Advances in melon breeding (*Cucumis melo* L.): An update

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Abstract Melon (*Cucumis melo* L.) a member of family Cucurbitaceae is extensively cultivated for its fleshy fruits. Based upon the agroclimatic zones of cultivation as well as concerning the regional preferences, melon displays significant variability phenotypic and biochemical attributes. Below, an effort is put forth to considerably evaluate the scope of achievements while in the growth as well as the enactment of melon breeding programs by employing the newest solutions. Melon breeding has achieved critical milestones throughout the previous century, and we hope this trend will go on to persist down the road. However, experiments have to understand new genetic information for genes associated with the challenges imposed by climate change. The identification of valuable hereditary and also metabolic variability in the form of landraces and melon wild relatives will be useful for harvest diversification and also for the broadening of the cultivated melon genetic base. Whereas, considerable information on genomics, and melon metabolomics, is beneficial for dissecting the basis of the inheritance of important traits. Overall, we hope the manuscript is going to serve as a crucial resource for the melon breeders.

Keywords: Breeding, Diversity, Genetic engineering, Genomics, Male sterility, Melon, QTLs

INTRODUCTION

Melon (*Cucumis melo* L.) ($2n = 2x = 20$ four) a member of family Cucurbitaceae is a crucial eudicot diploid with a genome size of 454 Mb (Garcia-Mas et al., 2012). It is extensively cultivated all over the globe, in temperate, subtropical and tropical areas. The prominent melon producing nations are China, USA, Spain, Turkey and Iran (FAO, 2019). Based on the climatic zones and also concerning the local preferences, melon displays extreme variability in physical, biochemical and phenotypic characteristics (Silberstein et al., 2003). The wild relatives of melon are distributed in Asia, Africa and Australia (Luan et al., 2008; Kerje and Grum, 2000; Sebastian et al., 2010; Endl et al., 2018). There is an extensive perturbation in the morphology of the fresh fruits of melon, in shape, colour, texture and flavour (Kirkbride, 1993). Melon fruit can reach a size of up to 20 kg, while the shape can vary from spherical to long type. Whereas, in flavour, fruits can be from bland to sweet, sour, or maybe bitter (Kirkbride, 1993; Stepansky et al., 1999; Liu et al., 2004; Monforte et al., 2004).

The recent breeding effort has developed several hybrids aiming to enhance storage and shelf life, disease resistance and resistance to abiotic stresses. Generally, cultivars with a longer shelf life (LSL types) are thought of by customers as having low fruit quality and therefore, present minimal acceptability (Wolff and Dunlap, 1995). Although, most of the breeders concur that powdery mildew resistance and fusarium are essential and fundamental demands of farmers for the modern melon varieties (Capel et al., 2010; Branham et al., 2018). Also, insect pest management is a significant component which benefits commercial yield by providing a much better yield safety measures, reduced waste along with much better fruit quality (Ramamurthy and Waters, 2015). Melon leaf curl New Delhi virus, which is transmitted by whiteflies is causing a considerable yield loss throughout Asia and Europe. More recently, a QTLs are identified for the disease resistance in melon (Saez et al., 2017).

Similarly, the quantitative genes of yield and also yield-related traits in melon are also thoroughly studied. Additionally, many researchers have reported on the merging ability and heterosis benefits in fruit yield along with other morphological characteristics of melon under even under biotic and abiotic stress conditions (Kamer et al., 2015; Varinder and Vashisht, 2018). Recently, due to its very affordable cost and high sensitivity, the next-generation sequencing is possible for melon. Especially GBS (genotyping by sequencing) and RAD sequencing of multiplexed samples are reproducible, fast, and accessible (Ganal et al., 2014; Shang et al., 2020; Zhang et al., 2016). Below, an attempt is put forth to significantly assess the scope of accomplishments while in the development and enactment of melon breeding programs by employing the latest technologies. We hope this manuscript will serve as an important resource for the melon breeders.

DIVERSITY

Cucumis melo belongs to family Cucurbitaceae is a horticultural crop of great economic importance and showed a wide range of diversity for agro-morphological and fruit traits (Zitter et al., 1996; Silberstein et al., 2003). Leaves are simple, three or five-lobed, borne singly at nodes, have significant variation for colour, shape and size (Kirkbride, 1993). Tendrils are simple and borne on leaf axils. Melons fruits are classified as Pepo with three ovary sections (Font-Quer, 1979). Variations in melon fruits were observed for shape, size, internal and external colour. Flesh color varied from orange, light orange, pink, white, green; rind color varied from green, white, orange, yellow and red grey; rind texture as smooth, striped, warty, rough and netted; shape from round, elongated, flattened; size 4cm in *C. melo var. agrestis* to 200 cm in *C. melo var. flexuosus* (Kirkbride, 1993). Melon fruits are generally climacteric type, but non-climacteric type was observed in inodorus variety (Aggelis et al., 1997; Zheng and Wolf, 2000; Perin et al., 2002; Liu et al., 2004).

Almost all melon fruits have 1:1 ratio of length/breadth, while, measurements recognize flexuosus types to width ratio of around 4:1 (Burger et al., 2010). Because so many wild species of Cucumis appeared in Africa, it has been suggested the centre of origin of cultivated melon is Africa. Nevertheless, recent reports suggested the closest wild relatives of melon are found in India and Australia (Luan et al., 2008; Kerje et al., 2000; Sebastian et al., 2010; Endl et al., 2018). Melons are divided *C. melo* ssp. melo along with *C. melo* ssp. agrestis reliant on ovary pubescence (Jeffrey, 1980). It includes fifteen different groups or varieties of which ten variations are belonging to the ssp. melo, for example, cantalupensis, reticulatus, adana, chandalak, ameri, inodorus, chate, flexuosus, dudaim and tibish and five variations are belonging to the ssp. agrestis like momordica, conomon, chinensis, makuwa, as well as acidulous (Zhao et al., 2019).

FLORAL BIOLOGY AND MALE STERILITY

Muskmelon produces several kind of flowers structures such as hermaphrodite or perfect (bisexual) flowers, andromonoecious (staminate and perfect flowers), gynomonoecious (pistillate and perfect flowers), monoecious (both staminate and pistillate) and gynoecious (pistillate) flowers (Munshi and Alvarez, 2005; Choudhary and Pandey, 2016). However, andromonoecious is the predominant sex form in muskmelon. Staminate flowers are borne either singly, or clusters of two or rarely three but hermaphrodite flowers appear separately (Kiill et al., 2016; Revanasidda and Belavadi, 2019; Munshi and Alvarez, 2005). The ratio of staminate to hermaphrodite flowers ranged from 6 to 19:1 (Siqueira et al., 2011 and Tschoeke et al., 2015). Flowers are yellow, epigynous and actinomorphic. Flowering in muskmelon starts 40-45 days after sowing (Choudhary and Pandey, 2016; Revanasidda and Belavadi, 2019). Anthesis takes place in the early morning between 5.30 to 6.30 am, and anther dehiscence occurs 5.00 to 6.00 am. Pollens remains viable between 5.00 am to 2 pm (Choudhary and Pandey, 2016) and stigma become receptive 2 hr before and 2 -3 hr after anthesis (Munshi and Alvarez, 2005). Two significant genes A and G determine the sex expression in musk melon. Allele G is responsible for the production of unisexual male flower, either andromonoecious or monoecious (Kubicki, 1969; Kenigsbuch and Cohen 1990). Allele A with G produces monoecious flowers and with gg has gynoecious flowers (Kubicki 1962; Kenigsbuch and Cohen 1990). According to Choudhary and Pandey, the different genotypes produced by the combination of two genes can be represented as aagg-hermaphrodite, aaG_-andromonoecious, A_gg-gynomonoecious and A_G_monoecious.

Now a day's use male sterility for heterosis exploitation is a major area of interest for plant breeders to develop high yielding commercial hybrids. Use of male sterility reduces the total cost of hybrid seed production by eliminating the need for labors for the emasculation of female parents (Dhillon and Kumar 2008). All of these five genes are recessive, non-allelic and have unique phenotype (Pitrat, 1991). The first gene for genetic male sterility was reported in 1949 by Bohn and Whitaker. The second gene for male sterility was identified by Bohn and Principe (1964) in powdery mildew resistant line La Jolla 40460. Plants with ms-2 gene produced hermaphrodite and staminate flowers are with small anthers having empty pollen walls. It differed from ms-1 for spindle orientation during meiotic metaphase-2, cell size and shape (Bohn and Principe, 1964). The third male sterility gene was reported by McCreight and Elmstrom (1983) in PI321005 a cross of Georgia 47 × Smith's perfect. The segregation ratio in F2 indicated monogenic recessive inheritance of this gene. The anthers of ms-3 plants are waxy, dull, and translucent. The fifth male sterility gene was observed first in 1966 while developing a powdery mildew resistant line. However, its inheritance was published by Lecouviour et al., (1990). The fourth male sterility gene was identified by Lozanov (1983). This gene was used for hybrid seed production by Clause Seed Company. On hermaphrodite and staminate flowers, the anthers are empty and of reduced size. Two hybrids namely Punjab hybrid (MS-1 x Hara Madhu) and Punjab Anmol were developed in India by using male sterility ms-1 gene (Nandpuri et al., 1982; Lal et al., 2007).

Five Male sterility genes have been identified, but commercialization of ms- based hybrid to a significant level is still waiting. There are some reasons why GMS based hybrids are utilized a limited extent. Transfer of male sterility to a new line by the conventional back cross method is time taking. As the inheritance of male sterility gene is monogenic recessive, the identification of homozygous (MsMs) and heterozygous (Msms) plants in the backcross population is difficult. One generation of selfing is required to select the plants homozygous for ms allele.

Male fertile plants are identified and removed, and remaining plants are used for hybrid seed production. The identification of the male fertile plant is very tedious and laborious. However, the efficiency of the GMS system can be enhanced by the use of morphological markers linked with the male sterile genes. A linkage between ms-1 and red stem gene was reported by McCreight (1983) and between ms-2 and yellow-green by Pitrat (1991). Similarly, Whereas, 3 SSRs on chromosome 6 linked to ms-1 gene were reported by Singh et al. (2019) and a SCAR marker SOAM08.644 linked to ms-3 gene was developed by Park et al. (2004). These molecular markers can be employed to select the male-sterile plants at the seedling stage.

GYNOECIOUS LINE

Gynoecious breeding lines provides several advantages for hybrid seed production as it reduces the cost of emasculation, manual pollination, rouging and use of chemical treatment and ensures 100% purity of hybrid seed production. Gynoecious lines also found advantageous over genetic male sterile lines as it avoids the need for identification and rouging of 50% male fertile plants. The use of gynoecious lines for hybrid seed production was also suggested by Frankel and Galun (1977) and Loy et al. (1979). Kenigsbuch and Cohen (1990) proposed possible genotype and sex expression. Kenigsbuch and Cohen (1990) suggested that for stable gynoecious condition, genotype AAgg and recessive mm combination is needed. At very first, Peterson et al. (1983) identified durable gynoecious plants from Wisconsin-998 population. Three gynoecious breeding lines were developed by More et al., (1987) at IARI, New Delhi (India). An improved gynoecious line named as ‘Gylan’ was developed from a cross of line 36 and GY-4. Fruits of Gylan are round to oval with orange flesh and weight from 0.9 to 1.1 kg. This line produced good F1 with an andromonoecious Vedrantais and Tam-Uvalde (Cohen et al., 1993). A cross between W321 (gynoecious line) and N233 showed earliness in picking and 50% higher yield than Punjab hybrid (Dhaliwal and Lal, 1996). To induce perfect flowers for the maintenance of gynoecious lines, silver thiosulphate, Ethral and Alar had been suggested by Rudich et al. 1970 and More and Seshadri, 1987. Ma et al., (2010) identified two SSR markers MU5549-1and MU14723-2 linked with gene ‘a’ and ‘m’, respectively. However, instability of gynoecious lines under high-temperature conditions limits their utilization for hybrid seed production.

HETEROSIS

The primary breeding objectives in muskmelon include early maturity, medium to long vine length, high female flower to male flower ratio, high total fruit yield, fruit size, fruit shape, i.e., round to flattish to oval, outer skin colour, hard netted skin, small seed cavity, adequate flesh thickness, flesh texture, attractive flesh colour, total soluble solids, good resistance against downy mildew, powdery mildew, viral disease, fruit fly, red pumpkin beetle etc. Due to vigorous growth, early maturity, high yield and good quality of hybrids, heterosis breeding is the commonly used method in muskmelon (Banga and Banga, 2000). A good level of heterosis for different traits has been reported by various researchers working on muskmelon. The first study for heterosis in muskmelon was done by Munger (1942) who noticed uniformity for fruits and 30% increment in yield of hybrid in comparison to parents. Heterosis for earliness was reported by several research workers in melon (Dhaliwal and Lal, 1996; Gaurav et al., 2000; Choudhary et al., 2003; Vishwanatha, 2003; Kamer et al., 2015; Choudhary et al., 2018), flesh thickness (Chadha and Nandpuri, 1980; Choudhary et al., 2003; Tomar and Bhalala, 2006; Kamer et al., 2015) fruit yield (Chadha and Nandpuri, 1977; Munshi and Verma, 1997; Tomar and Bhalala, 2006; Subramanian, 2008; Kamer et al., 2015; Selim, 2019) vine length, number of leaves and number of branches (Kamer et al., 2015; Duradundi et al., 2018) average fruit (Kamer et al., 2015 and Selim, 2019), fruit length, fruit girth (Tomar and Bhalala, 2006; Subramanian, 2008) leaf area index, netting, seed cavity (Selim, 2019), total soluble solids (Subramanian, 2008; Selim, 2019) number of fruit per plant (Tomar and Bhalala, 2006; Subramanian, 2008; Kamer et al., 2015) fruit shape index, fruit skin color, b-carotene, vitamin C (Kamer et al., 2015) rind thickness (Varinder and Vashisht, 2018) germination percentage, seed number per fruit and empty seeds (Nerson, 2012) powdery mildew resistance (Kesavan and More 1991).

QTLian BREEDING

In muskmelon, many economically important characters such as yield, quality traits and resistance against diseases showed polygenic inheritance, and the genetic variation for these characters is controlled by several genes known as quantitative trait loci. Identification of QTLs for these traits using conventional breeding approaches is not so easy due to complex nature and their interaction with the environment (Lynch and Walash, 1998). However, with the advent of DNA marker techniques and linkage mapping, it is possible to dissect the complex nature of quantitatively inherited characters. Different mapping populations such as F2 generation, $F_{2:3}$, recombinant inbred lines (RILs), near-isogenic lines (NILs) and Double haploids (DHs) are used for QTL mapping. These populations are created by crossing two parents differing for the trait (s) of interest. Each mapping populations have their advantage and disadvantage. Earlier several QTLs have been mapped in the different genetic background of muskmelon using diverse mapping populations and molecular markers. In muskmelon QTLs for different traits have been mapped using molecular markers such as cleaved amplified polymorphism sequence AFLP, RFLP (CAPS) Simple sequence repeat (SSR), Random amplification of polymorphic DNA (RAPD) (Baudracco-Arnas and Pitrat, 1996; Oliver et al., 2001; Zalapa et al., 2007; Cuevas et al., 2008, 2009; Wang et al., 2016; Baloch et al., 2016; Amanullah et al., 2018).

Earlier linkage maps in muskmelon are prepared on using segregating population such as F2 and BC1 which are unsaturated and related with few economically important characters (Baudracco-Arnas and Pitrat 1996; Liou et al. 1998; Oliver et al. 2001; Silberstein et al. 2003). However, recently linkages maps are constructed using immortal population such as RILs (Perin et al. 2002a, b; Cuevas et al., 2008; Paris et al., 2008; Fukino et al. 2008; Zalapa et al. 2007b; Pereira et al., 2018), NILs (Moreno et al., 2008) and DHs (Monforte et al. 2004). A wide range of variation was observed for fruit shape, size, external skin colour, acidity, flesh colour and fruit weight which provide ample scope for investigation of genetic and molecular basis fruit external and quality traits (Burger et al., 2006). Flesh colour in muskmelon is controlled by two genes gf (green flesh) and wf (white flesh) which interacts with each other to produce green, white and orange flesh colour (Hughes 1948; Iman et al. 1972; Clayberg 1992). Monforte et al., (2004) hypothesized that three putative loci control expression of orange flesh colour in musk melon, *i.e.* ofc2.1 and ofc12.1 and ofc3.1 on linkages group LG2, LG12 and LG3, a however large population is required to know the complexity of this trait (Gross, 1987; Navazio, 1994). For beta-carotene, seven QTLs were identified using RIL and three by using F3 population (Cuevas et al., 2008; Cuevas et al., 2009).

For fruit shape two QTL were identified by Paris et al., (2008), eight QTL by Moreno et al., (2008), two by Baloch et al., (2016), five by Pereira et al., (2018) and four by Amanullaha et al. (2018); for fruit weight four QTL by Amanullaha et al., (2018), two QTL by Wang et al., (2016), two by Zalapa et al., (2007), six by Monforte et al., (2004) and two by Pereira et al., (2018); for fruit diameter two QTL were detected by Wang et al., (2016) two by Dıaz et al., 2014 and two by Pereira et al., (2018); for fruit length five QTL were identified by Dıaz et al., 2014 three by Wang et al., (2016) and 4 by Pereira et al., (2018). Fruit maturity is an important trait in muskmelon as early maturity increase the total number of harvests. However, its inheritance is complex and affected favourably by environmental conditions (Monforte et al. 2004; Zalapa et al. 2006). Monforte et al identified nine QTLs for fruit maturity; three QTL for flesh thickness, four for Netting density and four for netting width; five QTL for fruit firmness and two QTL for flesh firmness; one QTL for seed number and 4 for seed weight., (2004), Moreno et al., (2008), Cuevas et al. (2009); Wang et al., (2016), Amanullaha et al. (2018) and Pereira et al., (2018), respectively. Fukino et al identified two QTL for resistance against powdery mildew., (2008), one by Capel et al., 2010 one QTL by Yuste-Lisbona et al., (2011), one by Wang et al., (2016) and one by Li et al., (2017). Two QTLs were identified against Alternaria leaf blight, four QTL for *Fusarium oxysporum* f. sp. *Melonis*, three QTL for Sulfur tolerance and three QTL for Tomato leaf curl Daley et al identified new Delhi virus (ToLCNDV)., 2017, Branham et al., 2018, Branham et al., 2020 and Saez et al., 2017, respectively. Major QTLs for different traits can be used for the genetic improvement of muskmelon using marker-assisted breeding approaches. The list of QTLs identified for the important traits of melon is provided in Table 1.

Table 1. QTLs identified for important morphological and biochemical traits along with important disease resistance traits.

Trait	Generation	Parents	No. of QTLs	Linkage Group	References
Fruit weight	F2:3	M4-7 × MR-1	4	LG2, LG5, LG10	Amanullaha et al., (2018)

Fruit firmness			5	LG2, LG3, LG5, LG8	
Fruit width			6	LG5, LG8, LG9	
Flesh firmness			2	LG3, LG6	
Brix			3	LG7, LG9, LG10	
Fruit shape			4	LG5, LG8, LG9	
beta-carotene mesocarp	F3	Q 3-2-2 × Top Mark	3	LG, LG8, LG9	Cuevas et al., (2009)
Fruit maturity			3	LG2, LG6, LG11	
beta-carotene	RIL	USDA 846-1 × Top Mark	7	LG1, LG2, LG4, LG6	Cuevas et al. (2008)
Powdery mildew	RIL	AR 5 × Earl's Favourite	2	LG IIA, LGXII	Fukino et al., (2008)
Fruit weight	F2		2	LG5, LG11	Wang et al., (2016)
Fruit diameter			2	LG5, LG11	
Fruit length			3	LG2, LG7, LG8	
Flesh thickness			3	LG5, LG11, LG12	
Netting density			4	LG2, LG4, LG6, LG7	
Netting width			4	LG2, LG4, LG6, LG7	
Powdery mildew			1	LG2	
Primary branches number	RIL	USDA 846-1 × Top Mark	4	LG1, LG2, LG10	Zalapa et al., (2007)

Fruit number per plot			5	LG1, LG2, LG8	
Average weight per fruit			2	LG1, LG8	
Percentage of mature fruit			1	LG10	
Powdery mildew	F2	TGR-1551 × ‘Bola de Oro	1	LG5	Yuste-Lisbona et al., (2011)
Soluble solids content	RIL	USDA-846-1 × Top Mark	2	LG7, LG10	Paris et al., (2008)
Mesocarp pressure			3	LG7, LG10	
Seed cell diameter			3	LG1, LG5, LG8	
Seed cell diameter: Fruit diameter			1	LG2	
Percent netting at full-slip			1	LG2	
Fruit shape			2	LG1, LG2	
Climacteric ripening	NIL	PI 161375 × Piel de Sapo	1	LG3	Moreno et al., (2008)
Earliness	F2 and DHs	Piel de Sapo × PI 161375	9	LG1, LG2, LG9, LG10, LG12	Monforte et al., (2004)
Fruit shape			8	LG1, LG3, L5, LG6, LG7, LG9, LG11	Monforte et al., (2004)
Fruit weight			6	LG3, LG4,	

				LG5, LG12	
Sugar content			5	LG1, LG2, LG4, LG8	
Powdery mildew resistance	F2	MR-1 × Top Mark	1	LG12	Li et al., (2017)
Fruit shape	F2	MR-1 × Top mark	2	LG4, LG12	Baloch et al., (2016)
SSC	RIL	Védrantais × Piel de Sapo	6	LG8, LG9, LG10	Pereira et al., (2018)
Fruit weight			2	LG5, LG8	
Fruit diameter			2	LG2, LG5	
Fruit shape			5	LG2, LG6, LG11	
Fruit length			4	LG5, LG6, LG11	
Fruit perimeter			4	LG5, LG6, LG7, LG11	
Seed number			1	LG5	
Seed weight			4	LG3, LG5, LG7, LG8	
Fruit length	F2	Piel de Sapo × PI124112	5	LG2, LG3b, LG6a, LG8, LG10b	Dıaz et al., 2014
Fruit diameter			2	LG3a, LG12	
Fruit shape			3	LG2, LG8, LG12	
Days to maturity	Introgression lines (ILs)	Ginsen makuwa × Vedrantais	2	LG1, LG6	Perpina et al., 2016
Fruit weight			4	LG1, LG2,	

				LG6, LG11	
Fruit length			5	LG1, LG2, LG6, LG7, LG11	
Fruit diameter			5	LG1, LG5, LG6, LG11	
Fruit shape			2	LG7, LG11	
Cavity width			1	LG2	
Fesh firmness			2	LG7, LG10	
Aroma			2	LG7, LG10	
Rind thickness			2	LG2, LG6	
Netting			3	LG5, LG6, LG7	
Color of the inner rind			3	LG6, LG8, LG12	
Soluble solids content			1	LG10	
Sucrose content			4	LG1, LG5, LG10, LG11	
Glucose content			3	LG1, LG5, LG11	
Fructose content			3	LG5, LG10, LG11	
Fruit area	F2	PS × TRI	4	LG2, LG4, LG6, LG8	Diaz et al., 2017
Fruit length			4	LG2, LG4, LG6, LG8	
Fruit diameter			2	LG4, LG8	
Fruit shape			3	LG2, LG4, LG6	

Fruit weight			4	LG2, LG4, LG6, LG8	
Distal fruit blockiness			1	LG11	
Pulp area			3	LG5, LG6, LG8	
Pulp thickness			2	LG5, LG8	
Total fruit weight per plant			1	LG2	Ramamurthy and Waters, 2015
Seed cell diameter			1	LG4	
Fruit shape			2	LG4, LG12	
Ovary shape			1	LG11	
Flesh color			1	LG4	
Soluble solid concentration			1	LG2	
Chlorosis			1	LG8	
Alternaria leaf blight	RIL	MR-1 × Ananas Yokneum	2	LG10, LG12	Daley et al., 2017
Fusarium oxysporum f. sp. *melonis*	RIL	MR-1 × AY	4	LG2, LG7, LG11, LG12	Branham et al., 2018
Powdery mildew	F2	TGR-1551 × Bola de Oro	1	LG5	Capel et al., 2010
Sulfur tolerance	RIL	MR-1 × AY	3	LG1, LG8, LG12	Branham et al., 2020
Tomato leaf curl New Delhi virus (ToLCNDV)	F2and BC1	WM-7 × PS	3	LG11, LG2, LG12	Saez et al., 2017

GENETIC ENGINEERING

Traditional breeding played a significant role in the genetic improvement of musk melon for yield, quality improvements, resistance against diseases and insects pests. It made substantial progress in the varietal development process. However, there are some limitations, such as sexual incompatibility for inter-specific and inter-generic crosses (Robinson and Decker-Walters, 1999) more time taking programs (Pitrat et al., 1999) production of interspecific hybrids with low-quality characters (Seshadri and More, 2002) etc. Now a day's most popularizing technology such marker-assisted breeding and genetic engineering contributed significantly to genetic improvement and varietal development by reducing the risks and limitations of traditional breeding approaches (Li et al., 2009). Transgenic technology has been used successfully in many crops, including musk melon (Bezirganoglu et al., 2014).

Muskmelon is affected by several fungal diseases, viral diseases and insects-pests leads to a considerable loss in production (Kwon et al. 2001). Leaf fungal diseases such downy mildew and powdery mildew and soil-borne fungus such *Rhizoctonia solani* causing damping-off, root and stem rot and Fusarium oxysporum causing wilting are severe threats to melon production (Gaba et al., 2004; Bezirganoglu et al., 2013). Viruses are the major limitation to cause colossal damage to melon crops. From the past three decades, two most common approaches have been used in muskmelon to develop resistance against viruses one is coat-protein mediated resistance.

Transgenic genotypes in muskmelon have been developed by overexpressing the using coat protein gene of WMV, PRSV, ZYMV and WMV. Coat-protein mediated protection or resistance against different viruses have reported by several workers (Yoshioka et al., 1992; Fang and Grumet, 1993; Gonsalves et al., 1994; Clough and Hamm, 1995; Wu et al., 2010). The expression of amino-truncated core portion or antisense CP-ZYMV provides limited protection while plants expressing the full length of CP-ZYMV gene were highly resistant (Fang and Grumet, 1993). Similarly, ribozyme-mediated resistance in musk melon was observed by Plages et al., 1997 against CMV and by Huttner et al., 2001 against ZYMV and WMV. This type of resistance is based on the ability of ribozymes, small RNA molecules, to cleave viral RNA with high specificity. An enhanced level of salt tolerance was observed in muskmelon by the use of a transgene HAL 1 from *Saccharomyces cerevisiae* (Bordas et al., 1997). Overexpression of HAL 1 maintained a high K, low Na content and increased K/Na ratio (Serrano, 1996).

Melon fruit is rich in vitamins and folic acid and these nutrients act as potent antioxidants and essential compounds in human metabolic reactions. Ripening process in musk melon involves a series of changes in texture, colour, aroma, firmness, flavour (Lelievre et al., 1997; Jiang and Fu, 2000) and ethylene is known as ripening factor in climacteric fruits (Giovannoni, 2001). Two critical enzymes involve in ethylene biosynthesis pathway, enzyme ACC synthase (ACS) converts the S-adenosyl methionine into 1-aminocyclopropane-1-carboxylate (ACC) which is then oxidized to ethylene by ACC oxidase (ACO) (Fluhr and Mattoo 1996; Johnson and Ecker 1998). To improve the fruit quality, reduced ethylene production and delayed ripening in muskmelon was achieved by using antisense technology for ACS and ACO gene by (Ayub et al., 1996; Guis et al., 1997; Silva et al., 2004; Nunez-Palenius et al., 2006). The transgenic approach has also been utilized for the genetic improvement of other important traits such as fruit development, sucrose content, aroma and female flower development (Yu et al., 2008; Tian et al., 2010; Zhang et al., 2014; Kocaman et al., 2016). The list of trangenics developed in melon is provided in Table 2.

Table 2. List of transgenics developed in melon for quality, biotic and abiotic stress related traits.

Trait (s) improved	**Transgene**	**Transformation method**	**References**
Quality traits			
Ripening behavior	ACC oxidase gene	*Agrobacterium tumefaciens*	Silva et al., 2004
Sex expression	ACS synthase	*Agrobacterium tumefaciens*	Papadopoulou et al., 2005
Improved shelf life	ACC oxidase gene	*Agrobacterium tumefaciens*	Ayub et al., 1996
Ripening behavior	SAMase (S-adenosylmethionine hydrolase)	*Agrobacterium tumefaciens*	Clendennen et al., 1999
Reduced ethylene production	ACC Oxidase gene	*Agrobacterium tumefaciens*	Guis et al., 2000

Reduced ethylene production	pAP4 gene	*Agrobacterium tumefaciens*	Nora et al., 2001
Ripening behavior	ACC oxidase gene	*Agrobacterium tumefaciens*	Silva et al., 2004
Sex expression	ACS synthase	*Agrobacterium tumefaciens*	Papadopoulou et al., 2005
Improved shelf life	ACC oxidase gene	*Agrobacterium tumefaciens*	Nunez-Palenius et al.,2006
Fruit development and sucrose content	MAI1 (acid invertase gene)	*Agrobacterium tumefaciens*	Yu et al., 2008
Bisexual and female flowers	CmACS-7	*Agrobacterium tumefaciens*	Zhang et al., 2014
Aroma	Two ADH genes	*Agrobacterium tumefaciens*	Kocaman et al., 2016
Biotic stress			
CMV resistance	CP gene of CMV	*Agrobacterium tumefaciens*	Yoshioka et al., 1992
Potyvirus resistance	ZYMV-CP gene	*Agrobacterium tumefaciens*	Fang and Grumet, 1993
CMV resistance	CP gene of CMV–WL	*Agrobacterium tumefaciens*	Gonsalves et al., 1994
Resistance against ZYMV and WMV	CP gene of ZYMV, WMV and CMV	_	Clough and Hamm, 1995
CMV resistance	Polyribozyme against CMV	*Agrobacterium tumefaciens*	Plages et al., 1997
Potyvirus resistance	Polyribozyme	-	Huttner et al., 2001
Downy mildew resistance	eR genes At1 and At2	*Agrobacterium tumefaciens*	Taler et al., 2004
Potyvirus resistance	CP genes of ZYMV and	*Agrobacterium*	Wu et al., 2010

	PRSV-W	*tumefaciens*	
Fungal disease resistance	Chitinase and β-Glucanase genes	*Agrobacterium tumefaciens*	Akbari et al., 2013
Resistance against glufosinate ammonium-based herbicides.	bar gene	ZYMV-AGII (Potyvirus based vector)	Shiboleth et al., 2001
Abiotic stress			
Salt tolerance	HAL1 gene	*Agrobacterium tumefaciens*	Bordas et al., 1997
Salt tolerance	HAL1 gene	*Agrobacterium tumefaciens*	Serrano et al., 1999

GENOMICS

Genomics is widely used in melon research because of its affordable price and very high sensitivity, and the next-generation sequencing is doable for melon and its diverse wild relatives (Ganal et al., 2014). Especially RAD-sequencing and GBS (genotyping by sequencing) of multiplexed samples is easy, fast, and reproducible (Shang et al., 2020; Zhang et al., 2016). Furthermore, low cost and the flexibility of these tools in creating high-density genetic maps rendered their usage in genome-wide association studies (GWAS) (Nimmakayala et al., 2016). The melon genome was sequenced and annotated for the first time in the year 2012 (Garcia-Mas et al., 2012). A genomic platform had been built in an attempt to host the genome sequence (available at http://melonomics.net). Over the years, the melon genome was eventually changed to improve the anchoring and orientation3 of the scaffold assembly with a particular SNP selection strategy, acquiring the v3.5.1 assembly10 (available at http://melonomics.net). In this new genome version, 98.2 % together with 90 % of the scaffold assembly was anchored and oriented to some SNP genetic chart, respectively, which stand for a considerable enhancement of the pseudomolecules. 27.8 Mb of scaffold assembly remained unanchored in the genome and pseudomolecule zero annotation utilized in the melon genome discharge v3.5.1 was the same as in v3.5 (Castanera et al., 2020).

CONCLUSIONS AND FUTURE DIRECTIONS

Melon breeding has achieved several milestones during the last century, and we hope this trend will continue to persist in the future. Although, studies are required to recognize new genetic resources for genes related to the unique challenges imposed by climate change. Researchers need to dissect and elucidate the molecular basis for resistance, yield traits and fruit quality by gaining insight into the regulatory factors, that synchronize at different development stages for contributing traits. Nevertheless, a sturdy, durable resistance strategy is required against plant pathogens as pathogens can overcome resistance by building new races. The recent sequencing of the melon genomes at a large scale is going to provide the ability to get, reliable information for disease resistance genes to different diseases and also genes for important biochemical attributes. Lates techniques like speed breeding have to be tailored for the cucurbits keep in view the different sex forms temperature requirement for flowering induction.

As the genome sequencing costs decreasing the use of RAD-sequencing, and DNA microarrays, will accelerate genome mapping and tagging of new QTLs. These QTLs might be used to send the resistance into high yielding melon genotypes and combine different QTL with substantial resistance genes to the other races. Moreover, in melon, GWAS (genome-wide association studies) are used for mapping traits to the one candidate gene level. This procedure continues to be recently called mGWAS (metabolite genome-wide association study). The identification of useful genetic and also metabolic variability forms the foundation for directed harvest diversification as well as genetic enhancement by breeding.

References

1. Aggelis, A., John, I., and Grierson, D. 1997. Analysis of physiological and molecular changes in melon (*Cucumis melo* L) varieties with different rates of ripening. J. Exp. Bot. 48: 769–778.
2. Akbari, M., Nadaf, E., Lotfi, M., & Tohidfar, M. (2013). Transformation of Iranian melon for increasing resistance to fungal diseases. Research in Plant Sciences, 1, 1–3.
3. Amanullaha, S, Liua, S., Gao, P., Zhua, Z., Zhua,Q., Fana,C., Luana, F. (2018). QTL mapping for melon (*Cucumis melo* L.) fruit traits by assembling and utilization of novel SNPs based CAPS markers. Scientia Horticulturae, 236: 18–29. https://doi.org/10.1016/j.scienta.2018.02.041

4. Ayub, R.; Guis, M.; BenAmor, M.; Gillot, L.; Roustan, J. P.; Latche, A.; Bouzayen, M.; Pech, J. C. Expression of ACC oxidase antisense gene inhibits ripening of cantaloupe melon fruits. Nat. Biotechnol. 14:862–866; 1996.
5. Baloch, A.M., Baloch, A.W., Liu, S., Gao, P., Baloch, M.J.,Wang, X., Davis, A.R., Ali, M., Luan, F. (2016). Linkage map construction and qtl analysis of fruit traits in melon (*Cucumis melo* L.) Based on caps markers. Pak. J. Bot., 48(4):1579-1584.
6. Banga, S.S. and Banga, S. K. (ed) (2000) Hybrid Cultivar Development. pp. 17- 31 Narosa Publishing House, New Delhi.
7. Baudracco-Arnas S and Pitrat M (1996) A genetic map of melon (*Cucumis me*lo L.) with RFLP, RAPD, isozyme, disease resistance and morphological markers. Theor Appl Genet 93: 57-64.
8. Bezirganoglu I, Hwang S, Fang TJ, Shaw J (2013). Transgenic lines of melon (*Cucumis melo* L. var. makuwa cv. 'Silver Light') expressing antifungal protein and chitinase genes exhibit enhanced resistance to fungal pathogens. Plant Cell Tiss Organ Cult (2013) 112:227–237. DOI 10.1007/s11240-012-0227-5
9. Bohn G W and Principe J A (1964) A second male-sterility gene in the muskmelon. J Hered 55: 211-15.
10. Bohn G W and Whitaker T W (1949) A gene for male sterility in muskmelon (*Cucumis melo* L.). P Am Soc Hortic Sci 53: 309-14.
11. Bordas M, Montesinos C, Dabauza M, Salvador A, Roig LA, Serrano R, Moreno V (1997) Transfer of the yeast salt tolerance gene HAL1 to *Cucumis melo* L. cultivars and in vitro evaluation of salt tolerance. Transgenic Res 6:41–50
12. Branham SE, Daley J, Levi A, Hassell R and Wechter W.P. (2020). QTL Mapping and Marker Development for Tolerance to Sulfur Phytotoxicity in Melon (*Cucumis melo*). Frontiers in Plant Science, 11, doi: 10.3389/fpls.2020.01097
13. Branham,S.E., Levi,A., Katawczik,M.,Fei,Z., andWechter,W.P. (2018).Construction of a genome-anchored, high-density genetic map for melon (Cucumis melo L.) and identification of Fusarium oxysporum f. sp. melonis race 1 resistance QTL. Theor. Appl. Genet. 131, 829–837. doi: 10.1007/s00122-017-3039-5
14. Burger Y, Paris HS, Cohen R, Katzir N, Tadmor Y, Lewinsohn E, Schaffer AA. Genetic diversity of *Cucumis melo*. Hortic Rev. 2010: 36:165–98.
15. Burger Y, Saar U, Paris HS, Lewinsohn E, Katzir N, Tadmor Y & Schaffer AA (2006). Genetic variability for valuable fruit quality traits in *Cucumis melo*. Israel Journal of Plant Sciences, 54:3, 233-242.
16. Castanera, R., Ruggieri, V., Pujol, M., Garcia-Mas, J., Casacuberta, J.M., 2020. An Improved Melon Reference Genome With Single-Molecule Sequencing Uncovers a Recent Burst of Transposable Elements With Potential Impact on Genes. Front. Plant Sci. 10. https://doi.org/10.3389/fpls.2019.01815
17. Chadha, M.L. and K.S. Nandpuri. 1980. Hybrid vigour studies in muskmelon. Indian J. Hort, 37 (3): 276-282.
18. Chadha, M.L. and Nandpuri, K.S. 1977. Estimation of top cross performance in some muskmelon (*Cucumis melo* L.) varieties. J. of Hort., 34: 40-43.
19. Choudhary BR and Pandey S (2016). Muskmelon Genetics, Breeding, and Cultural Practices. Handbook of Cucurbits: Growth, Cultural Practices, and Physiology.

20. Choudhary BR, Haldhar SM and Maheshwari SK. (2018). Identification and possibility of monoecious inbred of muskmelon (*Cucumis melo* L.) for heterosis breeding. Vegetable Science (2018) 45 (1) : 118-120.
21. Choudhary, BR, Dhaka RS, Fageria, MS. (2003) Heterosis for yield related attributes in muskmelon (*Cucumis melo* L.). Ind. J. Genet., 63: 91-92.
22. Clayberg, C.D. 1992. Interaction and linkage tests of flesh color genes in *Cucumis melo* L. Cucurbit Genetics Cooperative. 15:53–54.
23. Clendennen, S., Kellogg, K.J.A., Wolff, K.A., Matsumura, W., Peters, S., Vanwinkle, J.E., Copes, B., Pieper, M., Kramer, M.G., 1999. Genetic engineering of cantaloupe to reduce ethylene biosynthesis and control ripening. In: Kanellis, A.K., Chang, C., Klee, H., Bleecker, A.B., Pech, J.P., Grierson, D. (Eds.), Biology and Biotechnology of the Plant Hormone Ethylene. Part II. Kluwer Academic Publishers, Dordrecht, pp. 371–380.
24. Clough, G. H.; Hamm, P. B. Coat protein transgenic resistance to watermelon mosaic and zucchini yellow mosaic virus in squash and cantaloupe. Plant Dis. 79:1107–1109; 1995.
25. Cohen Y, Eyal H and Cohen A. (1993). ‘Gylan’—A Gynoecious Muskmelon. HORT SCIENCE 28(8):855.
26. Cuevas HE, Staub JE, Simon PW, Zalapa JE, McCreight JD (2008) Mapping of genetic loci that regulated quantity of -carotene in fruit of U.S. Western Shipping melon (*Cucumis melo* L.). Theor Appl Genet 117:1345–1359. DOI 10.1007/s00122-008-0868-2
27. Cuevas, H. E., Staub, J. E., Simon, P.W., Zalapa, J.E. (2009). A consensus linkage map identiWes genomic regions controlling fruit maturity and beta-carotene-associated flesh color in melon (*Cucumis melo* L.). Theor Appl Genet, 119:741–756. DOI 10.1007/s00122-009-1085-3
28. Daley J., Branham S., Levi A., Hassell R., Wechter P. (2017). Mapping resistance to Alternaria cucumerina in *Cucumis melo*. Phytopathology 107: 427:432.
29. Dhaliwal M S and Lal T (1996) Genetics of some important characters using line x tester analysis in muskmelon. Indian J Genet Pl Br 56: 207-13.
30. Dhillon N P S and Kumar J (2008) Assessment of stability of expression of various malesterile genes in muskmelon in sub-tropical field conditions. Pitrat M (ed): Proc 9th EUCARPIA meeting on Genetics and Breeding of Cucurbitaceae. Pp 535-8 Avignon, France.
31. Díaz, A., A. M. Martín-Hernández, R. Dolcet-Sanjuan, A. Garcés-Claver, J. M.Álvarez, J. Garcia-Mas, B. Picó, and A. J. Monforte. 2017. Quantitative trait loci analysis of melon (*Cucumis melo* L.) domestication-related traits. Theoretical and Applied Genetics 130: 1837–1856.
32. Diaz, A., Zarouri, B., Fergany, M., Eduardo, I., Alvarez, J.M., Pico, B. and Monforte, A.J. (2014) Mapping and introgression of QTL involved in fruit shape transgressive segregation into ’Piel de Sapo’ melon (*Cucumis melo* L.). PLoS One, 9, 8.
33. Duradundi SK, Gasti VD, Mulge R, Kerutagi MG, Masuthi DA (2018). Heterosis studies in muskmelon (*Cucumis melo* L.) for growth, earliness and yield traits. International Journal of Chemical Studies, 6(4): 3079-3086.
34. Endl, J., E. G. Achigan-Dako, A. K. Pandey, A. J. Monforte, B. Pico, and H. Schaefer. 2018. Repeated domestication of melon (*Cucumis melo*) in Africa and Asia and a new close relative from India. American Journal of Botany 105(10): 1–10.

35. Fang, G. W.; Grumet, R. Genetic engineering of potyvirus resistance using constructs derived from the zucchini yellow mosaic virus coat protein gene. Mol. Plant Microbe Interact. 6:358–367; 1993.
36. FAO, 2017. Statistics Division of Food and Agriculture Organization of the United Nations. FAOSTAT Accessed 30 May 2020. http://faostat.fao.org/.
37. Fluhr R, Mattoo AK (1996) Ethylene - biosynthesis and perception. Crit Rev Plant Sci 15:479–523
38. Font-Quer, P. 1979. Diccionario de Botanica. Editorial Labor.Mexico.
39. Frankel R., and Galun E. 1977. Pollination mechanisms, reproduction and plant breeding. Monogr. Theor. Appl. Genet., vol 8. Springer, Berlin Heidelberg New York, 281 pp.
40. Fukino N, Ohara T, Monforte AJ, Sugiyama M, et al. (2008). Identification of QTLs for resistance to powdery mildew and SSR markers diagnostic for powdery mildew resistance genes in melon (*Cucumis melo* L.). Theor. Appl. Genet. 118: 165-175.
41. Ganal, M.W., Wieseke, R., Luerssen, H., Durstewitz, G., Graner, E.-M., Plieske, J., Polley, A., 2014. High-throughput SNP profiling of genetic resources in crop plants using genotyping arrays, in: Genomics of Plant Genetic Resources. Springer, pp. 113–130.
42. Garcia-Mas, J., Benjak, A., Sanseverino, W., Bourgeois, M., Mir, G., González, V.M., Hénaff, E., Câmara, F., Cozzuto, L., Lowy, E., 2012. The genome of melon (*Cucumis melo* L.). Proceedings of the National Academy of Sciences 109, 11872–11877.
43. Giovannoni, J.J., 2001. Molecular biology of fruit maturation and ripening. Annu. Rev. Plant Physiol. Plant Mol. Biol. 52, 725–749.
44. Gonsalves, C.; Xue, B.; Yepes, M.; Fuchs, M.; Ling, K.; Namba, S.; Chee, P.; Slingtom, J. L.; Gonsalves, D. Transferring cucumber mosaic viruswhite leaf strain coat protein gene into Cucumis melo L. and evaluating transgenic plants for protection against infections. J. Am. Soc. Hort. Sci. 119:345–355; 1994.
45. Gross J (1987) Carotenoids. In: Schweigert BS (ed) Pigments in fruits. Academic Press, London, New York, pp 87–186.
46. Guis, M., BenAmor, M., Latche, A., Pech, J.C., & Roustan J.P. (2000). A reliable system for the transformation of cantaloupe Charentais melon (*Cucumis melo* L. var. cantalupensis) leading to a majority of diploid regenerants. Scientia Horticulturae, 84, 91–99. doi:10.1016/S0304-4238(99)00101-6
47. Guis, M., Botondi, R., Ben-Amor, M., Ayub, R., Bouzayen, M., Pech, J.C., Latche´, A., 1997a. Ripening-associated biochemical traits of Cantaloupe Charentais melons expressing an antisense ACC oxidase transgene. J. Am. Soc. Hortic. Sci. 122, 748–751.
48. Gurav, S. B., Wavhal, K. N. and Navale, P. A. 2000. Heterosis and combining ability on muskmelon. J Maharashtra Agric Univ 25: 149-52. (Original not seen. Abstr. in Biological Abstracts, 14: Entry No. 20013067327, 2000).
49. Hughes, M.B. 1948. The inheritance of two characters of *Cucumis melo* and their interrelationship. Procedures of the American Society for Horticultural Sciences. 52:399-402.
50. Huttner, E., Tucker, W., Vermeulen, A., Ignart, F., Sawyer, B., & Birch, R. (2001). Ribozyme genes protecting transgenic melon plants against potyviruses. Current Issues in Molecular Biology, 3, 27–34.
51. Imam MKL, Abo-Bakr MA, Hanna HY (1972) Inheritance of some economic characters in crosses between sweet melon and snake cucumber. I. Inheritance of qualitative characters. Assiut J Ag Sco 3:363–380.

52. Jeffrey C (1980) Further notes on Cucurbitaceae V. The Cucurbitaceae of the Indian subcontinent. Kew Bull 34:789–809.
53. Jiang, Y. M., and Fu, J. R. 2000. Ethylene regulation of fruit ripening: Molecular aspects. Plant Growth Regul. 30: 193–200.
54. Johnson, P. R., and Ecker, J. R. 1998. The ethylene gas signal transduction pathway: A molecular perspective. Annu. Rev. Genet. 32: 227–254.
55. Kamer A, Mona M. E, Yousry M. and El-Gamal M. A. (2015). Heterosis and Heritability Studies for Fruit Characters and Yield in Melon (*Cucumis melo*, L.). Middle East Journal of Applied Sciences, 5: 262-273.
56. Kenigsbuch D and Cohen Y (1990) The inheritance of gynoecy in muskmelon. Genome 33: 317-20.
57. Kerje T, GrumM (2000) The origin of melon, *Cucumis melo*: A review of the literature. Acta Hortic 510:34–37.
58. Kesavan PK, More TA. Use of monoecious lines in heterosis breeding in muskmelon (*Cucumis melo* L.). Veg. Sci. 1991; 18(1):59-64.
59. Kiill, L.H.P., de Edsângela, A.F., de Siqueira, K.M.M., de Ribeiro, M.F., da Silva, E.M.S., 2016. Evaluation of floral characteristics of melon hybrids (*Cucumis melo* L.) in pollinator attractiveness. Rev. Bras. Frutic. Jaboticabal SP 38 (2), 531
60. Kirkbride, J. H. 1993. Biosystematic monograph of the genus Cucumis (Cucurbitaceae). Parkway Publishers, Boone, NC, USA.
61. Kocaman E, Mendi Y Y, Latche A, Izgu T and El-Sharkawy I. (2016). Transformation of Cm-ADH gene to melon genotype. Acta Hortic. 1145. ISHS 2016. DOI 10.17660/ActaHortic.2016.1145.22
62. Kubicki B (1962) Inheritance of some characters in muskmelons (*Cucumis melo* L.). Genetica Polonica 3, 265-274
63. Kubicki B (1969) Comparative studies on sex determination in cucumber (*Cucumis sativus* L.) and muskmelon (Cucumis melo L.). Genetica Polonica 10, 167-183
64. Kwon KM, Hong RJ, Kim HY, Kim CK (2001) Soil-environmental factors involved in the development of root rot/vine on cucurbit caused by *Monosporascus cannonballus*. Plant Pathol J 17: 45–51
65. Lal T, Vashisht V K and Dhillon N P S (2007) Punjab Anmol-a new hybrid of muskmelon (Cucumis melo L.). J Res Punjab Agric Univ 44: 83.
66. Lecouviour M, Pitrat M, Risser G (1990) A fifth gene for male sterility in Cucumis melo. Cucurbit Genet Coop Rpt 13: 34-5.
67. Lelievre, J.M., Latche, A., Jones, B., Bouzayen, M., Pech, J.C., 1997. Ethylene and fruit ripening. Physiol. Plantarum. 101, 727–739.
68. Li P, Pei Y, Sang X, Ling Y, Yang Z, He G (2009) Transgenic indica rice expressing a bitter melon (Momordica charantia) class I chitinase gene (McCHIT1) confers enhanced resistance to Magnaporthe grisea and Rhizoctonia solani. Eur J Plant Pathol 125:533–543
69. Li, B., Zhaoa, Y., Zhu, Q., Zhanga, Z., Fan, C., Amanullaha, S., Gaoa, P., Luana, F. (2017). Mapping of powdery mildew resistance genes in melon (Cucumis melo L.) by bulked segregant analysis. Scientia Horticulturae, 220: 160–167.
70. Liou PC, Chang YM, Hsu WS, Cheng YH, Chang HR, Hsiao CH (1998) Construction of a linkage map in *Cucumis melo* (L.) using random amplified polymorphic DNA markers. In: RA Drew (eds) Proceedings of the international symposium in biotechnololy: tropical and subtropical species, pp 123–131.

71. Liu, L., F. Kakihara and M. Kato (2004) Characterization of six varieties of *Cucumis melo* L. based on morphological and physiological characters, including shelf-life of fruit. Euphytica 135: 305–313.
72. Loy, J.B., T.A. Natti, C.D. Zack, and S.K. Fritts. 1979. Chemical regulation of sex expression in gynomonoecious line of muskmelon. J. Am. Soc. Hort. Sci. 104(1): 100–101.
73. Lozanov P (1983) Selekcija na mazkosterilni roditelski komponenti za ulesnjavana na proizvodstvoto na hibridni semena ot papesi. In Dokl na parva naucna konferencija po genetika i selekapa, Razgrad.
74. Luan, F.S., Delannay, I. and Staub, J.E. (2008) Chinese melon (*Cucumis melo* L.) diversity analysis provides strategies for germplasm curation, genetic improvement, and evidentiary support of domestication patterns. Euphytica, 164, 445–461.
75. Lynch M, Walsh B (1998) Genetic and analysis of quantitative traits. Sinauer association, Inc, Sunderland, MA
76. Ma H, Luan F, Sheng Y and Gao M (2010). Inheritance and Molecular Mapping of Andromonoecious and Gynoecious Sex Determining Genes in Melon (*Cucumis melo* L.). Proc. 4th IS on Cucurbits Ed.: Xiaowu Sun, Acta Hort. 871, ISHS 2010.
77. McCreight J D (1983) Linkage of red stem and male sterility-1 in muskmelon. Cucurbit Genet Coop Rpt 6: 48.
78. McCreight J D and Elmstrom G W (1983) A Third Male Sterile Gene in Muskmelon. Cucurbit Genet Coop Rpt 6: 46.
79. Monforte, A.J., Oliver, M., Gonzalo, M.J., Alvarez, J.M., Dolcet-Sanjuan, R., Arffls, P. (2004). Identification of quantitative trait loci involved in fruit quality traits in melon (*Cucumis melo* L.). Theor. Appl. Genet., 108: 750–758. DOI 10.1007/s00122-003-1483-x
80. More T A and Seshadri V S (1987) Maintenance of gynoecious muskmelon with silver thiosulphate. Veg Sci 14: 138-42.
81. More, T.A., Mishra, J.P., Seshadri, V.S., Doshi, S.P. and Sharma, J.C. (1987). Association of fruit shape with flesh area and flesh proportion in muskmelon. Ann. Agrl. Res., 8 (2): 237-242.
82. Moreno, J., Obando, J.M., Dos-Santos, N., Fernández-Trujillo, J.P., Monforte, A.J., Garcia-Mas, J. (2008). Candidate genes and QTLs for fruit ripening and softening in melon. Theor Appl Genet (2008) 116:589–602. DOI 10.1007/s00122-007-0694-y
83. Munger H M (1942) The possible utilization of first generation muskmelon hybrids and improved methods of hybridization. Proc Amer Soc Hortic Sci 40: 405-10.
84. Munshi A D and Alvarez J M (2005) Hybrid melon development. J New Seeds 6: 321-60.
85. Munshi AD and Verma VK (1997). Studies on heterosis in muskmelon (*Cucumis melo* L.). Veg Sci., 24: 103-106.
86. Nandapuri K S, Singh S and Lal T (1982) 'Punjab Hybrid' a variety of muskmelon. Prog Farming 18: 3-4.
87. Navazio JP (1994) Utilization of high carotene cucumber germplasm for genetic improvement of nutritional quality. PhD Thesis. University of Wisconsin-Madison.
88. Nerson, H (2012). Heterosis in fruit and seed characters of muskmelon. The Asian and Australasian Journal of Plant Science and Biotechnology, 6: 24-27.
89. Nimmakayala, P., Tomason, Y.R., Abburi, V.L., Alvarado, A., Saminathan, T., Vajja, V.G., Salazar, G., Panicker, G.K., Levi, A., Wechter, W.P., 2016. Genome-wide

differentiation of various melon horticultural groups for use in GWAS for fruit firmness and construction of a high-resolution genetic map. Frontiers in plant science 7, 1437.

90. Nora, F.R., Peters, J.A., Schuch, M.W., Lucchetta, L., Marini, L., Silva, J.A., & Rombaldi, C.V. (2001). Melon regeneration and transformation using an apple ACC oxidase antisense gene. Revistabrasileira de Agrociencia, 7, 201–204.
91. Nu˜nez-Palenius, H., Cantliffe, D. J., Huber, D. J., Ciardi, J., and Klee, H. J. 2006. Transformation of a muskmelon 'Galia' hybrid parental line (*Cucumis melo* L. var. reticulatus Ser.) with an antisense ACC oxidase gene. Plant Cell Rep. 25: 198–205.
92. Oliver M, Garcia-Mas J, Cardus M, Pueyo N, López-Sesé AI, Arroyo M, Gomez-Paniagua H, Arus P, Vicente M D (2001). Construction of a reference linkage map for melon. Genome 44: 836-45.
93. Papadopoulou, E., Little, H.A., Hammar, S.A., & Grumet, R. (2005). Effect of modified endogenous ethylene production on sex expression, bisexual flower development, and fruit production in melon (*Cucumis melo* L.). Sexual Plant Reproduction, 18, 131–142. doi:10.1007/s00497-005-0006-0
94. Paris, M.K., Zalapa, J.E., McCreight, J.D., Staub, J.E. (2008). Genetic dissection of fruit quality components in melon (*Cucumis melo* L.) using a RIL population derived from exotic 3 elite US Western Shipping germplasm. Mol Breeding, 22:405–419. DOI 10.1007/s11032-008-9185-3
95. Park SO, Crosby KM, Huang RF and Mirkov TE (2004). Identification and confirmation of RAPD and SCAR markers linked to the ms-3 gene controlling male sterility in melon (*Cucumis melo* L.). J. Am. Soc. Hort. Sci. 129: 819-825.
96. Pereira L, Ruggieri V., Pérez S., Alexiou K. G., Fernández M., Jahrmann T., Pujol M. and Garcia-Mas J. (2018). QTL mapping of melon fruit quality traits using a high-density GBS-based genetic map. BMC Plant Biology (2018) 18:324. https://doi.org/10.1186/s12870-018-1537-5.
97. Perin C, Hagen L, De Conto V, Katzir N, Danin-Poleg Y, Portnoy V, Baudracco-Arnas S, Chadoeuf J, Dogimont C and Pitrat M (2002a) A reference map of *Cucumis melo* based on two recombinant inbred line populations. Theor Appl Genet 104: 1017-34
98. Perin C, Hagen L, Giovinazzo N, Besombes D, Dogimont C and Pitrat M (2002b) Genetic control of fruit shape acts prior to anthesis in melon (*Cucumis melo* L.). Mol Genet Genomics 266: 933-41.
99. Perpina, G., Esteras, C., Gibon, Y., Monforte, A.J. and Pico, B. (2016) A new genomic library of melon introgression lines in a cantaloupe genetic background for dissecting desirable agronomical traits. BMC Plant Biol. 16, 154.
100. Peterson C E, Owens K W and Rowe P R (1983) Wisconsin 998 muskmelon germplasm. Hortscience 18: 116.
101. Pitrat M (1991) Linkage groups in Cucumis melo L. J Hered 82: 406-11.
102. Pitrat M, Hanelt P, Hammer K (2000) Some comments on infraspecific classification of cultivars of melon. Acta Hortic 510:29–36.
103. Pitrat, M., Chauvet, M., and Foury, C. 1999. Diversity, history and productivity of cultivated cucurbits. In: First International Symposium on Cucurbits, pp. 21–28. Abak, K., and B¨uy¨ukalaca, S., Eds., ISHS, Adana, Turkey.
104. Plages JN (1997). Lavenir des varietes genetiqement modifies pour la resistance aux virus (unexemple developpe par limagrain) CR Acad Agric Fr 83: 161-164.

105. Ramamurthy, R.K. and Waters, B.M. (2015) Identification of fruit quality and morphology QTLs in melon (Cucumis melo) using a population derived from flexuosus and cantalupensis botanical groups. Euphytica, 204, 163–177.
106. Revanasidda and Belavadi, V.V. (2019). Floral biology and pollination in Cucumis melo L., a tropical andromonoecious cucurbit. Journal of Asia-Pacific Entomology 22: 215–225.
107. Robinson, R.W. and Decker-Walters, D. Curcurbits. 1999. CABInternational, Walling ford, Oxon, OX108DE, U.K.
108. Saez C, Esteras C, Martınez C, Ferriol M., Dhillon NPS, Lopez C., Pico B. (2017). Resistance to tomato leaf curl New Delhi virus in melon is controlled by a major QTL located in chromosome 11. Plant Cell Rep DOI 10.1007/s00299-017-2175-3
109. Sebastian, P., H. Schaefer, I. R. H. Telford, and S. S. Renner. 2010. Cucumber (*Cucumis sativus*) and melon (*C. melo*) have numerous wild relatives in Asia and Australia, and the sister species of melon is from Australia. Proceedings of the National Academy of Sciences, USA 107: 14269–14273.
110. Selim M.A.M.(2019). Heterosis and combining ability for some fruit quality traits of egyptian melon inbred lines using line × tester analysis. Egypt. J. Agric. Res., 97 (1): 317-342.
111. Serrano, R., 1996. Salt tolerance in plants and microorganisms: Toxicity targets and defence responses. Int. Rev. Cytol. 165, 1±51.
112. Serrano, R., Culianz-Macia, F.A., & Moreno, V. (1999). Genetic engineering of salt and drought tolerance with yeast regulatory genes. Scientia Horticulture-Amsterdam, 78, 261–269. doi:10.1016/S0304-4238(98)00196-4
113. Shang, J., Kong, S., Li, Na, Wang, J., Zhou, D., Li, Nannan, Ma, S., 2020. Genetic mapping and localization of major QTL for bitterness in melon (Cucumis melo L.). Scientia Horticulturae 266, 109286.
114. Sheshadri VS and More TA 2002. Indian land races in Cucumis melo. Acta Horticulturae 588: 187-193.
115. Shiboleth, Y. M., Arazi, T., Wang, Y., & Gal-On, A. (2001). A new approach for weed control in a cucurbit field employing an attenuated potyvirus-vector for herbicide resistance. J. Biotech, 92, 37–46.
116. Silberstein L, Kovalski I, Brotman Y, Perin C, Dogimont C, Pitrat M, Klingler J, Thompson G, PortnoyV,KatzirN, Perl-Treves R (2003) Linkage map of Cucumismelo including phenotypic traits and sequence-characterized genes. Genome 46:761–773.
117. Silva JA, da Costa TS, Lucchetta L, Marini LJ, Zanuzo MR, Nora L, Nora FR, Twyman RM, Rombaldi CV (2004) Characterization of ripening behavior in transgenic melons expressing an antisense 1-aminocyclopropane-1-carboxylate (ACC) oxidase gene from apple. Postharvest Biol Technol 32:263–268
118. Singh M, Sharma, SP, Navraj Kaur Sarao, Simranjot Kaur & Parveen Chhuneja (2019): Molecular mapping of nuclear male-sterility gene ms-1 in muskmelon (*Cucumis melo* L.), The Journal of Horticultural Science and Biotechnology, DOI: 10.1080/14620316.2019.1652119
119. Singh V and Vashisht V.K. (2018). Heterosis and Combining Ability for Yield in Muskmelon (*Cucumis melo* L.). Int.J.Curr.Microbiol.App.Sci, 7(8): 2996-3006.
120. Siqueira, K.M.M., Kiill, L.H.P., de Siqueira, K.M.M., Gama, da Silva, D.R., Araújo, E.M.S., Dos, D.C., Coelho, S., 2011. Comparação do padrão de floração e de

visitação do meloeiro do tipo amarelo em Juazeiro-BA. E. Revista Brasileira de Fruticultura, Jaboticabal, pp. 473–478 (Volume Especial).

121. Stepansky, A., Kovalski, I., Perl-Treves, R., 1999. Intraspecific classification of melons (*Cucumis melo* L.) in view of their phenotypic and molecular variation. Plant Syst. Evol. 217, 313–332.

122. Subramanian D. Studies on heterosis expression and association of fruit yield and yield component characters among five intervarietal crosses of vellari melon (*Cucumis melo* L.). Madras Agric. J., 2008; 95(1-6):24-31.

123. Taler, D., M. Galperin, I. Benjamin, Y. Cohen, and D. Kenigsbuch. 2004. Plant eR genes that encode photorespiratory enzymes confer resistance against disease. Plant Cell 16: 172–184.

124. Tomar RS and Bhalala M. K. (2006). Heterosis studies in muskmelon (*Cucumis melo* L.). J. Hort. Sci., 1 (2): 144-147.

125. Tschoeke, P.H., Oliveira, E.E., Dalcin, M.S., Silveira-Tschoeke, M.C.A.C., Santos, G.R., 2015. Diversity and flower-visiting rates of bee species as potential pollinators of melon (*Cucumis melo* L.) in the Brazilian Cerrado. Sci. Horticult. Amster. 186, 207–216.

126. Varinder S and Vashisht V.K. (2018). Heterosis and Combining Ability for Yield in Muskmelon (*Cucumis melo* L.). Int.J.Curr.Microbiol.App.Sci, 7(8): 2996-3006.

127. Vishwanatha PD. Genetic variability and heterosis studies in muskmelon (*Cucumis melo* L.). M. Sc. (Hort.) Thesis, Univ. Agric. Sci., Dharwad, 2003.

128. Wang, Y.H., Wu, D.H., Huang, J.H., Tsao, S.J., Hwu, K.K. and Lo, H.F. (2016). Mapping quantitative trait loci for fruit traits and powdery mildew resistance in melon (*Cucumis melo*). Bot Stud (2016) 57:19. DOI 10.1186/s40529-016-0130-1

129. Wolff, D.W., Dunlap, J.R., 1995. Ethylene Production Rate and Postharvest Shelf-life Diversity in Melon (*Cucumis melo* L.) Germplasm. HortScience 30, 827A–827.

130. Wu, H.-W., Yu, T.-A., Raja, J. A. J., Christopher, S. J., Wang, S.-L., and Yeh, S.-D. 2010. Double- virus resistance of transgenic oriental melon conferred by untranslatable chimeric construct carrying partial coat protein genes of two viruses. Plant Dis. 94:1341-1347.

131. Yoshioka, K., Hanada, K., Nakazaki, Y., Minobe, Y., Yakuwa, T., and Oosawa, K. (1992). Successful transfer of the cucumber mosaic-virus coat protein gene to *Cucumis melo* L. Jap. J. Breed. 42 :277-285.

132. Yu X, Wang X, Zhang W, Qian T, Tang G, Guo Y and Zheng C (2008). Antisense suppression of an acid invertase gene (MAI1) in muskmelon alters plant growth and fruit development. Journal of Experimental Botany, 59:2969–2977

133. Yuste-Lisbona, F.J., Capel, C., Sarria, E., Torreblanca, R., Marıa, L. Guillamon, G., Capel, J., Lozano, R. and Lo´pez-Sese, A.I. (2011). Genetic linkage map of melon (*Cucumis melo* L.) and localization of a major QTL for powdery mildew resistance. Mol Breeding, 27:181–192. DOI 10.1007/s11032-010-9421-5

134. Zalapa JE, Staub JE, McCreight JD (2006) Generation means analysis of plant architectural traits and fruit yield in melon. Plant Breed 125:482–487.

135. Zalapa, J. E., Staub, J. E., McCreight, J. D., Chung, S. M., Cuevas, H. (2007). Detection of QTL for yield-related traits using recombinant inbred lines derived from exotic and elite US Western Shipping melon germplasm. Theor. Appl. Genet., 114: 1185–1201. DOI 10.1007/s00122-007-0510-8

136. Zarembinski, T. I., and A. Theologis. 1994. Ethylene biosynthesis and action: A case of conservation. Plant Mol. Biol. 26:1579–1597.

137. Zhang H.J., Gao1 P., Wang X.Z. and Luan F.S. (2014). An efficient regeneration protocol for Agrobacterium-mediated transformation of melon (*Cucumis melo* L.). Genetics and Molecular Research 13 (1): 54-63.

138. Zhang, H., Yi, H., Wu, M., Zhang, Y., Zhang, X., Li, M., Wang, G., 2016. Mapping the flavor contributing traits on" Fengwei melon"(*Cucumis melo* L.) chromosomes using parent resequencing and super bulked-segregant analysis. PLoS One 11, e0148150.

139. Zhao, G., Lian, Q., Zhang, Z., Fu, Q., He, Y., Ma, S., Ruggieri, V., Monforte, A et al., 2019. A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. Nat. Genet. 51, 1607–1615.

140. Zheng XY, Wolff DW. Ethylene production, shelf-life and evidence of RFLP polymorphisms linked to ethylene genes in melon (*Cucumis melo* L.). TAG Theor Appl Genet. 2000;101: 613–24.

141. Zitter, T. A., Hopkins, D. L., and Thomas, C. E. 1996. Compendium of Cucurbit Diseases. APS Press, St. Paul, MN.