	55.56	183.89
37	51.11	175.56	91	58.89	177.50	142	50.00	164.72
39	46.67	149.72	94	53.89	168.61	143	51.11	163.89
40	50.56	165.28	95	52.22	172.78	144	55.00	181.39
43	51.67	168.33	96	41.67	138.89	146	48.33	157.22
44	51.67	168.33	97	41.67	146.67	147	50.56	165.28
45	51.67	170.28	101	42.22	145.28	148	51.67	168.33
49	56.11	194.17	102	46.67	151.67	149	51.67	168.33
51	46.67	149.72	104	51.11	169.72	150	51.67	170.28
54	54.44	180.83	105	49.44	156.39	151	50.00	164.72
55	55.00	181.39	106	52.22	170.83	152	51.11	163.89
56	48.89	157.78	108	48.33	155.28			
57	52.78	171.39	109	45.00	140.28			
Highly susceptible lines								
F$_2$. No	**PDI**	**AUDPC**	**F$_2$. No**	**PDI**	**AUDPC**	**F$_2$. No**	**PDI**	**AUDPC**
19	68.89	240.00	42	66.11	235.28	64	81.67	280.00
23	79.44	270.00	47	65.56	230.83	65	68.89	232.22
24	70.56	230.00	48	78.89	267.50	P1	75.56	258.98
38	63.33	216.94	50	72.78	240.00			
41	66.67	231.94	52	60.56	202.50			

P1-Kashi Madhu
P2 - COHB38
F1 - Kashi Madhu X COHB38
PDI - Percent disease index
AUDPC-Area under disease progress curve

Table 4: Reaction of parents, F$_1$ and F$_2$ lines of Kashi Madhu x COHB38 for powdery mildew disease.

Reaction	**Percent Disease Index**	**Powdery mildew (152 lines)**
Resistant	0-25%	COHB38, F$_1$ and 25 F$_2$s
Moderately resistant	25.1-40.0%	27 F$_2$s
Susceptible	40.1-60.0%	88 F$_2$s
Highly susceptible	>60%	Kashi Madhu and 12 F$_2$s

Table 5: Genetic parameters of variability in F_2 population of Kashi Madhu × COHB38 for Percent disease index (PDI) of powdery mildew disease.

Particulars	**PDI of Powdery mildew**
Mean	44.38
Minimum	0
Maximum	81.67
PCV	33.96
GCV	24.11
h^2	70.99
GA	21.73
GAM	48.96

PCV- Phenotypic co-efficient of variation
GA- Genetic advance
GCV- Genotypic co-efficient of variation
GAM- Genetic advance as per cent mean
h^2 - Broad sense heritability

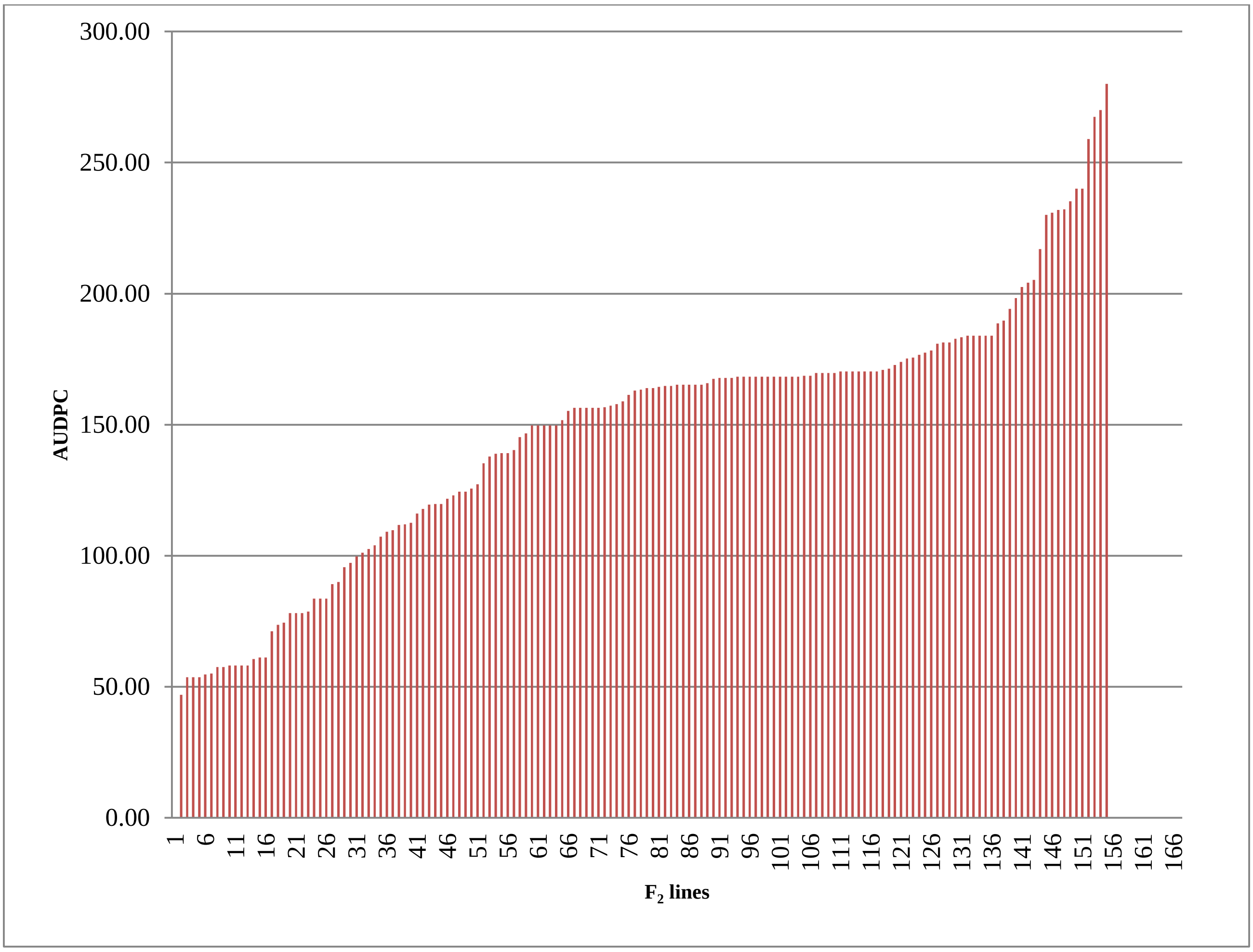

Fig. 1: Distribution of 152 F_2 lines of Kashi Madhu and COHB38 for powdery mildew disease area.

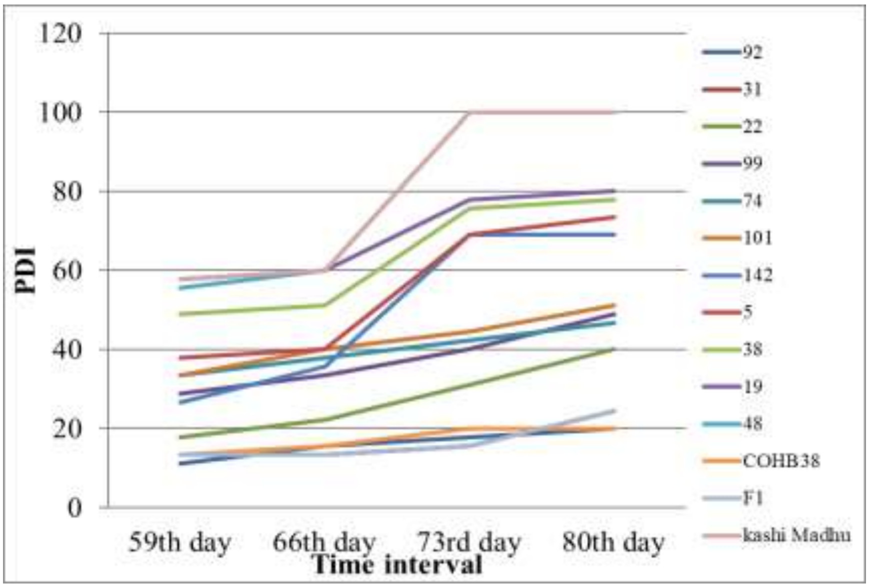

Fig. 2: Disease progress curve of different categories of F_2 population for powdery mildew incidence.

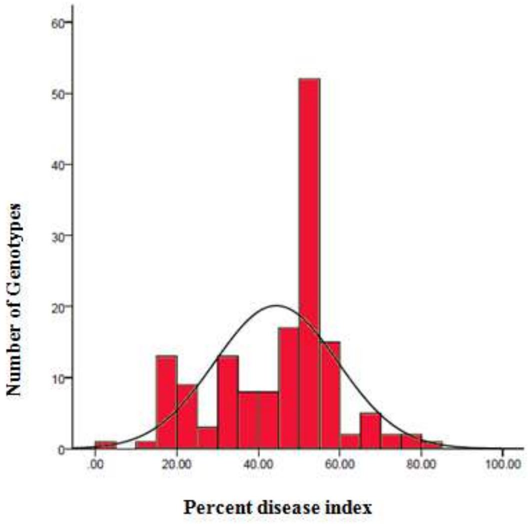

Fig. 3: Frequency distribution of F_2 lines of Kashi Madhu X COHB38 for powdery mildew disease.

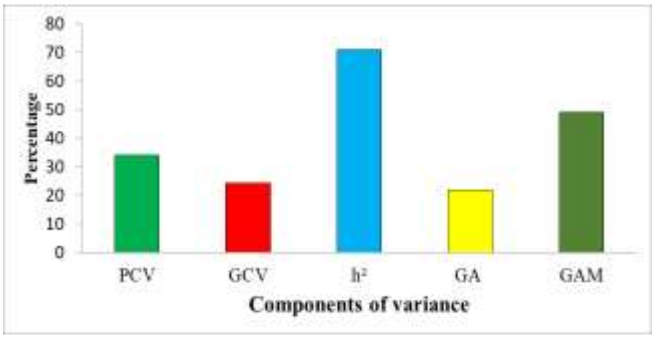

Fig. 4: Components of variance, heritability and genetic advance as percent mean for powdery mildew disease.

PCV- Phenotypic co-efficient of variation
GCV- Genotypic co-efficient of variation
GA- Genetic advance
GAM- Genetic advance as pecent mean

Conclusion

Among 152 F_2 s screened for powdery mildew disease, 25 were resistant and 27 were moderately resistant. Powdery mildew disease reaction also showed a continuous distribution from highly resistant to highly susceptible phenotypes and indicated the polygenic nature of resistance. The PCV, GCV, heritability and genetic advance as percent mean values were also high for resistance to powdery mildew.

Author’s Contribution

Both authors contributed equally in all steps of research work, manuscript preparation and approval of final form of the manuscript.

Conflict of Interest

The authors declare that there is no conflict of interest with present publication.

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