

2002 Gene List for Melon

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Gene lists of melon have been published previously, the last one in 1998 (109, 17, 18, 93, 95, 96). They included different types of genes: disease and pest resistance genes, isozymes, leaf, stem, flower, fruit and seed characters.. The 2002 list includes a total number of 162 loci, QTLs for Cucumber Mosaic Virus resistance, ethylene production during fruit maturation and ovary and fruit shape, and one cytoplasmic mutant (*cyt-Yt*) (Table 1).

Genes have also been cloned in melon (mRNA or complete gene with eventually intron...). Only genes with complete sequences are listed in Table 2. Most of them are related to fruit maturation. About 50 partial clones, for instance Resistance Gene Homologues, are also available in databases.

Genetic maps using different types of molecular markers have been published (4, 12, 25, 26, 86, 92, 122). Linkages between isozymes (114) and between phenotypic mutants (94) have also been reported. These maps have been constructed using different melon genotypes as parents and some markers cannot be transferred easily from one map to another or are not polymorphic between all the parents (Table 3). There is not yet a reference saturated map of melon. Moreover very few phenotypic traits have been mapped.

Allelism tests have often not been performed, inflating the number of described genes. This is particularly clear for *Powdery mildew resistance* but also for many other traits. This could be because accessions previously described with this trait are not (or no more) available. It is strongly recommended to send seed samples along with reports of new genes to the melon gene curators. They should consult the lists and the rules of gene nomenclature for the *Cucurbitaceae* (110, 17) before proposing a gene name and symbol.

Table 1. Gene list of melon. In **bold characters** are the genes which are maintained by the curators or which are very common in collections (like *andromonoecious* or *white testa*). In light characters are genes which either have been apparently lost, are not yet maintained by curators, or have uncertain descriptions. In the second part of the table are QTL and in the third part one cytoplasmic factor.

Gene symbol		Character	LG ^z	References
Prefered	Synonym			
<i>a</i>	<i>M</i>	<i>andromonoecious</i>. Mostly staminate, fewer perfect flowers; on <i>A</i>_ plants, pistillate flowers have no stamens; epistatic to <i>g</i>.	4, II	103, 111, 121
<i>ab</i>	-	<i>abrachiate</i> . Lacking lateral branches. Interacts with <i>a</i> and <i>g</i> (e.g. <i>ab ab a a G</i> _ plants produce only staminate flowers).		39
<i>Ac</i>	-	<i>Alternaria cucumerina</i> resistance (in MR-1).		116
<i>Aco-1</i>	<i>Ac</i>	<i>Aconitase-1</i>. Isozyme variant with two alleles, each regulating one band, in PI 218071, PI 224769.	A	114
<i>Acp-1</i>	<i>APS-11</i> , <i>Ap-1</i> ¹	<i>Acid phosphatase-1</i> . Isozyme variant with two codominant alleles, each regulating one band. The heterozygote has two bands.		36

<i>Acp-2</i>	<i>Acp-1</i>	<i>Acid phosphatase-2</i>. Isozyme variant with two alleles, each regulating one band, in PI 194057, PI 224786. Relationship with <i>Acp-1</i> is unknown.	114
<i>Acp-4</i>	-	<i>Acid phosphatase-4</i>. Isozyme variant with two alleles, each regulating one band, in PI 183256, PI 224786. Relationship with <i>Acp-1</i> unknown, different from <i>Acp-2</i>.	114
<i>Af</i>	-	<i>Aulacophora foveicollis</i> resistance. Resistance to the red pumpkin beetle.	119
<i>Ag</i>	-	<i>Aphis gossypii</i> tolerance. Freedom of leaf curling following aphid infestation (in PI 414723).	11
<i>Ak-4</i>	-	<i>Adenylate kinase</i>. Isozyme variant with two alleles, each regulating one band, in PI 169334.	114
<i>Ala</i>	-	<i>Acute leaf apex</i> . Dominant over obtuse apex, linked with <i>Lobed</i> leaf. (<i>Ala</i> in Maine Rock, <i>ala</i> in PV Green).	43
<i>alb</i>	-	<i>albino</i>. White cotyledons, lethal mutant (in Trystorp).	5
<i>Al-1</i>	<i>Al₁</i>	<i>Abscission layer-1</i> . One of two dominant genes for abscission layer formation. See <i>Al-2</i> . (<i>Al-1 Al-2</i> in C68, <i>al-1 al-2</i> in Pearl).	115
<i>Al-2</i>	<i>Al₂</i>	<i>Abscission layer-2</i> . One of two dominant genes for abscission layer formation. See <i>Al-1</i> .	115
<i>Al-3</i>		<i>Abscission layer-3</i>. One dominant gene for abscission layer formation (in PI 161375). Relationship with <i>Al-1</i> or <i>Al-2</i> is unknown.	VIII 91
<i>Al-4</i>		<i>Abscission layer-4</i>. One dominant gene for abscission layer formation (in PI 161375). Relationship with <i>Al-1</i> or <i>Al-2</i> is unknown.	IX 91
<i>bd</i>	-	<i>Brittle dwarf</i> . Rosette growth with thick leaf. Male fertile, female sterile (in TAM-Perlita45).	20
<i>Bi</i>	-	<i>Bitter</i>. Bitter seedling (common in honeydew or in Charentais type while most American cantaloupes are <i>bi</i>).	69
<i>Bif-1</i>	<i>Bif</i>	<i>Bitter fruit-1</i> . Bitterness of tender fruit in wild melon. Relations with <i>Bi</i> are unknown.	88
<i>Bif-2</i>	-	<i>Bitter fruit-2</i> . One of two complementary independent genes for bitter taste in young fruit: <i>Bif-2_ Bif-3_</i> are bitter. (Relationships with <i>Bi</i> and <i>Bif-1</i> are unknown).	73
<i>Bif-3</i>	-	<i>Bitter fruit-3</i> . One of two complementary independent genes for bitter taste in young fruit: <i>Bif-2_ Bif-3_</i> are bitter. (Relationships with <i>Bi</i> and <i>Bif-1</i> are unknown).	73
<i>cab-1</i>	-	<i>cucurbit aphid borne yellows virus resistance-1</i>. One of two complementary independent genes for resistance to this polerovirus: <i>cab-1 cab-1 cab-2 cab-2</i> plants are resistant. (in PI 124112).	29

<i>cab-2</i>	-	<i>cucurbit aphid borne yellows virus resistance-2. One of two complementary independent genes for resistance to this polerovirus: cab-1 cab-1 cab-2 cab-2 plants are resistant. (in PI 124112).</i>		29
<i>cb</i>	<i>cb1</i>	<i>cucumber beetle</i> resistance. Interacts with <i>Bi</i> , the nonbitter <i>bi bi cb cb</i> being the more resistant (in C922-174-B).		84
<i>cf</i>	-	<i>cochleare folium. Spoon-shaped leaf with upward curling of the leaf margins (spontaneous mutant in Galia).</i>		68
<i>cl</i>	-	<i>curled leaf.</i> Elongated leaves that curl upward and inward. Usually male and female sterile.		20
<i>Cys</i>	-	<i>Cucurbit Yellow Stunting Disorder virus</i> resistance. One dominant gene for resistance to this crinivirus in TGR-1551.		70
<i>dc-1</i>	-	<i>Dacus cucurbitae-1</i> resistance. One of two complementary recessive genes for resistance to the melon fruitfly. See <i>dc-2</i> .		112
<i>dc-2</i>	-	<i>Dacus cucurbitae-2</i> resistance. One of two complementary recessive genes for resistance to the melon fruitfly. See <i>dc-1</i> .		112
<i>dl</i>	-	<i>dissected leaf (in URSS 4). Highly indented leaves.</i>	10	31
<i>dl'</i>	<i>cl</i>	<i>dissected leaf Velich. First described as cut leaf in Cantaloup de Bellegarde. Allelic to dl.</i>	10	120
<i>dl-2</i>	-	<i>dissected leaf-2.</i> First described as «hojas hendidas».		35
<i>dlet</i>	<i>dl</i>	<i>delayed lethal.</i> Reduced growth, necrotic lesions on leaves and premature death.		129
<i>Ec</i>	-	<i>Empty cavity. Carpels are separated at fruit maturity leaving a cavity. Ec in PI 414723, ec in Védreantais.</i>	III	90
<i>ech</i>	-	<i>exaggerated curvature of the hook. Triple response of seedlings germinating in darkness in presence of ethylene. ech in PI 161375, Ech in Védreantais.</i>	I	91
<i>f</i>	-	<i>flava.</i> Chlorophyll deficient mutant. Growth rate reduced (in K 2005).	8	100
<i>fas</i>	-	<i>fasciated stem (in Vilmorin 104).</i>		40
<i>Fdp-1</i>	-	<i>Fructose diphosphate-1. Isozyme variant with two alleles, each regulating one band, in PI 218071, PI 224688.</i>		114
<i>Fdp-2</i>	-	<i>Fructose diphosphate-2. Isozyme variant with two alleles, each regulating one band, in PI 204691, PI 183256.</i>		114
<i>fe</i>	-	<i>fe (iron) inefficient mutant. Chlorotic leaves with green veins. Turns green when adding iron in the nutrient solution.</i>		83
<i>Fn</i>	-	<i>Flaccida necrosis. Semi-dominant gene for wilting and necrosis with F pathotype of Zucchini Yellow Mosaic Virus (Fn in Doublon, fn in Védreantais).</i>	2, V	108

<i>Fom-1</i>	<i>Fom₁</i>	<i>Fusarium oxysporum melonis</i> resistance. Resistance to races 0 and 2 and susceptibility to races 1 and 1,2 of <i>Fusarium</i> wilt (<i>Fom-1</i> in Doublon, <i>fom-1</i> in Charentais T).	5, IX	107
<i>Fom-2</i>	<i>Fom_{1,2}</i>	<i>Fusarium oxysporum melonis</i> resistance. Resistance to races 0 and 1 and susceptibility to races 2 and 1,2 of <i>Fusarium</i> wilt. (<i>Fom-2</i> in CM 17187, <i>fom-2</i> in CharentaisT).	6, XI	107
<i>Fom-3</i>	-	<i>Fusarium oxysporum melonis</i> resistance. Same phenotype as <i>Fom-1</i> but segregates independently from <i>Fom-1</i> . (<i>Fom-3</i> in Perlita FR, <i>fom-3</i> in CharentaisT).		130
<i>G</i>	-	<i>gynomonoecious</i> . Mostly pistillate, fewer perfect flowers. Epistatic to <i>a a A_ G_</i> monoecious; <i>A_ g g</i> gynoeceious; <i>a a G_</i> andromonoecious; <i>a a g g</i> hermaphrodite.		103
<i>gf</i>	-	<i>green flesh</i> color. Recessive to salmon. (<i>gf</i> in honeydew, <i>Gf</i> in Smiths' Perfect cantaloupe).	IX	51
<i>gl</i>	-	<i>glabrous</i> . Trichomes lacking (in Arizona glA).	3	38
<i>gp</i>	-	<i>green petals</i> . Corolla leaf like in color and venation.		79
<i>Gpi</i>	-	<i>Glucosephosphate isomerase</i> . Isozyme variant with two alleles, each regulating one band, in PI 179680.		114
<i>Gs</i>	-	<i>Gelatinous sheath</i> around the seeds. Dominant to absence of gelatinous sheath.		41
<i>gyc</i>	-	<i>greenish yellow corolla</i> .		128
<i>gy</i>	<i>n, M</i>	<i>gynoeceious</i> . Interacts with <i>a</i> and <i>g</i> to produce stable gynoeceious plants (<i>A_ g g gy gy</i>) (in WI 998).		60, 62
<i>h</i>	-	<i>halo</i> cotyledons. Yellow halo on the cotyledons, later turning green.	4, II	82
<i>Idh</i>	-	<i>Isocitrate dehydrogenase</i> . Isozyme variant with two alleles, each regulating one band, in PI 218070, PI 224688.	A	114
<i>Imy</i>	-	<i>Interveinal mottling and yellowing</i> resistance. Resistance to a complex of viruses in PI 378062.		49
<i>jf</i>	-	<i>juicy flesh</i> . Segregates discretely in a monogenic ratio in segregating generations.		13
<i>L</i>	-	<i>Lobed</i> leaf. Dominant on non lobed, linked with <i>Acute leaf apex</i> . (<i>L</i> in Maine Rock, <i>l</i> in P.V. Green).		43
<i>lmi</i>	-	<i>long mainstem internode</i> . Affects internode length of the main stem but not of the lateral ones (in 48764).	8	74
<i>Liy</i>	-	<i>Lettuce infectious yellows</i> virus resistance. One dominant gene for resistance to this crinivirus in PI 313970.		75

<i>Lt</i>	-	<i>Liriomyza trifolii</i> (leafminer) resistance (in Nantais Oblong).		28
<i>M-Pc-5</i>	-	<i>Modifier of Pc-5</i> . Gene <i>Pc-5</i> for downy mildew resistance (see <i>Pc-5</i>) is dominant in presence of <i>M-Pc-5</i> , recessive in the absence of <i>M-Pc-5</i> .		2
<i>Mc</i>	-	<i>Mycosphaerella citrullina</i> resistance. High degree of resistance to gummy stem blight (in PI 140471).		104
<i>Mc-2</i>	<i>Mci</i>	<i>Mycosphaerella citrullina</i> resistance-2. Moderate degree of resistance to gummy stem blight (in C-1 and C-8.)		104
<i>Mc-3</i>	-	<i>Mycosphaerella citrullina</i> resistance-3. High level of resistance to gummy stem blight in PI 157082, independent from <i>Mc</i> .		131
<i>Mc-4</i>	-	<i>Mycosphaerella citrullina</i> resistance-4. High level of resistance to gummy stem blight in PI 511890. Relationships with <i>Mc</i> and <i>Mc-3</i> unknown.		131
<i>Mca</i>	-	<i>Macrocalyx</i> . Large, leaf like structure of the sepals in staminate and hermaphrodite flowers (<i>Mca</i> in makuwa, <i>mca</i> in Annamalai).		42
<i>Mdh-2</i>	-	<i>Malate dehydrogenase-2</i>. Isozyme variant with two alleles, each regulating one band, in PI 224688, PI 224769.	B	114
<i>Mdh-4</i>	-	<i>Malate dehydrogenase-4</i>. Isozyme variant with two alleles, each regulating one band, in PI 218070, PI 179923.	B	114
<i>Mdh-5</i>	-	<i>Malate dehydrogenase-5</i>. Isozyme variant with two alleles, each regulating one band, in PI 179923, PI 180283.	B	114
<i>Mdh-6</i>	-	<i>Malate dehydrogenase-6</i>. Isozyme variant with two alleles, each regulating one band, in P 179923, PI 180283.	B	114
<i>Me</i>	-	<i>Mealy</i> flesh texture. Dominant to crisp flesh. (<i>Me</i> in <i>C. callosus</i> , <i>me</i> in makuwa).		41
<i>Me-2</i>	-	<i>Mealy</i> flesh texture-2 (in PI 414723).		90
<i>Mpi-1</i>	-	<i>Mannosephosphate isomerase-1</i>. Isozyme variant with two alleles, each regulating one band, in PI 183257, PI 204691.	A	114
<i>Mpi-2</i>	-	<i>Mannosephosphate isomerase-2</i>. Isozyme variant with two alleles, each regulating one band, in PI 183257, PI 204691.	A	114
<i>ms-1</i>	<i>ms¹</i>	<i>male sterile-1</i>. Indehiscent anthers with empty pollen walls in tetrad stage.	3	8
<i>ms-2</i>	<i>ms²</i>	<i>male sterile-2</i>. Anthers indehiscent, containing mostly empty pollen walls, growth rate reduced.	6, XI	10
<i>ms-3</i>	<i>ms-L</i>	<i>male sterile-3</i>. Waxy and translucent indehiscent anthers, containing two types of empty pollen sacs.	12	77
<i>ms-4</i>	-	<i>male sterile-4</i>. Small indehiscent anthers. First male flowers abort at bud stage (in Bulgaria 7).	9	71

<i>ms-5</i>	-	male sterile-5. Small indehiscent anthers. Empty pollen (in Jivaro, Fox).	13	67
<i>Mt</i>	-	<i>Mottled</i> rind pattern. Dominant to uniform color. Epistatic with <i>Y</i> (not expressed in <i>Y_</i>) and <i>st</i> (<i>Mt_ st st</i> and <i>Mt_ St_ mottled</i> ; <i>mt mt st st</i> striped, <i>mt mt St_</i> uniform). (<i>Mt</i> in Annamalai, <i>mt</i> in makuwa).		41
<i>Mt-2</i>	-	Mottled rind pattern (in PI 161375). Relationship with <i>Mt</i> unknown.	II	90
<i>Mu</i>	-	<i>Musky</i> flavour (olfactory). Dominant on mild flavor (<i>Mu</i> in <i>C. melo callosus</i> , <i>mu</i> in makuwa or Annamalai).		41
<i>Mvd</i>	-	<i>Melon vine decline</i> resistance. Semi-dominant gene for partial resistance to <i>Acremonium cucurbitacearum</i> and <i>Monosporascus cannonballus</i> (in Pat 81 <i>agrestis</i> melon).		52
<i>My</i>	-	<i>Melon yellows</i> virus resistance. Semi-dominant gene, in Nagata Kin Makuwa, for partial resistance to this crinivirus.		37, 81
<i>n</i>	-	nectarless. Nectaries lacking in all flowers (in 40099).		6
<i>Nm</i>	-	Necrosis with Morocco strains of Watermelon Mosaic Virus, a potyvirus (<i>Nm</i> in Védreantais, <i>nm</i> in Ouzbèque).		105
<i>nsv</i>	-	Melon necrotic spot virus resistance. One recessive gene for resistance to this carmovirus in Gulfstream, Planters Jumbo.	7, XII	19
<i>O</i>	-	Oval fruit shape. Dominant to round; associated with <i>a</i>.		121
<i>Org-1</i>	-	<i>Organogenic</i> response for <i>in vitro</i> shoot regeneration. Partially dominant. Interacts with an additive model with <i>Org-2</i> .		80
<i>Org-2</i>	-	<i>Organogenic</i> response for <i>in vitro</i> shoot regeneration. Partially dominant. Interacts with an additive model with <i>Org-1</i> .		80
<i>p</i>	-	pentamerous. Five carpels and stamens; recessive to trimerous (in Casaba).	XII	111
<i>Pa</i>	-	Pale green foliage. <i>Pa Pa</i> plants are white (lethal); <i>Pa pa</i> are yellow (in 30567).	3	76
<i>Pc-1</i>	-	<i>Pseudoperonospora cubensis</i> resistance. One of two complementary incompletely dominant genes for downy mildew resistance (in PI 124111). See <i>Pc-2</i>.		16, 117
<i>Pc-2</i>	-	<i>Pseudoperonospora cubensis</i> resistance. One of two complementary incompletely dominant genes for downy mildew resistance (in PI 124111). See <i>Pc-1</i>.		16, 117
<i>Pc-3</i>	-	<i>Pseudoperonospora cubensis</i> resistance. Partial resistance to downy mildew (in PI 414723).		33
<i>Pc-4</i>	-	<i>Pseudoperonospora cubensis</i> resistance. One of two complementary genes for downy mildew resistance in PI 124112. Interacts with <i>Pc-1</i> or <i>Pc-2</i>.		63

<i>Pc-5</i>	-	<i>Pseudoperonospora cubensis</i> resistance. One gene in Line 5-4-2-1 which interacts with <i>M-Pc-5</i> in the susceptible line K15-6 (<i>Pc-5</i> is dominant in presence of <i>M-Pc-5</i> , recessive in the absence of <i>M-Pc-5</i>).		2
<i>Pep-gl</i>	-	Peptidase with glycyl-leucine. Isozyme variant with two alleles, each regulating one band, in PI 218070.	B	114
<i>Pep-la</i>	-	Peptidase with leucyl-alanine. Isozyme variant with two alleles, each regulating one band, in PI 183256.		114
<i>Pep-pap</i>	-	Peptidase with phenylalanyl-proline. Isozyme variant with two alleles, each regulating one band, in PI 183256.		114
<i>Pgd-1</i>	<i>6-PGDH-2l</i> <i>Pgd-2l</i>	<i>Phosphoglucose dehydrogenase-1</i> . Isozyme variant with two alleles, each regulating one band. The heterozygote has one intermediate band.		36
<i>6-Pgd-2</i>	-	6-Phosphogluconate dehydrogenase. Isozyme variant with two alleles, each regulating one band, in PI 161375, Védtrantais. Relationship with <i>Pgd-1</i> is unknown.	IX	4
<i>Pgd-3</i>	<i>Pgd</i>	6-Phosphogluconate dehydrogenase. Isozyme variant with two alleles, each regulating one band, in PI 218070. Relationship with <i>Pgd-1</i> and <i>6-Pgd-2</i> is unknown.	A	114
<i>Pgi-1</i>	<i>PGI-1l</i>	<i>Phosphoglucoisomerase-1</i> . Isozyme variant with two alleles, each regulating two bands. The heterozygote has three bands.		36
<i>Pgi-2</i>	<i>PGI-2l</i>	<i>Phosphoglucoisomerase-2</i> . Isozyme variant with two alleles, each regulating two bands. The heterozygote has three bands.		36
<i>Pgm-1</i>	<i>PGM-2l</i> <i>Pgm-2l</i>	<i>Phosphoglucomutase-1</i> . Isozyme variant with two alleles, each regulating two bands. The heterozygotes has three bands.		36
<i>Pgm-2</i>	<i>Pgm</i>	Phosphoglucomutase. Isozyme variant with two alleles, each regulating one band, in PI 218070, PI 179923. Relationship with <i>Pgm-1</i> is unknown.	A	114
<i>pH</i>	-	pH(acidity) of the mature fruit flesh. Low pH value in PI 14723 dominant to high pH value in Dulce	VIII	25
<i>pin</i>	-	pine-seed shape (in PI 161375).	III	92
<i>Pm-1</i>	<i>Pm¹</i> <i>Pm-A ?</i>	Powdery mildew resistance-1. Resistance to race 1 of <i>Sphaerotheca fuliginea</i> (in PMR 45).		55
<i>Pm-2</i>	<i>Pm²</i> <i>Pm-C ?</i>	Powdery mildew resistance-2. Interacts with <i>Pm-1</i>. Resistance to race 2 of <i>Sphaerotheca fuliginea</i> (in PMR 5 with <i>Pm-1</i>).		9
<i>Pm-3</i>	<i>Pm³</i>	Powdery mildew resistance-3. Resistance to race 1 of <i>Sphaerotheca fuliginea</i> (in PI 124111).	7	47, 48
<i>Pm-4</i>	<i>Pm⁴</i>	Powdery mildew resistance-4. Resistance to <i>Sphaerotheca fuliginea</i> (in PI 124112).		47, 48
<i>Pm-5</i>	<i>Pm⁵</i>	Powdery mildew resistance-5. Resistance to <i>Sphaerotheca fuliginea</i> (in PI 124112).		47, 48

<i>Pm-6</i>	-	<i>Powdery mildew</i> resistance-6. Resistance to <i>Sphaerotheca fuliginea</i> race 2 (in PI 124111).	61
<i>Pm-7</i>	-	<i>Powdery mildew</i> resistance-7. Resistance to <i>Sphaerotheca fuliginea</i> race 1 (in PI 414723).	1
<i>Pm-E</i>	-	<i>Powdery mildew</i> resistance-E. Interacts with <i>Pm-C</i> in PMR5 for <i>Erysiphe cichoracearum</i> resistance.	34
<i>Pm-F</i>	-	<i>Powdery mildew</i> resistance-F. Interacts with <i>Pm-G</i> in PI 124112 for <i>Erysiphe cichoracearum</i> resistance.	34
<i>Pm-G</i>	-	<i>Powdery mildew</i> resistance-G. Interacts with <i>Pm-F</i> in PI 124112 for <i>Erysiphe cichoracearum</i> resistance.	34
<i>Pm-H</i>	-	<i>Powdery mildew</i> resistance-H. Resistance to <i>Erysiphe cichoracearum</i> and susceptibility to <i>Sphaerotheca fuliginea</i> (in Nantais oblong).	34
<i>Pm-w</i>	<i>Pm-B ?</i>	<i>Powdery mildew</i> resistance in WMR 29. Resistance to <i>Sphaerotheca fuliginea</i> race 2.	2, V 94
<i>Pm-x</i>	-	<i>Powdery mildew</i> resistance in PI 414723. Resistance to <i>Sphaerotheca fuliginea</i> .	4, II 94
<i>Pm-y</i>	-	<i>Powdery mildew</i> resistance in VA 435. Resistance to <i>Sphaerotheca fuliginea</i>	7, XII 94
<i>Prv¹</i>	<i>Wmv</i>	<i>Papaya Ringspot virus</i> resistance. Resistance to W strain of this potyvirus (formerly Watermelon Mosaic Virus 1) (in B 66-5, WMR 29, derived from PI 180280). Dominant to <i>Prv²</i> .	5, IX 98, 123
<i>Prv²</i>	-	<i>Papaya Ringspot virus</i> resistance. Allele at the same locus as <i>Prv¹</i> but different reaction with some strains of the virus (in 72-025 derived from PI 180283). Recessive to <i>Prv¹</i> .	5, IX 57, 98
<i>Prv-2</i>	-	<i>Papaya Ringspot virus</i> resistance-2 (in PI 124112). Relationship with <i>Prv</i> is unknown.	78
<i>Px-1</i>	<i>PRX-1I</i>	<i>Peroxidase-1</i> . Isozyme variant with two codominant alleles, each regulating a cluster of four adjacent bands. The heterozygote has five bands.	36
<i>Px-2</i>	<i>Px2A</i> <i>Prx2</i>	<i>Peroxidase-2</i> . Isozyme variant with two codominant alleles, each regulating a cluster of three adjacent bands. The heterozygote has 4 bands.	14, 22
<i>r</i>	-	red stem. Red pigment under epidermis of stems, especially at nodes; tan seed color (in PI 157083).	3 7, 76
<i>ri</i>	-	<i>ridge</i> . Ridged fruit surface, recessive to ridgeless. (<i>ri</i> in C68, <i>Ri</i> in Pearl).	115
<i>s</i>	-	<i>sutures</i> . Presence of vein tracts on the fruit (« sutures »); recessive to ribless.	3
<i>s-2</i>	-	<i>sutures-2</i> on the fruit rind (in PI 161375). Relationship with <i>s</i> is unknown.	XI 90
<i>Sfl</i>	<i>S</i>	<i>Subtended floral leaf</i> . The floral leaf bearing the hermaphrodite flowers is sessile, small and encloses the flower. (<i>Sfl</i> in makuwa, <i>sfl</i> in Annamalai).	42

<i>si-1</i>	<i>b</i>	<i>short internode-1</i>. Extremely compact plant habit (bush type) (in UC Topmark bush).	1	27
<i>si-2</i>	-	<i>short internode-2</i>. Short internodes from ‘birdnest’ melon (in Persia 202).		87
<i>si-3</i>	-	<i>short internode-3</i>. Short internodes in Maindwarf.		64
<i>Skdh-1</i>	-	<i>Shikimate dehydrogenase-1</i> . Isozyme variant with two codominant alleles, each regulating one band. The heterozygote has three bands.		14, 44
<i>slb</i>	<i>sb</i>	<i>short lateral branching</i> . Reduction of the elongation of the lateral branches, in LB.		85
<i>So</i>	-	<i>Sour</i> taste. Dominant to sweet.		65
<i>So-2</i>	-	<i>Sour</i> taste-2 (in PI 414723). Relationship with <i>So</i> is unknown.		90
<i>sp</i>	-	<i>spherical</i> fruit shape. Recessive to obtuse; dominance incomplete.		3, 72
<i>spk</i>	-	<i>speckled fruit epidermis</i> (<i>spk</i> in PI 161375 or PI 414723, <i>Spk</i> in Védraçais).	VII	92
<i>st</i>	-	<i>striped</i> epicarp. Recessive to non-striped.		46
<i>st-2</i>	<i>st</i>	<i>striped epicarp-2</i>. Present in Dulce, recessive to non-striped in PI 414723. Relationship with <i>st</i> is unknown.	XI	25
<i>v</i>	-	<i>virescent</i>. Pale cream cotyledons and hypocotyls; yellow green foliage (mainly young leaves).	11	50
<i>v-2</i>	-	<i>virescent-2</i>.		32
<i>v-3</i>	-	<i>virescent-3</i>. White cotyledons which turn green, light green young leaves which are normal when they are older.		101
<i>Vat</i>	-	<i>Virus aphid transmission</i> resistance. Resistance to the transmission of several viruses by <i>Aphis gossypii</i> (in PI 161375).	2, V	97
<i>w</i>	-	<i>white</i> color of mature fruit. Recessive to dark green fruit skin. (<i>w</i> in honeydew, <i>W</i> in Smiths’ Perfect cantaloupe).		51
<i>wf</i>	-	<i>white flesh</i>. Recessive to salmon. <i>Wf</i> epistatic to <i>Gf</i>.		15, 53
<i>Wi</i>	-	White color of <i>immature</i> fruit. Dominant to green.		65
<i>Wmr</i>	-	<i>Watermelon Mosaic virus 2</i> (potyvirus) resistance (in PI 414723).	II	45
<i>Wt</i>	-	<i>White testa</i>. Dominant to yellow or tan seed coat color.		46
<i>Wt-2</i>	-	<i>White testa-2</i> (in PI 414723). Relationship with <i>Wt</i> unknown.	IV	90
<i>Y</i>	-	<i>Yellow</i> epicarp. Dominant to white fruit skin.		46
<i>yg</i>	-	<i>yellow green</i> leaves. Reduced chlorophyll content.	6, XI	124

<i>yg</i> ^W	<i>lg</i>	<i>yellow green Weslaco</i> . First described as <i>light green</i> in a cross Dulce x TAM-Uvalde. Allelic to <i>yg</i> .	21
<i>yv</i>	-	<i>yellow virescence</i> . Pale cotyledons; yellow green young leaves and tendrils; bright and yellow petals and yellow stigma; etiolated; older leaves becoming green.	1 127
<i>yv-2</i>	<i>yv-X</i>	<i>yellow virescence-2</i> . Young leaves yellow green, old leaves normal green.	5, IX 102
<i>Zym</i>	<i>Zym-1</i>	<i>Zucchini Yellow Mosaic virus</i> resistance. Resistance to pathotype 0 of this potyvirus (in PI 414723).	4, II 99
<i>Zym-2</i>	-	<i>Zucchini Yellow Mosaic</i> potyvirus resistance. One of three complementary genes (see <i>Zym</i> and <i>Zym-3</i>) for resistance to this potyvirus (in PI 414723).	24
<i>Zym-3</i>	-	<i>Zucchini Yellow Mosaic</i> potyvirus resistance. One of three complementary genes (see <i>Zym</i> and <i>Zym-2</i>) for resistance to this potyvirus (in PI 414723).	24

Quantitative Trait Loci (QTLs)

<i>cmv</i>	-	<i>cucumber mosaic virus</i> resistance. Three recessive genes have been described in the cross Freemans's cucumber x Noy Amid. Seven QTLs are involved in resistance to three different strains of this cucumovirus in the cross Védrañtais x PI 161375.	30, 58
<i>eth</i>		<i>ethylene</i> production in fruit (climacteric crisis). Four QTLs described in the cross Védrañtais x PI 161375.	91
<i>fl</i>	-	<i>fruit length</i> . Four QTL described in the cross Védrañtais x PI 161375 and 4 QTLs in the cross Védrañtais x PI 414723, one is common to both crosses.	89
<i>fs</i>	-	<i>fruit shape</i> (ratio fruit length/fruit width). Six QTL described in the cross Védrañtais x PI 161375 and 2 QTLs in the cross Védrañtais x PI 414723, which are common to both crosses.	89
<i>fw</i>	-	<i>fruit width</i> . Five QTL described in the cross Védrañtais x PI 161375 and 1 QTLs in the cross Védrañtais x PI 414723.	89
<i>ovl</i>	-	<i>ovary length</i> . Six QTL described in the cross Védrañtais x PI 161375.	89
<i>ovs</i>	-	<i>ovary shape</i> (ratio ovary length/ovary width). Six QTL described in the cross Védrañtais x PI 161375.	89
<i>ovw</i>	-	<i>ovary width</i> . Eight QTL described in the cross Védrañtais x PI 161375.	89

Cytoplasmic Factors

<i>cyt-Yt</i>	-	<i>cytoplasmic yellow tip</i> . Chlorophyll deficient mutant with yellow young leaves, turning green when becoming older. Maternally inherited	106
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^z Linkage group to which this gene belongs: Letters correspond to (114), arabic numbers to (94) and roman numbers to (92). See Table 3.

Table 2. List of cloned genes in melon and their putative function. Sequences can be submitted directly to databases or can be published in journals (Ref.). A few genes have been mapped (Linkage Groups).

Gene symbol	Gene accession	(Putative) Function	Submitted by	LG^z	Ref.
<i>Cm-AAT</i>	AB075227	Alcohol acetyltransferase GeAAT	Ishimaru M.		
<i>Cm-AAT2</i>	AF468022	Putative alcohol acyltransferase (AT2)	El Yahyaoui F. <i>et al</i>		
<i>Cm-ACO1</i>	X95551	1-aminocyclopropane-1- carboxylate (ACC) oxidase 1	Lasserre E. <i>et al</i>	V	66
<i>Cm-ACO2</i>	X95552	1-aminocyclopropane-1- carboxylate (ACC) oxidase 2	Lasserre E. <i>et al</i>	VIII	66
<i>Cm-ACO3</i>	X95553	1-aminocyclopropane-1- carboxylate (ACC) oxidase 3	Lasserre E. <i>et al</i>		66
<i>Cm-ACS1</i>	AB025906	1-aminocyclopropane-1- carboxylate (ACC) synthase 1	Yamamoto M. <i>et al</i>	XI	126
<i>Cm-ACS1</i>	AB032935	1-aminocyclopropane-1- carboxylate (ACC) synthase	Shiomi S. <i>et al</i>	XI	
<i>Cm-ACS2</i>	D86242	1-aminocyclopropane-1- carboxylate (ACC) synthase 2	Ishiki Y. <i>et al</i>		54
<i>Cm-ACS2</i>	AB032936	1-aminocyclopropane-1- carboxylate (ACC) synthase 2	Shiomi S. <i>et al</i>		
<i>Cm-AGPP-mlf2</i>	AF030383 AF030384	ADP-glucose pyrophosphorylase large subunit (mlf2)	Park S.-W. <i>et al</i>		
<i>Cm-AGPP-msf1</i>	AF030382	ADP-glucose pyrophosphorylase small subunit (msf1)	Park S.-W. <i>et al</i>		
<i>Cm-AmT1</i>	AY066012	Aminotransferase 1	Taler D. <i>et al</i>		
<i>Cm-AmT2</i>	AF461048	Aminotransferase 2	Taler D. <i>et al</i>		
<i>Cm-AO1</i>	AF233593	Ascorbate oxidase AO1	Sanmartin M. <i>et al</i>		
<i>Cm-AO3</i>	Y10226	Ascorbate oxidase AO3	Pateraki I. <i>et al</i>		
<i>Cm-AO4</i>	AF233594	Ascorbate oxidase AO4	Sanmartin M. <i>et al</i>		
<i>Cm-AOS</i>	AF081954	Allene oxide synthase (AOS)	Tijet N. <i>et al</i>		
<i>Cm-ASR1</i>	AF426403 AF426404	Abscisic acid response protein (Asr1)	Hong S.-H. <i>et al</i>		

<i>Cm-CCM</i>	D32206	Cucumisin (serine protease)	Yamagata H. <i>et al</i>	125
<i>Cm-CHI1</i>	AF241266	Chitinase 1	Zou X. <i>et al</i>	
<i>Cm-CHI2</i>	AF241267	Chitinase 2	Zou X. <i>et al</i>	
<i>Cm-E8</i>	AF241538 AB071820	Regulator of ethylene synthesis, similar to <i>Le-E8</i>	Fujimori A. <i>et al</i>	
<i>Cm-EIL1</i>	AB063191	Transcription factor Ethylene Insensitive 1 for At-EIN3-like protein	Sato T. <i>et al</i>	
<i>Cm-EIL2</i>	AB063192	Transcription factor Ethylene Insensitive 2 for At-EIN3-like protein	Sato T. <i>et al</i>	
<i>Cm-ERS1</i>	AF037368	Putative ethylene receptor ERS1	Sato Nara K. <i>et al</i>	I 113
<i>Cm-ERS1</i>	AB049128	Ethylene receptor ERS1	Furukawa H.	
<i>Cm-ETR1</i>	AF054806	Putative ethylene receptor (ETR1)	Sato Nara K. <i>et al</i>	113
<i>Cm-ETR1</i>	AB052228	Ethylene receptor (ETR1)	Furukawa H.	
<i>Cm-GAS1</i>	AY077642	Galactinol synthase (GAS1)	Volk G.M. <i>et al</i>	
<i>Cm-GAS2</i>	AY077641	Galactinol synthase (GAS2)	Volk G.M. <i>et al</i>	
<i>Cm-GLD</i>	AF252339	L-galactono-1,4-lactone dehydrogenase	Pateraki I. and Kanellis A.K.	
<i>Cm-HMG-CoA</i>	AB021862	3-hydroxy-3-methylglutaryl coenzyme A reductase	Kato-Emori S. <i>et al</i>	59
<i>Cm-HPL</i>	AF081955	Fatty acid 9-hydroperoxide lyase (HPL)	Tijet N. <i>et al</i>	118
<i>Cm-ITS1</i>	AF006802	Internal Transcribed Spacer 1	Jobst J. <i>et al</i>	56
<i>Cm-ITS2</i>	AF013333	Internal Transcribed Spacer 2	Jobst J. <i>et al</i>	56
<i>Cm-Lec17</i>	AF520577	17 kDa phloem lectin (Lec17)	Dinant S. <i>et al</i>	
<i>Cm-Lec17-1</i>	AF517156	17 kDa phloem lectin Lec17-1	Dinant S. <i>et al</i>	
<i>Cm-Lec17-3</i>	AF517157	17 kDa phloem lectin Lec17-3 mRNA	Dinant S. <i>et al</i>	
<i>Cm-Lec26</i>	AF517154	26 kDa phloem lectin (Lec26)	Dinant S. <i>et al</i>	
<i>Cm-MPP</i>	AF297643	Mitochondrial processing peptidase beta subunit	He C. <i>et al</i>	

<i>Cm-PG1</i>	AF062465	Polygalacturonase precursor (MPG1)	Hadfield K.A. <i>et al</i>
<i>Cm-PG2</i>	AF062466	Polygalacturonase precursor (MPG2)	Hadfield K.A. <i>et al</i>
<i>Cm-PG3</i>	AF062467	Polygalacturonase precursor (MPG3)	Hadfield K.A. <i>et al</i>
<i>Cm-ProETRI</i>	E51774	Promoter of melon ethylene receptor	Ezura H. <i>et al</i> Patent JP 2001037484-A 14 13-FEB-2001
<i>Cm-PSY1</i>	Z37543	Phytoene synthase	Karvouni Z. <i>et al</i>
<i>Cm-TCTP</i>	AF230211	Translationally controlled tumor protein-related protein	Gomez-Lim M.A. <i>et al</i>

^z Linkage group to which this gene belongs according to 92.

Table 3. Genes and QTLs localization and correspondance between linkage groups using common markers such as phenotypic traits or molecular markers (mainly SSR according to 23).

94 ^z	4 ^z	122 ^z	114 ^z	12 ^z	86 ^z	92 ^z	25 ^z	Genes	QTLs
1	-	-	-	-	-	-	-	<i>si-1, yv</i>	
2	2+ K	-	-	6	4	V	-	<i>Cm-ACO1, Fn, Pm-w, Vat</i>	<i>fl5.1, fw5.2</i>
3	-	-	-	-	-	-	-	<i>gl, ms-1, Pa, r</i>	
4	D	-	-	3	8	II	IV	<i>a, h, mt-2, Pm-x, Zym</i>	<i>cmv2.1, cmv2.2, eth2.1, fl2.1, fs2.1, fs2.2, fw2.1, ovl2.1, ovl2.2, ovs2.1, ovs2.2, ovw2.1</i>
5	5	-	-	11	7	IX	II	<i>Al-4, Fom-1, gf, 6-Pgd2, Prv, yv-2</i>	<i>cmv9.1, fw9.1, ovl9.1, ovs9.1</i>
-	-	-	A	-	-	-	-	<i>Aco-1, Idh, Mpi-1, Mpi-2, Pgd-3, Pgm-2</i>	
6	6	III	-	1	5	XI	III	<i>Cm-ACSI, Fom-2, ms-2, s-2, yg</i>	<i>eth11.1, fs11.1</i>
7	7	-	-	3	11	XII	-	<i>nsv, p, Pm-Y</i>	<i>cmv12.1, cmv12.2, fs12.1, fw12.1, ovs12.1, ovw12.1</i>
8	-	-	-	-	-	-	-	<i>f, lmi</i>	
9	-	-	-	-	-	-	-	<i>dl</i>	
10	-	-	-	-	-	-	-	<i>ms-3</i>	
11	-	-	-	-	-	-	-	<i>ms-4</i>	
12	-	-	-	-	-	-	-	<i>ms-5</i>	
13	-	-	-	-	-	-	-	<i>V</i>	
-	C	-	-	10	10	IV	-	<i>Wt-2</i>	<i>fl4.1, fw4.1, ovl4.1</i>
-	E	-	-	3+8+ 13 (+17?))	1	VIII	I	<i>Al-3, Cm-ACO2, pH</i>	<i>cmv8.1, fl8.1, fl8.2, fs8.1, fs8.2, ovl8.1, ovs8.1, ovs8.2, ovw8.1</i>
-	F	-	-	-	3	VII	VI	<i>Spk</i>	<i>fw7.1, ovl7.1, ovs7.1</i>

-	G	-	-	3+12	6	I	VIII	<i>ech, Cm-ERS1</i>	<i>eth1.1, fl1.1, fs1.1, ovs1.1</i>
-	J	-	-	-	2	III	V	<i>Cm-ACS5, Ec, pin</i>	<i>cmv3.1, cmv3.2, eth3.1</i>
-	-	-	B	-	-	-	-	<i>Mdh-2, Mdh-4, Mdh-5, Mdh-6, Pep-gl</i>	
-	A	-	-	4+7	9	X	-		<i>ovw10.1</i>
-	B	-	-	9	12	VI	-		<i>fl6.1</i>

N.B. If *6-Pgd-2* (4) and *Pgd-3* (114) correspond to the same locus, which is probable but not yet demonstrated, lines 5 and 6 of this table can be merged.

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