

# **Snampelon (*Cucumis melo* L. *Momordica* Group), an indigenous cucurbit from India with immense value for breeding**

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6 **Snapmelon (*Cucumis melo* L. Momordica Group), an indigenous cucurbit**

7 **from India with immense value for breeding**

8

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21

22 **Keywords:** Disease resistance, pest resistance, molecular markers, resistance to abiotic  
23 stress, fruit quality

24 **Abstract**

25 **Snampmelon**(*Cucumis melo* L. Momordica Group;  $2n = 2x = 24$ ) is native to India,  
26 where it is widely cultivated and is commonly called ‘phut,’ which means to split.

27 **Immature fruits are cooked or eaten raw. In this paper we review the wealth of genetic**  
28 **resources in Indian snampmelon landraces for resistance to fungal and viral diseases,**  
29 **nematodes, and insects, and tolerance to drought, soil salinity, and high temperature.**

30 **Global melon breeding programs have transferred many of these qualities into open-**  
31 **pollinated and hybrid varieties of sweet melon cultivated in Africa, Asia, Australia,**

32 **Europe, and the Americas. Snampmelons are sources of high fruit acidity, a trait that has**  
33 **been utilized to breed uniquely flavored melon cultivars. High frequencies of unique**  
34 **alleles have been identified in snampmelon collections from various parts of India.**

35 **Snampmelon can serve as a source of new resistance genes to combat pathogens and**  
36 **pests, and to strengthen crop resilience against climate change. More effort is needed to**  
37 **collect, characterize, evaluate and preserve snampmelon diversity in genebanks.**

38

## 39 INTRODUCTION

40 Snapmelon is native to India, which is considered the center of domestication of  
41 melon by some researchers with the earliest melon remains at the Indus Valley site of  
42 Harappa dated between 2300 and 1600 BC (Vishnu-Mittre, 1974). It is widely cultivated in  
43 various Indian states such as Rajasthan, Gujarat, Punjab, Haryana, Uttar Pradesh, West  
44 Bengal and some other northeastern states. It is also cultivated in other countries of South-  
45 East Asia, for instance Myanmar (Yi et al., 2009) and Vietnam (Phan et al., 2010). It is  
46 commonly called ‘phut,’ which means to split. Fruit cracking is either longitudinal or random  
47 starting in the middle of fruit, though in some instances only skin peeling (longitudinal or  
48 random) occurs (Dhillon et al., 2007). It is also known by other names such as ‘phoot kakari’  
49 or ‘kakadia.’ Several types of fruit shape are found in snapmelon viz. round, acorn, oblate,  
50 ovate, elongated, elliptical and pyriform (Dhillon et al., 2007). Fruit flesh color varies from  
51 cream and yellow to orange. Vines are monoecious. Immature fruits may be eaten raw or  
52 cooked, or pickled or dehydrated for off-season use. After removing the coat, seeds are used  
53 in bakery products and the traditional drink ‘thandai’. Fruits are sources of vitamin C, iron  
54 and calcium (Goyal and Sharma, 2009). We review the wealth of genetic resources in Indian  
55 snapmelon landraces for resistances to fungal and viral diseases, nematodes and insects,  
56 tolerance to drought and salinity, genes for unique flavors, and the present status of genetic  
57 diversity of snapmelons in different parts of India.

## 58 Fungal disease resistance

59 Powdery mildew is a serious foliar disease of melon worldwide (Sitterly, 1978). It  
60 affects the plant canopy and subsequently the fruit yield and quality. Cucurbit powdery

61 mildew is mainly incited by two fungal species: *Podosphaera xanthii* (syn. *Sphaerotheca*  
62 *fuliginea* auct.p.p.) and *Golovinomyces cichoracearum* (syn. *Erysiphe cichoracearum*  
63 auct.p.p.), the first species being the most frequent on melon. More than 30 races of each  
64 pathogen have been identified on melon (Lebeda and Sedláková, 2004; McCreight et al.,  
65 2012). Powdery mildew was first noted on an epidemic scale in 1925 in the melon production  
66 area in the Imperial Valley of California where it remained a serious problem for several  
67 successive years (Jagger, 1926; Jagger and Scott, 1937). A source of genetic resistance was  
68 identified in accession Calif. 525, which was a self-pollinated increase of 'Big Round' that  
69 was brought to the United States by D.N. Mehta (Second Economic Botanist, Nagpur  
70 Provinces, India) an Indian student of J.T. Rosa (Swarup, 2000; Kathleen R. Reitsma,  
71 personal communication; I.C. Jagger, unpublished pedigree note). This germplasm was  
72 collected from Kathiawar region of Gujarat state in India. Powdery mildew-susceptible,  
73 orange flesh 'Hale's Best' melon (*C. melo* Reticulatus group) was crossed with Calif. 525  
74 and the F<sub>1</sub> was resistant to the local strain of powdery mildew. A resistant F<sub>2</sub> selection that  
75 produced large elongated fruits was backcrossed to 'Hale's Best' to recombine powdery  
76 mildew resistance with superior horticultural qualities of 'Hale's Best'. Seven generations of  
77 inbreeding and selection led to the development and release of 'Powdery Mildew Resistant  
78 Cantaloupe No. 45' ('PMR 45') to the western United States melon industry in 1935 (Jagger  
79 and Scott, 1937).

80 Race 2 of *P. xanthii* overcoming the resistance of 'PMR 45' appeared in Imperial  
81 Valley in 1938 (Jagger et al., 1938). Resistance to this new race was identified in 'Piria', that  
82 was donated by D. Mehta of Nagpur, Madhya Pradesh, India to the United States in 1929 and

83 designated PI 79376 (Pryor et al., 1946; USDA, ARS, 2014). Resistance to race 2 was  
84 combined with resistance to race 1 in melon cultivars ‘PMR 5’ and ‘PMR 6’, released in  
85 1942, and ‘Campo’ and ‘Jacumba’ released in 1964 in the United States (Bohn et al., 1965).  
86 PI 124111 (MR-1) from the Bihar state of India, was resistant to 26 races of *P. xanthii*  
87 (McCreight et al., 2012). This accession was also resistant to several races of *G.*  
88 *cichoracearum* (Pitrat et al., 1998; Lebeda et al., 2012).

89 Powdery mildew resistance genes identified in Calif. 525 and PI 79376 were introgressed in  
90 many melon breeding lines and cultivars (Harwood and Markarian, 1968) and are still  
91 prevalent in modern melon releases in United States: ‘Georgia 47’ (Anon. 1954), ‘Home  
92 Garden’ (Ivanoff, 1957), ‘Gulfstream’ and ‘Planter Jumbo’ (Nugent, 1994), ‘Mainstream’  
93 and ‘Edisto 47’ (Nugent et al., 1979), and recently released ‘Chujuc’ and ‘Pacal’ (Crosby et  
94 al., 2007, 2008). Moderately powdery mildew-resistant melon cultivar ‘Punjab Sunehri’,  
95 released in 1975 in Punjab state of India (Nandpuri et al., 1975; Waraitch et al., 1977), has  
96 ‘Edisto’ in its pedigree. This orange flesh powdery mildew-resistant cultivar remained  
97 popular with Indian growers and consumers for two decades. Race 1 and race 2 powdery  
98 mildew-resistant Reticulatus Group cultivars PMR 5, Dulce, Gulfstream and Jacumba were  
99 resistant to a race-unknown population of powdery mildew in India in a controlled  
100 inoculation experiment (Waraitch et al., 1977). PI 414723 was also resistant to many races of  
101 *P. xanthii* (McCreight et al., 2012). Several race-specific genes have been described in these  
102 accessions (Dogimont, 2010-2011). Fergany et al. (2011) reported two additional snapmelon  
103 accessions resistant to powdery mildew: AM 22 to races 1 (strain Sm3) and 3 (strain  
104 00Sm39) and AM 86 resistant to races 1 and 5 (strain 98Sm65). A large number of powdery

105 mildew resistance genes have been described (Dogimont 2010-2011), most of them are likely  
106 allelic. Several QTLs conferring resistance to different races have been mapped in melon  
107 Linkage Groups (LG) II, V and XII (Perchepped et al., 2005; Fukino et al., 2008; Zhang et al.,  
108 2013)

109 Downy mildew caused by *Pseudoperonospora cubensis* (Berk. & Curtis) Rostov. is a  
110 common foliar disease of melons in humid production areas of the world. Six pathotypes  
111 have been identified: 1 and 2 in Japan, 3 and 6 in Israel, and 4 and 5 in the United States  
112 (Cohen et al., 2003). These pathotypes do not colonize *Luffa* ssp. (Thomas et al., 1987),  
113 whereas the Indian and Chinese isolates of cucurbit downy mildew are able to colonize *Luffa*  
114 ssp. and are considered as distinct races. Shetty et al. (2002) confirmed that the downy  
115 mildew races in U.S. are distinct from the race in Asia, whereas the race in Poland is similar  
116 to the races in the U.S. Four partially dominant resistance genes have been identified in three  
117 accessions of snapmelon: PI 124111 (*Pc-1*, *Pc-2*), PI 414723 (*Pc-3*), and 5-4-2-1 (*Pc-5*)  
118 (Dogimont, 2010-2011). Resistance to *P. cubensis* races 3 and 6 in Israel has been found in  
119 PI 124111F controlled by two R genes, *At1* and *At2* (Taler et al., 2004). Interestingly, PI  
120 124111F, reported resistant to six pathotypes of *P. cubensis*, was susceptible to an Indian  
121 isolate of *P. cubensis* (More, 2002), but IC 267353, IC 274029, KP7, and B-159 were  
122 resistant to this Indian isolate (Dhillon et al., 2007; Pandey et al., 2008). It will be interesting  
123 to test the reaction of these genotypes to the six pathotypes of *P. cubensis* available in the  
124 other parts of the world.

125 Melon Fusarium wilt (MFW) is caused by the soil-borne fungal pathogen *Fusarium*  
126 *oxysporum* Schlechtend:Fr.f.sp.*melonis* (H.N. Hansen) W.C. Snyder & H.N. Hans (*Fom*).

127 The pathogen survives in the soil as chlamydospores and is able to colonize crop residues and  
128 roots of most of crops cultivated in rotation with melon (Gordon et al., 1989), thus rendering  
129 crop rotation as a limited tool to manage this disease. Soil solarization can reduce soil  
130 inoculum but is limited by local climate factors, i.e., temperature and relative humidity  
131 (Tamietti and Valentino, 2006) and it is not suitable for intensive vegetable farming systems  
132 where there is insufficient time for effective soil solarization. Grafting of susceptible melon  
133 scions onto Fusarium wilt-resistant rootstocks is an effective control strategy for MFW, but  
134 the additional cost limits this approach to very high value melon cultivars. Use of resistant  
135 varieties is regarded as the most effective strategy to control this disease. MFW isolates have  
136 been designated into four physiological races: 0, 1, 2, and 1.2. Two dominant resistance  
137 genes, *Fom-1* and *Fom-2*, control resistance to races 0 and 2, and 0 and 1, respectively and  
138 were identified in PI 124111F and its derivative MR-1 (Cohen and Eyal, 1987; Zink and  
139 Thomas, 1990). *Fom-2* has also been reported in PI 414723. Using MR-1 and PI 414723,  
140 these two genes have been cloned using chromosome walking strategies and belong to the  
141 NB-LRR family (TIR subfamily for *Fom-1* and non-TIR for *Fom-2*) (Joobeur et al., 2004;  
142 Brotman et al., 2013). These *Fom* genes along with cucurbit powdery mildew resistance  
143 genes are routinely deployed in modern melon commercial hybrids. Accession AM 27  
144 exhibited uniform resistance to race 2 and segregated for resistance to race 1 (Fergany et al.,  
145 2011). Resistance to race 1.2 seems to have a complex genetic control what is hampering the  
146 development of reliable molecular markers and subsequent cloning (Oumouloud et al., 2013)

147 MFW and leafminer (*Liriomyza* spp) are the most devastating disease and insect pests  
148 of melon in India. The prevailing melon cultivars grown by Indian farmers (NS 7475, Punjab



149 Sunehri, Punjab Hybrid 1, Durgapur Madhu, Kashi Madhu, Pusa Madhurus, Arka Jeet, Arka  
150 Rajhans) are susceptible to MFW. Existing global melon genetic resources, including recent  
151 releases of seed companies, have been found susceptible in Indian field conditions (N.P.S.  
152 Dhillon, unpublished data; Arvind Kapur, personal communication).

153         There was a much lower incidence of MFW or *Monosporascus* sudden wilt, which is  
154 incited by *Monosporascus cannonballus* (Pollack & Uecker), exhibited by snapmelon  
155 germplasm compared with 100% loss of muskmelon (*Reticulatus* Group) landraces and  
156 varieties during melon germplasm collection expeditions in farmer's fields in the arid and  
157 semi-arid areas of Rajasthan and southern Punjab in India (N.P.S. Dhillon, unpublished data).  
158 Snapmelon accessions may have additional genes for resistance to MFW and *M.*  
159 *cannonballus*.

160         *Alternaria* leaf blight of melons caused by *Alternaria cucumerina* (Ellis & Everh.) is  
161 widespread in wet and warm conditions (20 to 30°C) areas having sandy soil such as  
162 southern India and southeastern United States (Thomas, 1996). Resistance to this fungal  
163 pathogen is controlled by the single dominant gene *Ac* in MR-1, which was derived from PI  
164 124111 (Thomas et al., 1990).

### 165 **Viral disease resistance**

166         Numerous viruses affect melons worldwide. Three kinds of virus symptoms generally  
167 appear on the vines: 1) mosaic on leaves associated with leaf and fruit discolorations and  
168 deformation, 2) yellowing of leaves coupled with leaf thickening, and 3) necrotic spots or

169 progressive necrosis resulting in vine death (Lecoq et al., 1998). Melon fields may be  
170 infected with more than one virus.

171 *Cucumber mosaic virus* (CMV) causes economic losses in melon worldwide.  
172 Resistance to CMV was first reported in accessions belonging to the Conomon Group from  
173 East Asia and is controlled by recessive oligogenes (Karchi et al., 1975; Dogimont et al.,  
174 2000; Essafi et al., 2008; Guiu-Aragonés et al., 2014). This resistance is effective against  
175 some CMV strains and is, thus, not easy to use for the development of commercial F<sub>1</sub>  
176 hybrids. Resistance to a broad spectrum of CMV strains likely will need the combination of  
177 genes from different CMV resistance sources.

178 Snapmelon accessions AM 25, AM 82, IC 274014, SM 67, SM 72, SM 73, SM 82,  
179 MM 3974, MM 3982 and MM 3994 were highly resistant to CMV (Dhillon et al., 2007,  
180 2009; Fergany et al., 2011; Malik et al., 2014). These accessions may contribute to a broad-  
181 based resistance against different strains of CMV prevailing in different parts of the world.

182 *Zucchini yellow mosaic virus* (ZYMV) is a serious virus of cucurbits worldwide  
183 (Desbiez and Lecoq, 1997). Three complementary, dominant genes in PI 414723 (*Zym-1*,  
184 *Zym-2*, and *Zym-3*) impart resistance to ZYMV (Pitrat and Lecoq, 1984; Danin-Poleg et al.,  
185 1997). Accessions IC 274007, IC 274014, and PI 179905 are potentially useful sources of  
186 resistance to ZYMV (Dhillon et al., 2007).

187 *Papaya ringspot virus* watermelon strain (PRSV-W), formerly *Watermelon mosaic*  
188 *virus 1*, is very common in the tropics (Lecoq et al., 1980). Two alleles, *Prv<sup>1</sup>* and *Prv<sup>2</sup>*, found  
189 in the weedy type melons PI 180280 and PI 180283, respectively, condition resistance to

190 PRSV-W (Kaan, 1973; Webb, 1979; Pitrat and Lecoq, 1983). PI 414723 has the *Prv*<sup>2</sup> allele  
191 (M. Pitrat, unpublished data) and this gene has been recently isolated from the Indian  
192 accession PI 414723, encoding for a NBS-LRR type protein (Brotman et al., 2013). Nine  
193 accessions from northern India segregated for resistance to PRSV-W: IC 267360, IC 267363,  
194 IC 267374, IC 267384, IC 274006, IC 274007, IC 274010, IC 274011 and IC 274013  
195 (Dhillon et al., 2007). The genetic relationships between genes in these accessions and *Prv*  
196 have not been established. Twenty-nine landraces from Kerala and Tamil Nadu states in  
197 southern India, exhibited necrotic symptoms in response to artificial inoculation with the  
198 potyvirus *Moroccan watermelon mosaic virus* (MWMV) (Fergany et al., 2011).

199 *Watermelon mosaic virus* (WMV), formerly *Watermelon mosaic virus 2*, is another  
200 widespread potyvirus of melons. Genetic resistance to WMV was reported in PI 414723  
201 (Munger, 1991) and is controlled by a single dominant gene, *Wmr* (Gilbert et al., 1994).

202 *Cucurbit aphid-borne yellow virus* (CABYV) is a worldwide important polerovirus of  
203 melons transmitted by aphids. 'Faizabadi phoont', and PI 414723 were reported resistant to  
204 CABYV (Dogimont et al., 1997).

205 *Watermelon chlorotic stunt virus* (WmCSV) is economically important in Yemen,  
206 Sudan, and Iran (Yousif et al., 2007). PI 414723 provided resistance during graft inoculation  
207 experiments and multiple field trials in Sudan (Yousif et al., 2007).

208 *Cucurbit leaf crumple virus* (CuLCrV) is a sweetpotato whitefly-transmitted  
209 begomoviruses of melon that have appeared in commercial melon fields in the southwestern  
210 United States, western Mexico, and Central America since 1977. PI124111, PI 179901, and

211 PI 414723 exhibited partial resistance to CuLCrV in naturally-infected field and controlled  
212 inoculation greenhouse tests. Resistance in PI 313970 (*Acidulus* Group) was conditioned by  
213 a single recessive gene and appeared allelic to that in the snapmelon accessions (McCreight  
214 et al., 2008).

215 *Cucumber green mottle mosaic virus* (CGMMV) is economically significant in  
216 greenhouse production (Hollings et al., 1975) and has been reported in Europe and Asia. A  
217 biological vector of this melon virus is unknown, but CGMMV is transmitted mechanically  
218 and through growing media (Lecoq et al., 1998). In early 1980s, CGMMV affected 70% to  
219 80% of plants in peri-urban cucurbit fields of Delhi, India (Raychaudhury and Varma, 1978).  
220 Identification of resistance to CGMMV in ‘Phoot’ led to the development of five Indian lines  
221 (VRM 5-10, VRM 29-1, VRM 31-1-2, VRM 42-4, and VRM 43-6) that had high-level  
222 resistance to CGMMV along with improved yield and sweetness (More et al., 1993).

223 *Kyuri green mottle mosaic virus* (KGMMV) is economically significant in Japan,  
224 Korea, and Indonesia (Daryono et al., 2005). It is mechanically transmitted and seed-borne.  
225 PI 414723 is resistant to KGMMV (Daryono et al., 2005).

226 Spring (dry season) melons in the trans-Gangetic plains of India are threatened by  
227 CMV, CGMMV, SqMV, PRSV, and ZYMV, whereas whitefly transmitted begomoviruses  
228 predominate during the rainy season in this region (Sharma et al., 2007). Landrace IC 274014  
229 is an asymptomatic host of CMV that also exhibited field resistance to an unidentified  
230 begomovirus (Sharma and Kang, 2009).

231 **Root-knot nematode and insect resistance**

232           Root-knot nematode (RKN), *Meloidogyne* spp, is found in melon fields worldwide,  
233 particularly in sandy soils. Its impact on melon yield depends upon the RKN population  
234 density in the field. Current melon cultivars are susceptible to RKN. High-level resistance to  
235 *M. incognita* has been identified in landrace IC 274023 (Dhillon et al., 2007) which should  
236 be exploited to develop the first RKN-resistant melon variety.

237           Melon aphid, also called cotton melon aphid (CMA), *Aphis gossypii* Glover, is found  
238 throughout most of the temperate, subtropic and tropic regions of the world. Younger plants  
239 are more susceptible to feeding. CMA is also an efficient vector of viruses including CMV  
240 and potyviruses. Strong resistance to CMA biotype D (McCreight et al., 1992) available in PI  
241 414723 was used in conventional breeding to develop orange flesh melon breeding lines AR  
242 Topmark, AR-5, and AR Hale's Best Jumbo (McCreight et al., 1984). These breeding lines  
243 exhibited different levels of resistance to virus transmission by CMA (Kishaba et al., 1992).  
244 PI 414723 has three components of resistance to CMA: antibiosis, antixenosis, and tolerance  
245 (Bohn et al., 1972). Tolerance to CMA in PI 414723 is expressed as freedom from curling of  
246 leaves and is governed by the single dominant gene *Ag* (Bohn et al., 1973). Snapmelon  
247 landraces IC 267353, IC 267384, and IC 274010 have resistance to virus transmission by  
248 CMA (Dhillon et al., 2007).

249           Cucumber beetles (CB) infest melon seedlings and fruit (Kishaba et al., 1998).  
250 Seedling and fruit resistance to western striped CB [*Acalymma trivittata* (Mannerheim)] and  
251 spotted CB [*Diabrotica undecimpunctata* (Mannerheim)] has been identified in PI 414723  
252 but genetic basis of resistance not determined.

253 Sweetpotato whitefly (SPWF), *Bemisia tabaci* Gennadius, is another economically  
254 important insect pest in the desert southwestern United States. It has several biotypes. SPWF-  
255 A is a vector of *Lettuce infectious yellow virus* (LIYV) whereas SPWF-B is a vector of  
256 *Cucurbit yellow stunting disorder virus* (CYSDV) and *Cucurbit leaf crumple virus*  
257 (CuLCrV). Resistance to SPWF-B was reported in PI 414723 (Boissot et al., 2003).

### 258 **Melon flavor enrichment**

259 Accumulation of sugar and acid in melon fruit imparts unique taste and flavor.  
260 Titrable acidity of Indian commercial melons ranges 0.12% to 0.2% (N.P.S. Dhillon,  
261 unpublished data). High acidity sources have been reported in snapmelon landraces IC  
262 274021 (0.61%) and IC 267360 (0.57%) (Dhillon et al., 2007). The low-pH gene derived  
263 from snapmelon accession IND-35 was exploited using marker-assisted selection by  
264 Syngenta in 2008 to develop the pleasant-tasting F<sub>1</sub> hybrid melon 'GWANIPA' that was  
265 commercialized in UK, Germany and Holland by Kernel Export (Jordi Garcia-Mas, personal  
266 communication). This melon has a lemon flavor and contains 700-800 mg citric acid per 100  
267 g fruit fresh weight (FW) with a pH level of 4.5 (patent no. EP 1587933 B1) (Casanueva et  
268 al., 2010).

### 269 **Vitamin and Mineral content**

270 Higher concentrations (up to 34.1 mg•100 g<sup>-1</sup> FW) of vitamin C were detected in  
271 snapmelon landraces of northern India compared to the germplasm from eastern India (upto  
272 19.4 mg•100g<sup>-1</sup> FW) and southern India (up to 9.0 mg•100g<sup>-1</sup>FW) (Dhillon et al., 2007;  
273 Fergany et al., 2011; Malik et al., 2014).

274 Iron and zinc deficiency is recognized as a nutritional problem worldwide (Uauy et  
275 al., 2006). Wide variation for P (2.6 to 21.4 mg•100g<sup>-1</sup>FW), K (19.7 to 232.4 mg•100g<sup>-1</sup>FW),  
276 Fe (0.5 to 0.89 mg•100g<sup>-1</sup>FW) and Zn (0.12 to 0.68 mg•100 g<sup>-1</sup>FW) have been identified in  
277 landraces (Fergany et al., 2011). This genetic variation for vitamins and minerals is important  
278 for breeding of new mineral- and vitamin-rich snapmelon varieties. Snapmelons are  
279 consumed by poor and middle-class consumers, and the fruit are available in the market for  
280 nearly five months of the spring and rainy season. Snapmelon fruits were used as food in the  
281 two Japanese islands (Hachijo and Fukue) during the two World Wars (Fujishita, 2004).

## 282 **Snapmelon genetic diversity**

283 Based on the variability at nine simple sequence repeat loci (160 alleles,  
284 polymorphism information content value 0.81), clear genetic differentiation was observed  
285 among gene pools of snapmelon germplasm from northern, southern and eastern region of  
286 India (Dhillon et al., 2013). Global melon reference populations were distinct from this  
287 germplasm; clearly snapmelon landraces possessed unique alleles when compared with  
288 international reference accessions. Snapmelon germplasm offers opportunity to widen the  
289 genetic base of melons inhabiting the secondary centers of diversity (eastern Asia, western  
290 Mediterranean area) and proximal parts (e.g., Turkey) of the primary center of diversity.

## 291 **Snapmelons for developing climate-smart melons**

292 To maintain and increase crop productivity in increasingly hostile environments,  
293 novel sources of genetic variation must be sought for adapting crops to unstable climate.  
294 Snapmelons were little explored gene pools and are readily available to the sweetmelon

295 genepools through conventional hybridization. Snapmelons are drought hardy, and are  
296 cultivated by small-scale farmers in arid and semiarid regions of India during the rainy  
297 season (Pareek and Samadia, 2002). Two highly drought and heat tolerant snapmelon  
298 selections, AHS 10 and AHS 82, were bred from local landraces from the arid region of  
299 Rajasthan, India (Pareek and Samadia, 2002). Snapmelon accession RSM 50 was highly  
300 drought tolerant compared to Reticulatus Group cultivars in a controlled (water deficit)  
301 irrigation field experiment (Dhillon et al., 2013). Accession Calif. 525 was acknowledged for  
302 contributing high-levels tolerances to salt and high temperature along with resistance  
303 to powdery mildew in 'PMR 45', the first modern western U.S. shipping-type melon (Jagger  
304 and Scott, 1937). Grafted melons are more tolerant to salinity than non-grafted controls  
305 (Orsini et al., 2013). Snapmelon landraces from the coastal, arid areas of India (Gujarat,  
306 Karnataka, Kerala, Andhra Pradesh, Tamil Nadu, Odisha) are potential sources of new salt,  
307 drought and heat tolerant rootstocks for melon grafting.

## 308 **Conclusion**

309 Snapmelons originated in India. This horticultural group has provided yeoman service  
310 to sweetmelon breeding programs worldwide. For example, PI 414723 was used in breeding  
311 as source of resistance to eight fungal and viral diseases and two insect pests. PI 124111  
312 (MR-1) is resistant to powdery and downy mildew, Alternaria and Fusarium wilt. More than  
313 1000 snapmelon accessions are maintained in four national genebanks in India (National  
314 Bureau of Plant Genetic Resources, New Delhi; Central Institute for Arid Horticulture,  
315 Bikaner; Central Horticultural Experiment Station, Bhubaneswar; Punjab Agricultural  
316 University, Ludhiana), but they have not been comprehensively evaluated against various



317 biotic and abiotic stresses. Erosion of snapmelon genetic diversity in India is a real threat  
318 because of rapid urbanization, and swift adoption and spread of commercial F<sub>1</sub> hybrid  
319 sweetmelons across India. International, collaborative research efforts should be launched to  
320 collect, characterize and evaluate the snapmelon germplasm available in the many different  
321 agro-ecological regions of India. This will result in identification of unique and useful genes  
322 to broaden the narrow gene pool of sweetmelons, provide new sources for resistance to  
323 various diseases and insects of melons, and help in meeting the challenges of climate change  
324 to sustainable production of melon crop worldwide.

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326 **Literature Cited**

- 327 Anon. 1954. New vegetable varieties. Proc. Am. Soc. Hort. Sci. 63:503-525.
- 328 Bohn, G.W., Davis, G.N., Foster, R.E. and Whitaker, T.W. 1965. Campo and Jacumba. New  
329 cantaloupe varieties for the southwest. Calif. Agr. 19:8-10.
- 330 Bohn, G.W., Kishaba, A.N. and Toba, H.H. 1972. Mechanisms of resistance to melon aphid  
331 in a muskmelon line. HortScience 7:281-282.
- 332 Bohn, G.W., Kishaba, A.N., Principe, J.A. and Toba, H.H. 1973. Tolerance to melon aphid in  
333 *Cucumis melo* L. J. Am. Soc. Hort. Sci. 98:37-40.
- 334 Boissot, N., Lafortune, D., Pavis, C. and Sauvion, N. 2003. Field resistance to *Bemisia tabaci*  
335 in *Cucumis melo*. HortScience 38:77-80.
- 336 Brotman, Y., Normantovich, M., Goldenberg, Z., Zvirin, Z., Kovalski, I., Stovbun, N.,  
337 Doniger, T., Bolger, A.M., Troadec, C., Bendahmane, A., Cohen, R., Katzir, N., Pitrat,  
338 M., Dogimont, C. and Perl-Treves, R. 2013. Dual resistance of melon to *Fusarium*  
339 *oxysporum* races 0 and 2 and to *Papaya ring-spot virus* is controlled by a pair of head-to-  
340 head oriented NB-LRR genes of unusual architecture. Molecular Plant Physiology 6:235-  
341 238.
- 342 Casanueva, A., Foncelle, B., Nicolet, J.E., Van Doon, J.E. and Oliver, S.M. 2010.  
343 <http://www.faqs.org/patents/app/20100034952>.
- 344 Cohen, Y. and Eyal, H. 1987. Downy mildew, powdery mildew and Fusarium wilt-resistant  
345 muskmelon breeding line PI 124111F. Phytoparasitica 15:187-195.

346 Cohen, Y., Meron, I., Mor, N. and Zuriel, S. 2003. A new pathotype of *Pseudoperonospora*  
347 *cubensis* causing downy mildew in cucurbits in Israel. *Phytoparasitica* 31:458-466.

348 Crosby, K., Jifon, J. and Leskovar, D. 2007. 'Pacal' orange-casaba, and 'Chujuc' western-  
349 shipper cantaloupe: two new melon cultivars from the Texas Agricultural Experiment  
350 Station. *HortScience* 42:1013 [abstr.].

351 Crosby, K.M., Jifon, J.L. and Leskovar, D.I. 2008. 'Chujuc', a new powdery mildew-  
352 resistant U.S. western-shipper melon with high sugar and  $\beta$ -carotene content. *HortScience*  
353 43:1904-1906.

354 Daryono, B.S., Somowiyarjo, S. and Natsuaki, K.T. 2005. Screening for resistance to *Kyuri*  
355 *green mottle mosaic virus* in various melons. *Plant Breed.* 124:487-490.

356 Danin-Poleg, Y., Paris, H.S., Cohen, S., Rabinowitch, H.D. and Karchi, Z. 1997. Oligogenic  
357 inheritance of resistance to *Zucchini yellow mosaic virus* in melons. *Euphytica* 93:331-  
358 337.

359 Desbiez, C. and Lecoq, H. 1997. *Zucchini yellow mosaic virus*. *Plant Pathology* 46:809-829.

360 Dhillon, N.P.S., Ranjana, R., Singh, K., Eduardo, I., Monforte, A.J., Pitrat, M., Dhillon, N.K.  
361 and Singh, P.P. 2007. Diversity among landraces of Indian snapmelon (*Cucumis melo* var.  
362 *momordica*). *Genet. Resources Crop Evol.* 54:1267-1283.

363 Dhillon, N.P.S., Singh, J., Fergany, M., Monforte, A.J. and Sureja, A.K. 2009. Phenotypic  
364 and molecular diversity among landraces of snapmelon (*Cucumis melo* var. *momordica*)  
365 adopted to the hot and humid tropics of eastern India. *Plant Genet. Resources.* 7:291-300.

366 Dhillon, N.P.S., Monforte, A.J., Pitrat, M., Pandey, S., Singh, P.K., Reitsma, K.R., Garcia-  
367 Mas, J., Sharma, A. and McCreight, J.D. 2013. Melon landraces of India: Contributions  
368 and importance. *Plant Breed. Rev.* 35:85-150.

369 Dogimont, C. 2010-2011. Gene list 2011 for melon. *Cucurbit Genet. Coop. Rep.* 33-34:104-  
370 133.

371 Dogimont, C., Bussemakers, A., Martin, J., Slama, S., Lecoq, H. and Pitrat, M. 1997. Two  
372 complementary recessive genes conferring resistance to *Cucurbit aphid borne yellows*  
373 *luteovirus* in an Indian melon line (*Cucumis melo* L.). *Euphytica* 96:391-395.

374 Dogimont, C., Lecomte, L., Périn, C., Thabuis, A., Lecoq, H. and Pitrat, M. 2000.  
375 Identification of QTLs contributing to resistance to different strains of cucumber mosaic  
376 cucumovirus in melons. *Acta Hort.* 510:391-398.

377 Essafi, A., Pendon Diaz, J.A., Moriones, E., Monforte, A.J., Garcia-Mas, J. and Martin-  
378 Hernandez, A.M. 2008. Dissection of the oligogenic resistance to *Cucumber mosaic virus*  
379 in the melon accession PI 161375. *Theor. Appl. Genet.* 118:275-284.

380 Fergany, M., Kaur, B., Monforte, A.J., Pitrat, M., Lecoq, H., Dhillon, N.P.S. and Dhaliwal,  
381 S.S. 2011. Variation in melon (*Cucumis melo* L.) landraces adapted to the humid tropics  
382 of southern India. *Genet. Resources Crop Evol.* 55:225-243.

383 Fujishita, N. 2004. Pedigree of melon (*Cucumis melo* L.) in ancient Japan - International  
384 symposium on Asian Plant Diversity and Systematics, Sakura, Japan, July 29 - August 1,  
385 2004.

386 Fukino, N., T. Ohara, A. Monforte, M. Sugiyama, Y. Sakata, M. Kuniyama, and S.  
387 Matsumoto, 2008: Identification of QTLs for resistance to powdery mildew and SSR  
388 markers diagnostic for powdery mildew resistance genes in melon (*Cucumis melo* L.).  
389 Theoretical and Applied Genetics 118:165-175.

390 Gilbert, R.Z., Kyle, M.M., Munger, H.M. and Gay, S.M. 1994. Inheritance of resistance to  
391 watermelon mosaic virus in *Cucumis melo* L. HortScience 29:107-110.

392 Gordon, T.R., Okamoto, D. and Jacobson, D.J. 1989. Colonization of muskmelon and non-  
393 host crops by *Fusarium oxysporum* f.sp. *melonis* and other species of *Fusarium*.  
394 Phytopathology. 79:1095-1100.

395 Goyal, M. and Sharma, S.K. 2009. Traditional wisdom and value addition prospects of arid  
396 foods of desert regions of North West India. Indian J. Traditional Knowledge 8:581-585.

397 Guiu-Aragonés, C., Monforte, A.J., Saladié, M., Corrêa, R.X., Garcia-Mas, J. and Martín-  
398 Hernández, A.M. 2014. The complex resistance to cucumber mosaic cucumovirus (CMV)  
399 in the melon accession PI 161375 is governed by one gene and at least two quantitative  
400 trait loci. Mol. Breed. DOI : 10.1007/s11032-014-0038-y

401 Harwood, R.R. and Markarian, D. 1968. A genetic survey of resistance to powdery mildew in  
402 muskmelon. J. Hered. 59:213-217.

403 Hollings, M., Komuro, Y. and Tochigara, H. 1975. *Cucumber green mottle mosaic virus*.  
404 Descriptions of plant viruses No. 154. Kew, Surrey, U.K: Commonwealth Mycol.  
405 Inst./Assn. Appl. Biol. [www.dpvweb.net/dpv/showdpv.php?dpvno=154](http://www.dpvweb.net/dpv/showdpv.php?dpvno=154).

406 Ivanoff, S.S. 1957. The Home garden Cantaloupe, a variety with combined resistance to  
407 downy mildew, powdery mildew, and aphids. *Phytopathology* 47:552-556.

408 Jagger, I. 1926. Powdery mildew of muskmelon in the Imperial valley of California in 1925.  
409 *Phytopathology* 16:1009-1010.

410 Jagger, I.C. and Scott, G.W. 1937. Development of powdery mildew resistant cantaloup No  
411 45. USDA Circ. 441:6.

412 Jagger, I.C., Whitaker, T.W. and Porter, D.R. 1938. Inheritance in *Cucumis melo* of  
413 resistance to powdery mildew (*Erysiphe cichoracearum*). *Phytopathology* 28:761.

414 Joobeur, T., King, J.J., Nolin, S.J., Thomas, C.E. and Dean, R.A. 2004. The Fusarium wilt  
415 resistance locus *Fom-2* of melon contains a single resistance gene with complex features.  
416 *Plant J.* 39:283-297.

417 Kaan, J.F. 1973. Recherches sur la résistance du melon aux maladies, notamment à la  
418 mosaïque de la pastèque et au *Pseudoperonospora*, appliquées au type variétal "Cantaloup  
419 Charentais". EUCARPIA meeting on melon. Avignon, France 19-22 June 1973. p 41-49.

420 Karchi, Z., Cohen, S. and Govers, A. 1975. Inheritance of resistance to *Cucumber mosaic*  
421 *virus* in melons. *Phytopathology* 65:479-481.

422 Kishaba, A.N., S. Castle, D.L. Coudriet, J.D. McCreight, and G.W. Bohn. 1992. Virus  
423 transmission by *Aphis gossypii* Glover to aphid-resistant and susceptible muskmelons.  
424 *J. Amer. Soc. Hort. Sci.* 117:248-254.

425 Kishaba, A.N., Castle, S.I., Coudriet, D.L., McCreight, J.D. and Bohn, G.W. 1998.  
426 Resistance to western spotted and striped cucumber beetle in melon. *Cucurbitaceae*' 98:

427 Evaluation and enhancement of cucurbit germplasm. Pacific Grove, California (USA) 30  
428 Nov-4 Dec. 1998p. 101-105.

429 Lebeda, A. and Sedláková, B. 2004. Disease impact and pathogenicity variation in Czech  
430 populations of cucurbit powdery mildews. Progress in cucurbit genetics and breeding  
431 research. Olomouc, Czech Republic 12-17 July 2004. p. 281-287.

432 Lebeda, A., Sedláková, B., Křístková, E., Vajdová, M. and McCreight, J.D. 2012.  
433 Application of a new approach for characterization and denomination of races of cucurbit  
434 powdery mildews—a case study of Czech pathogen populations. Cucurbitaceae 2012,  
435 Proceedings of the X<sup>th</sup> EUCARPIA meeting on genetics and breeding of Cucurbitaceae.  
436 Antalya, Turkey 15-18 October 2012. p. 172-180.

437 Lecoq, H., Labonne, G. and Pitrat, M. 1980. Specificity of resistance to virus transmission by  
438 aphids in *Cucumis melo*. Ann. Phytopathol. 12:139-144.

439 Lecoq, H., Wisler, G. and Pitrat, M. 1998. Cucurbit viruses: The classic and the emerging.  
440 Cucurbitaceae' 98: Evaluation and enhancement of cucurbit germplasm. Pacific Grove,  
441 California (USA) 30 November-4 December 1998. p. 126-142.

442 Malik, A.A., Vashisht, V.K., Singh, K., Sharma, A., Singh, D.K., Singh, H., Monforte, A.J.,  
443 McCreight, J.D. and Dhillon, N.P.S. 2014. Diversity among melon (*Cucumis melo* L.)  
444 landraces from the Indo-Gangetic plains of India and their genetic relationship with USA  
445 melon cultivars. Genet. Resources Crop Evol. DOI 10.1007/s10722-014-0101-x.

446 McCreight, J.D., Bohn, G.W. and Kishaba, A.N. 1992. "Pedigree" of PI 414723 melon.  
447 Cucurbit Genet. Coop. Rpt. 15:51-52.

448 McCreight, J.D., M.D. Coffey, B. Sedlakova, and A. Lebeda. 2012. Cucurbit powdery  
449 mildew of melon incited by *Podosphaera xanthii*: Global and western U.S. perspectives.  
450 Cucurbitaceae 2012, Proceedings of the X<sup>th</sup> EUCARPIA meeting on genetics and breeding  
451 of Cucurbitaceae. Antalya, Turkey 15-18 October, 2012. p. 181-189.

452 McCreight, J.D., Kishaba, A.N. and Bohn, G.W. 1984. AR Hale's Best Jumbo, AR 5, and  
453 AR Topmark, melon aphid-resistant muskmelon breeding lines. HortScience. 19:309-310.

454 McCreight, J.D., Liu, H.-Y. and Turini, T.A. 2008. Genetic resistance to *Cucurbit leaf*  
455 *crumple virus* in melon. HortScience 43:122-126.

456 More, T.A. 2002. Enhancement of muskmelon resistance to disease via breeding and  
457 transformation. Acta Hort. 588:205-211.

458 More, T.A., Varma, A., Seshadri, V.S., Somkuwar, R.G. and Rajamony, L. 1993. Breeding  
459 and development of *Cucumber green mottle mosaic virus* (CGMMV) resistant lines in  
460 melon (*Cucumis melo* L.). Cucurbit Genet. Coop. Rpt. 16:44-46.

461 Munger, H.M. 1991. Progress in breeding melons for watermelon mosaic resistance.  
462 Cucurbit Genet. Coop. Rept. 14: 43-44.

463 Nandpuri, K.S., Singh, S. and Lal, T. 1975. Punjab Sunehri: A new variety of muskmelon.  
464 Progressive Farming, November issue, p. 21-23.

465 Nugent, P.E. 1994. Tetraploid 'Planters Jumbo' melon lines C883-M6-4X and 67-M6-  
466 1004X. HortScience 29:48-49.

467 Nugent, P.E., Hoffman, J.C. and Andrus, C.F. 1979. 'Mainstream' muskmelon. HortScience  
468 14:192.



469 Orsini, F., Sanoubar, R., Oztekin, G.B., Kappel, N., Tepecik, M., Quacquarelli, C., Tuzal, Y.,  
470 Bona, S. and Gianquinto, G. 2013. Improved stomatal regulation and ion partitioning  
471 boosts salt tolerance in grafted melons. *Functional Plant Biol.* 40:628-636.

472 Oumouloud, A., M. El-Otmani, H. Chikh-Rouhou, A.G. Claver, R.G. Torres, R. Perl-Treves,  
473 and J.M. Alvarez, 2013: Breeding melon for resistance to Fusarium wilt: recent  
474 developments. *Euphytica* 192:155-169.

475 Pandey, S., Rai, M., Prassanna, H.C. and Kalloo, G. 2008. Kashi Madhu: A new muskmelon  
476 cultivar with high total soluble solids. *HortScience* 43:245-246.

477 Pareek, O.P. and Samadia, O.K. 2002. Promising indigenous cucurbit varieties. *Indian Hort.*  
478 July-Sept.p.15-18.

479 Perchepied, L., Bardin, M., Dogimont, C. and Pitrat, M. 2005. Relationship between loci  
480 conferring downy mildew and powdery mildew resistance in melon assessed by  
481 quantitative trait loci mapping. *Phytopathology.* 95:556-565.

482 Phan, T.P.N., Akashi, Y., Tran, T.M.H., Tanaka, K., Aierken, Y., Yamamoto, T., Nishida,  
483 H., Long, C.L. and Kato, K. 2010. Genetic diversity in Vietnamese melon landraces  
484 revealed by the analyses of morphological traits and nuclear and cytoplasmic molecular  
485 markers. *Breeding Science* 60:255-266.

486 Pitrat, M., Dogimont, C. and Bardin, M. 1998. Resistance to fungal diseases of foliage in  
487 melon. *Cucurbitaceae '98: Evaluation and enhancement of cucurbit germplasm.* Pacific  
488 grove, California (USA) 30 November-4 December 1998. p. 167-173.

489 Pitrat, M. and Lecoq, H. 1983. Two alleles for *Watermelon mosaic virus 1* resistance in  
490 melon. *Cucurbit Genet. Coop. Rept.* 6:52-53.

491 Pitrat, M. and Lecoq, H. 1984. Inheritance of *Zucchini mosaic virus* resistance in *Cucumis*  
492 *melo* L. *Euphytica* 33:57-61.

493 Pryor, D.E., Whitaker, T.W. and Davis, G.N. 1946. The development of powdery mildew  
494 resistant cantaloupes. *Proc. Am. Soc. Hort. Sci.* 47:347-356.

495 Raychaudhury, M. and Varma, A. 1978. Mosaic diseases of muskmelon, caused by a minor  
496 variant of *Cucumber green mottle mosaic virus*. *Phytopath. Z.* 93:120-125.

497 Sharma, A., Kang, S.S., Thiara, S.K. and Kaur, S.I. 2007. Occurrence of cucurbit viruses in  
498 Punjab. *Proceedings of 10<sup>th</sup> International Plant Virus Epidemiology Symposium on*  
499 *Controlling Epidemics of Emerging and established Plant Virus Diseases - The Way*  
500 *Forward.* Hyderabad India 15-19 October 2007. p. 151.

501 Sharma, A. and Kang, S.S. 2009. Cucurbits: A new host for begomovirus in Punjab. *Plant*  
502 *Dis.* 24:51-53.

503 Shetty, N.V., Wehner, T.C., Thomas, C.E., Doruchowski, R.W. and Shetty, K.P.V. 2002.  
504 Evidence for downy mildew races in cucumber tested in Asia, Europe, and North  
505 America. *Sci. Hort.* 94:231-239.

506 Sitterly, W.R. 1978. Powdery mildew of cucurbits.p. 359-379. In: Spencer, D. (ed.), *The*  
507 *powdery mildews*, Academic Press, New York.

508 Swarup, V. 2000. Genetic resources in vegetable crops in India. p.346-355. In: Kallo, G. and  
509 Singh, K. (eds.), Emerging scenario in vegetable research and development. Research  
510 Periodicals and Book Publishing Home, India.

511 Taler, D., Galperin, M., Benjamin, I., Cohen, Y. and Kenigsbuch, D. 2004. Plant R genes that  
512 encode photorespiratory enzymes confer resistance against disease. *Plant Cell* 16:172-184.

513 Tamietti, G. and Valentino, D. 2006. Soil solarization as an ecological method for the control  
514 of *Fusarium* wilt of melon in Italy. *Crop Prot.* 25:389-397.

515 Thomas, C.E. 1996. *Alternaria* leaf blight, p.23-24. In: Zitter, T.A., Hopkins, D.L. and  
516 Thomas, C.E. (eds.), *Compendium of Cucurbit Diseases*. APS Press, St. Paul, MN.

517 Thomas, C.E., Inaba, T. and Cohen, Y. 1987. Physiological specialization in  
518 *Pseudoperonospora cubensis*. *Phytopathology*. 77:1621-1624.

519 Thomas, C.E., McCreight, J.D. and Jourdain, E.L. 1990. Inheritance of resistance to  
520 *Alternaria cucumerina* in *Cucumis melo* line MR-1. *Plant Dis.* 74:868-870.

521 Uauy, C., Distelfeld, A., Fahima, T., Blechi, A. and Dubcovsky, J. 2006. A NAC gene  
522 regulating senescence improves grain protein, zinc and iron content in wheat. *Science*  
523 314:1298-1301.

524 USDA, ARS. 2014. National Genetic Resources Program. Germplasm Resources  
525 Information Network—(GRIN).[Online database]. National Germplasm Resources  
526 Laboratory, Beltsville, MD. [http://http://www.ars-grin.gov/cgi-](http://http://www.ars-grin.gov/cgi-bin/npgs/acc/display.pl?1743283)  
527 [bin/npgs/acc/display.pl?1743283](http://http://www.ars-grin.gov/cgi-bin/npgs/acc/display.pl?1743283)

- 528 Vishnu-Mittre. 1974. Palaeobotanical evidence in India.p.3-30. In: Hutchinson, J. (ed.),  
529 Evolutionary studies in world crops, diversity and changes in Indian subcontinent.  
530 Cambridge Univ. Press, Cambridge, UK.
- 531 Waraitch, K.S., Munshi, G.D., Nandpuri, K.S. and Lal, T. 1977. Screening of muskmelon,  
532 wildmelon and snapmelon for resistance to powdery mildew (*Sphaerotheca fuliginea*).  
533 Phytopathol. Mediterranea 16:37-39.
- 534 Webb, R.E. 1979. Inheritance of resistance to watermelon mosaic virus in *Cucumis melo* L.  
535 HortScience 14:265-266.
- 536 Yi, S.S., Akashi, Y., Tanaka, K., Cho, T.T., Khaing, M.T., Yoshino, H., Nishida, H.,  
537 Yamamoto, T., Win, K. and Kato, K. 2009. Molecular analysis of genetic diversity in  
538 melon landraces (*Cucumis melo* L.) from Myanmar and their relationship with melon  
539 germplasm from East and South Asia.Genet. Resources Crop Evol. 56:1149-1161.
- 540 Yousif, M.T., Kheyr-Pour, A., Gronenborn, B., Pitrat, M. and Dogimont, C. 2007. Sources of  
541 resistance to *Watermelon chlorotic stunt virus*. Plant Breed. 126:422-427.
- 542 Zhang, C., Y. Ren, S. Guo, H. Zhang, G. Gong, Y. Du, and Y. Xu, 2013: Application of  
543 comparative genomics in developing markers tightly linked to the Pm-2F gene for  
544 powdery mildew resistance in melon (*Cucumis melo* L.). Euphytica 190:157-168.
- 545 Zink, F.W. and Thomas, C.E. 1990. Genetics of resistance to *Fusarium oxysporum* f.sp.  
546 *melonis* races 0, 1, and 2 in muskmelon line MR-1. Phytopathology. 80:1230-1232.

547