

Gene List for *Cucurbita* species, 2009

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The genus *Cucurbita* L. contains 12 or 13 species (50). As far as is known, all have a complement of 20 pairs of chromosomes ($2n = 40$).

This gene list for *Cucurbita* contains detailed sources of information, being modeled after the one for cucumber presented by Wehner and Staub (103) and its update by Xie and Wehner (109). In order to more easily allow confirmation of previous work and as a basis for further work, information has been included concerning the genetic background of the parents that had been used for crossing. Thus, in addition to the species involved, the cultivar-group (for *C. pepo*), market type (for *C. maxima*, *C. moschata*), and/or cultivar name are included in the description wherever possible.

Genes affecting phenotypic/morphological traits are listed in **Table 1**. The data upon which are based identifications and concomitant assignment of gene symbols vary considerably in their content. No attempt is made here to assess the certainty of identifications, but gene symbols have been accepted or assigned only for cases in which at least some data are presented. The genes that are protein/isozyme variants are listed in **Table 2**. It can be seen from Tables 1 and 2 that approximately 70 genes have been identified for *C. pepo* L, for *C. moschata* Duchesne 25 and for *C. maxima* Duchesne 19. For the interspecific cross of *C. maxima* × *C. ecuadorensis* Cutler & Whitaker, 29 genes have been identified, of which 25 are isozyme variants. A few genes have also been identified in four of the wild species (*C. okechobeensis* Bailey, *C. lundelliana* Bailey, *C. foetidissima* HBK and *C. ecuadorensis*) and in several other interspecific crosses.

Some genes are listed as occurring in more than one species. This does not necessarily indicate that these genes reside at identical locations in the genome of different species.

New additions to the list of *Cucurbita* genes include a number of omissions as well as a number of new genes published after the last update. Those that had been omitted are three unnamed genes for fruit bitterness (3). They are herein designated *Bitter fruit-1*, *-2*, and *-3*, symbols *Bi-1*, *Bi-2*, and *Bi-3*. This has necessitated the modi-

fication of the symbols for the two previously identified genes (12, 30, 32) for *Bitter fruit* as *Bi^{max}* and *Bi-0*. Newly identified genes that have been published since the last update are: *ae* (*androecy enhancer*), *Crr-1*, *Crr-2*, and *Crr-3* (*Crown rot resistance-1*, *-2*, and *-3*), *gl-2* (*glabrous-2*), and *l-2^R* (*light type-2 Reverse striping*). The symbols *ae*, *Crr-1*, *Crr-2*, and *Crr-3* are herein assigned for the first time. Before choosing a gene name and symbol, researchers are urged to consult this Gene List as well as the rules of Gene Nomenclature for the Cucurbitaceae that appears near the end of this Cucurbit Genetics Cooperative Report in order to avoid confusion arising from duplication of gene names and symbols. Please contact us if you find omissions or errors in this Gene List.

Several cases of genetic linkage have been reported: *D - mo-2* (61) and *M - Wt* (*C. pepo*) (72) and *Bi - Lo-2* (*C. ecuadorensis* × *C. maxima*) (32). Some of the isozyme variants observed by Weeden & Robinson (102) were also found to be linked to one another. RAPD markers have been categorized and organized into linkage groups and are not listed here but can be found in Brown and Myers (5) and Zraidi and Lelley (111). These two maps cannot be easily compared, as they were constructed using different mapping populations; RAPD markers are population-specific. Neither map gives complete coverage of the *Cucurbita* genome. Both maps contain morphological traits, either as single genes or as quantitative trait loci (QTLs), which are listed in **Table 3**. More recently, a map for *Cucurbita pepo* has been constructed using RAPDs, AFLPs, and SSRs (27, 113). Over 300 markers were mapped, with coverage of some 2,200 cM of the genome, 20 linkage groups and a map density of 2.9 cM.

Sequenced genes can be valuable to breeders and geneticists, as the differences in the gene sequences that result in the phenotypes of interest can be used in marker-assisted selection. Unlike random markers, these gene-specific, allele-specific markers are completely linked to the genes of interest. Most of the genes sequenced in *Cucurbita* have been isolated by researchers doing comparative studies of specific genes across plant families; usually only a single allele is available. Nonetheless, we have included a list of the sequenced genes as **Table**

4 because the sequences could be useful as a starting point for breeders interested in isolating the genes from lines of differing phenotype. In addition to the genes listed here, there exists a collection of partial sequences from mRNA for genes differentially expressed during

seed development in *C. pepo*. These expressed sequence tags were identified in a study of the naked seed trait. The Gene Accession numbers for these sequences are CD726806 through CD726832.

Table 1. Phenotypic/Morphologic Characteristics

Gene Symbol				
Preferred	Synonym	Character	Species	Reference(s)
<i>a</i>		<i>androecious</i> . Found in ‘Greckie’; produces only male flowers, recessive to <i>A</i> .	<i>pepo</i>	41
<i>ae</i> *		<i>androecy enhancer</i> . From cross between two vegetable-marrow cultivars, the strongly male ‘Vegetable Spaghetti’, <i>ae/ae</i> , and ‘Bolognese’, <i>Ae/Ae</i> .	<i>pepo</i>	48
<i>B</i>		<i>Bicolor</i> . Precocious yellow fruit pigmentation; pleiotropic, affecting fruit and foliage, modified by <i>Ep-1</i> , <i>Ep-2</i> and <i>Ses-B</i> . Originally from ‘Vaughn’s Pear Shaped’ ornamental gourd. <i>B</i> in <i>C. moschata</i> ‘Precocious PI 165561’ derived from <i>C. pepo</i> through backcrossing. Complementary to <i>L-2</i> for intense orange, instead of light yellow, fruit-flesh color.	<i>pepo, moschata</i>	57, 74, 84, 91, 93
<i>B</i> ^{max}	<i>B-2</i>	<i>Bicolor</i> . Precocious yellow fruit pigmentation, from subsp. <i>andreana</i> PI 165558	<i>maxima</i>	92, 95
<i>Bl</i> ^{max} *	<i>Bi</i>	<i>Bitter</i> fruit. High cucurbitacin content in fruit. <i>Bl</i> from <i>C. maxima</i> subsp. <i>andreana</i> and <i>C. ecuadorensis</i> ; <i>bi</i> from <i>C. maxima</i> subsp. <i>maxima</i> , including ‘Queensland Blue’. Linked to <i>Lo-2</i> .	<i>maxima, maxima</i> × <i>ecuadorensis</i>	12, 32
<i>Bi-0</i> *	<i>Bi</i>	<i>Bi-0</i> from wild Texan gourd; <i>bi-0</i> from zucchini squash. Might be identical with either <i>Bi-1</i> or <i>Bi-2</i> .	<i>pepo</i>	30
<i>Bi-1</i> *		In cross of <i>C. pepo</i> × <i>C. argyrosperma</i> , three complementary dominant alleles are needed for bitterness. <i>Bi-1</i> from <i>C. pepo</i> straightneck ‘Goldbar’, <i>bi-1</i> from <i>C. argyrosperma</i> ‘Green Striped Cushaw’.	<i>pepo</i> × <i>argyrosperma</i>	3
<i>Bi-2</i> *		In cross of <i>C. pepo</i> × <i>C. argyrosperma</i> , three complementary dominant alleles are needed for bitterness. <i>Bi-2</i> from <i>C. pepo</i> straightneck ‘Goldbar’, <i>bi-2</i> from <i>C. argyrosperma</i> ‘Green Striped Cushaw’.	<i>pepo</i> × <i>argyrosperma</i>	3
<i>Bi-3</i> *		In cross of <i>C. pepo</i> × <i>C. argyrosperma</i> , three complementary dominant alleles are needed for bitterness. <i>Bi-3</i> from <i>C. argyrosperma</i> ‘Green Striped Cushaw’, <i>bi-3</i> from <i>C. pepo</i> straightneck ‘Goldbar’.	<i>pepo</i> × <i>argyrosperma</i>	3
<i>bl</i>		<i>blue</i> fruit color. Incompletely recessive to <i>Bl</i> for green fruit color, in hubbard squash.	<i>maxima</i>	33
<i>Bn</i>		<i>Butternut fruit shape</i> , from ‘New Hampshire Butternut’, dominant to <i>bn</i> for crookneck fruit shape, as in ‘Canada Crookneck’.	<i>moschata</i>	52
<i>Bu</i>	<i>D</i>	<i>Bush</i> habit. Short internodes; dominant to vine habit, <i>bu</i> , in young plant stage. In <i>C. pepo</i> , <i>Bu</i> in ‘Giant Yellow Straightneck’ and near-isogenic line of ‘Table Queen’, <i>bu</i> in ‘Table Queen’ acorn. In <i>C. maxima</i> , <i>Bu</i> from inbred line, <i>bu</i> from ‘Delicious’. In <i>C. moschata</i> , <i>Bu</i> from inbred line, <i>bu</i> from undisclosed parent.	<i>pepo, maxima, moschata</i>	18, 31, 66, 90, 106

Gene Symbol				
Preferred	Synonym	Character	Species	Reference(s)
<i>Cmv</i>		<i>Cucumber mosaic virus resistance</i> , from Nigerian Local. Dominant to <i>cmv</i> for susceptibility, from 'Waltham Butternut'.	<i>moschata</i>	4
<i>cr</i>		<i>cream corolla</i> . Cream to nearly white petals, <i>cr</i> from <i>C. okeechobeensis</i> ; <i>Cr</i> from <i>C. moschata</i> 'Butternut' incompletely dominant (yellow petals for <i>Cr/cr</i> , and orange for <i>Cr/Cr</i>)	<i>moschata</i> × <i>okeechobeensis</i>	81
<i>Crr-1*</i>		<i>Crown rot</i> resistance. Resistance to <i>Phytophthora capsici</i> , introgressed from <i>C. lundelliana</i> and <i>C. okeechobeensis</i> subsp. <i>okeechobeensis</i> into a breeding line of <i>C. moschata</i> . One of three complementary dominant genes for resistance. Genotype of the susceptible <i>C. moschata</i> 'Butterbush' is <i>crr-1/crr-1</i> .	<i>moschata</i>	56
<i>Crr-2*</i>		<i>Crown rot</i> resistance. Resistance to <i>Phytophthora capsici</i> , introgressed from <i>C. lundelliana</i> and <i>C. okeechobeensis</i> subsp. <i>okeechobeensis</i> into a breeding line of <i>C. moschata</i> , One of three complementary dominant genes for resistance. Genotype of the susceptible <i>C. moschata</i> 'Butterbush' is <i>crr-2/crr-2</i> .	<i>moschata</i>	56
<i>Crr-3*</i>		<i>Crown rot</i> resistance. Resistance to <i>Phytophthora capsici</i> , introgressed from <i>C. lundelliana</i> and <i>C. okeechobeensis</i> subsp. <i>okeechobeensis</i> into a breeding line of <i>C. moschata</i> . One of three complementary dominant genes for resistance. Genotype of the susceptible <i>C. moschata</i> 'Butterbush' is <i>crr-3/crr-3</i> .	<i>moschata</i>	56
<i>cu</i>		<i>cucurbitacin-B</i> reduced; <i>cu</i> for reduced cucurbitacin-B content of cotyledons of 'Early Golden Bush Scallop'; <i>Cu</i> for high cucurbitacin content of cotyledons of 'Black Zucchini'.	<i>pepo</i>	89
<i>D</i>		<i>Dark stem</i> . Series of three alleles observed in <i>C. pepo</i> : <i>D</i> for dark stem and dark intermediate-age fruit, <i>D^s</i> for dark stem but fruit not affected, and <i>d</i> for light stem and fruit not affected, with dominance $D > D^s > d$. <i>D</i> from 'Fordhook Zucchini', <i>D^s</i> from 'Early Prolific Straightneck'; <i>d</i> from 'Vegetable Spaghetti'. Epistatic to genes <i>l-1</i> and <i>l-2</i> when either is homozygous recessive; linked to <i>mo-2</i> . In <i>C. maxima</i> , only the fruit was observed: <i>D</i> for dark intermediate-age fruit from the zapallito 'La Germinadora'; <i>d</i> for light intermediate-age fruit from a variant zapallito breeding stock.	<i>pepo, maxima</i>	26, 45, 60, 61, 64, 66, 73, 86
<i>de</i>		<i>determinate</i> plant habit; stem lacking tendrils and terminating with female flowers. Recessive to <i>De</i> for indeterminate plant habit. <i>De</i> from 'Jeju' and 'Sokuk', <i>de</i> from inbred designated "Det".	<i>moschata</i>	42
<i>Di</i>		<i>Disc</i> fruit shape. From scallop squash, dominant to spherical or pyriform.	<i>pepo</i>	97, 104

Gene Symbol				
Preferred	Synonym	Character	Species	Reference(s)
<i>Ep-1</i>		<i>Extender of pigmentation-1</i> ; modifier of <i>B. Ep-1</i> incompletely dominant to <i>ep-1</i> and additive with <i>Ep-2. Ep-1</i> from 'Small Sugar 7 × 7' pumpkin; <i>ep-1</i> from 'Table King' acorn.	<i>pepo</i>	96
<i>Ep-2</i>		<i>Extender of pigmentation-2</i> ; modifier of <i>B. Ep-2</i> incompletely dominant to <i>ep-2</i> and additive with <i>Ep-1. Ep-2</i> from 'Table King' acorn; <i>ep-2</i> from 'Small Sugar 7 × 7' pumpkin.	<i>pepo</i>	96
<i>Fr</i>		<i>Fruit fly (Dacus cucurbitae)</i> resistance. <i>Fr</i> from 'Arka Suryamukhi', dominant to <i>fr</i> for susceptibility.	<i>maxima</i>	53
<i>fv</i>		<i>fused vein</i> . Fusion of primary leaf veins, subvital male gametophyte; found in hull-less-seeded pumpkin breeding line.	<i>pepo</i>	8, 9
<i>G</i>	<i>a, m</i>	<i>Gynoecious</i> sex expression; dominant to <i>g</i> for monoecious sex expression.	<i>foetidissima</i>	19, 24
<i>Gb</i>		<i>Green band</i> on inner side of base of petal, from a scallop squash; dominant to <i>gb</i> , for no band, from a straightneck squash.	<i>pepo</i>	20
<i>gc</i>		<i>green corolla</i> . Green, leaf-like petals, sterile; in unspecified F2 population.	<i>pepo</i>	99
<i>gl-1*</i>	<i>gl</i>	<i>glabrous</i> , lacking trichomes	<i>maxima</i>	39
<i>gl-2</i>		<i>glabrous</i> , lacking trichomes; <i>gl-2</i> mutant found in straightneck squash	<i>pepo</i>	108
<i>Gr</i>	<i>G</i>	<i>Green rind</i> . Dominant to buff skin of mature fruit. <i>Gr</i> from 'Long Neapolitan', <i>gr</i> from 'Butternut'.	<i>moschata</i>	77
<i>grl</i>		<i>gray leaf</i> . Recessive to green leaf. Recessive <i>grl</i> derived from cross of zapallito-type line of <i>C. maxima</i> and a butternut-type line of <i>C. moschata</i> . Dominant <i>Grl</i> from zapallito-type <i>C. maxima</i> .	<i>maxima</i> × <i>moschata</i>	44
<i>Hi</i>		<i>Hard rind inhibitor</i> . <i>Hi</i> , for hard-rind inhibition, from <i>C. maxima</i> 'Queensland Blue'; <i>hi</i> , for no hard-rind inhibition, from <i>C. ecuadorensis</i> .	<i>maxima</i> × <i>ecuadorensis</i>	32
<i>Hr</i>		<i>Hard rind</i> . <i>Hr</i> for hard (lignified) rind in ornamental gourd, straightneck squash, and zucchini; <i>hr</i> for soft (non-lignified) rind in 'Small Sugar' pumpkin and 'Sweet Potato' ('Delicata'). Complementary to <i>Wt</i> for <i>Warty</i> fruit.	<i>pepo</i>	47, 85
<i>i</i>		<i>intensifier</i> of the <i>cr</i> gene for cream flowers. <i>Cr</i> /- <i>I</i> /- for intense orange or yellow flowers, <i>Cr</i> /- <i>i</i> / <i>i</i> for light orange or yellow flowers, <i>cr</i> / <i>cr</i> <i>I</i> /- for cream flowers, <i>cr</i> / <i>cr</i> <i>i</i> / <i>i</i> for white flowers. <i>I</i> from <i>C. moschata</i> 'Butternut', <i>i</i> from <i>C. okeechobeensis</i> .	<i>moschata</i> × <i>okeechobeensis</i>	81
<i>I-mc</i>	<i>I_{mc}</i>	<i>Inhibitor</i> of mature fruit color; dominant to <i>i-mc</i> for no inhibition. <i>I-mc</i> in a scallop squash.	<i>pepo</i>	10

Gene Symbol				
Preferred	Synonym	Character	Species	Reference(s)
<i>I-T</i>		<i>Inhibitor</i> of the <i>T</i> gene for trifluralin resistance. <i>I-T</i> from 'La Primera'; <i>i-t</i> from 'Ponca' and 'Waltham Butternut'.	<i>moschata</i>	1
<i>l-1</i>	<i>c, St</i>	<i>light fruit coloration-1</i> . Light intensity of fruit coloration. Series of five alleles observed in <i>C. pepo</i> which, in complementary interaction with the dominant <i>L-2</i> allele, give the following results: <i>L-1</i> for uniformly intense/dark fruit coloration, from 'Fordhook Zucchini'; <i>l-1^{BSI}</i> for broad, contiguous intense/dark stripes, from 'Cocozelle'; <i>l-1St</i> for narrow, broken intense/dark stripes, from 'Caserta'; <i>l-1^{iSt}</i> for irregular intense/dark stripes, from 'Beirut' vegetable marrow; <i>l-1</i> for light coloration, from 'Vegetable Spaghetti', with dominance of $L-1 > (l-1^{BSI} > l-1^{St}) \geq l-1^{iSt} > l-1$. In <i>C. maxima</i> , <i>L-1</i> from the zapallito 'La Germinadora'; <i>l-1</i> from a variant zapallito breeding stock.	<i>pepo, maxima</i>	26, 45, 62, 67, 63, 66, 67, 73, 82, 91
<i>l-2</i>	<i>r</i>	<i>light fruit coloration-2</i> . Light intensity of fruit coloration. Series of four alleles observed in <i>C. pepo</i> , which, in complementary interaction with dominant alleles at the <i>l-1</i> locus, give the following results: <i>L-2</i> for intense/dark fruit coloration, with <i>L-1</i> from 'Fordhook Zucchini', and intense/dark fruit stripes with <i>l-1^{BSI}</i> from 'Cocozelle'; allele <i>L-2^w</i> has delayed and weaker effect than <i>L-2</i> , from <i>C. pepo</i> subsp. <i>fraterna</i> ; <i>l-2^R</i> confers reversal of color, that is, stripes lighter than the background in combination with any of the striping alleles at the <i>l-1</i> locus, or completely light fruit in the presence of <i>L-1</i> , from <i>C. pepo</i> subsp. <i>texana</i> 'Delicata'; <i>l-2</i> for light coloration, from 'Vegetable Spaghetti', with dominance of $(L-2 = l-2^R) > L-2$. Dominant <i>L-2</i> is also complementary with <i>B</i> for intense orange, instead of light yellow, fruit-flesh color and with recessive <i>qi</i> for intense exterior color of young fruit. In <i>C. maxima</i> , <i>L-2</i> from the zapallito 'La Germinadora'; <i>l-2</i> from a variant zapallito breeding stock.	<i>pepo, maxima</i>	26, 45, 57, 65, 68, 69, 73
<i>lo-1</i>	<i>l</i>	<i>lobed leaves-1</i> ; recessive to <i>Lo-1</i> for non-lobed leaves	<i>maxima</i>	21
<i>Lo-2</i>		<i>Lobed leaves-2</i> . <i>Lo-2</i> for lobed leaves in <i>C. ecuadorensis</i> dominant to <i>lo-2</i> for unlobed leaves in <i>C. maxima</i> . Linked to <i>Bi</i> .	<i>ecuadorensis</i> × <i>maxima</i>	32
<i>lt</i>		<i>leafy tendril</i> . Tendrils with laminae; <i>lt</i> found in ornamental gourd.	<i>pepo</i>	83
<i>ly</i>		<i>light yellow corolla</i> . Recessive to orange yellow; <i>ly</i> found in ornamental gourd.	<i>pepo</i>	83

Gene Symbol				
Preferred	Synonym	Character	Species	Reference(s)
<i>M</i>		<i>Mottled</i> leaves. <i>M</i> for silver-gray areas in axils of leaf veins, dominant to <i>m</i> for absence of silver-gray. For <i>C. maxima</i> , <i>M</i> in ‘Zuni’ and <i>m</i> in ‘Buttercup’ and ‘Golden Hubbard’. For <i>C. pepo</i> , <i>M</i> in ‘Caserta’ and inbred of ‘Striato d’Italia’ cocozelle; <i>m</i> in ‘Early Prolific Straightneck’ and ‘Early Yellow Crookneck’. For <i>C. moschata</i> , <i>M</i> in ‘Hercules’ and ‘Golden Cushaw’, <i>m</i> in butternut type. Weakly linked to <i>Wt</i> .	<i>pepo, maxima, moschata</i>	14, 72, 82, 87
<i>Mldg</i>		<i>Mottled light</i> and <i>dark green</i> immature fruit color; germplasm unspecified. Dominant to <i>mldg</i> for non-mottled.	<i>moschata</i>	6
<i>mo-1</i>		<i>mature orange-1</i> ; complementary recessive gene for loss of green fruit color prior to maturity. <i>Mo-1</i> from ‘Table Queen’ acorn; <i>mo-1</i> from ‘Vegetable Spaghetti’.	<i>pepo</i>	61
<i>mo-2</i>		<i>mature orange-2</i> ; complementary recessive gene for loss of green fruit color prior to maturity. <i>Mo-2</i> from ‘Table Queen’ acorn; <i>mo-2</i> from ‘Vegetable Spaghetti’. Linked to <i>D</i> .	<i>pepo</i>	61
<i>ms-1</i>	<i>ms₁</i>	<i>male sterile-1</i> . Male flowers abort before anthesis, derived from a cross involving ‘Golden Hubbard’, recessive to <i>Ms-1</i> for male fertile.	<i>maxima</i>	88
<i>ms-2</i>	<i>ms₂</i>	<i>male sterile-2</i> . Male flowers abort, sterility expressed as androecium shrivelling and turning brown; <i>ms-2</i> from ‘Eskandarany’ (PI 228241).	<i>pepo</i>	23
<i>ms-3</i>	<i>ms-2</i>	<i>male sterile-3</i> .	<i>maxima</i>	39
<i>m-zym^{mos}</i>		<i>modifier</i> of dominance of <i>zucchini yellow mosaic</i> virus resistance; confers resistance to otherwise susceptible <i>Zym^{mos}/zym^{mos}</i> heterozygotes. <i>M-zym^{mos}</i> in ‘Soler’, <i>m-zym^{mos}</i> in ‘Waltham Butternut’ and ‘Nigerian Local’.	<i>moschata</i>	55
<i>n</i>	<i>h</i>	<i>naked</i> seeds. Lacking a lignified seed coat, <i>n</i> from oil-seed pumpkin.	<i>pepo, moschata</i>	29, 86, 107, 112, 113
<i>pl</i>		<i>plain light</i> fruit color, <i>pl</i> from ‘Beirut’ vegetable marrow and ‘Fordhook Zucchini’; <i>Pl</i> in ‘Vegetable Spaghetti’.	<i>pepo</i>	58
<i>Pm</i>		<i>Powdery mildew</i> resistance. Resistance to <i>Podosphaera xanthii</i> ; <i>Pm</i> from <i>C. lundelliana</i> .	<i>lundelliana</i>	76
<i>Pm-0</i>		<i>Powdery mildew</i> resistance. Resistance to <i>Podosphaera xanthii</i> ; <i>Pm-0</i> from <i>C. okechobeensis</i> and in <i>C. pepo</i> .	<i>okechobeensis, pepo</i>	11, 13, 37
<i>pm-1</i>		<i>powdery mildew</i> resistance in <i>C. moschata</i> . Series of three alleles: <i>pm-1^P</i> for susceptibility from ‘Ponca’ dominant to <i>pm-1^L</i> for resistance from ‘La Primera’, which is dominant to <i>pm-1^W</i> for susceptibility in ‘Waltham Butternut’.	<i>moschata</i>	2
<i>pm-2</i>		<i>powdery mildew</i> resistance in <i>C. moschata</i> ‘Seminole’, recessive to <i>Pm-2</i> for susceptibility	<i>moschata</i>	2

Gene Symbol				
Preferred	Synonym	Character	Species	Reference(s)
<i>prv</i>		<i>papaya ringspot virus resistance</i> , in Nigerian Local, recessive to <i>Prv</i> for susceptibility, in 'Waltham Butternut'.	<i>moschata</i>	4
<i>qi</i>		<i>quiescent intense</i> . Recessive to <i>Qi</i> for not intense and complementary to <i>L-2</i> for intense young fruit color; little or no effect on mature fruit. <i>Qi</i> from 'Vegetable Spaghetti'; <i>qi</i> from 'Jack O'Lantern' pumpkin and 'Verte non-coureuse d'Italie' cocozelle.	<i>pepo</i>	63, 66
<i>Rd</i>		<i>Red skin</i> . Red external fruit color; dominant to green, white, yellow and gray. <i>Rd</i> from 'Turk's Cap'; <i>rd</i> from 'Warted Hubbard'.	<i>maxima</i>	46
<i>ro</i>		<i>rosette leaf</i> . Lower lobes of leaves slightly spiraled, <i>ro</i> derived from an ornamental gourd.	<i>pepo</i>	47
<i>s-1</i>	<i>s</i>	<i>sterile</i> . Male flowers small, without pollen; female flower sterile. Derived from crossing 'Greengold' with 'Banana'.	<i>maxima</i>	34
<i>s-2</i>		<i>sterile</i> . Male flowers small, without pollen and female flower sterile; mutant in powdery mildew resistant, straightneck squash breeding line.	<i>pepo</i>	7
<i>Ses-B</i>		<i>Selective suppression</i> of gene <i>B</i> . Suppression in foliage of precocious yellowing conferred by <i>B</i> . <i>Ses-B</i> in straightneck breeding line dominant to <i>ses-B</i> in 'Jersey Golden Acorn'.	<i>pepo</i>	94
<i>sl</i>		<i>silverleaf resistance</i> . Recessive to <i>Sl</i> for susceptibility. In <i>C. moschata</i> , <i>Sl</i> from 'Soler'; <i>sl</i> from PI 162889 and butternut types. In <i>C. pepo</i> , <i>Sl</i> from 'Black Beauty' zucchini and <i>sl</i> from Zuc76 breeding line.	<i>moschata, pepo</i>	28, 110
<i>slc</i>		<i>Squash leaf curl virus resistance</i> ; derived from <i>C. moschata</i> .	<i>pepo</i>	50
<i>sp</i>		<i>spaghetti flesh</i> , breaking into strands after cooking	<i>pepo</i>	49
<i>T</i>		<i>Trifluralin resistance</i> . Dominant to susceptibility to the herbicide; modified by <i>I-T</i> . <i>T</i> in 'La Primera'; <i>t</i> in 'Ponca' and 'Waltham Butternut'.	<i>moschata</i>	1
<i>uml</i>		<i>umbrella-like</i> ; leaves shaped like partially opened umbrella. Recessive <i>uml</i> derived from a cross of <i>C. maxima</i> 'Warzywna' and a <i>C. pepo</i> inbred; dominant <i>Uml</i> from 'Warzywna'.	<i>maxima</i> × <i>pepo</i>	75
<i>v</i>		<i>virescent</i> . Yellow-green young leaves, <i>v</i> found in 'Golden Delicious'.	<i>maxima</i>	22
<i>W</i>		<i>Weak fruit coloration</i> . Dominant to <i>w</i> for intense-pigmented mature fruit; <i>W</i> from scallop squash. Complementary to <i>Wf</i> for white external fruit color.	<i>pepo</i>	59, 91, 97
<i>wc</i>		<i>white corolla</i> . Derived from 'Ispanskaya' × 'Emerald'. Recessive to <i>Wc</i> for normal orange-yellow corolla	<i>maxima</i>	40
<i>Wf</i>		<i>White flesh</i> . Dominant to <i>wf</i> for colored flesh. <i>Wf</i> in a scallop squash, <i>wf</i> in a straightneck squash. Complementary to <i>W</i> for white external fruit color.	<i>pepo</i>	20, 59, 97

Gene Symbol				
Preferred	Synonym	Character	Species	Reference(s)
<i>Wmv</i>		<i>Watermelon mosaic virus resistance</i> . From “Menina” and “Nigerian Local”, dominant to <i>wmv</i> for susceptibility in ‘Musquée de Provence’ and ‘Waltham Butternut’. May be linked with or identical to <i>Zym-1</i> .	<i>moschata</i>	4, 25
<i>Wmv^{ecu}</i>		<i>Watermelon mosaic virus resistance</i> . From <i>C. ecuadorensis</i> , in a cross with an unspecified <i>C. maxima</i> .	<i>maxima</i> × <i>ecuadorensis</i>	101
<i>Wt</i>		<i>Warty fruit</i> . Dominant to non-warted, <i>wt</i> , and complementary to <i>Hr</i> , with fruit wartiness being expressed only in the presence of the dominant <i>Hr</i> allele. <i>Wt</i> in straightneck, crookneck, and ‘Delicata’; <i>wt</i> in zucchini, cocozelle, and ‘Small Sugar’ pumpkin. Weakly linked to <i>M</i> .	<i>pepo</i>	72, 85, 97
<i>wyc</i>		<i>white-yellow corolla</i> ; isolated in ‘Riesen-Melonen’. Recessive to <i>Wyc</i> for normal orange-yellow corolla.	<i>maxima</i>	40
<i>Y</i>		<i>Yellow fruit color</i> . <i>Y</i> for yellow fruit color of intermediate-age fruits, from straightneck and crookneck squash, dominant to <i>y</i> for green intermediate-age fruit color, from vegetable marrow, ornamental gourd, and cocozelle.	<i>pepo</i>	72, 82, 90, 91, 97
<i>yg</i>		<i>yellow-green leaves and stems</i>	<i>maxima</i>	39
<i>Ygp</i>		<i>Yellow-green placenta</i> . Dominant to yellow placental color. <i>Ygp</i> in a scallop squash, <i>ygp</i> in a straightneck squash.	<i>pepo</i>	20
<i>ys</i>		<i>yellow seedling</i> . Lacking chlorophyll; lethal	<i>pepo</i>	47
<i>zym^{ecu}</i>		<i>zucchini yellow mosaic virus resistance</i> , recessive to susceptibility; <i>zym^{ecu}</i> from <i>C. ecuadorensis</i> , <i>Zym^{ecu}</i> from <i>C. maxima</i> ‘Buttercup’.	<i>ecuadorensis</i>	80
<i>zym^{mos}</i>		<i>zucchini yellow mosaic virus resistance</i> , recessive to susceptibility; <i>zym^{mos}</i> from ‘Soler’, <i>Zym^{mos}</i> from ‘Waltham Butternut’.	<i>moschata</i>	55
<i>Zym-0</i>		<i>Zucchini yellow mosaic virus resistance</i> . <i>Zym-0</i> from <i>C. moschata</i> ‘Nigerian Local’ dominant to <i>zym-0</i> for susceptibility from ‘Waltham Butternut’. Perhaps one of two separate genes for resistance in ‘Nigerian Local’.	<i>moschata</i>	4, 51, 55
<i>Zym-1</i>		<i>Zucchini yellow mosaic virus resistance</i> . <i>Zym-1</i> from <i>C. moschata</i> ‘Menina’ dominant to <i>zym-1</i> for susceptibility from <i>C. moschata</i> ‘Waltham Butternut’. <i>Zym-1</i> transferred via backcrossing to <i>C. pepo</i> ‘True French’ zucchini, in which it confers resistance through complementary interaction with <i>Zym-2</i> and <i>Zym-3</i> . <i>Zym-1</i> is either linked with <i>Wmv</i> or also confers resistance to watermelon mosaic virus.	<i>moschata, pepo</i>	25, 55, 70, 71
<i>Zym-2</i>		<i>Zucchini yellow mosaic virus resistance-2</i> . Dominant to susceptibility and complementary to <i>Zym-1</i> . <i>Zym-2</i> from <i>C. moschata</i> ‘Menina’. <i>Zym-2</i> in <i>C. pepo</i> derived from <i>C. moschata</i> , in near-isogenic resistant line of ‘True French’ zucchini; <i>zym-2</i> from <i>C. pepo</i> ‘True French’.	<i>moschata, pepo</i>	70

Gene Symbol				
Preferred <i>Zym-3</i>	Synonym	Character <i>Zucchini yellow mosaic virus resistance-3.</i> Dominant to susceptibility and complementary to <i>Zym-1</i> . <i>Zym-3</i> from <i>C. moschata</i> 'Menina'. <i>Zym-3</i> in <i>C. pepo</i> derived from <i>C. moschata</i> , in near-isogenic resistant line of 'True French' zucchini; <i>zym-3</i> from <i>C. pepo</i> 'True French'.	Species <i>moschata, pepo</i>	Reference(s) 70

*Proposed new gene symbol.

Table 2. Isozyme Variants

Gene Symbol					
Preferred	Synonym	No. alleles observed	Character	Species	Reference(s)
<i>Aat-1</i>	<i>Aat</i>	8	<i>Aspartate aminotransferase-1</i> . Variant among accessions.	<i>pepo</i>	17, 36
<i>Aat-3</i>		2	<i>Aspartate aminotransferase-3</i> . Variant among wild populations.	<i>pepo</i>	17
<i>Aat-4</i>		3	<i>Aspartate aminotransferase-4</i> . Variant among wild populations.	<i>pepo</i>	17
<i>Aat-mb</i>		2	<i>Aspartate aminotransferase – microbody</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Aat-m1</i>		2	<i>Aspartate aminotransferase mitochondria-1</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Aat-m2</i>		2	<i>Aspartate aminotransferase mitochondria-2</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Aat-p2</i>		2	<i>Aspartate aminotransferase plastid-2</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Acp-1</i>		2	<i>Acid phosphatase-1</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Acp-2</i>		2	<i>Acid phosphatase-2</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Adh</i>		2	<i>Alcohol dehydrogenase</i>	<i>pepo</i>	105
<i>Aldo-p</i>		2	<i>Aldolase – plastid</i>	<i>maxima</i> × <i>ecuadorensis</i>	101
<i>Est-1</i>	<i>Est</i>	2	<i>Esterase</i>	<i>maxima</i> × <i>ecuadorensis</i>	100, 102
<i>Gal-1</i>		2	<i>β-galactosidase-1</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Gal-2</i>		2	<i>β-galactosidase-2</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>G2d-1</i>		3	<i>Glycerate dehydrogenase-1</i> . Variant among wild populations.	<i>pepo</i>	17
<i>G2d-2</i>		2	<i>Glycerate dehydrogenase-2</i> . Variant among wild populations.	<i>pepo</i>	17
<i>Got-1</i>		5	<i>Glutamine oxaloacetate-1</i> . Variant among accessions, wild populations, and among <i>Cucurbita</i> species.	<i>pepo</i>	15, 16, 38, 105
<i>Got-2</i>		3	<i>Glutamine oxaloacetate-2</i> . Variant among species.	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Gpi</i>		2	<i>Glucosephosphate isomerase</i> . Variant among accessions.	<i>pepo</i>	36
<i>Gpi-3</i>		2	<i>Glucosephosphate isomerase-3</i> . Variant among wild populations.	<i>pepo</i>	17

Gene Symbol					
Preferred	Synonym	No. alleles observed	Character	Species	Reference(s)
<i>Gpi-c1</i>		2	<i>Glucosephosphate isomerase cytosolic-1</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Gpi-c2</i>		2	<i>Glucosephosphate isomerase cytosolic-2</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Idh-1</i>		4	<i>Isocitrate dehydrogenase-1</i> . Variant among accessions, wild populations, and <i>Cucurbita</i> species.	<i>pepo</i>	15, 16, 17, 38, 105
<i>Idh-2</i>		2	<i>Isocitrate dehydrogenase-2</i> . Variant among accessions, wild populations, and <i>Cucurbita</i> species.	<i>pepo</i>	15, 16, 17, 38, 105
<i>Idh-3</i>		2	<i>Isocitrate dehydrogenase-3</i> . Variant among accessions and populations.	<i>pepo</i>	15, 16, 17, 38
<i>Lap-1</i>	<i>Lap</i>	4	<i>Leucine aminopeptidase</i> . Variant among <i>C. pepo</i> accessions.	<i>maxima</i> × <i>ecuadorensis</i> ; <i>pepo</i>	17, 36, 100, 102
<i>Mdh-1</i>	<i>Mdh</i>	7	<i>Malate dehydrogenase</i> . Variant among accessions.	<i>pepo</i>	36
<i>Mdh-2</i>		3	<i>Malate dehydrogenase-2</i> . Variant among accessions, wild populations, and <i>Cucurbita</i> species.	<i>pepo</i>	15, 16, 17, 38, 105
<i>Mdh-3</i>		3	<i>Malate dehydrogenase-3</i> . Variant among accessions, wild populations, and <i>Cucurbita</i> species.	<i>pepo</i>	15, 16, 17, 38, 105
<i>Mdh-m1</i>		2	<i>Malate dehydrogenase mitochondria-1</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Mdh-m2</i>		2	<i>Malate dehydrogenase mitochondria-2</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Mdh-c2</i>		2	<i>Malate dehydrogenase cytosolic-2</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Per-1</i>		2	<i>Peroxidase-1</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Per-2</i>		3	<i>Peroxidase-2</i> . Variant among accessions and wild populations.	<i>pepo</i>	15, 16, 38
<i>Per-3</i>		2	<i>Peroxidase-3</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Pgi-1</i>		2	<i>Phosphoglucose isomerase-1</i>	<i>pepo</i>	15
<i>Pgi-2</i>		2	<i>Phosphoglucose isomerase-2</i> . Variant among <i>Cucurbita</i> species.	<i>pepo</i>	15, 38, 105
<i>Pgi-3</i>		4	<i>Phosphoglucose isomerase-3</i> . Variant among accessions, wild populations, and <i>Cucurbita</i> species.	<i>pepo</i>	15, 16, 38, 105
<i>Pgm-1</i>	<i>Pgm</i>	2	<i>Phosphoglucomutase</i> . Variant among accessions.	<i>pepo</i>	36

Gene Symbol					
Preferred	Synonym	No. alleles observed	Character	Species	Reference(s)
<i>Pgm-2</i>		4	<i>Phosphoglucomutase-2</i> . Variant among accessions, wild populations, and <i>Cucurbita</i> species.	<i>pepo</i>	15, 16, 38, 105
<i>Pgm-5</i>		2	<i>Phosphoglucomutase-5</i> . Variant among wild populations.	<i>pepo</i>	17
<i>Pgm-6</i>		2	<i>Phosphoglucomutase-6</i> . Variant among wild populations.	<i>pepo</i>	17
<i>Pgm-c2</i>		2	<i>Phosphoglucomutase cytosolic-2</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Pgm-p</i>		2	<i>Phosphoglucomutase plastid</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Skd-1</i>		6	<i>Shikimate dehydrogenase</i> . Variant among wild populations.	<i>pepo</i>	17
<i>Skdh</i>		5	<i>Shikimate dehydrogenase</i> . Variant among <i>C. pepo</i> accessions.	<i>maxima</i> × <i>ecuadorensis</i> ; <i>pepo</i>	36, 102
<i>Sod-1</i>		2	<i>Superoxide dismutase-1</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Tpi-c2</i>		2	<i>Triosephosphatase isomerase cytosolic-2</i>	<i>maxima</i> × <i>ecuadorensis</i>	102
<i>Tpi-p2</i>		2	<i>Triosephosphatase isomerase plastid-2</i>	<i>maxima</i> × <i>ecuadorensis</i>	102

Table 3. Mapped Phenotypic/Morphological Characteristics

Trait	Symbol	Linked Marker(s)	Recombination Distance (cM)	Reference(s)
Precocious yellow fruit	<i>B</i>	I10_1700	27.1	5
Bush growth habit	<i>Bu</i>	CMTp131	7.8	27
Dwarf	<i>Bu</i>	S1225_548, SCAR3_398	2.29	43
Leaf Mottle	<i>M</i>	H14_600 U489_1200	13.0 16.3	5
Seed Coat	<i>n</i>	AK11_340	4.4	111
Hull-less seed	<i>n</i>	CMTp58, CMTp151, CMTm115, CMTm239	1.5 - 3.6	27
Mature Fruit Color	[none given]	G17_700	9.7	5
Fruit Length	(QTL)	AE07_165, AC10_490, AJ20_420, P13_750, J01_600, AO20_1200, T08_460, AB08_540, AE09_1600		111
Fruit Width	(QTL)	AE07_165, AJ20_420, AM10_950, AG08_440		111
Fruit Length/width Ratio	(QTL)	AE07_165, AC10_490, AJ20_420, P13_750, J01_600		111
No. of Fruit Chambers	(QTL)	P13_950, AE08_470		111
Leaf Indentation	(QTL)	F10_400, K11_950, G2_400		5
Fruit Shape	(QTL)	F8_1050, B8_900, H19_500		5

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Table 4. Genes with known DNA sequence

Gene Symbol*	Gene Accession	(Putative) Function	Source	Ref.
AIG-2	AY666083	aspartic protease inhibitor	<i>C. maxima</i>	**
PRB1	AY326308	phloem RNA-binding protein	<i>C. maxima</i> 'Big Max'	**
GAIP	AY32630, AY326307	gibberellic acid insensitive phloem protein (two very similar genes)	<i>C. maxima</i> 'Big Max'	**
FAD2	AY525163	omega-6 fatty acid desaturase	<i>C. pepo</i> zucchini	**
NIP1	AJ544830	Nod26-like protein	<i>C. pepo</i> zucchini	35
PP2	AY312402	phloem protein 2 lectin (includes promoter region)	<i>C. moschata</i> crookneck	**
PP2	AF150627	phloem protein 2 lectin	<i>C. moschata</i> crookneck	**
PP2	Z22647	phloem protein 2 lectin	<i>C. pepo</i> 'Autumn Gold'	61
PP2	Z17331	phloem protein 2 lectin	<i>C. maxima</i> 'Big Max'	5
PP2	L31550, L31551, L31552	phloem protein 2 (three alleles)	<i>C. maxima</i>	**
GA2OX, GA20OX, GA3OX	AJ315663, AJ302041, AJ308480, AJ302040	gibberellin oxidases (two sequences for GA2OX)	<i>C. maxima</i> 'Riesenmelone'	**
	U61385	gibberellin 20-oxidase	<i>C. maxima</i> 'Riesenmelone'	38
	U63650	gibberellin 2 beta,3 beta hydroxylase	<i>C. maxima</i> 'Riesenmelone'	39
	AJ006453	gibberellin 3 beta hydroxylase	<i>C. maxima</i> 'Riesenmelone'	**
	U61386	gibberellin dioxygenase	<i>C. maxima</i> 'Riesenmelone'	37
Moschatin 1 through 5	AF462349, AF504011, AY25646, AY27921, AY279217	ribosome-inactivating protein	<i>C. moschata</i> crookneck	**
CPS1	AB109763	copalyl diphosphate synthase; gibberellin biosynthesis	<i>C. maxima</i>	**
CPS	AF049905, AF049906	copalyl diphosphate synthase; gibberellin biosynthesis (2 genes)	<i>C. maxima</i>	55
Hsc70	AF527794, AF527795, AF527796	cell-autonomous heat shock protein; chaperonin 70 (multiple sequences)	<i>C. maxima</i>	1
	AB061204	thioredoxin h	<i>C. maxima</i>	**
Puga, Pugb, PUGC	AB055116, AB055117, AB055118	glutathione S-transferase	<i>C. maxima</i>	**
CYP88A	AF212990, AF212991	cytochrome P450; ent-kaurenoic acid oxidase (multiple alleles)	<i>C. maxima</i> 'Queensland Blue'	23

Gene Symbol*	Gene Accession	(Putative) Function	Source	Ref.
PP2	AF520583	phloem protein 2	<i>C. digitata</i> PI 240879	**
PP2	AF520582	phloem lectin	<i>C. argyrosperma</i> subsp. <i>sororia</i>	**
	L32700, L32701	phloem lectin	<i>C. argyrosperma</i>	5
	X56948	malate synthase	<i>Cucurbita</i> sp.*** 'Kurokawa Amakuri Nankin'	44
pMCPN60	X70867, X70868	chaperonin 60	'Kurokawa Amakuri Nankin'	59
PCPK	AY07280, AY072802	phloem calmodulin-like protein kinases	<i>C. maxima</i> 'Big Max'	66
	X55779	ascorbate oxidase	<i>C. maxima</i> 'Ebisu Nankin'	14
AAO	D55677	ascorbate oxidase	<i>C. maxima</i>	33
chitP1	AB015655	chitinase	<i>C. maxima</i> 'Ebisu Nankin'	**
PLC	AF082284	chitinase	<i>C. moschata</i> crookneck	32
PV72	AB006809	vacuolar sorting receptor	'Kurokawa Amakuri Nankin'	54
	D88420	stromal ascorbate peroxidase	'Kurokawa Amakuri Nankin'	42
	D78256	isocitrate lyase	'Kurokawa Amakuri Nankin'	41
	D70895	3-ketoacyl-CoA thiolase	'Kurokawa Amakuri Nankin'	31
	D83656	thylakoid ascorbate peroxidase	'Kurokawa Amakuri Nankin'	64
	D49433	hydroxypyruvate reductase	'Kurokawa Amakuri Nankin'	21
MP28	D45078	membrane protein	'Kurokawa Amakuri Nankin'	28
	D38132	glyoxysomal citrate synthase	'Kurokawa Amakuri Nankin'	30
	D29629	aconitase	'Kurokawa Amakuri Nankin'	19
	D16560	prepro2S albumin	'Kurokawa Amakuri Nankin'	17
	D14044	glycolate oxidase	'Kurokawa Amakuri Nankin'	58
	AF002016	acyl CoA oxidase	'Kurokawa Amakuri Nankin'	18
PP36	AF274589	cytochrome b5 reductase	<i>C. maxima</i> 'Big Max'	**
pAPX	AB070626	peroxisomal ascorbate peroxidase	'Kurokawa Amakuri Nankin'	48
CM-ACS3	AB038559	ACC synthase	<i>C. maxima</i>	62
CmATS	AB049135	acyl-(acyl-carrier protein); acyltransferase	<i>C. moschata</i> 'Shirogikuza'	**
	Y00771	glycerol-3-phosphate acyltransferase transit peptide	<i>C. moschata</i> 'Shirakikuza'	29
	AB002695	aspartic endopeptidase	<i>C. pepo</i>	24
PS-1	AF284038	phloem serpin	<i>C. maxima</i>	65
SLW	AF170086, AF170087	silverleaf whitefly-induced protein (multiple genes)	<i>C. pepo</i> zucchini 'Chefini'	60
aprX	Y17192	anionic peroxidase	<i>C. pepo</i> zucchini 'Black Beauty'	6

Gene Symbol*	Gene Accession	(Putative) Function	Source	Ref.
cpCPK1	U90262	calcium-dependent calmodulin-independent protein kinase	<i>C. pepo</i> zucchini	13
PP16	AF079170, AF079171	mRNA movement protein; phloem transport (multiple alleles)	<i>C. maxima</i> 'Big Max'	63
AOBP	D45066	transcription factor binding to ascorbate oxidase	<i>C. maxima</i>	34
accW	D01032	auxin-induced 1-aminocyclopropane-1-carboxylate synthase	<i>C. maxima</i> 'Ebisu'	47
	U37774	auxin-induced 1-aminocyclopropane-1-carboxylic acid synthase	<i>C. maxima</i>	46
ACC1	M58323	1-aminocyclopropane-1-carboxylate synthase	<i>C. pepo</i>	52
ACC1A, ACC1B	M61195	1-aminocyclopropane-1-carboxylate synthase (2 genes, tightly linked)	<i>C. pepo</i> zucchini	26
PHP-1	D86306	proton-translocating inorganic pyrophosphatase	<i>C. moschata</i> crookneck	**
PP1	U66277	phloem filament protein	<i>C. maxima</i> 'Big Max'	9
pfiAF4	X81647	trypsin inhibitor	<i>C. maxima</i> 'Supermarket Hybrid'	45
pfiBM7	X81447	chymotrypsin inhibitor	<i>C. maxima</i> 'Supermarket Hybrid'	45
	M15265	phytochrome	<i>C. pepo</i> zucchini 'Black Beauty'	53
NADH	M33154	nitrate reductase	<i>C. maxima</i>	11
	M36407	11S globulin beta-subunit	'Kurokawa Amakuri Nankin'	20
	AF206895	18S ribosomal RNA	<i>C. pepo</i>	**
	AF479108	26S ribosomal RNA	<i>C. pepo</i>	56
	AJ488214 EF595858 FJ915115 FJ915114 FJ915113 FJ915112 FJ915111 FJ915110 FJ915109 FJ915108 FJ915107 FJ915106 FJ915105 FJ915104 FJ915101 AM981172 AM981170 AM981169 AM981168	5.8S ribosomal RNA	<i>C. moschata</i> <i>C. ficifolia</i> <i>C. pepo</i> <i>C. lundelliana</i>	** , 7
	AY396415	5S ribosomal RNA	<i>C. pepo</i>	12
	FJ263619	16S ribosomal RNA	<i>C. moschata</i>	**

Gene Symbol*	Gene Accession	(Putative) Function	Source	Ref.
	DQ298735 AY357209 AY357208	18S ribosomal RNA	<i>C. pepo</i> <i>C. moschata</i>	** ₄
	AF017158	25S ribosomal RNA	<i>C. maxima</i>	**
GID1b	AM745267	gibberellin receptor	<i>C. maxima</i>	**
APRX	DQ518906	class III peroxidase precursor	<i>C. pepo</i> zucchini 'Black Beauty'	10
RBP50	EU793994	polypyrimidine tract binding protein	<i>C. maxima</i> 'Big Max'	16
	AJ829947	reverse transcriptase	<i>C. pepo</i>	**
rbcL	AF206756 L21938 DQ535804 EU309692	ribulose 1,5-bisphosphate carboxylase	<i>C. pepo</i> <i>C. ficifolia</i> <i>C. moschata</i>	36,57
NACP1	FJ151402	NAC-domain containing protein	<i>C. maxima</i>	50
DNCED1	EU391616	9-cis-epoxycarotenoid dioxygenase	<i>C. moschata</i>	**
PhoH1	AB435244	alpha-1,4-glucan phosphorylase H isozyme	<i>C. maxima</i>	**
PhoL1	AB435243	alpha-1,4-glucan phosphorylase L isozyme	<i>C. maxima</i>	**
PP16-1	EU430061	16kDa phloem protein 1	<i>C. maxima</i> × <i>C. moschata</i> 'Ribenzhenmu'	**
PP16-2	EU430062	16kDa phloem protein 2	<i>C. maxima</i> × <i>C. moschata</i> 'Ribenzhenmu'	**
PP16-1	EF055181	phloem protein 1	<i>C. pepo</i>	**
PP16-2	EF055182	phloem protein 2	<i>C. pepo</i>	**
	D01033	1-aminocyclopropane-1-carboxylate synthase	<i>C. maxima</i> 'Ebisu'	27
	EF103124	mitochondrial alternative oxidase	<i>C. pepo</i>	**
matK	DQ536666 DQ536665 DQ536664	maturase K	<i>C. pepo</i> <i>C. digitata</i> <i>C. ficifolia</i>	36
trnG	EF595908	tRNA-Gly	<i>C. pepo</i>	15
	EF202177	aquaporin	<i>C. ficifolia</i>	**
	EU056338	chitinase	<i>C. moschata</i>	**
cat1	D55645	catalase	<i>C. pepo</i>	**
cat2	D55646	catalase	<i>C. pepo</i>	**
cat3	D55647	catalase	<i>C. pepo</i>	**
	AF260737	catalase	<i>C. pepo</i>	**
FTL1	EF462211 DQ865290	flowering locus T protein 1	<i>C. moschata</i> PI441726 <i>C. maxima</i> 'Big Max'	40

Gene Symbol*	Gene Accession	(Putative) Function	Source	Ref.
FTL2	DQ865291	flowering locus T protein 2	<i>C. maxima</i> 'Big Max'	40
	AB303333	glyoxalase I	<i>C. maxima</i>	**
	EF062594	Cu-Zn SOD	<i>C. ficifolia</i>	**
	EF101660 EF101661 EF101662 EF101663 EF101664 EF101665 EF101666 EF101667 EF199760 EF199759 EF199758 EF199757 EF199756 EF199755	NBS resistance protein	<i>C. moschata</i>	**
	AB002695	aspartic endopeptidase	<i>C. pepo</i>	24
DHAR	EF122791	dehydroascorbate reductase	<i>C. ficifolia</i>	**
API	DQ286449 DQ286448 DQ286447 DQ286445 DQ286444 DQ286443 DQ287856	aspartic acid proteinase inhibitor	<i>C. pepo</i> <i>C. maxima</i>	7
	EF055184 EF055183 EF055180	16 kDa phloem protein 2	<i>C. moschata</i> <i>C. ficifolia</i>	**
PP16	DQ088368 DQ088369 DQ088370 DQ088371 DQ088372 DQ088373	16 kDa. phloem protein 2	<i>C. maxima</i> 'Lefki kolokytha'	**
PATL1	DQ251455	patellin 1	<i>C. pepo</i> 'Fordhook'	49
	E02079	glycerol-3-phosphate acyltransferase	<i>C. moschata</i>	**
	AJ628045 AJ630372	histidine kinase	<i>C. maxima</i>	**
A215	X76086	14-3-3 protein endonuclease	<i>C. pepo</i>	43
EIN3	DQ023224 DQ023223	EIN3-like protein	<i>C. moschata</i>	**
aprx	Y17192	peroxidase	<i>C. pepo</i> zucchini 'Black Beauty'	**
pfiAF4	X81647	fruit trypsin inhibitor	<i>C. maxima</i> 'Supermarket Hybrid'	**

Gene Symbol*	Gene Accession	(Putative) Function	Source	Ref.
pfiBM7	X81447	chymotrypsin inhibitor	<i>C. maxima</i> 'Supermarket Hybrid'	**
	X73314	Gibberellin 20-oxidase	<i>C. maxima</i> 'Riesenm Elone, Gelb Genetzt'	**
	X55779	ascorbate oxidase	<i>Cucurbita</i> spp. 'Ebisu Nankin'	**
pMCPN60-2	X70867 X70868 X68606	chaperonin 60	<i>Cucurbita</i> spp. 'Kurokawa Amakuri'	**
	AJ829946 AJ829945 AJ829944	reverse transcriptase	<i>C. pepo</i>	**
NIP1	AJ544830	Nod26-like protein	<i>C. pepo</i>	35
GAIP-B	AY326307 AY326306	gibberellic acid insensitive phloem B	<i>C. maxima</i>	22
	AY663852	serine/threonine kinase-like protein	<i>C. ficifolia</i>	**
CPR	AB116239	oxidosqualene cyclase	<i>C. pepo</i>	**
CPQ	AB116238	cucurbitadienol synthase	<i>C. pepo</i>	**
	AY672635	chymotrypsin protease inhibitor	<i>C. maxima</i>	**
	AY672634	aspartic protease inhibitor	<i>C. maxima</i>	**
AIG-2	AY666083	aspartic protease inhibitor	<i>C. maxima</i>	**
AIG-1	AY666082	aspartic protease inhibitor	<i>C. maxima</i>	**
rpl2	AY396281	ribosomal protein L2	<i>C. pepo</i>	12
rpl23	AY396396	ribosomal protein L23	<i>C. pepo</i>	12
rps19	AY396376	ribosomal protein S19	<i>C. pepo</i>	12
psbC	AY396185	photosystem II protein	<i>C. pepo</i>	12
rpoB	AY396320	polymerase beta subunit	<i>C. pepo</i>	12
rps2	AY396301	ribosomal protein S2	<i>C. pepo</i>	12
FAD2	AY525163	omega-6 fatty acid desaturase	<i>C. pepo</i>	**
matR	AY453101	maturase	<i>C. pepo</i>	3
GAS1	AY379783	galactinol synthase	<i>C. pepo</i>	2
atpB	AF209573	ATP synthase beta subunit	<i>C. pepo</i>	**
Pugf	AB059484	glutathione S-transferase	<i>C. maxima</i>	25

Gene Symbol*	Gene Accession	(Putative) Function	Source	Ref.
nad1 nad2	AF453584 through AF453645	NADH dehydrogenase subunit 1 and 2	<i>C. pepo</i> ssp. <i>pepo</i> <i>C. pepo</i> ssp. <i>fraterna</i> <i>C. pepo</i> ssp. <i>ovifera</i> <i>C. pepo</i> var. <i>texana</i> <i>C. pepo</i> var. <i>ozarkana</i> <i>C. moschata</i> <i>C. maxima</i> <i>C. foetidissima</i> <i>C. argyrosperma</i> <i>C. sororia</i> <i>C. ecuadorensis</i> <i>C. andreana</i> ; <i>C. okeechobeensis</i> ssp. <i>martinezii</i>	51
CmMP73	AB062669	preproMP73	<i>C. maxima</i> ‘Kurokawa Amakuri Nankin’	**
CmATS1;2	AB042401 AB042400	glycerol-3-phosphate acyltransferase	<i>C. moschata</i>	**
	AF260736	glucose-6-phosphate dehydrogenase	<i>C. pepo</i>	**
	AF260735 AF260734 AF260733 AF260732	NADP-dependent malic enzyme	<i>C. pepo</i>	**
	AF260731	heat shock protein 70	<i>C. pepo</i>	**
API-2 API-1	AF038167 AF038166	aspartic proteinase inhibitor	<i>C. maxima</i>	8

* Gene symbols were assigned by the researchers isolating the gene; they have no correspondence to the official *Cucurbita* gene symbols.

**Unpublished: Genes can be submitted directly to Genbank, without being published in a journal.

*** ‘Kurokawa Amakuri Nankin’ was identified only as “*Cucurbita* sp.”

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