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Screening of Muskmelon (*Cucumis melo* L.) Germplasm Against Fusarium wilt (*Fusarium oxysporum* f. sp. *melonis*) and its Utilization in Hybrid Development

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ABSTRACT

Fusarium wilt is serious disease of muskmelon throughout globe. Fifty accessions of muskmelon and its relatives (*Fom* differentials, snapmelon and wild melon) were used for hybrid making in half diallel manner. Fifty accessions were screened at expanded cotyledonary stage after inoculation with local *Fom* isolate under artificial conditions. Based on disease severity, eight accessions were found highly resistant (0.00-21.67%) and three moderately resistant (28.33-36.67%).The *Fom* resistant differentials; Hemed (AUDPC 850; severity 91.67%) and F-65 (AUDPC 983.33; severity 88.33%) showed susceptible reaction, which signifies the presence of new *Fom* pathogenic race. Further, eight highly resistant and two susceptible genotypes were crossed to generate 45 hybrids. These hybrids were screened under wilt sick plot for two consecutive years for fusarium wilt disease incidence and other important yield traits. Out of 45 hybrids, KP_4HM-15 × MM-202, KP_4HM-15 × Kajri Sel. 1, MM-314 × KP_4HM-15, and Kajri Sel. 1 × MM-202 were best performing resistant hybrids for yield and quality traits with least incidence of fusarium wilt disease. Based on the results, we concluded that, novel putative resistant genes prevail in Indian germplasm which can further be mapped for the identification of linked markers to strengthen the hybrid development program against newly evolving pathogenic races in muskmelon and cantaloupe.

Keywords: Fusarium wilt, *Fusarium oxysporum* f.sp. *melonis*, Hybrid development, F-65, Hemed, Snapmelon

INTRODUCTION

Muskmelon, a member of genus *Cucumis* and family Cucurbitaceae is considered as "wholesome food" due to magical health benefits (Gul and Monga, 2014; Maran and Priya, 2015; Guruvayoorappan *et al*., 2015). Short crop duration, high crop production potential and sweet taste, it is designated as commercial dessert fruit signature (Mallick *et al*., 1984) with rich source of dietary fiber, vitamins, and minerals, *viz*., Ca, P, and Fe (Pitrat, 2008). Melon exhibits a wide biochemical, morphological, and physiological diversity (Eduardo *et al*., 2007).

Muskmelon is prone to many diseases which affect yield and quality of fruits. Among all, fusarium wilt (*Fusarium oxysporum* f. sp. *melonis*) (*Fom*) (Kalia *et al*., 2017) is the most devastating disease which causes 80-100 percent yield loss (Sherf and Macnab, 1986; Appel and Gordon, 1995; Zitter, 1999). Muskmelon wilt pathogen is a cosmopolitan species (Booth, 1971) and comprises of both pathogenic and non-pathogenic isolates (Gordon and Martyn, 1997). After penetration, the fungi grow inside the xylem vessels and later invade entire plant that produces typical wilt symptoms (Gordon and Okamoto, 1990). Disease development is enhanced by high nitrogen, low Ca and K levels in the sick soil (Sherf and Macnab, 1986). Therefore, from last half-century, host resistance breeding is an effective and economically viable strategy against newly developed or unidentified *Fom* races.

Many Indian germplasm (MR-1 (PI 124111), PI 164323, PI 164723, PI 124112, IC 274014, WM 7, WM 9) are being utilized in various resistant breeding strategies around the continents (Yousif *et al*., 2007; McCreight *et al*., 2008; Lopez *et al*., 2015; Romay *et al*., 2019). Though India is a secondary center of origin with a sizable diversity (Ganesan, 1991), there are no reports of using resistant melon germplasm for hybrid generation against unknown race(s) of *Fom* from India (Patel *et al*., 2017). Hence, the present study was designed with an objective to screen and identify resistant sources against local *Fom* isolate and their use in development of hybrids and testing under wilt sick plot for disease and yield related traits.

MATERIALS AND METHODS

Experimental location

The artificial screening and field experiment were conducted at Vegetable Research Farm, Punjab Agricultural University, Ludhiana, India (30º 54' North latitude, 75º 48' East longitude and 247 m

above MSL). The location falls under Indo-Gangetic plains and comprises of sub-tropical climate with 755 mm annual rainfall. The farm soil was sandy loam with low available N and organic matter, medium amount of available P and high K with normal pH range of 6.5-7.5.

Plant material

Fifty melon (*Cucumis melo* L.) accessions (37 accessions of var. *melo*, seven var. *momordica*, two each of *reticulatus* and *inodorus* and one each of *cantalupensis* and *callosus* were obtained from diverse sources (**Table 1**). It includes *Fom* differential Hemed (resistance against *Fom* race 0 and 2), and F-65 (resistance against *Fom* race 0 and 1) and EinDor (susceptible).

Table 1: List of melon germplasm, their source, and AUDPC score

S. No.	Designation	Var group	Source Country	AUDPC	Sr	Designation	Var group	Source Country	AUDPC
1	PS	*melo*	India	837.50	26	IC-267375	*melo*	India	0.00
2	Kajri Sel. 1	*melo*	India	0.00	27	IC-267379	*melo*	India	837.50
3	MS-5	*melo*	USA	1004.17	28	IC-267397	*melo*	India	866.67
4	NDM-18	*melo*	India	841.67	29	IC-320114	*melo*	India	1037.50
5	NDM-21	*melo*	India	0.00	30	MS-1	*melo*	India	820.83
6	PM	*melo*	India	704.17	31	MM-201	*melo*	India	608.33
7	KP_4HM-15	*melo*	India	0.00	32	MM-202	*melo*	India	225.00
8	Hara Madhu	*melo*	India	616.67	33	MM-136	*melo*	India	658.33
9	Hari Patti	*melo*	India	695.83	34	MM-137	*melo*	India	1033.33
10	Narika Col-1	*melo*	India	987.50	35	MM-312	*melo*	India	904.17
11	Canary Yellow	*melo*	Canada	850.00	36	MM-314	*melo*	India	204.17
12	MM-28	*melo*	India	562.50	37	MM-321	*melo*	India	225.00
13	MM-315	*melo*	India	1008.33	38	Hemed	*cantalupensis*	Israel	850.00
14	MM-601	*melo*	India	658.33	39	EinDor	*reticulatus*	Israel	600.00
15	MM-3864	*melo*	India	537.50	40	F-65	*reticulatus*	Israel	983.33
16	MM-3917	*melo*	India	745.83	41	MM-3013-1	*inodorus*	Afghanistan	1033.33
17	MM-3968	*melo*	India	541.67	42	MM-3013-2	*inodorus*	Afghanistan	733.33
18	MM-4021	*melo*	India	654.17	43	IC-267364	*momordica*	India	512.50
19	MM-4216	*melo*	India	262.50	44	IC-267378	*momordica*	India	1070.83
20	MM-4276	*melo*	India	770.83	45	IC-274034	*momordica*	India	562.50
21	MM-4279	*melo*	India	866.67	46	IC-320165	*momordica*	India	441.67
22	MM-4305	*melo*	India	420.83	47	KP-9	*momordica*	India	858.33
23	IC-255414	*melo*	India	904.17	48	SM-2012-12	*momordica*	India	120.83
24	IC-267357	*melo*	India	775.00	49	SM-2013-1	*momordica*	India	395.83
25	IC-267359	*melo*	India	862.50	50	WM-2014-1	*callosus*	India	25.00

Note: PS = Punjab Sunehri and PM = Pusa Madhuras

Artificial screening experiment

The pathogen was isolated from muskmelon disease plant and pure culture was maintained and identified on morphological basis. For artificial screening, sowing of seed in sterilized vermiculite media was done in two sets i.e., inoculated and non-inoculated (control) treatment with four replications. The concentration of conidia in the suspension culture was adjusted to 10^6 spore ml^{-1} (Yang *et al*., 2022) using hemacytometer for plant inoculation with sterile distilled water. At cotyledonary stage, the roots were washed and dipped into the inoculum for 5 minutes (Sekhon and Singh, 2009). Disease symptoms were assessed by using descriptive scale proposed by Najafinia and Sharma (2009) with 0 to 4 disease rating scale (0 = healthy; 1 = leaf chlorosis and browning of lower vessels; 2 = initial leaf necrosis and internal browning of upper vessels; 3 = Complete necrosis and initial wilting and 4 = death of the plant). Using the disease rating scale, Area Under Disease Progress Curve (AUDPC) was also calculated.

Field Experiment

Eight resistant and two susceptible lines identified after artificial screening were used for hybrid breeding programme (hand emasculation and pollination except in male sterile line) in half-diallel mating design. These hybrids were screened for disease, yield, and quality traits under wilt sick plot for two consecutive years in three replications. Three samples of each treatment were processed for assessment of quality traits. Different procedures were followed for the assessment of quality traits i.e., titrable acidity by Srivastava and Kumar (2006), ascorbic acid by Heinze *et al*. (1944), β-carotene content by Watanabe *et al*. (1991), and total soluble solids (TSS) was estimated by hand refractometer (Erma 0-32˚Brix).

Statistical analysis

AUDPC was computed as suggested by Shaner and Finney (1977).

$$\text{AUDPC} = \sum_{i=1}^{n-1}\left[\frac{(t_{i+1}-t_i)(d_i+d_{i+1})}{2}\right]$$

Where, t = days after transplanting, d = percentage of disease severity caused by *F. oxysporum* on each recording date (i) and n = number of estimations.

The percent disease severity and disease incidence was computed using the formulae:

$$\text{Disease Severity (\%)} = \frac{\sum \text{Sum of all numerical rating}}{\text{Total number of plant observed} \times \text{Maximum rating}} \times 100$$

$$\text{Disease Incidence (\%)} = \frac{\text{Number of infected plants}}{\text{Total number of plant observed}} \times 100$$

The ANOVA (pooled) was performed and mean were weighed using Scott-Knott cluster test (Scott and Knott, 1974). The genetic component analysis was carried out using Windostat software (Version 8.6). The mean performance of parents was compared with Duncan test using SPSS software (Version 27).

RESULTS

Artificial screening against fusarium wilt disease

In muskmelon, artificial inoculation at cotyledonary stage with 10^6 spores ml^{-1} clearly differentiated the resistant and susceptible genotypes (**Figure 1**). Initial symptoms were observed in Punjab Sunehri (PS) after 10 dpi (days post-inoculation) which got intensified and complete death of plants occurred 20 dpi. *Cucumis melo* var. *momordic*a was assumed to be resistant while in our investigation out of seven, one accession (SM-2012-12) was found highly resistant, another (SM-2013-1) moderately resistant and five accessions (IC-207364, IC-267378, IC-274034, IC-320165 and KP-9) were susceptible to fusarium wilt disease.

Diseases severity at 15 dpi was zero in Kajri Sel-1, NDM-21, KP_4HM-15, MM-601, IC-267375, SM-2012-12, and WM-2014-1, while, it was less than 10% in MM-314 (1.67%), MM-202 (5.00%), MM-321 (5.00%), IC-320165 (6.67%), MM-4216 (6.67%), and SM-2013-1 (8.33%). Further scoring at 30 dpi, nine accessions viz., Kajri Sel-1 (0.00%), NDM-21 (0.00%), KP_4HM-15 (0.00%), IC-267375 (0.00%), WM-2014-1 (3.33%), SM-2012-12 (15.00%), MM-314 (20.00%), MM-202 (21.67%), and MM-321 (21.67%) exhibited low disease severity (< 25 %), while, three accessions viz., MM-4216 (28.33%), MM-4305 (35.00%), and SM-2013-1 (36.67%) recorded intermediate (25-50 %) at 30 dpi (**Figure 1**) and considered as resistant and moderately resistant, respectively.

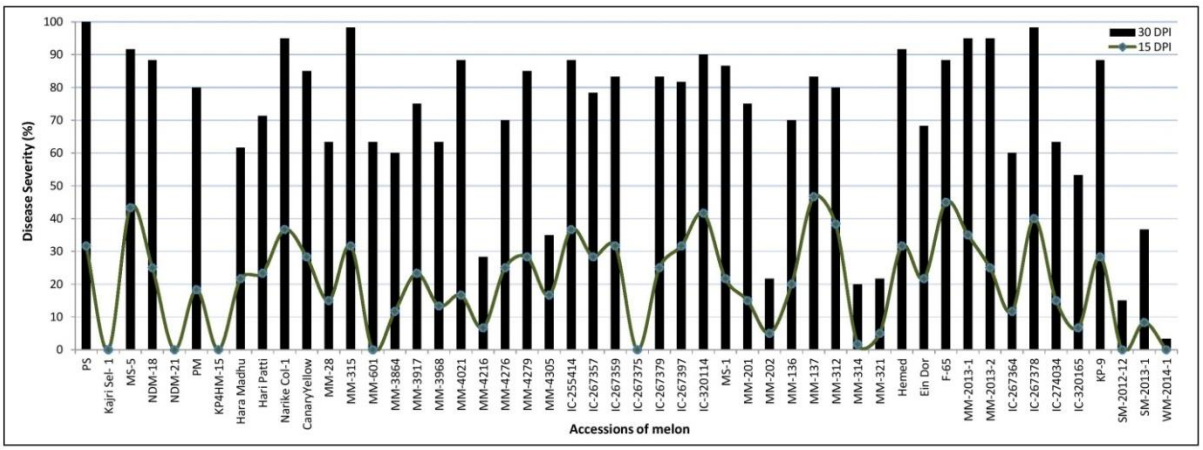

Figure 1: Fusarium wilt disease severity (%) at 15 and 30 dpi in accessions of melon.

As per AUDPC value, eight percent of the accessions scored zero and rest scored maximum value (**Table 1**). Kajri Sel-1, KP_4HM-15, NDM-21, and IC-267375 exhibited high resistance among all accessions while five accessions showing 200-400 AUDPC values were moderately resistant. The per

cent disease severity and AUDPC value have positive significant correlation with above resistance class, except that of MM-4305, which showed 35.00% disease severity and 420.83 AUDPC value. However, MM-4305 was statistically *at par* with SM-2013-1, MM-202, MM-314, MM-321, SM-2012-12, MM-4216, and IC-320165 on the basis of disease severity at 30 dpi (**Figure 1**).

Field experiment

The pooled ANOVA for the experimental design has been given in **Table 2** for all the traits. The mean square (environment) was non-significant for all the traits except β-carotene content. Mean squares (treatment: genotype) were found significant for all the studied traits. The mean square due to genotype × environment, variance due to parents × environment and the hybrids × environment portraying non-significant performance of parents and hybrids across environment for all the traits. The mean values of hybrids for all the studied traits showed desirable increase over parental mean.

Quadratic component of variance is illustrated in **Table 3**. The GCA variance (σ^2g) was lower than SCA variance (σ^2s) for all the studied traits. Thus the ratio of variance due to GCA and SCA (σ^2g /σ^2s) was less than unity. In present study, dominance variance was higher for the traits fruit yield, average fruit weight, number of fruits vine^{-1}, titrable acidity and ascorbic acid content. Low to moderate range of heritability (h^2) was observed for most of the traits except β-carotene content (61.41%) since these traits have higher additive variance as compared to dominance variance. The correlation study (**Figure 2**) revealed that fusarium wilt incidence (FWI) under field (sick plot) condition was positively correlated with TSS, β-carotene content and titrable acidity while negatively with fruit yield, average fruit weight, number of fruits and ascorbic acid content.

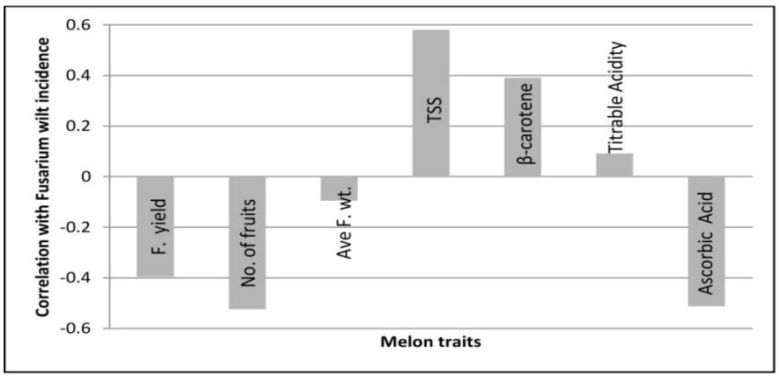

Figure 3: Correlation of Fusarium wilt incidence with other important melon traits.

Parents and hybrids performance under sick plot

The mean performance (pooled) of parents involved in half diallel program and superior hybrids (based on FWI and others traits) along with two standard check is concealed in **Table 4**. Fusarium wilt incidence in standard checks *viz*., MH-27 and Farmers' Glory was 3.74 and 3.75, respectively. Among parents, MS-1 have high disease incidence (3.98) which is *at par* with Punjab Sunehri (3.70) while MM-321 has no disease incidence followed by SM-2012-12 (0.50). During two-year evaluation of 45 hybrids under wilt sick plot, only six hybrids i.e., MM-321× Kajri Sel. 1, MM-321 × SM-2012-12, MM-314 × MM-202, MM-314 × SM-2012-12, KP_4HM-15 × MM-202, and Kajri Sel. 1 × SM-2012-12 were symptomless (**Figure 3**). The disease scale was ≤1 in twelve, 1.01-2 in eleven, and ≥2 in 16 hybrids.

Among parents, SM-2012-12 has maximum yield (36.56 kg plot^{-1}), number of fruits vine^{-1} (4.37) and ascorbic acid (37.18 mg 100^{-1} ml) whilst NDM-21 has highest average fruit weight (0.97kg) and titrable acidity (31.78 mg 100^{-1} ml). Though being susceptible parents, Punjab Sunehri have high TSS (11.63˚Brix) and β-carotene content (2.73 mg 100^{-1} g). Among 45 hybrids, four best performing hybrids were illustrated (**Table 4**) on the groundwork of yield and quality traits. Out of them, KP_4HM-15 × MM-202 have no disease incidence along with highest average fruit weight (0.74kg), β-carotene content (2.98 mg 100^{-1} g), and good TSS (12.28˚Brix) while KP_4HM-15 × KajriSel 1 have maximum fruit yield (24.14 kg plot^{-1}), number of fruits (3.52) and TSS (13.56˚Brix) and negligible (0.25) disease incidence. The other two hybrids [Kajri Sel. 1 × MM-202 (DI = 0.25) and MM-314 × KP_4HM-15 (DI = 0.50)] have less disease incidence with good yield and quality traits. The above identified hybrids were better than standard checks (MH-27 and Farmers' Glory) in terms of disease incidence and important quality traits.

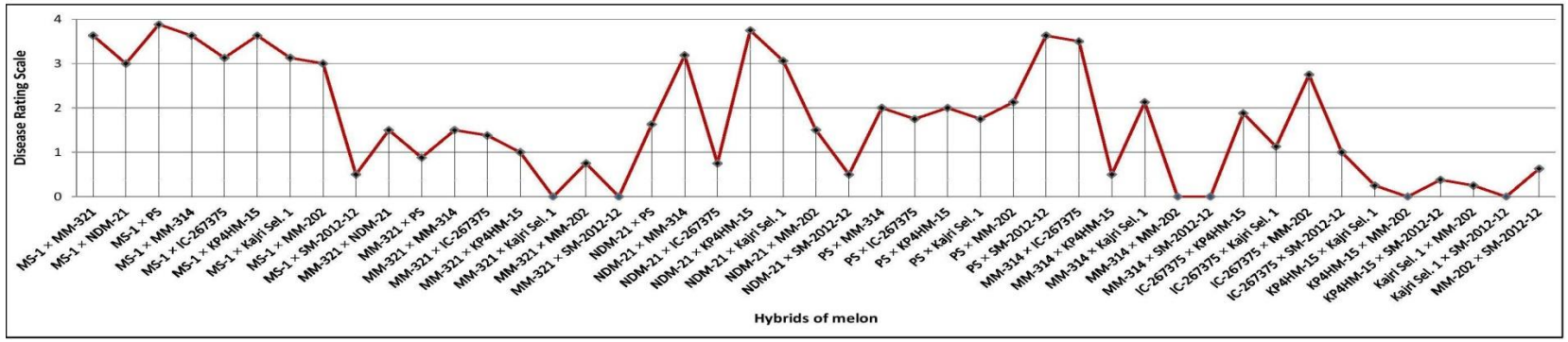

Figure 3: Fusarium wilt incidence in 45 hybrids of melon under wilt sick plot.

Table 2: ANOVA (pooled) for the experimental design, mean and range of eight important horticultural traits of melon evaluated in half-diallel for two consecutive years at PAU, Ludhiana, India.

Source of variation	d.f.	Fusarium wilt incidence	Fruit yield (kg plot^{-1})	Number of fruit vine^{-1}	Average fruit weight (kg)	Total soluble solids (°Brix)	β-carotene content (mg 100^{-1} g)	Titrable Acidity (mg 100^{-1} ml)	Ascorbic acid (mg 100^{-1} ml)
					Mean sum of squares				
Environments	1	0.55	1.05	0.02	0.004	0.03	0.062*	21.11	16.57
Replication within environments	2	0.05	1.56	15.39	0.004	0.70	0.008*	61.99**	5.27
Genotype	54	8.23**	184.73**	157.34**	0.08**	17.87**	2.784**	298.35**	344.04**
Genotype × environment	54	0.04	0.61	3.57	0.002	0.42	0.001	2.44	1.10
Parents × environment	9	0.04	1.29	1.25	0.001	0.22	0.002	5.15	1.21
Hybrids × environment	44	0.03	0.49	4.13	0.002	0.45	0.001	1.92	1.07
Parents vs Hybrids × environment	1	0.03	0.06	0.06	0.002	0.80	0.000	0.75	1.56
Error	108	0.20	2.80	6.23	0.002	0.40	0.002	3.09	2.01
					Mean and range values				
General mean		1.92	24.40	35.18	0.70	9.26	0.95	20.19	18.45
Parent mean		2.05	22.02	33.42	0.67	8.85	0.71	18.53	17.85
Hybrid mean		1.77	25.02	36.22	0.69	9.31	1.01	20.68	18.09
Range Minimum value		0.00	12.22	19.00	0.39	4.57	0.07	5.25	2.90
Maximum value		4.87	40.03	48.75	1.03	13.56	2.98	40.50	37.17

Table 3: Genetic analysis of eight important horticultural traits of melon evaluated in half-diallel for two consecutive years

Character	Genetic components						
	σ^2_{GCA}	σ^2_{SCA}	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ_e^2	σ^2_A	σ^2_D	h^2_{bs} (%)
Fusarium wilt incidence	0.65	0.86	0.75	0.10	1.29	0.86	59.79
Fruit yield (kg plot^{-1})	7.75	35.98	0.22	1.4	15.5	35.98	30.00
Number of fruit vine^{-1}	4.44	34.68	0.13	3.12	8.88	34.68	19.62
Average fruit weight (kg)	0.00	0.01	0.33	0.00	0.01	0.01	38.27
Total soluble solids (°Brix)	1.37	1.96	0.70	0.2	2.73	1.96	55.79
β-carotene content (mg 100^{-1} g)	0.23	0.29	0.80	0.00	0.46	0.29	61.41
Titrable acidity (mg 100^{-1} ml)	16.96	47.86	0.35	1.54	33.93	47.86	40.91
Ascorbic acid (mg 100^{-1} ml)	8.11	83.16	0.10	1.01	16.21	83.16	16.23

Table 4: Pooled mean performance of parents involved in hybrid breeding program, superior hybrids and checks under wilt sick plot

Traits	Fusarium wilt incidence	Fruit yield(kg plot^{-1})	Number of fruits vine^{-1}	Ave Fruit weight (kg)	Total soluble solids (°Brix)	β-carotene content (mg 100^{-1}g)	Titrable Acidity (mg 100^{-1} ml)	Ascorbic Acid (mg 100^{-1} ml)
Parents								
MS-1	3.98 f	17.98 e	3.00 e	0.59 de	9.88 c	1.14 c	12.38 c	14.90 e
MM-321	0.00 a	16.54 ef	3.92 b	0.42 f	6.40 f	0.24 d	13.45 c	28.78 c
NDM-21	2.63 e	24.65 c	2.52 f	0.97 a	9.39 cd	0.12 ef	31.78 a	5.39 h
Punjab Sunehri	3.70 f	12.22 g	3.20 d	0.39 f	11.63 a	2.73 a	28.86 a	16.93 d
MM-314	2.63 e	21.38 d	3.45 c	0.63 cd	7.63 e	0.12 ef	7.26 d	8.25 g
IC-267375	1.63 d	28.51 b	3.55 c	0.79 b	8.76 d	0.21 de	21.28 b	11.71 f
KP_4HM-15	1.25 cd	15.93 f	2.37 f	0.68 c	9.75 c	0.12 ef	13.38 c	32.55 b
Kajri Sel. 1	1.63 d	24.24 c	3.00 e	0.82 b	9.53 cd	0.11 ef	13.38 c	15.53 de
MM-202	0.88 bc	22.26 d	4.02 b	0.56 e	10.79 b	2.20 b	12.76 c	7.25 g
SM-2012-12	0.50 b	36.56 a	4.37 a	0.84 b	4.73 g	0.08 f	30.75 a	37.18 a
Best identified Hybrids								
KP_4HM-15 × MM-202	0.00	19.99	2.73	0.74	12.28	2.98	11.18	18.98
KP_4HM-15 × Kajri Sel. 1	0.25	24.14	3.52	0.67	13.56	0.10	11.03	5.65
Kajri Sel. 1 × MM-202	0.25	21.88	3.42	0.68	11.01	1.23	12.48	11.26
MM-314 × KP_4HM-15	0.50	23.04	3.40	0.69	10.84	0.90	23.38	26.51
Standard Check								
MH-27	3.74	26.61	2.67	0.88	9.50	0.69	18.43	8.72
Farmers Glory	3.75	19.51	1.90	1.03	10.55	1.26	13.28	35.29

Duncan's test: same letter indicates no significant difference between treatments ($P < 0.05$)

DISCUSSION

The artificial screening was done at cotyledonary stage as being most fragile growing period (Eid, 2019; Zink, 1992) of any crop plant. The used concentration for artificial inoculation with 1×10^6spores ml^{-1} was also documented by Yang *et al*., (2022) and differentiated the studied germplasm into various resistant and susceptible classes. Such variability within germplasm was observed against local *Fusarium oxysporum* and been reported by Gallo *et al*. (2012) and those putative resistant sources with many resistant gene(s) (Patel *et al*., 2017) can be utilized. Similar variable reaction of germplasm to Fusarium wilt results were quoted by Park *et al*. (2013) who screened 65 melon germplasm and found 35 highly resistant, one moderately resistant, and rest were having susceptible reaction. This variation could be due to production of some organic chemicals via plant defense mechanism that induces resistance against *Fom* (Rajsree *et al*., 2016; Kalia *et al*., 2017).

The variation in disease progress in resistant and susceptible lines was due to higher thickness of epidermis and cortex tissue (Kalia *et al*., 2017). The rapid progression of disease curve increased AUDPC value at faster rate in susceptible germplasm and these findings were identical with those of Chauhan *et al*. (2020) for white mold disease in common bean. Thus, lower AUDPC values have significant relation with resistant classes. The accessions Hemed and F-65 possess *Fom*-1 and *Fom*-2 gene, respectively (Deol *et al*., 2022) were found susceptible to local *Fusarium oxysporum* isolate, this implies that the new race or pathotype can be present under Punjab, India conditions. Consequently, it shows that accessions IC-267375, NDM-21, KP_4HM-15, and Kajri Sel-1 may possess some different resistant gene other than *Fom*-1 and *Fom*-2. As like other Indian germplasm (MR-1), these can be useful in strengthening fusarium wilt resistance breeding programme of muskmelon under national and global level.

Germplasm from *Cucumis melo* var *momordica* group was reported to be resistant to fusarium wilt disease (Deol *et al*., 2022) and thus, have higher yield and number of fruits as compared to other germplasm (Dhillon *et al*., 2015). Ozbahce *et al*. (2021) stated that fusarium wilt resistant rootstock improves yield and quality traits. Among 45 hybrids, the best identified hybrids have higher resistance and good TSS along with comparable yield with the standard checks which could be due to uninterrupted plant growth. Resistant hybrids have higher yield and better-quality traits (Kalia *et al*., 2017) as compared to susceptible ones (Choudhary *et al*., 2020). Similarly, Kaur *et al*., (2022) observed noticeable correlation between ascorbic acid and disease resistance. Thus, resistant parent involved in hybrid program will improve yield and quality parameter.

The mean square (environment) was non-significant for all the traits except β-carotene content which depicts that environment in 2 years were almost similar. In the present study, high dominance variance for fruit yield, average fruit weight, number of fruits $vine^{-1}$, titrable acidity, and ascorbic acid content denotes non-additive gene action thus, improvement *via* heterosis breeding can be done whereas fusarium wilt incidence, TSS and β-carotene content have higher additive variance and hence, can be improved via selection methods.

The pooled ANOVA with non-significant mean square due to environment depicts that environment was more or less similar in two studied years and β-carotene content was greatly affected by slight change in environment (Wibowo *et al*., 2022). Significant mean squares due to genotypes showed potential genetic variability among parents and their hybrids that prove hybrid breeding can be effective for the studied traits. The mean square due to treatment × environment (i.e., parents × environment and hybrids × environment) was non-significant for all the studied traits, which illustrates uniform response pattern across the environment (Iqbal *et al*., 2022) due to stable genetic combination of plant. Contrarily, Mohammadi *et al*. (2014) found significant interaction which suggested that the genotypes were influenced by environment.

The variance due to GCA (σ^2_{GCA}) was lower than SCA (σ^2_{SCA}) indicating significance of heterosis breeding rather than single plant selection. Pouyesh *et al*. (2017) and Akrami and Arzani (2019) also found dominant or non-additive gene effect for fruit yield, average fruit weight, number of fruits $vine^{-1}$, titrable acidity and ascorbic acid content. The ratio σ^2_D/σ^2_A is more than unity suggesting predominance of non-additive effects (Islam *et al*., 2022). In traits like β-carotene content and FWI, both additive (major effect) and dominance variance were present thus mass selection with open pollination can be followed.

It was concluded that AUDPC value of *Fom* differential (Hemed, EinDor, and F-65) was > 600 with higher disease severity against local *Fom* isolate. This signifies presence of new *Fom* pathogenic race or pathotype. Out of 45 hybrids generated from eight resistant and two susceptible accessions, KP_4HM-15 × MM-202, KP_4HM-15 × Kajri Sel. 1, MM-314 × KP_4HM-15, and Kajri Sel. 1 × MM-202 were best performing resistant hybrids for yield and quality traits with least incidence of fusarium wilt disease. The novel

resistant gene may prevail in Indian germplasm that can be used to strengthen the hybrid development program and development of novel markers against newly evolving pathogenic races in muskmelon and cantaloupe.

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