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(54) RESTORER FACTOR FOR THE BACCATUM CYTOPLASMIC MALE STERILITY SYSTEM IN PEPPER

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(57) **ABSTRACT**

The present disclosure provides *Capsicum annuum* BCMS plants comprising a male fertility restoration locus. Such plants comprise novel introgressed genomic regions associated with male fertility from *Capsicum annuum* on chromosome 6. In certain aspects, compositions and methods for producing, breeding, identifying, and selecting plants or germplasm with a male fertility phenotype are provided.

Specification includes a Sequence Listing.

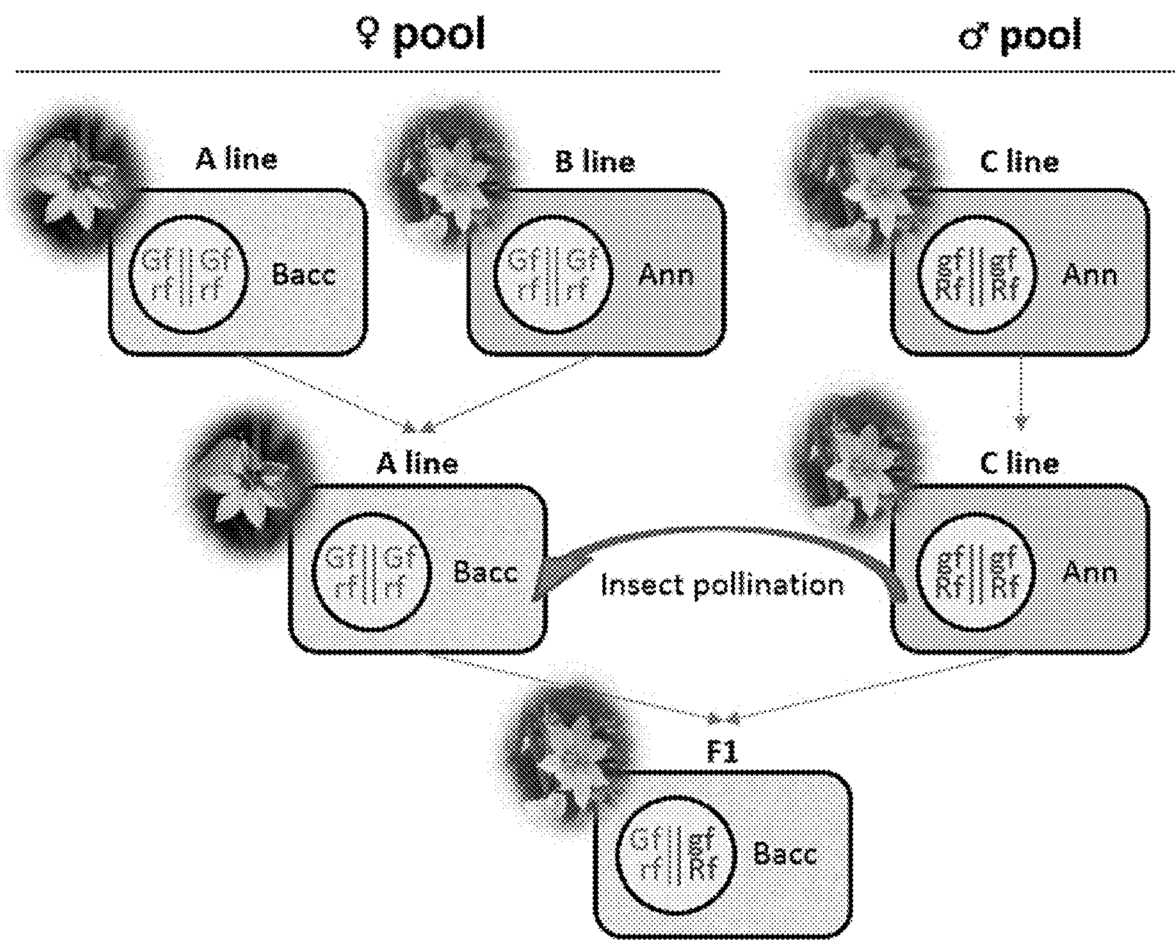
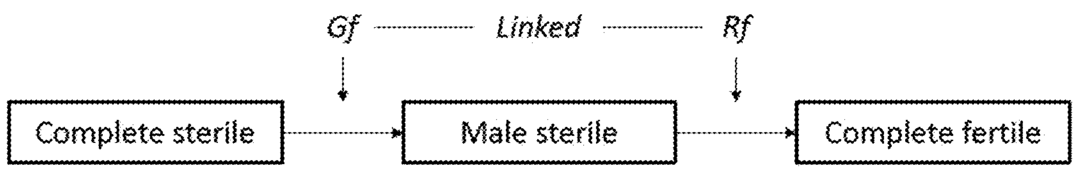


FIG. 1



gfRf = annuum restoration haplotype *gfrf* = annuum non-restoration haplotype

Gfrf = baccatum haplotype

Possible genotypes	Female fertility	Male fertility	Flower class
Gfrf/Gfrf	Fertile	Sterile	Male sterile
Gfrf/gfrf	Fertile	Sterile	Male sterile
Gfrf/gfRf	Fertile	Fertile	Complete fertile
gfrf/gfrf	Sterile	Sterile	Complete sterile
gfrf/gfRf	Sterile	Sterile	Complete sterile
gfRf/gfRf	Sterile	Sterile	Complete sterile

FIG. 2

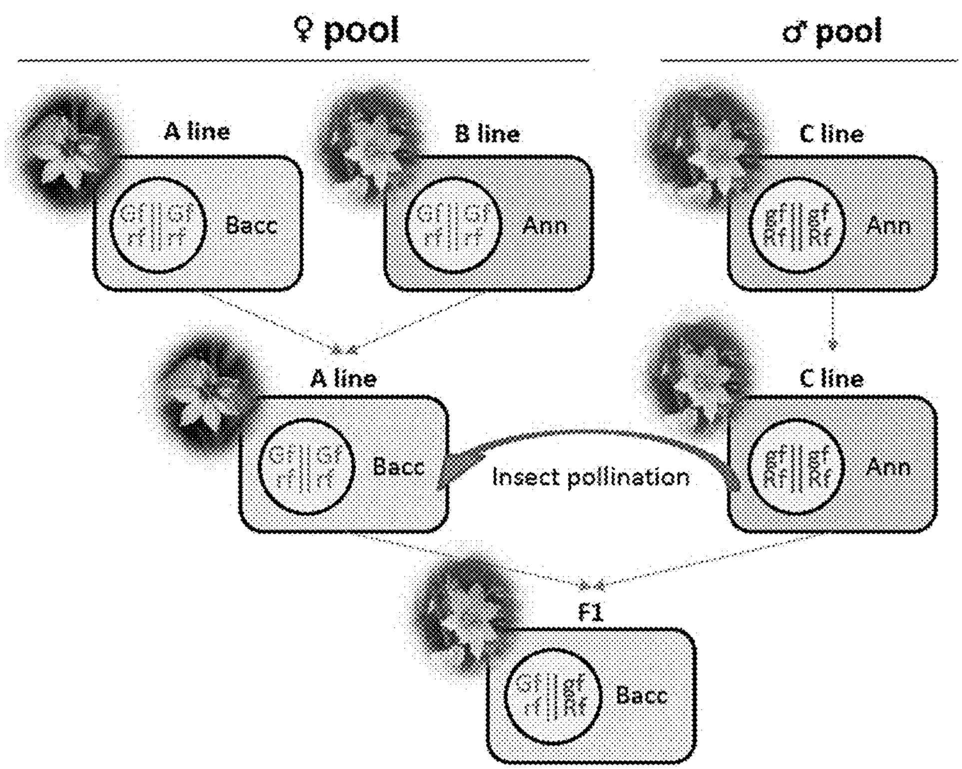

♀ pool
♂ pool
A line
Gf Gf rf rf
Bacc
B line
Gf Gf rf rf
Ann
C line
gf gf Rf Rf
Ann
A line
Gf Gf rf rf
Bacc
C line
gf gf Rf Rf
Ann
Insect pollination
F1
Gf gf rf Rf
Bacc

FIG. 3

Parental cross: BCMS Donor Line 1: (S)*Gfrf/gfrf* x 'Flame Fountain' (N)*gfRf/gfRf*

→ F_1: ½(S)*Gfrf/gfRf* (completely fertile) + ~~½(S)*gfrf/gfRf*~~ (completely sterile)

→ F_2: ½(S)*Gfrf/gfRf* (completely fertile) + ~~½(S)*Gfrf/Gfrf*~~ (male sterile)

→ …

→ F_n: ½(S)*Gfrf/gfRf* (completely fertile) + ½(S)*Gfrf/Gfrf* (male sterile)

* note that (S)*Gfrf/Gfrf* plants cannot be selfed and do not contribute to next selfing generation.

RESTORER FACTOR FOR THE BACCATUM CYTOPLASMIC MALE STERILITY SYSTEM IN PEPPER

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of priority of U.S. Provisional Appl. Ser. No. 62/690,728, filed Jun. 27, 2018, the disclosure of which is hereby incorporated by reference in its entirety.

INCORPORATION OF SEQUENCE LISTING

[0002] The sequence listing that is contained in the file named "SEMB035US_ST25.txt", which is 50.8 kilobytes as measured in Microsoft Windows operating system and was created on Jun. 25, 2019, is filed electronically herewith and incorporated herein by reference.

FIELD OF THE INVENTION

[0003] The present invention relates to the field of agriculture and more specifically to methods and compositions for producing pepper plants exhibiting restored male fertility.

BACKGROUND OF THE INVENTION

[0004] The goal of vegetable breeding is to combine various desirable traits in a single variety/hybrid. Production of hybrid peppers may be carried out by hand-emasculation or by using male sterility. A number of male sterility systems have been identified for use in pepper production, however each system has limitations. Efforts to overcome these limitations are hindered by a lack of specific markers linked to the alleles associated with male sterility phenotypes. The use of marker-assisted selection (MAS) in plant breeding methods has made it possible to select plants based on genetic markers linked to traits of interest. However, accurate markers for identifying or tracking desirable traits in plants are frequently unavailable even if a gene associated with the trait has been characterized. These difficulties are further complicated by factors such as polygenic or quantitative inheritance, epistasis and an often incomplete understanding of the genetic background underlying expression of a desired phenotype.

SUMMARY OF THE INVENTION

[0005] In one aspect, the present invention provides a *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm and comprising a chromosomal segment on chromosome 6 that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment. In some embodiments, the chromosomal segment is flanked by Marker M29 (SEQ ID NO: 29) and a marker selected from the group consisting of Marker M14 (SEQ ID NO: 14), Marker M15 (SEQ ID NO: 15), Marker M16 (SEQ ID NO: 16), and Marker M17 (SEQ ID NO: 17) in said plant. In further embodiments, the chromosomal segment comprises a marker locus selected from the group consisting of Marker M18 (SEQ ID NO: 18), Marker M19 (SEQ ID NO: 19), Marker M20 (SEQ ID NO: 20), Marker M21 (SEQ ID NO: 21), Marker M22 (SEQ ID NO: 22), Marker M23 (SEQ ID NO: 23), Marker M24 (SEQ ID NO: 24), Marker M25 (SEQ ID NO: 25), Marker M26 (SEQ ID NO: 26), Marker M27 (SEQ ID NO: 27), and Marker M28 (SEQ ID NO: 28) on chromosome 6. In some embodiments, the chromosomal segment is located between 26,405 bp and 213,924,156 bp on chromosome 6 of public pepper genome sequence Pepper CM334 v.1.55. In some embodiments, the chromosomal segment comprises the haplotype of variety Ganti, wherein a representative sample of seed of said variety has been deposited under NCIMB accession number 43055. In other embodiments, the chromosomal segment comprises the haplotype of variety Flame Fountain, wherein a representative sample of seed of said variety has been deposited under NCIMB accession number 43054.

[0006] The present invention also provides a seed that produces a *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm and comprising a chromosomal segment on chromosome 6 that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment.

[0007] Additionally, the present invention provides a plant part of a *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm and comprising a chromosomal segment on chromosome 6 that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment. In certain embodiments, the plant part is a cell, a seed, a root, a stem, a leaf, a flower, a fruit, or pollen.

[0008] The present invention also provides a *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm and comprising a chromosomal segment on chromosome 6 that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment, wherein the plant is a sweet pepper variety.

[0009] Additionally, the present invention provides a *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm and comprising a chromosomal segment on chromosome 6 that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment, wherein the plant has a blocky type fruit shape.

[0010] The present invention also provides a *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm and comprising a chromosomal segment on chromosome 6 that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment, wherein said plant further comprises a chromosomal segment from *Capsicum baccatum* on chromosome 6 that confers uniform female fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment, wherein said chromosomal segment from *Capsicum baccatum* is flanked by Marker A12 (SEQ ID NO: 35) and Marker A35 (SEQ ID NO: 36) in said plant.

[0011] In another aspect, the present invention provides a method for producing a *Capsicum annuum* plant that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm, comprising introgressing into said plant a chromosomal segment on chromosome 6 that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment. In some embodiments, the introgressing comprises crossing a plant comprising said chromosomal segment with itself or with a second *Capsicum annuum* plant of a different genotype to produce one or more progeny plants, and selecting a progeny plant comprising said chromosomal segment. In further embodiments, the selecting a progeny plant comprises detecting at least one allele flanked by Marker M29 (SEQ ID NO: 29) and a marker selected from the group consisting of Marker M14 (SEQ ID NO: 14), Marker M15 (SEQ ID NO: 15), Marker M16 (SEQ ID NO: 16), and Marker M17 (SEQ ID NO: 17) on chromosome 6. In other embodiments, the progeny plant is an F_2-F_6 progeny plant. In particular embodiments, the crossing comprises backcrossing, which in certain embodiments comprises from 2-7 generations of backcrosses.

[0012] The present invention also provides a *Capsicum annuum* plant produced by a method comprising introgressing into said plant a chromosomal segment on chromosome 6 that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment. Thus, the present invention also provides a method of producing food or feed comprising obtaining a *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm and comprising a chromosomal segment on chromosome 6 that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment, or a part thereof, and producing said food or feed from said plant or part thereof.

[0013] In another aspect, the present invention provides a *Capsicum annuum* plant obtainable by a method comprising the step of introgressing into a plant a male fertility restoration locus allele for *Baccatum* cytoplasmic male sterility, wherein said male fertility restoration locus allele is defined as located in a chromosomal segment flanked by Marker M29 (SEQ ID NO: 29) and a marker selected from the group consisting of Marker M14 (SEQ ID NO: 14), Marker M15 (SEQ ID NO: 15), Marker M16 (SEQ ID NO: 16), and Marker M17 (SEQ ID NO: 17) on chromosome 6. In certain embodiments, the introgressing comprises backcrossing. In other embodiments, the introgressing comprises marker-assisted selection.

BRIEF DESCRIPTION OF THE DRAWINGS

[0014] FIG. **1**: Shows an overview of the genetic model for the functioning of the *Baccatum* cytoplasmic male sterility (CMS) system. The phenotypic predictions are for plants with *Capsicum baccatum* cytoplasm.

[0015] FIG. **2**: Shows a schematic of the hybrid production concept with CMS, based on *Capsicum baccatum* cytoplasm. The female pool comprises two lines that lack the male fertility restorer locus: the A-line, which is a male sterile line that serves as the female parent in the hybrid cross; and the B-line, which is a male fertile line that serves as the maintainer and enables crosses within the female breeding pool. The C-line serves as the male parent of the hybrid cross and generally is a normal *Capsicum annuum* line that lacks the Gf locus, but is fixed for the male fertility restorer locus allele Rf. "Bacc" indicates plants with a *Capsicum baccatum* cytoplasm, while "Ann" indicates plants with a *Capsicum annuum* cytoplasm.

[0016] FIG. **3**: Shows a schematic of the genetic model for Gf and Rf transmission in pepper plants having a *Capsicum baccatum* or a *Capsicum annuum* cytoplasm. The "(S)" denotes a *Capsicum baccatum* cytoplasm and the "(N)" denotes a *Capsicum annuum* cytoplasm. Fn progeny derived from restored F1 plants (e.g. BCMS Donor Line 1×'Flame Fountain') segregate for 50% completely fertile and 50% male sterile plants.

DETAILED DESCRIPTION

[0017] Male sterility is used by breeders for two basic product concepts in a variety of crops. The first product concept is seedless fruit. Plants comprising the male sterility trait are crossed with plants comprising parthenocarpy genes to produce hybrid seed. This hybrid seed produces plants bearing seedless fruit. Under normal circumstances, male sterile plants cannot set fruit in the absence of pollination. However, if the plant also contains parthenocarpy genes, then fruit set occurs in the absence of pollination. In this product concept, it is possible to use different forms of male sterility without a restorer locus. However, only cytoplasmic male sterility will allow for production of seed from which 100% of the plants grown from this seed are sterile and bear seedless fruit. Using genic male sterility for this product concept requires an intermediate seedling selection step after showing the hybrid seed, followed by transplanting or grafting of the selected sterile plants. The second product concept is one where male sterility is used to easily develop hybrid seed. In the development of hybrid seed it is important to ensure genetic purity of a seed batch. This entails minimizing the number of seed that are the result of self-fertilization. Self-fertilization is prevented during seed production through physical removal of male sex organs in the flower before the flower opens, a process referred to as emasculation. This is a labor-intensive procedure that is not only costly, but also is not 100% effective. Genetic emasculation of the female line overcomes these limitations and ensures the genetic purity of the hybrid seed. However, successful hybrid production requires that the male sterility system used can be restored in the hybrid. Thus, the male parent of the hybrid will typically contain a dominant male fertility restorer locus. When a male parent comprising the restorer locus is crossed with the male sterile female parent, fully fertile hybrid plants will be produced. Given that resultant hybrid plants are heterozygous, it is essential that the restorer locus be dominant.

[0018] Genetic (or genic) male sterility (GMS) systems utilize male sterility loci that are often inherited in a recessive manner and encoded within the nuclear genome. An exception to this is, for example, a GMS system in rapeseed where both the sterility and sterility suppressor genes are dominant. A primary disadvantage with the genetic male sterility system is that only half of the progeny plants will be male sterile. A breeder would therefore have to select which plants are suitable for hybrid/seedless fruit production post-germination, resulting in at least half of the seedlings being discarded. A system that does not have this problem is the cytoplasmic male sterility (CMS) system. In this system, the male sterility loci are coded in the mitochondrial DNA and, in the absence of a nuclear male fertility restoration gene, 100% of the progeny plants are male sterile. In pepper, the Peterson's CMS system is widely used because a dominant male fertility restoration locus is available, making this system suitable for both hybrid production and the seedless fruit concept. The restorer locus for Peterson's CMS is often referred to as the CMS restorer locus or Rf. The CMS restorer allele (Rf) was identified in pungent *Capsicum annuum* germplasm and has been mapped to a locus on the short arm of chromosome 6. Transferring a functioning restorer locus to sweet pepper types has proven difficult and remains the subject of much study and breeding efforts because the Peterson's CMS system is known to be unstable with respect to environmental conditions and genetic background.

[0019] An environmentally-stable alternative to the Peterson's CMS system is the *Baccatum* cytoplasmic male sterility (BCMS) system. This system was created by crossing a female *Capsicum baccatum* plant with a male *Capsicum annuum* plant. The resulting hybrid, which was obtained through a step of embryo rescue, contained a *Capsicum baccatum* cytoplasm and was male sterile. Through extensive backcrossing to the *Capsicum annuum* parent, the *Capsicum baccatum* genome was replaced with *Capsicum annuum* DNA. However, the BCMS system has some limitations. First, female sterility segregates within the population of BCMS lines and efforts to eliminate this negative trait through crossing and selection has not been successful. Second, there does not appear to be a dominant restorer locus for the BCMS, in the absence of a nuclear male fertility restoration gene.

[0020] The present inventors have found that the limitation of use of the BCMS system due to the lack of a dominant restorer locus can be overcome by use of a chromosomal segment from certain *Capsicum annuum* lines on the short arm of chromosome 6 that confers male fertility in BCMS pepper lines. This locus was identified in the varieties 'Ganti' (NCIMB 43055) and 'Flame Fountain' (NCIMB 43054) in a study of BCMS male fertility restoration using *Capsicum annuum* accessions. The variety 'Ganti' is a landrace from Hungary that is best described as a sweet Hungarian-white or Hungarian-wax type pepper. The variety 'Flame Fountain' is a hot Indian-type pepper that is characterized by a long and thin fruit that colors green to red. Surprisingly, although the novel male fertility restoration locus of the invention is located on the same chromosome as the CMS restorer allele used in the Peterson's CMS system, it was found that they are distinct, as crosses between BCMS plants and plants with the Peterson's CMS fertility restorer locus did not result in male fertility restoration. The invention therefore provides methods and compositions for restoring male fertility in BCMS pepper plants, as well as markers for tracking and identifying the novel chromosomal segment in plants during breeding. A non-limiting summary of useful markers is provided in Table 1. The chromosomal segment is located between markers M1 (SEQ ID NO: 1) and M34 (SEQ ID NO: 34), while markers M2 to M33 can also be used to select the chromosomal segment in subsequent germplasm. The specific selected markers used depends on the polymorphism between the male fertility locus donor ('Ganti' or 'Flame Fountain') and the non-donor parent (recurrent parent). Therefore, a combination of markers listed in Table 1 may be used for benefit in a first selection, while markers can be limited to a polymorphic subset in a given cross for further selections.

I. GENOMIC REGIONS, ALLELES, AND POLYMORPHISMS ASSOCIATED WITH MALE FERTILITY IN BCMS LINES

[0021] The inventors identified a novel chromosomal segment on chromosome 6 from *Capsicum annuum* that confers male fertility in a *Baccatum* cytoplasmic male sterile plant, together with polymorphic nucleic acids and linked markers for tracking and introgressing the chromosomal segment into potentially any variety during plant breeding. The newly identified chromosomal segment on chromosome 6 from donor line 'Ganti' covers a region of 31.7 cM and is flanked by marker M1, a SNP change [A/G] at 213,924,156 bp on genome sequence version 1.55 of pepper line CM334, which can be found at solgenomics.net, and marker M34, a SNP change [G/C] at 21,133,217 bp. Interstitial markers, such as M2, a SNP change [C/T] at 213,907,080 bp, M3, a SNP change [A/G] at 213,907,920 bp, M4, a SNP change [T/C] at 427,239 bp, M6, a SNP change [T/C] at 87,022 bp, M8, a SNP change [C/T] at 89,795 bp, M12, a SNP change [A/C] at 3,009,771 bp, M13, a SNP change [C/T] at 2,999,718 bp, M14, a SNP change [G/T] at 3,504,248 bp, M18, a SNP change [A/G] at 3,475,770 bp, M19, a SNP change [G/T] at 3,422,765 bp, M20, a SNP change [A/T] at 4,276,008 bp, M23, a SNP change [A/G] at 70,994,266 bp, M27, a SNP change [T/G] at 8,522,176 bp, M28, a SNP change [A/G] at 9,799,932 bp, and M33, a SNP change [C/T] at 11,592,142 bp, can be used in any possible combination as flanking markers to select for the restorer locus on chromosome 6 from Ganti or another donor line.

[0022] The newly identified chromosomal segment on chromosome 6 from donor line 'Flame Fountain' covers a region of 24.9 cM and is flanked by marker M5, a SNP change [A/G] at 428,143 bp on genome sequence version 1.55 of pepper line CM334, which can be found at solgenomics.net, and marker M33, a SNP change [C/T] at 11,592,142 bp. Interstitial markers, such as M7, a SNP change [C/T] at 125,861 bp, M8, a SNP change [C/T] at 89,795 bp, M11, a SNP change [A/G] at 3,055,268 bp, M12, a SNP change [A/C] at 3,009,771 bp, M13, a SNP change [C/T] at 2,999,718 bp, M14, a SNP change [G/T] at 3,504,248 bp, M15, a SNP change [C/A] at 3,500,133 bp, M16, a SNP change [A/G] at 3,505,583 bp, M17, a SNP change [C/T] at 3,308,938 bp, M18, a SNP change [A/G] at 3,475,770 bp, M19, a SNP change [G/T] at 3,422,765 bp, M20, a SNP change [A/T] at 4,276,008 bp, M25, a SNP change [G/A] at 6,240,565 bp, and M26, a SNP change [C/T] at 6,241,544 bp, can be used in addition to the flanking markers to select for the restorer locus on chromosome 6 from Flame Fountain or another donor line.

[0023] Additionally, interstitial markers, such as M5, a SNP change [A/G] at 428,143 bp, M7, a SNP change [C/T] at 125,861 bp, M9, a SNP change [T/C] at 386,489 bp, M10, a SNP change [C/A] at 26,405 bp, M21, a SNP change [G/A] at 4,240,789 bp, M22, a SNP change [G/C] at 4,245,699 bp, M24, a SNP change [A/T] at 4,240,551 bp, M29, a SNP change [C/T] at 10,670,362 bp, M30, a SNP change [T/C] at 10,664,163 bp, M31, a SNP change [G/T] at 10,664,630 bp, and M32, a SNP change [T/C] at 11,108,817 bp, can be used in addition to the flanking markers to select for the restorer locus on chromosome 6 from either donor line 'Ganti' or 'Flame Fountain' or another donor line. Thus, the present disclosure provides a *Capsicum annuum* plant comprising a chromosomal segment on chromosome 6 of *Capsicum annuum* flanked by markers M1 and M34 that confers male fertility to BCMS pepper plants. In certain embodiments, one or both of the flanking markers are interstitial markers between M1 and M34, such as markers M2, M3, M4, M5, M6, M7, M8, M9, M10, M11, M12, M13, M14, M15, M16, M17, M18, M19, M20, M21, M22, M23, M24, M25, M26, M27, M28, M29, M30, M31, M32, or M33 and comprise an allele from ‘Ganti’ or ‘Flame Fountain’ at said marker(s). In some embodiments, the chromosomal segment on chromosome 6 of *Capsicum annuum* comprises a plurality of the markers listed in Table 1, including any possible combination thereof. In some embodiments, the chromosomal segment on chromosome 6 of *Capsicum annuum* restoring fertility in plants with *Capsicum baccatum* cytoplasmic male sterility from ‘Ganti’ is flanked by markers M14 and M29, wherein interstitial markers M15, M16, M17, M18, M19, M20, M21, M22, M23, M24, M25, M26, M27, M28 or any combination thereof are used to select this region. In some embodiments, the chromosomal segment on chromosome 6 of *Capsicum annuum* restoring fertility in plants with *Capsicum baccatum* cytoplasmic male sterility from ‘Flame Fountain’ is flanked by markers M17 and M29, wherein interstitial markers M18, M19, M20, M21, M22, M23, M24, M25, M26, M27, M28 or any combination thereof are used to select this region.

II. INTROGRESSION OF GENOMIC REGIONS ASSOCIATED WITH RESTORATION OF MALE FERTILITY

[0024] Marker-assisted introgression involves the transfer of a chromosomal region defined by one or more markers from a first genetic background to a second. Offspring of a cross that contain the introgressed genomic region can be identified by the combination of markers characteristic of the desired introgressed genomic region from a first genetic background and both linked and unlinked markers characteristic of the second genetic background.

[0025] The invention provides a *Capsicum annuum* plant comprising an introgressed allele on chromosome 6 that confers male fertility in a pepper plant with BCMS, wherein said allele is located between marker M2 and marker M33, or preferably between marker M14 and marker M29. In addition, the invention provides a *Capsicum annuum* plant with a cytoplasm from *Capsicum baccatum*, in which male fertility is restored due to the presence of a male fertility restoration allele on chromosome 6, wherein said allele is located between marker M2 and marker M33, or preferably between marker M14 and marker M29. In some embodiments, the plant is a variety selected from the group consisting of Anaheim, Ancho/Poblano, Asian Long Slim, Asian Short, Blocky or Bell, Capia, Cascabel, Cayenne, Chiltepins or Small Hots, Corno di Toro, Cubanelle, ‘Fresno Chili’, Hungarian Wax/Banana/Hungarian White, Jalapeno, Ornamental, Pasilla, Pimiento, Santa Fe Grande, Serrano, and Waxy peppers. In certain embodiments, the plant has a blocky type fruit shape, a ¾ long type fruit shape, or a half long type fruit shape. For example, the fruit of the plant may have a length to width ratio less than 2.5:1, such as a length to width ratio of less than 2:1, or a length to width ratio of between 0.8 to 1.2. As used herein, blocky type pepper refers to a pepper wherein the length of the fruit is about the same as the width of the fruit. For example, the length of the fruit is about 0.8, about 0.9, about 1.0, about 1.1, or less than 1.2 of the width of the fruit. As used herein, ¾ long type pepper, often known as lamuyo, refers to a pepper wherein the length of the fruit is more than about 1.5 of the width of the fruit. These peppers can have a variety of different colors, for example white, purple, and green at the immature stage, and for example red, yellow, green, orange, and brown at the mature fruit stage. It is also well-known that definitions vary regionally. For example, in the United States peppers with a length to with ratio of 1.2 to 1.4 are often referred to as “deep blocky”, while the terms half long and lamuyo are used interchangeably for sweet peppers with a length to width ratio over 1.4.

[0026] In certain embodiments, the genomic regions identified herein may be introgressed from any *Capsicum annuum* type into any *Capsicum annuum* type. Types of *Capsicum annuum* include, but are not limited to Anaheim, Ancho/Poblano, Asian long slim, Asian short, Blocky or Bell, Capia, Cascabel, Cayenne, Chiltepins or Small Hots, Corno di Toro, Cubanelle, ‘Fresno Chili’, Jalapeno, Ornamental, Pasilla, Pimiento, Santa Fe Grande, Serrano, and Waxy peppers, including Hungarian wax/Banana/Hungarian white.

[0027] In certain embodiments, the identified genomic regions are introduced into a jalapeno variety. Pepper fruit shapes are well-known to those skilled in the art of pepper breeding. Jalapeno peppers are a type of *Capsicum annuum* that have a characteristic fruit shape. Jalapeno fruits are typically bullet-shaped and have a length to width ratio of about 2.5 to 1. For example, a fruit having a length of about 10 cm would be expected to be about 4 cm wide. The fruit typically has thick walls of about 5-6 mm and the dry matter content is normally around 7%. The fruit of most plants develops from a medium green at the immature stage to red at the mature stage. As a commercial product, the fruits are harvested at the green stage. The pungency of jalapeno peppers varies from 0 units to over 5000 units on the Scoville scale.

[0028] The present invention provides novel markers for identifying and tracking introgression of one or more of the genomic regions from a donor plant comprising male fertility restoration alleles into *Baccatum* cytoplasmic male sterility lines. The invention further provides markers for identifying and tracking the novel introgressions disclosed herein during plant breeding, including the markers set forth in Table 1.

[0029] Markers within or linked to any of the genomic intervals of the present invention can be used in a variety of breeding efforts that include introgression of genomic regions associated with male fertility into a desired genetic background. For example, a marker within 30 cM, 25 cM, 20 cM, 16 cM, 15 cM, 10 cM, 5 cM, 2 cM, or 1 cM of a marker associated with male fertility described herein can be used for marker-assisted introgression of genomic regions associated with a male fertility phenotype.

[0030] Pepper plants comprising one or more introgressed regions associated with a desired phenotype wherein at least 10%, 25%, 50%, 75%, 90%, or 99% of the remaining genomic sequences carry markers characteristic of the germplasm are also provided. Pepper plants comprising an introgressed region comprising regions closely linked to or adjacent to the genomic regions and markers provided herein and associated with a male fertility phenotype are also provided.

III. DEVELOPMENT OF PEPPER PLANTS THAT PROVIDE MALE FERTILITY

[0031] For most breeding objectives, commercial breeders work within germplasm that is “cultivated type” or “elite.” This germplasm is easier to breed because it generally performs well when evaluated for horticultural performance. For example, *Capsicum annuum* is an agronomically elite, cultivated pepper adapted to commercial use. However, the performance advantage a cultivated germplasm provides can be offset by a lack of allelic diversity. Breeders generally accept this tradeoff because progress is faster when working with cultivated material than when breeding with genetically diverse sources.

[0032] In contrast, when a breeder makes either intraspecific crosses, or interspecific crosses, a converse tradeoff occurs. In these examples, a breeder typically crosses germplasm of an economically important species with a non-cultivated or commercially unacceptable species. The breeder can gain access to novel alleles from the non-cultivated species, but may have to overcome genetic drag or interspecific hybridization barriers associated with such crosses. Because of the difficulty with this breeding strategy, this approach often fails because of fertility and fecundity problems. The difficulty with this breeding approach extends to many crops, and is exemplified with an important disease resistant phenotype that was first described in tomato in 1944 (Smith, *Proc. Am. Soc. Hort. Sci.* 44:413-16). In this cross, a nematode disease resistance was transferred from *L. peruvianum* (PI128657) into a cultivated tomato. Despite intensive breeding, it was not until the mid-1970's before breeders could overcome the genetic drag and release successful lines carrying this trait. Indeed, even today, tomato breeders deliver this disease resistance gene to a hybrid variety from only one parent. This allows the remaining genetic drag to be masked. The inventiveness of succeeding in this breeding approach has been recognized by the USPTO (U.S. Pat. Nos. 6,414,226, 6,096,944, 5,866,764, and 6,639,132).

[0033] The process of introgressing desirable genes from one species into another while avoiding problems with linkage drag or low heritability is a long and often arduous process. Success in deploying alleles derived from related species therefore strongly depends on minimal or truncated introgressions that lack detrimental effects and reliable marker assays that replace phenotypic screens. Success is further defined by simplifying genetics for key attributes to allow focus on genetic gain for quantitative traits. Moreover, the process of introgressing genomic regions from non-cultivated lines or different species can be greatly facilitated by the availability of informative markers.

[0034] One of skill in the art would therefore understand that the alleles, polymorphisms, and markers provided by the invention allow the tracking and introduction of any of the genomic regions identified herein into any genetic background. In addition, the genomic regions associated with male fertility disclosed herein can be introgressed from one genotype to another and tracked phenotypically or genetically. Thus, Applicants' discovery of accurate markers associated with male fertility restoration locus will facilitate the development of pepper plants having beneficial phenotypes. For example, plants and seeds can be genotyped using the markers of the present invention in order to develop varieties comprising desired male fertility. Moreover, marker-assisted selection (MAS) allows identification of plants which are homozygous or heterozygous for the desired introgression.

[0035] Meiotic recombination is essential for plant breeding because it enables the transfer of favorable alleles across genetic backgrounds, the removal of deleterious genomic fragments, and pyramiding traits that are genetically tightly linked. In the absence of accurate markers, limited recombination forces breeders to enlarge segregating populations for progeny screens. Moreover, phenotypic evaluation is time-consuming, resource-intensive and not reproducible in every environment. The markers provided by the invention offer an effective alternative and therefore represent a significant advance in the art.

[0036] Phenotypic evaluation of large populations is time-consuming, resource-intensive and not reproducible in every environment. Marker-assisted selection offers a feasible alternative. Molecular assays designed to detect unique polymorphisms, such as SNPs, are versatile. However, they may fail to discriminate alleles within and among pepper species in a single assay. Structural rearrangements of chromosomes such as deletions impair hybridization and extension of synthetically labeled oligonucleotides. In the case of duplication events, multiple copies are amplified in a single reaction without distinction. The development and validation of accurate and highly predictive markers are therefore essential for successful MAS breeding programs.

[0037] Many desirable traits that are successfully introduced through introgression can also be introduced directly into a plant by the use of molecular techniques. One aspect of the invention includes plants with a genome that has been changed by any method using site-specific genome modification techniques. Techniques of site-specific genome modification include the use of enzymes such as, endonucleases, recombinases, transposases, helicases and any combination thereof. In one aspect, an endonuclease is selected from a meganuclease, a zinc-finger nuclease (ZFN), a transcription activator-like effector nucleases (TALEN), an Argonaute, and an RNA-guided nuclease, such as a CRISPR associated nuclease.

[0038] In another aspect, the endonuclease is a dCas9-recombinase fusion protein. As used herein, a "dCas9" refers to a Cas9 endonuclease protein with one or more amino acid mutations that result in a Cas9 protein without endonuclease activity, but retaining RNA-guided site-specific DNA binding. As used herein, a "dCas9-recombinase fusion protein" is a dCas9 with a protein fused to the dCas9 in such a manner that the recombinase is catalytically active on the DNA.

[0039] Non-limiting examples of recombinase include a tyrosine recombinase attached to a DNA recognition motif provided herein is selected from the group consisting of a Cre recombinase, a Gin recombinase a Flp recombinase, and a Tnp1 recombinase. In an aspect, a Cre recombinase or a Gin recombinase provided herein is tethered to a zinc-finger DNA-binding domain, or a TALE DNA-binding domain, or a Cas9 nuclease. In another aspect, a serine recombinase attached to a DNA recognition motif provided herein is selected from the group consisting of a PhiC31 integrase, an R4 integrase, and a TP-901 integrase. In another aspect, a DNA transposase attached to a DNA binding domain provided herein is selected from the group consisting of a TALE-piggyBac and TALE-Mutator.

[0040] Site-specific genome modification enzymes, induce a genome modification such as a double-stranded DNA break (DSB) or single-strand DNA break at the target site of a genomic sequence that is then repaired by the natural processes of homologous recombination (HR) or non-homologous end-joining (NHEJ). Sequence modifications then occur at the cleaved sites, which can include deletions or insertions that result in gene disruption in the case of NHEJ, or integration of exogenous sequences by homologous recombination.

[0041] Another aspect of the invention includes transgenic plant cells, transgenic plant tissues, transgenic plants, and transgenic seeds that comprise the recombinant DNA molecules and engineered proteins provided by the invention. These cells, tissues, plants, and seeds comprising the recombinant DNA molecules and engineered proteins exhibit resistance to *P. capsici*. Suitable methods for transformation of host plant cells for use with the current invention include virtually any method by which DNA can be introduced into a cell (for example, where a recombinant DNA construct is stably integrated into a plant chromosome) and are well known in the art. An exemplary and widely utilized method for introducing a recombinant DNA construct into plants is the *Agrobacterium* transformation system, which is well known to those of skill in the art. Another exemplary method for introducing a recombinant DNA construct into plants is insertion of a recombinant DNA construct into a plant genome at a pre-determined site by methods of site-directed integration. Transgenic plants can be regenerated from a transformed plant cell by the methods of plant cell culture. A transgenic plant homozygous with respect to a transgene (that is, two allelic copies of the transgene) can be obtained by self-pollinating (selfing) a transgenic plant that contains a single transgene allele with itself, for example an R0 plant, to produce R1 seed. One fourth of the R1 seed produced will be homozygous with respect to the transgene. Plants grown from germinating R1 seed can be tested for zygosity, using a SNP assay, DNA sequencing, or a thermal amplification assay that allows for the distinction between heterozygotes and homozygotes, referred to as a zygosity assay.

IV. MOLECULAR ASSISTED BREEDING TECHNIQUES

[0042] Genetic markers that can be used in the practice of the present invention include, but are not limited to, restriction fragment length polymorphisms (RFLPs), amplified fragment length polymorphisms (AFLPs), simple sequence repeats (SSRs), simple sequence length polymorphisms (SSLPs), single nucleotide polymorphisms (SNPs), insertion/deletion polymorphisms (Indels), variable number tandem repeats (VNTRs), and random amplified polymorphic DNA (RAPD), isozymes, and other markers known to those skilled in the art. Vegetable breeders use molecular markers to interrogate a crop's genome and classify material based on genetic, rather than phenotypic, differences. Advanced marker technologies are based on genome sequences, the nucleotide order of distinct, polymorphic genotypes within a species. Such platforms enable selection for horticultural traits with markers linked to favorable alleles, in addition to the organization of germplasm using markers randomly distributed throughout the genome. In the past, a priori knowledge of the genome lacked for major vegetable crops that now have been sequenced. Scientists exploited sequence homology, rather than known polymorphisms, to develop marker platforms. Man-made DNA molecules are used to prime replication of genome fragments when hybridized pair-wise in the presence of a DNA polymerase enzyme. This synthesis, regulated by thermal cycling conditions that control hybridization and replication of DNA strands in the polymerase chain reaction (PCR) to amplify DNA fragments of a length dependent on the distance between each primer pair. These fragments are then detected as markers and commonly known examples include AFLP and RAPD. A third technique, RFLP does not include a DNA amplification step. Amplified fragment length polymorphism (AFLP) technology reduces the complexity of the genome. First, through digestive enzymes cleaving DNA strands in a sequence-specific manner. Fragments are then selected for their size and finally replicated using selective oligonucleotides, each homologous to a subset of genome fragments. As a result, AFLP technology consistently amplifies DNA fragments across genotypes, experiments and laboratories.

[0043] Polymorphisms comprising as little as a single nucleotide change can be assayed in a number of ways. For example, detection can be made by electrophoretic techniques including a single strand conformational polymorphism, denaturing gradient gel electrophoresis, or cleavage fragment length polymorphisms, but the widespread availability of DNA sequencing often makes it easier to simply sequence amplified products directly. Once the polymorphic sequence difference is known, rapid assays can be designed for progeny testing, typically involving some version of PCR amplification of specific alleles or PCR amplification of multiple specific alleles.

[0044] Polymorphic markers serve as useful tools for assaying plants for determining the degree of identity of lines or varieties. These markers form the basis for determining associations with phenotypes and can be used to drive genetic gain. In certain embodiments of methods of the invention, polymorphic nucleic acids can be used to detect in a *Capsicum annuum* plant a genotype associated with male fertility, identify a *Capsicum annuum* plant with a genotype associated with male fertility, and to select a *Capsicum annuum* plant with a genotype associated with male fertility. In certain embodiments of methods of the invention, polymorphic nucleic acids can be used to produce a *Capsicum annuum* plant that comprises in its genome an introgressed locus associated with male fertility. In certain embodiments of the invention, polymorphic nucleic acids can be used to breed progeny *Capsicum annuum* plants comprising a locus associated with male fertility.

[0045] Genetic markers may include "dominant" or "codominant" markers. "Codominant" markers reveal the presence of two or more alleles (two per diploid individual). "Dominant" markers reveal the presence of only a single allele. Markers are preferably inherited in codominant fashion so that the presence of both alleles at a diploid locus, or multiple alleles in triploid or tetraploid loci, are readily detectable, and they are free of environmental variation, i.e., their heritability is 1. A marker genotype typically comprises two marker alleles at each locus in a diploid organism. The marker allelic composition of each locus can be either homozygous or heterozygous. Homozygosity is a condition where both alleles at a locus are characterized by the same nucleotide sequence. Heterozygosity refers to different conditions of the allele at a locus.

[0046] Nucleic acid-based analyses for determining the presence or absence of the genetic polymorphism (i.e., for genotyping) can be used in breeding programs for identification, selection, introgression, and the like. A wide variety of genetic markers for the analysis of genetic polymorphisms are available and known to those of skill in the art. The analysis may be used to select for genes, portions of genes, QTL, alleles, or genomic regions that comprise or are linked to a genetic marker that is linked to or associated with male fertility in BCMS plants.

[0047] As used herein, nucleic acid analysis methods include, but are not limited to, PCR-based detection methods (for example, TaqMan assays), microarray methods, mass spectrometry-based methods and/or nucleic acid sequencing methods, including whole genome sequencing. In certain embodiments, the detection of polymorphic sites in a sample of DNA, RNA, or cDNA may be facilitated through the use of nucleic acid amplification methods. Such methods specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis, fluorescence detection methods, or other means.

[0048] One method of achieving such amplification employs the polymerase chain reaction (PCR) using primer pairs that are capable of hybridizing to the proximal sequences that define a polymorphism in its double-stranded form. Methods for typing DNA based on mass spectrometry can also be used. Such methods are well known in the art.

[0049] Polymorphisms in DNA sequences can be detected or typed by a variety of effective methods well known in the art. The compositions and methods of the present invention can be used in conjunction with any polymorphism typing method to type polymorphisms in genomic DNA samples. These genomic DNA samples used include but are not limited to, genomic DNA isolated directly from a plant, cloned genomic DNA, or amplified genomic DNA.

[0050] For instance, polymorphisms in DNA sequences can be detected by hybridization to allele-specific oligonucleotide (ASO) probes. U.S. Pat. No. 5,468,613 discloses allele specific oligonucleotide hybridizations where single or multiple nucleotide variations in nucleic acid sequence can be detected in nucleic acids by a process in which the sequence containing the nucleotide variation is amplified, spotted on a membrane and treated with a labeled sequence-specific oligonucleotide probe. Target nucleic acid sequence can also be detected by probe ligation methods where sequence of interest is amplified and hybridized to probes followed by ligation to detect a labeled part of the probe.

[0051] Microarrays can also be used for polymorphism detection, wherein oligonucleotide probe sets are assembled in an overlapping fashion to represent a single sequence such that a difference in the target sequence at one point would result in partial probe hybridization. On any one microarray, it is expected there will be a plurality of target sequences, which may represent genes and/or noncoding regions wherein each target sequence is represented by a series of overlapping oligonucleotides, rather than by a single probe. This platform provides for high throughput screening of a plurality of polymorphisms.

[0052] Other well-known methods for detecting SNPs and Indels include single base extension (SBE) methods. In another method for detecting polymorphisms, SNPs and Indels can be detected by methods in which an oligonucleotide probe having a 5' fluorescent reporter dye and a 3' quencher dye covalently linked to the 5' and 3' ends of the probe. When the probe is intact, the proximity of the reporter dye to the quencher dye results in the suppression of the reporter dye fluorescence, e.g. by Forster-type energy transfer. During PCR forward and reverse primers hybridize to a specific sequence of the target DNA flanking a polymorphism while the hybridization probe hybridizes to polymorphism-containing sequence within the amplified PCR product. In the subsequent PCR cycle DNA polymerase with 5' 4 3' exonuclease activity cleaves the probe and separates the reporter dye from the quencher dye resulting in increased fluorescence of the reporter.

[0053] In another embodiment, a locus or loci of interest can be directly sequenced using nucleic acid sequencing technologies. Methods for nucleic acid sequencing are known in the art and include technologies provided by 454 Life Sciences (Branford, Conn.), Agencourt Bioscience (Beverly, Mass.), Applied Biosystems (Foster City, Calif.), LI-COR Biosciences (Lincoln, Nebr.), NimbleGen Systems (Madison, Wis.), Illumina (San Diego, Calif.), and VisiGen Biotechnologies (Houston, Tex.). Such nucleic acid sequencing technologies comprise formats such as parallel bead arrays, sequencing by ligation, capillary electrophoresis, electronic microchips, "biochips," microarrays, parallel microchips, and single-molecule arrays.

V. DEFINITIONS

[0054] The following definitions are provided to better define the present invention and to guide those of ordinary skill in the art in the practice of the present invention. Unless otherwise noted, terms are to be understood according to conventional usage by those of ordinary skill in the relevant art.

[0055] As used herein, the term "plant" includes plant cells, plant protoplasts, plant cells of tissue culture from which *Capsicum annuum* plants can be regenerated, plant calli, plant clumps and plant cells that are intact in plants or parts of plants such as pollen, flowers, seeds, leaves, stems, and the like.

[0056] As used herein, "blocky" type pepper refers to a pepper wherein the length of the fruit is about the same as the width of the fruit. For example, the length of the fruit is about 0.8, about 0.9, about 1.0, about 1.1, or less than 1.2 of the width of the fruit.

[0057] As used herein, "sweet" pepper refers to the fruit and the plant of the non-pungent chili pepper varieties. Sweet peppers belong to the genus *Capsicum*, of the nightshade family, Solanaceae. The term "sweet pepper" therefore includes bell peppers (*Capsicum annuum*), the "Thai sweet"—also a cultivar of *Capsicum annuum*, the "dulce"—a popular cultivar of *Capsicum baccatum*, as well as Numex Suave Orange (*Capsicum chinense*), an unusually sweet habanero-type pepper.

[0058] As used herein, the term "population" means a genetically heterogeneous collection of plants that share a common parental derivation.

[0059] As used herein, the terms "variety" and "cultivar" mean a group of similar plants that by their genetic pedigrees and performance can be identified from other varieties within the same species.

[0060] As used herein, an "allele" refers to one of two or more alternative forms of a genomic sequence at a given locus on a chromosome.

[0061] A "Quantitative Trait Locus (QTL)" is a chromosomal location that encodes for at least a first allele that affects the expressivity of a phenotype.

[0062] As used herein, a "marker" means a detectable characteristic that can be used to discriminate between organisms. Examples of such characteristics include, but are not limited to, genetic markers, biochemical markers, metabolites, morphological characteristics, and agronomic characteristics.

[0063] As used herein, the term "phenotype" means the detectable characteristics of a cell or organism that can be influenced by gene expression.

[0064] As used herein, the term "genotype" means the specific allelic makeup of a plant.

[0065] As used herein, the term "haplotype" means a chromosomal segment defined by the combination of alleles it carries.

[0066] As used herein, the term "introgressed," when used in reference to a genetic locus, refers to a genetic locus that has been introduced into a new genetic background, such as through backcrossing. Introgression of a genetic locus can be achieved through plant breeding methods and/or by molecular genetic methods. Such molecular genetic methods include, but are not limited to, marker assisted selection, various plant transformation techniques and/or methods that provide for homologous recombination, non-homologous recombination, site-specific recombination, and/or genomic modifications that provide for locus substitution or locus conversion.

[0067] As used herein, the term "linked," when used in the context of nucleic acid markers and/or genomic regions, means that the markers and/or genomic regions are located on the same linkage group or chromosome such that they tend to segregate together at meiosis.

[0068] As used herein, "cytoplasmic male sterility" refers to plants that are not usually capable of breeding from self-pollination due to the failure of the plant to produce functional anthers, pollen, or male gametes in absence of a male fertility restorer locus, but are capable of breeding from being cross-pollinated when used as the female parent. Furthermore, the male sterility is the result of an incompatibility between the cytoplasm and the nuclear genome.

[0069] As used herein, "*Baccatum* cytoplasmic male sterility" or "BCMS" refers to cytoplasmic male sterile plants wherein the cytoplasm is from a *Capsicum baccatum* plant and the nuclear genome from a *Capsicum annuum* plant.

[0070] As used herein, a "female parent" refers to a pepper plant that is the recipient of pollen from a male donor line, which pollen successfully pollinates an egg. A female parent can be any pepper plant that is the recipient of pollen. Such female parents can be male sterile, for example, because of genic male sterility, cytoplasmic male sterility, or because they have been subject to physical emasculation of the stamens. Genic or cytoplasmic male sterility can be manifested in different manners, such as sterile pollen, malformed or stamenless flowers, positional sterility, and functional sterility.

[0071] As used herein, "uniform female fertility" refers to the production of male sterile flowers that are otherwise developmentally normal (i.e. female fertile) and produce viable fruit and seed if fertilized with a male fertile pollen source. A locus that confers uniform female fertility means that all flowers of a *Baccatum* cytoplasmic male sterile plant carrying the locus will comprise functioning female organs and non-functioning male organs, in absence of a male fertility restoration locus.

[0072] As used herein, "good flower" refers to pepper plants comprising a flower that is female fertile and developmentally normal. Plants with good flowers can be male fertile or male sterile.

[0073] As used herein, "male parent plant" refers to a parent plant that provides pollen to (i.e. is a pollinator for) a female line. They may be useful for breeding of progeny pepper plants, such as parthenocarpic seedless progeny plants.

[0074] As used herein, "resistance allele" means the nucleic acid sequence associated with resistance or tolerance to disease.

[0075] As used herein "resistance" or "improved resistance" in a plant to disease conditions is an indication that the plant is less affected by disease conditions with respect to yield, survivability and/or other relevant agronomic measures, compared to a less resistant, more "susceptible" plant. Resistance is a relative term, indicating that a "resistant" plant survives and/or produces better yields in disease conditions compared to a different (less resistant) plant grown in similar disease conditions. As used in the art, disease "tolerance" is sometimes used interchangeably with disease "resistance." One of skill will appreciate that plant resistance to disease conditions varies widely, and can represent a spectrum of more-resistant or less-resistant phenotypes. However, by simple observation, one of skill can generally determine the relative resistance or susceptibility of different plants, plant lines or plant families under disease conditions, and furthermore, will also recognize the phenotypic gradations of "resistant."

[0076] The term "about" is used to indicate that a value includes the standard deviation of error for the device or method being employed to determine the value. The use of the term "or" in the claims is used to mean "and/or" unless explicitly indicated to refer to alternatives only or the alternatives are mutually exclusive, although the disclosure supports a definition that refers to only alternatives and to "and/or." When used in conjunction with the word "comprising" or other open language in the claims, the words "a" and "an" denote "one or more," unless specifically noted. The terms "comprise," "have" and "include" are open-ended linking verbs. Any forms or tenses of one or more of these verbs, such as "comprises," "comprising," "has," "having," "includes" and "including," are also open-ended. For example, any method that "comprises," "has" or "includes" one or more steps is not limited to possessing only those one or more steps and also covers other unlisted steps. Similarly, any plant that "comprises," "has" or "includes" one or more traits is not limited to possessing only those one or more traits and covers other unlisted traits.

VI. DEPOSIT INFORMATION

[0077] Deposits of seeds of *Capsicum annuum* lines designated 'Flame Fountain' and 'Ganti,' which are disclosed herein above and referenced in the claims, were made with NCIMB, Ferguson Building, Craibstone Estate, Bucksburn, Aberdeen, AB21 9YA, Scotland, U.K. The date of deposit was May 29, 2018 and the accession numbers for those deposited seeds of lines 'Flame Fountain' and 'Ganti' are NCIMB Accession Nos. 43054 and 43055, respectively. All restrictions upon the deposits have been removed, and the deposits are intended to meet all of the requirements of 37 C.F.R. § 1.801-1.809. The deposits will be maintained in the depository for a period of 30 years, or 5 years after the last request, or for the effective life of the patent, whichever is longer, and will be replaced if necessary during that period.

VII. EXAMPLES

[0078] The following examples are included to illustrate embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples that follow represent techniques discovered by the inventor to function well in the practice of the invention. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

Example 1. Creation of a BCMS *Capsicum annuum* Plant

[0079] The compatibility between *Capsicum annuum* and *Capsicum baccatum* for interspecific crosses is very low. To transfer genetic information between these two species, intermediate pepper species, such as *Capsicum chinense* or *Capsicum frutescens*, have been used as a 'genetic bridge'. However, this method only allows for the transfer of nuclear traits. To develop a BCMS plant where a *Capsicum annuum* genome is introduced into a *Capsicum baccatum* cytoplasm, it is necessary to pollenate a *Capsicum baccatum* flower with *Capsicum annuum* pollen. These combinations never led to viable hybrid seed and it was therefore necessary to use embryo rescue techniques to recover a *Capsicum baccatum*×*Capsicum annuum* hybrid. The method described herein was used to develop *Capsicum baccatum*×*Capsicum annuum* hybrids from several *Capsicum baccatum* accessions, such as PI497974, PI159242, and PI640880.

[0080] Plants of these *Capsicum baccatum* accessions were grown simultaneously with *Capsicum annuum* lines that served as pollen donors. Flowers on the *Capsicum baccatum* plants were emasculated before the anthers shed and subsequently pollinated with the *Capsicum annuum* pollen. One day after the first pollination, the pollinated flowers were dipped in 200 mg/L NAA (1-naphthylacetic acid) followed by a second pollination after the NAA solution (growth regulator) had dried. The flowers were then left to develop fruit. Ripe fruit were harvested and seeds were extracted from the fruit for embryo rescue. The embryo rescue was performed under aseptic conditions by dissecting the embryos from endosperms. The extracted embryos were cultured on MS media until seedlings had fully developed. These F_1 seedlings were checked for *Capsicum baccatum*× *Capsicum annuum* hybridization using polymorphic DNA markers. Seedlings that were true hybrids were selected for further backcrossing to the *Capsicum annuum* parent. Early backcross generations were selected phenotypically for male sterility and the *Capsicum annuum* recurrent parent phenotype and the genome was evaluated for *Capsicum annuum* percentage using polymorphic DNA markers. In later generations, additional horticultural traits were used to select plants for advancement.

Example 2. Mapping of the Male Fertility Restorer Locus

[0081] After extensive crossing and evaluation of F_1 progeny, two *Capsicum annuum* accessions were identified that can restore male fertility in BCMS lines: 'Flame Fountain' and 'Ganti'. The ability of 'Flame Fountain' and 'Ganti' to restore male fertility in BCMS lines was later validated by remaking the F_1 populations. Two F_2 populations, BCMS Donor Line 1×'Flame Fountain' and BCMS Donor Line 1×'Ganti', were developed by selfing male fertile lines from these F_1 crosses. These F_2 populations were used to map QTL associated with male fertility restoration.

[0082] Individual F_2 plants from both populations were genotyped and evaluated for fertility in the greenhouse. Fertility was determined by the presence or absence of normal anthers and visible pollen in the flowers, although flower formation, fruit set, and presence of seed in the selfed fruit were also noted. QTL Cartographer was used to run a single marker analysis on both mapping populations using the presence or absence of visible pollen to determine whether fertility was restored in individual F_2 plants.

[0083] The BCMS restorer locus (Rf) from the two *Capsicum annuum* lines mapped to the short arm of chromosome 6 in both populations, between the consensus positions 24.2-32.9 cM (2-LOD interval) in the BCMS Donor Line 1×'Flame Fountain' population and the consensus positions 17.2-45 cM (2-LOD interval) in the BCMS Donor Line 1×'Ganti' population. Rf was found to be completely dominant since the Rf/rf genotype provided male fertility and recombination was suppressed on the short arm of chromosome 6. The Rf locus can be tracked in the population via marker assisted selection by detecting the haplotype associated with the Rf locus (Table 1). Further fine mapping reduced the genomic interval restoring fertility in BCMS lines to a region flanked by M14 and M29. It was determined that markers M18, M19, M20, M21, M22, M23, M24, M25, M26, M27, and M28 are comprised within the region where the restorer factor is located. These markers should therefore comprise a haplotype corresponding to the Rf locus donor line. Markers M14/M15/M16/M17 and M29, which flank the chromosomal interval, may be used to select the recurrent parent allele. Depending on the Rf locus donor line used, M14 may be used if 'Ganti' is used as the Rf locus donor and M15, M16, or M17 may be used if 'Flame Fountain' is used as the Rf locus donor.

TABLE 1

List of markers and favorable alleles at each marker for tracking the Rf locus

Marker Name	Marker Sequence (SEQ ID NO)	Favorable Allele 'Flame Fountain'	Favorable Allele 'Ganti'	*C. annuum* Genetic Position (cM)	SNP Public Position CM334v1.55 (bp)	SNP Position in Marker (bp)	SNP Change
M1	1	—	G	17.2	213,924,156	93	A/G
M2	2	—	T	17.2	213,907,080	243	C/T
M3	3	—	G	17.9	213,907,920	2353	A/G

TABLE 1-continued

List of markers and favorable alleles at each marker for tracking the Rf locus

Marker Name	Marker Sequence (SEQ ID NO)	Favorable Allele 'Flame Fountain'	Favorable Allele 'Ganti'	*C. annuum* Genetic Position (cM)	SNP Public Position CM334v1.55 (bp)	SNP Position in Marker (bp)	SNP Change
M4	4	—	C	18.8	427,239	216	T/C
M5	5	G	G	19.1	428,143	287	A/G
M6	6	—	C	20.8	87,022	117	T/C
M7	7	T	T	20.8	125,861	93	C/T
M8	8	T	C	20.8	89,795	484	C/T
M9	9	C	C	21.8	386,489	313	T/C
M10	10	A	A	22.8	26,405	1149	C/A
M11	11	G	—	24.2	3,055,268	188	A/G
M12	12	A	C	24.2	3,009,771	387	A/C
M13	13	T	C	24.9	2,999,718	330	C/T
M14	14	T	G	25.7	3,504,248	294	G/T
M15	15	A	—	25.7	3,500,133	41	C/A
M16	16	G	—	25.7	3,505,583	98	A/G
M17	17	T	—	26.3	3,308,938	523	C/T
M18	18	G	A	26.4	3,475,770	779	A/G
M19	19	T	G	26.4	3,422,765	592	G/T
M20	20	A	T	30.2	4,276,008	279	A/T
M21	21	A	A	30.2	4,240,789	534	G/A
M22	22	C	C	30.2	4,245,699	279	G/C
M23	23	—	G	31.8	70,994,266	49	A/G
M24	24	T	T	32.4	4,240,551	287	A/T
M25	25	A	—	34.7	6,240,565	275	G/A
M26	26	T	—	34.7	6,241,544	30	C/T
M27	27	—	G	35.0	8,522,176	1140	T/G
M28	28	G	G	35.0	9,799,932	182	A/G
M29	29	T	T	40.8	10,670,362	246	C/T
M30	30	C	C	40.8	10,664,163	33	T/C
M31	31	T	T	42.2	10,664,630	142	G/T
M32	32	C	C	43.0	11,108,817	1613	T/C
M33	33	C	T	44.0	11,592,142	146	C/T
M34	34	—	C	48.9	21,133,217	285	G/C

[0084] In addition, to have uniform female fertile flowers, BCMS plants should have the Good Flowering (Gf) locus, which is a dominant *Capsicum baccatum* allele flanked by marker sequence SEQ ID NO: 35 and marker sequence SEQ ID NO: 36 on the short arm of chromosome 6. The Gf locus can be introgressed into BCMS plants from any *Capsicum baccatum* line and detected by using markers that flank the Gf locus (Table 2).

TABLE 2

Flanking markers and favorable alleles at each marker for tracking the Gf locus

Marker Sequence (SEQ ID NO)	Favorable Allele	*C. annuum* Genetic Position (cM)	SNP Public Position CM334v1.55 (bp)	SNP Position in Marker	SNP Change
35	G	1.9	3,064,350	358	A/G
36	G	35.7	21,133,217	285	C/G

[0085] The identification of the Gf locus and genetic markers associated with the locus is described in U.S. Provisional Appln. Ser. No. 62/690,722, filed concurrently herewith, the disclosure of which is incorporated herein by reference in its entirety.

[0086] F_1 progeny from the crosses BCMS Donor Line 1×'Flame Fountain' and BCMS Donor Line 1×'Ganti' have genotypic segregation of ½(S)Gfrf/gfRf+½(S)gfrf/gfRf and phenotypic segregation of ½ completely fertile+½ completely sterile. This segregation occurs in the F_1 because the plants of BCMS Donor Line 1 (or any other BCMS line) that have female fertile flowers to facilitate crossing have the heterozygous genotype ½(S)Gfrf/gfrf: The F_2 progeny are created by selfing F_1 plants with complete fertile flowers, (S)Gfrf/gfRf. Thus, the expected genotypic segregation in the F_2 progeny would be ¼(S)Gfrf/Gfrf+½(S)Gfrf/gfRf+¼(S)gfRf/gfRf and the expected phenotypic segregation would be ¼ male sterile+½ complete fertile+¼ complete sterile. However, the observed genotypic segregation in the F_2 progeny is ½(S)Gfrf/Gfrf+½(S)Gfrf/gfRf and the observed phenotypic segregation is ½ male sterile+½ completely fertile. The completely sterile plants are missing from the F_2 progeny both phenotypically and genotypically, indicating that the gfRf genotype is not transmissible via pollen (male gamete) from BCMS plants. The F_2 progeny in both mapping populations had normal germination rates of 92% which suggests that the underlying failure of gfRf transmission occurs early in the reproductive process, before seed formation.

Example 3. Genetic Model of the Male Fertility Restorer Locus for BCMS

[0087] There is a dominant nuclear allele present in some *Capsicum annuum* accessions, such as "Flame Fountain" and "Ganti", that restores male fertility in the presence of the *Capsicum baccatum* cytoplasm. The dominant *Capsicum annuum* allele is denoted as Rf, and the recessive allele is denoted as rf. Gf functions upstream of Rf, such that the gfgf genotype masks the male fertility restoration effect of Rf (i.e. recessive epistasis). This is consistent with the observation, represented by formula (I) below, where (S) denotes a *Capsicum baccatum* cytoplasm and (N) denotes a *Capsicum annuum* cytoplasm, that restored F_1 progeny from the BCMS Donor Line 1×'Flame Fountain' and BCMS Donor Line 1×'Ganti' crosses segregate for 50% completely fertile flowers and 50% completely sterile flowers, even though all of the F_1 progeny are heterozygous at the Rf locus:

Parental cross: BCMS Donor Line 1: (*S*)Gfrf/gfrf× 'Flame Fountain' (*N*)gfRf/gfRf→F_1:½(*S*)Gfrf/gfRf (completely fertile)+½(*S*)gfrf/gfRf(completely sterile) (I)

Example 4. Utilization of Uniform Female Fertility and the Male Fertility Restorer Locus for BCMS to Produce Hybrid Pepper Plants

[0088] Gf and Rf are tightly linked in repulsion on the short arm of chromosome 6. Therefore, the gametes Gfrf (*Capsicum baccatum* haplotype), gfrf (*Capsicum annuum* non-restorer haplotype), and gfRf (*Capsicum annuum* restorer haplotype) exist, but the recombinant gamete GfRf does not exist and cannot be recovered readily in segregating populations. Furthermore, the gfRf gamete is not pollen transmissible from plants that have the *Capsicum baccatum* cytoplasm, as these gametes are generally not viable. This is consistent with the observation, represented in FIG. **3**, where (S) denotes a *Capsicum baccatum* cytoplasm and (N) denotes a *Capsicum annuum* cytoplasm, that F_n progeny derived from restored F_1 plants (e.g. BCMS Donor Line 1×'Flame Fountain') segregate for 50% completely fertile and 50% male sterile plants.

[0089] Under this genetic model, the possible genotypic combinations and associated flowering phenotypes that can be observed are shown in FIG. **1**.

[0090] Using the genetic model of BCMS described herein, it is possible to design a breeding system that allows easier production of pepper hybrids. In the female pool, the breeder maintains two types of germplasm: an "A-line", which is a line that carries the *Baccatum* CMS trait and a "B-line", which is in the same breeding pool as the A-line, but comprises *Capsicum annuum* cytoplasm. The B-line is the backcross parent for the A-line. The male pool contains *Capsicum annuum* germplasm lines that are homozygous for the Rf allele. Fully fertile hybrids may be produced by crossing the A-line as the female parent and the C-line as male parent (FIG. **2**). Due to the male sterile nature of the A-line, it is possible to produce hybrids that do not contain off-types due to selfings. Furthermore, labor is reduced because the female plants do not need to be emasculated.

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gcaaggatta aactaagaaa tcaaactgaa tcagaaataa cagaaggaag caaaagactg 1800

ttacatgtga ttcatatttt aaaagcaact cttcatacac cctttgaagt tccaggaaat 1860

cactgtcttc ctgccaaaat taaaaaataa taacacaaca gtggtataat acaattttga 1920

aagaaagctg aaatagcagc gcgaagtgtg aaccattgag aagctttttt tcctagaggc 1980

tccttttctc ctgctagtga catgcaacaa agcccgcggg tcagggagag tacagtcttc 2040

agcttgatta ctccttgcat tgtcttcttg cttgccagag tctaaattga tgtcaacatc 2100

taatagttct tcaaaaggaa gtaagggtcc aatgtcacgt tcaagccttt tggctttgac 2160

<210> SEQ ID NO 11
<211> LENGTH: 493
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 11

accgtgaggg atgcttttgt atatactgta aagccagtct taagtccaaa tatctgaagt 60

tggtttcgcg acttgctatg cttattgttt ccaagtaatt ttgttctgaa tggttgtttt 120

tagtgttgta atttgtaaat gatgatatgt atgttcttct acagaccgaa agttctggag 180

gttcaccaga gcaggatttt gtccagaagg catttgagat tcatgacaag tatatggtgt 240

atgtgaaagg ctgttttgct gataacacta tctttcacaa ggtattccga ctgttaactg 300

ctgtacgctg atccctttta cgatgaatta cttgagacgt tatatagtta tgttcagtgt 360

tgtcgaaggt gcacataaga cctgaatcga ggctcaaatg tgtttgagag tttagcgtcg 420

cttaatgtgc acatattcct ctgaatggtt ctcttaggct gatgtataaa ctctttgact 480

ctcataggct ctg 493

<210> SEQ ID NO 12
<211> LENGTH: 516
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 12

tgctattgag gatacattgg ataaggtatg cacaaatttt acatctccga tcaatttggt 60

ggtcgaactt catatctttg ctcaaacatc gtcaaaattg tgtacttttg ttaggtggtc 120

aagcttgtga tgtacatcag cgacaaagat gtgtttgctg agttctacag gttggaattc 180

agtgccagca gttgttttga catctttaac catttgatat gctaactgtc ttaatactta 240

taggaagaag ctttctcgcc gattgctttt tgatagaagt ggcaatgaag aacatgaaag 300

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gcttatctta tcaaagctaa aacagcagtg tggtggacag tttacatcca agatggaggg    360

aatggtaagg attgttcaat ggacttagaa agttttgtct ctttaccgcg cttgagatat    420

ctgaaaacga atgactggaa atgtaaaaca ggtaacagat ttgtcattgg tgaaggaaaa    480

tcagactcac ttacaggaat atatcagtaa caaccc                              516
```

<210> SEQ ID NO 13
<211> LENGTH: 1880
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 13

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gttccatgta tttctggaaa acagatggta caagggtggg tttaaggaaa gggtaatttg     60

gtaaacaaac attttttac aaaatttata taaatatata ttatctttaa tacatcaaac    120

caaacaatgt gtaaaaacaa atgtatgtgt aactaatact agcattacta ctacttgcat    180

taataataca agcattacaa ataccccta tttagcatta ttcttataca ctctaccaaa    240

cgacacccta agcactttgg catgtacaaa tactacctac catacgatct tttttaacac    300

aaaactttca tgcttgcaac agttttttgc atgtcgtctc aatgaatgaa ccaagttcaa    360

attaaaatgg gaactcactg gcagagtttt gcagtgctgc tatagattct ccttgactgg    420

ttccgttcac catgcttgga gctgtctaat tctagtaagg aggcaccatg gagaaacttt    480

aatgccgctt ggaaatagat acccgtactt tcacttgatc cagaactctg aaccaaatag    540

ccaaagtcaa cataaaataa ataaatgaaa caaataagaa agcatatcca ccatattttg    600

tcccctcctt tcttaggaca taagtgtaaa ttcttttaac cttgagacga tctgccagat    660

gttttaggtt tgtggcttct tttatggcat ttgtagcagc ttgacttgat gaatccttct    720

gagcagggct gggaacatct tgatccctga ccttattagc agtattatta ggtaggtttc    780

catggtggct tttagctgtt ttaccctgtc ttgaagcatt tgacttttcc ctttcagaag    840

catcaactat aacacaattt gcctcgtttg cccgtccgga tccaggaact ggctctttaa    900

atacaaccgt ctcattctga actcttgtta atggaaactt ggaagagact tcaatctgct    960

cacttctgtt ggaaacaagc ttcttagatg atctctgatc atttcgatct ggtagtgcag   1020

cctggctttt atccaggcgg gatgcaacat ccgatcgagc ttctgcacca tcatgatgac   1080

caactcgtgg ttgattatca cctttaacat ttttgtccaa taattttcca gatgaatcct   1140

tcttagaact cttctttaat ctatctgaac caacaacatt ctcctgaaac ttgtttttc    1200

ctggtgccgt cttctcctcg tctaatggca tttgatctga agataaattt aaaatatcag   1260

gatttttggt gttacattgg tcagaatcag attctggagc ccgattcttc tctttgcgcc   1320

gtgacaaaga acctctttta ccatttgaga caaactcact atcctgacac tgatagtcat   1380

tctttctctc cttatcagag ccttggtctg agtttctgt cttgcaagaa aattgaccaa    1440

cttgacgtaa tggatcggca tttacatcag catccagatg agttgcataa ccagagacca   1500

tggtctttgc tttaactgtt gtatctgatt cacgatggac atctttctcc tctaaatcag   1560

cttcagctaa cacaacataa ctcgtgccat tgcatgcact atccttctta acaaaactgg   1620

attcatttga gaacccatca ttttcaccat cagaagacct cttgggactt gaagtgggaa   1680

cagctgatga ggcagcagca gaaggccgtg aattgcctag atcctttttg aagaatctgc   1740

agcttttaca ctctgcaaag atacagtgag atcttgccca gcctgctgtt ccttttaac    1800
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tcgacatgtt ccagcactac ctttgcttgc gctagtgtct ttccggtcag acttggagac 1860

ccttgctttc ttttccttcc 1880

<210> SEQ ID NO 14
<211> LENGTH: 2286
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 14

gttaggggaa gtacaaataa atcagcaagg aaaagacaag tccatttcat attgcagaaa 60

acatgttttc cacttcataa gtaggccatc atagatctat aagggattat tgatcattct 120

agtgatagtg ttcttaaccg ttactaacaa agatgaagga tatgtatagt tcttggtgtt 180

agtatgccca tgagaattgt aagatgggat tttagtttca ctataagctg catttttgtt 240

tcacctgtaa catcttctgc tatctagatt ggacattgtt ttggtctaca gctgatgaac 300

tttgagcagt ggactacgct tgaaatttta aaattatcca ctatgctgat ttttacgcat 360

taccataact aactgcattg cggtgaaaac tcaatgcatg tccttaagcc gtaggttgct 420

ttctaatcag caaacaagtt tggtgaacaa gttctctgaa tctatccatt ggttatcctt 480

gtctcgacaa gctagttctt tttccttttc tattctgttt gaattatatg agtcagcaaa 540

gtatagattt tgaaggagtt caagtaggaa atattaccgc tttggaaatt tacagatttg 600

cttttaaaac tttaattatg tgccacaagt ctagcttttg gaaatattta acatgcttct 660

tgaactgggt ttcataatgg tcaagtgccc atgaatttta ttttttctct tccgctgaat 720

acattatcaa acttcgaact tgaatcttca ttactttgca gacaactaga gtatttgctc 780

cttggctcaa taatgcaagc ttagagaatg aagaatcttg gcatgaaatt gctcgccctc 840

aagttcatgg tcatgacata aattgtgtga cagtaatcaa aggaaaagga aaccatcgtt 900

ttgttggcgg ggctgacgag aaagttgcca gagtttttga atctcctcta tcctttctga 960

agacattgag ccatgttact tcagacagct ctagtttttc tgccgacatt caagctgatg 1020

tgcagatatt aggggcaaat atgtctgctc taggtctatc gcagaaacct atatatgttc 1080

agggtgagtt ttccagtcta ttgtgtggta tcaattttgc ataataacat ataagatact 1140

cctattcatt tatgtttcca tcatcacttt tgatgttaca gggtgatata taactgagtt 1200

gttgacttgt caaaattaac tgtaaagacc ttctcttaac catgtattga attagaatta 1260

atgtgatgtg ttaccgactc tttctctaag tttgcttaaa gtgctgtgat atctgatgca 1320

aagtgttctg actttgatac aaacagcgat tatcctgaat atttcgtttg aggactctta 1380

tatgttataa tatctcatac atctaagcct atcttttgca gcagcatcga caccaacaga 1440

cagaagcaat acggaaggtt ttgatacact agaaactgtt cctgaagcag ttccagttgt 1500

cttgacagag ccacctattg aagagcagtt ggcatggcat actctatggc ccgagtcgca 1560

caaactttac ggtcatggga atgagatttt tgctctatgt tgtgatcagg agggaaagct 1620

tgtagcttca tcctgcaagg tttttctctc tttccctttt ctcctccttt cttttgggtg 1680

ttggcatggt tcttccttgt ctgtcttgaa tcttctgtta atagcattca acttgattgt 1740

acttttgcta agtgccctga taaagttggt ttttagtttc tggtcttaat atacttcgat 1800

agaaaaaaaa ggtagtactc cattccatat atggtgtcaa tttttttcaa tatcttgacc 1860

attagacgcc cctattttat tggtggatgg ggttagttaa ggaatagctg ggtttgatcc 1920

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tgcggcattt tctctcttat gagaaatcaa acgccaatct gctcatttta tataacttac   1980

tggtgatgct cactacctcg gacttttacg ttgttagaga cctctatgaa ctatagcaac   2040

acatgatgga attcacaata ttcttctaga tactcctttc aacttctaat gatttttttg   2100

ggggaagtct ttattttctt aattagttgt gtctatcaga aacactctct ctacctccga   2160

ggtaggggtg acgtgtgcgt gcgtacactc tacccttcct agacctcact ttgtgtgatt   2220

acactggaga tgtttttctg ttcttattta attgtgaata ctaattatgc tggggctata   2280

taatcc                                                              2286
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<210> SEQ ID NO 15
<211> LENGTH: 358
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 15

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gattccgtaa tcactctaac ggctgaaata tatctgattt agtgcttttc ggttcattat     60

aatcagtaat ccagccagta tgggtgacgg tcatgtcaat aatctgaaat gttatctgcc    120

tttttctgta atactatagt ctatagtatc atttatgtgc accaagagag cgaactaagc    180

atcaatccac gcagctattt ctgtttaaga atttaggcta agtagatttt tgtgccagta    240

aatgttttac tcttttagtt tctaagttga aggtgattca ttaattactc ttttagtttt    300

taggttggag gtaacctcta tgcagattta gttgggttta taaggatgca attatatg      358
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<210> SEQ ID NO 16
<211> LENGTH: 1273
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (470)..(470)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 16

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tgggggcatc tctatggccc gagtcgcaca aactttacgg tcatgggaat gagatttttg     60

ctctatgttg tgatcaggag ggaaagcttg tagcttcatc ctgcaaggtt tttctctctt    120

tccctttttct cctcctttct tttgggtgtt ggcatggttc ttccttgtct gtcttgaatc    180

ttctgttaat agcattcaac ttgattgtac ttttgctaag tgccctgata aagttggttt    240

ttagtttctg gtcttaatat acttcgatag aaaaaaaagg tagtactcca ttccatatat    300

ggtgtcaatt tttttcaata tcttgaccat tagacgcccc tattttattg gtggatgggg    360

ttagttaagg aatagctggg tttgatcctg cggcattttc tctcttatga gaaatcaaac    420

gccaatctgc tcattttata taacttactg gtgatgctca ctacctcggn acttttacgt    480

tgttagagac ctctatgaac tatagcaaca catgatggaa ttcacaatat tcttctagat    540

actcctttca acttctaatg attttttttgg gggaagtctt tattttctta attagttgtg    600

tctatcaaaa acactctctc tacctccgag gtaggggtga cgtgtgcgtg cgtacactct    660

acccttccaa aacctcattt tgtgtgatta acactgggga tgttttttct gtttctattt    720

aattgtgaat actaattatg ctggggctat tatatcctgc aggtcaatca ccaccattgt    780

tgaaatatgt tatgggcagt tgggttctgg aaaatcattt ggtcttttgg cattccaaat    840

ttaaaagtga ccccaaggga tttccccatg aaaccaattt ctcttggcct ttaaaaaaac    900
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ccctttttg ttttttaaat taatcaaaag gtttgaacat ttaccaccct cctttgccaa 960

aaattttaaa aaatacaaaa ccaaaaattt tttttccccc accccaatgt ttatatatac 1020

tgttaatata aaacttttct cccttttgga agtttttttt agaaaaacct ttctactttg 1080

gagagggaag agcctggcca actccccccc aaaacccccca cggtgtaaaa ttttattttc 1140

tttcctcccc cccctccacc ccccctcctc taccaccccc ctaaaataat ctcccttttt 1200

ttaatataaa aaacaaaaaa aaaaaaccct cctcttttta accccttccc cttaaatttt 1260

ttatttcccg cca 1273

<210> SEQ ID NO 17
<211> LENGTH: 1253
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 17

gcagaaatta aaatacacag gtaagataag tgggaagcaa catctaattg ggatttttct 60

tttcctttca tatttacaga ttgttttgta tttagacaaa ggagaaaaaa atctaaaaat 120

aacagatagt ggcggagcca cctttgctcc aggggttcat ctgaatccct cgatggaaaa 180

ttttaccgtt tttataatat ttttacatgg ttaaaaatat ttttattcat gtatagtaga 240

tgttgaaccc cgttcgacta gttcgtattt atacttccgt accccctcaa tgaaaaattt 300

ggctccgaca ctgataacag aatgtgatat agacaaacaa caccgtcaga ttttcctcta 360

tttataatgg acttgttgtt atttactgtg caatcaaact aacctttcct ggttagctct 420

tttcatgaaa cttatccaca tgcaagacta cagtacttga aacagataaa agtggtacac 480

ttgtcttagc agatcaacta atgttgcact ctggatacga ctccagtggc gggcttgtta 540

aaacctgcag gaataacatg tgaaatttca aaactttcaa gcattcaaca aatatcatct 600

caagtgttga aattccaaag tatatgtcct gaatcttgct ctaatatcca agaaatttaa 660

ataataaaaa aaaaactacc ctaggacgat atatgtagtc tgccgatatg atcttcttta 720

gagcagtctt ccaaggatgt gataggggat tgaaaatggg aacatagaag aattgatgaa 780

aaaatttcca agagttcaaa ttatttctac tggtgaggct gttcatagtt cagataagaa 840

gtgtaccaac aatgcaagtt gcagcaatat ctttgctgtg cctgcactca atattgagac 900

atccttcttt cgaatacatc tacgcattca caatgaaccg ataaataaaa gatttgttaa 960

atactgatca ttttcagatc aagattatcg aaagatcact tgaatggttg ttaattttaa 1020

aatggtaaca aaagggagat agcaagtcca tttcatgaaa ctccacaatt acagcgtatt 1080

tgacattgaa aaggcaacat atatgcaatt aaaaaaaaaa agaaatgagt ctacatcttt 1140

tcaaatacaa aagaaaatca aactcaccat ataaagtcta ccaaaagaaa gtgacatagc 1200

accgaagata tatggactcc ataccaccct ttactctgat aaagaagcag tcc 1253

<210> SEQ ID NO 18
<211> LENGTH: 1323
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 18

ctaaaatttt agcgtatttt tgtcaacctt tttaactgac atagcacctt tttagctaac 60

gtggcacctt tgacgtggcc cccattttta tgtaataaag gtgccacgtc agcacaaaag 120

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agtgacaaaa atacgctaaa attgagttcg ggggataata ggaccccgtg aagttggagt 180
gtgtcatagc aactttggtc ataatacaag gggtacaag atgcttatct cgaagaaaaa 240
tgaaaaatca caagcgcaac gtactttata tgtcagagtg tagcgagtgc acttcaagat 300
gtataataat ttgctcgagg atacagtact aattgaagcg aattacatcg tttcccctat 360
ctatttaata taagaaaggt tttgccgaag aattgggtga aggtgattag acatgacatg 420
acacaacttc aactgaccga ggacatgatc ctatatatga aggcatggag gtcgaggatt 480
agcgtcgaac gttaataggt agacacaagt tgtcatactt ctagtaggat gatttaggta 540
tcacgtagtt tttcccgcct atgttcatta ataactgttg ctatacttgt tttgtgtatt 600
gtttttctgt agtctctctt ttttctctta cttccttgct tttttgcgcc gagggtctat 660
cggaaacaac ctctctaccc cacaaagata gaggtaaggt ctgtttacac tcgatttact 720
gagctcggtc gaggttaagc tgatagctca gaacttgaat gtatattcgt tggtcataat 780
caatctccga accagatcaa cagctccgac accaaggtag ttgagttaag actagcacaa 840
ctttaactaa gctcgcaact tctagtaaag gacgcgtggt tgtgaaacat ggcctgtagg 900
ttctttgttt ttctttgaat aaccgagaaa tatgttgttt ttatcttcaa aactcggtgg 960
atgtttaagc cccttttctc tatctttctc cgtttaaata ccaaacttaa ttcaccgata 1020
gaatttgagc tcatgatgtg cgcctactac acattcttct tctaacaagc atgcgagtga 1080
caggaaaggg cagtaaggaa acaaagaaga tcatatcaaa agaaaatgtg ggcgaacctg 1140
gttgattcct cggtcctttt tccagcaatt ttgcccttgg gagccgctga caactgtaaa 1200
gattagaaca cgggatcttc aactcctctc ctccttgtaa gtaagaagac tagttgtttc 1260
actgtaacta ataatgaaac actaacctgt gaggcaatat cgattccaat ttcatcgagg 1320
acc 1323

<210> SEQ ID NO 19
<211> LENGTH: 786
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 19

actccatttg aactcatctc gttccaatgt tatgtcaata cagataaaag cttccacctt 60
gagtaggggc aattttctga aacatatccc ccgctacaaa gtccaaattt tcacttcctt 120
gcagattagc cacgacaggc ggaagatcaa gaacaataca tttcatgtca gggaattttt 180
ttgttatggc cattgcaaca gtaccatttc tcctccaaca tccactaaag atgtcaatcc 240
tctgaaaaca tccttaaact cgttgccaat cagtacgtta atgaatgatt gcgaatctct 300
agccatgttc gcgtgaaacc agttaccact actcgtatct ctcgaaagtt tactccagaa 360
taaatctcca tatgctgtgt aaaatgcatt tggatcctca tttctgaacc aatcacctaa 420
acagttcgat ccatgcttta aagaaaaatg aatcttgatc ttccatcaag ttccaaggcc 480
catccttcat tatatatcgg tcagctagtg caaccgaata ataccctttta ccatcatcac 540
catcgtccac attgttgtct tcatgttttt gtagaatcaa caagccataa cgaactacta 600
ttggtgtaag gcggtgaaag tcgggattat ttgaagggct aatagacagg gaagacatga 660
gttttgatag tgtcattggt tttccttgtt tggttaagtc attaggtatg cctaattgaa 720
gtgcacattt caatgttatg gtaaaagata tgatgaattc aacaaacgtt gacacttatt 780

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attttc 786

<210> SEQ ID NO 20
<211> LENGTH: 597
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 20

ggcaaattgg tacttctatc catggaaact attgcagatg ttccataacc aggtagatgt 60

gaagtagatg tttgagaagc aagtgagaag tgtgaactcc tctctcgaac agagggagaa 120

gtgtgtcgtt tatgaatact accatcttcc tcatttatga tctgcacaaa tcacaatagt 180

tccacacttt actccacaac atcggcctta aagactattt cggaaaagat gcccattatc 240

tgtcttggaa ggatgctggc agtaatttat aagagaaaag agagtaccct ttggatagca 300

ggatccaagg acgaaagcaa acgcctagaa cgttctggcc aagttcttgc aaacattctg 360

tacaaaattc ttgcagttga tcggacctgt tgttaaatcc aagggatatg aattgccaac 420

agatcttgaa tcgaattaaa gggggtatac atgcagataa ctatgccaaa atatgatact 480

cagagttcaa caagcatacc tcacccattg catcagagac acaacacttt ataaggtctt 540

catagagctc tgctgaacgt tgtacctcag atgcatcagg ccaatgttca aggatca 597

<210> SEQ ID NO 21
<211> LENGTH: 1085
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 21

ggatccacga acctaataag caccctccat ggatacctcc acaaccgctt cctcccatcc 60

acgcaacaac atgcctagtt caatcgcaca aaaggggtct agggagagta gagtatacgc 120

agaccttacc cctaccttgt agagataacc aaaaccctaa aacaatggat caaaactcct 180

gtttcatata gcctctaaaa ccccgcttag cccagtttct gcccctctga cctctggtcc 240

actgggacct tgcctaccca tatagccact tgccaatgga aaactggcta ctcagatgga 300

tgcaagacca atttgataat ggaaacctca tagcacgaaa ggcaaagttg ttggttatcc 360

taaaaataaa agcgattata ctcaaacgaa aaatgtcatg actgatatct tcataaaaat 420

cttggttcat ttacacattc atagtatact tacaacgaaa gtaataaaaa caaaggtaat 480

atactacctc aacagaaatg gggttgagtt tgagacagtc gaaactacaa tgaattttca 540

ccttcttgct ttcttttata gatttcttaa ctttttaaat gaagatgcac tagatacttg 600

tactaaatag tccaatagca agatgtatca ggagggactt tggtagcaga tctaatctag 660

ctgaggatgc tacattatcg aagttgcaag aggcgctaat acaataacaa cgacacacgt 720

atagcaaatc tggtttctcc gaaagagagg aggagccttg aaacaacgat aaagttgtct 780

ccatggttca agccgtggaa ttaaccgctg atgcttgtta gagtaggctg cctacattac 840

acccctcagt ttgcgaccct actcggacta tgcgtgaatg caggaagctt catgcaccga 900

actagctttt ttagttctcc ataaacccat acgtcaaaga gaaggcttgt tgagtatcaa 960

agttatcacc acaaatgcaa atggcaattg aatgcaatgc accatcacca gcaaaagaat 1020

agacaagcga caaccaaata cggcagcata aaacaccaag gcaataaact tcaatctaca 1080

gttgc 1085

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<210> SEQ ID NO 22
<211> LENGTH: 756
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (756)..(756)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 22

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gccaacaatg ggaatgaaca tggggatggg gatgagtatg gaaatgggca tgaatcggcc 120

aatagttcct tatcagccgt taatgccaag tccagcaatg cagaatgcag ctgcagtagc 180

acaaatggct cctagatatc ctcttccggc atatcatttg ccaccatttc ttgcacctga 240

ttcatccaga atccctgttg cgaatcagcc agatcctccg aggctaaact cacttgttgg 300

acataatacc aatcagccaa aacttccgca ttttgctgat tcatatgatc aatattttgg 360

tctccagcag gcacgactga tgttacccca ggcaagtcct tgttcttctc acacactata 420

tttatttatg tccttcaccc attgatattg caccttaacc tcattactgt tcacacccac 480

ctaattgtga gatactgatg aaactcacta acctgactaa tccaaattaa cgcatattta 540

tattatcgtc atgataacta cgttcatgta gaaattatca tctagaatat catcttgcaa 600

cataaactaa actctaaact gtggtcagct gcctacaaca gcttgtttca tcacctcaat 660

ttattgcacg ttcttccaag aaatcttttg acaattcatt gtattgaaat acaggataag 720

ggagtggaac agctgaactg cagtaaaccg aacagn 756

<210> SEQ ID NO 23
<211> LENGTH: 481
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 23

ggtgtcaaag aggcacctct ttgtccattt gttgtatccc ccgacacaac atgagtagaa 60

gttacttcct gatctccgtt ctcaccttgt ggtgcagcat ttagatccac atttagcacg 120

gtatttcttc tcgagttgga ccttgtacgc ttattttgtt gtgcccttct atctcgggta 180

ctcatgttat gctcagttgt accctaatta aaacaggaaa agacggaaaa atttgaagtc 240

atgatagggt ttatattctt aataatctat tacctcaaaa agcaagaata aaaagaagta 300

gtagtaatgc aagtatctca aatttactaa atatacttcc gcatgagcta ttacagtgga 360

ccttaacata caccacggcg atcaatgaat agacttgcaa attgtatgtt ttcaagaatt 420

ttagcaagtt gtatttacat tggctgcga tctggaaagc aaagcatgga catcggaagt 480

g 481

<210> SEQ ID NO 24
<211> LENGTH: 554
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (154)..(154)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (195)..(195)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (217)..(217)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (469)..(469)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 24

ggtgttttat gctgccgtat ttggttgtcg cttgtctatt cttttgctgg tgatggtgca 60

ttgcattcaa ttgccatttg catttgtggt gataactttg atactcaaca agccttctct 120

ttgacgtatg ggtttatgga gaactaaaaa aagntagttc ggtgcatgaa gcttcctgca 180

ttcacgcata gtccnagtag ggtcgcaaac tgagggntgt aatgtaggca gcctactcta 240

acaagcatca gcggttaatt ccacggcttg aaccatggag acaactatat cgttgtttca 300

aggctcctcc tctctttcgg agaaaccaga tttgctatac gtgtgtcgtt gttattgtat 360

tagcgcctct tgcaacttcg ataatgtagc atcctcagct agattagatc tgctaccaaa 420

gtccctcctg atacatcttg ctattggact atttagtaca agtatctant gcatcttcat 480

ttaaaaagtt aagaaatcta taaaagaaag caagaaggtg aaaattcatt gtagtttcga 540

ctgtctcaaa ctca 554

<210> SEQ ID NO 25
<211> LENGTH: 1216
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 25

gacaaagacc acaagaaagc tctactcatc ttatcttttg ctcttcttgc aatccttttc 60

catcatcctt gtatattctg attcaccatt ttgatcttca atcaattcat aataacatcc 120

aggcactcct tagagaattc acggagaaaa tatcgatggt atagagtttc agattgagta 180

ccacataata gggagccatc atcatcacta agtccaatat gcttcattct tgccttggtc 240

atgagtcgtt tatgcatggt tatctaacat ataaagctat gcgttggtat attggattta 300

ttccacactc ccctccattc aggccagcaa gagccaatcc ctatttacag atatagccac 360

tcagaatagt atattgtcat tccctttaag ccatccattg tgaacatgcc ctgccacaaa 420

tttagccttt agtccacaaa ttttcttcca gtggcaacat gaataagtag gggcatttaa 480

actttaccaa gacaaaaata gaagtcaatc ctcaacccca gatagctatg gtatagatgt 540

ctacctcaag tagctatggt ttctttctat caacagtgac aaaattaaaa tatacatctc 600

gtaatagagt tactttttag taaggtatat attacaaaaa gtggaagaag tcacgtaaca 660

aactatgatc agttagtgtg ctcaatcgta tactgttgta ccgactagct ctgatacaag 720

gctttttgt gtcactaatc tagatgcact agaaatacaa taggcagctc ctatcatcat 780

atccagcagc attaggcacc gaagtgccaa acccattgga gacgacaata actatcggca 840

tgaaacattc atggagaacc ctctttttct caatagttct ccccacgtct ctctctctct 900

ctctctttgg tgtgtatgta ataggtactc ttggaaaaag acaagttaac tctaagagaa 960

aggagtcatt caaaacttca aaccagaact tgcagcacac ggggctctcc tattatcctc 1020

agttaaagaa tgggtatcat caatctcaag tataaaatgc tcagcacata cgacatgtca 1080

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agtatctttg ttttggtcga cctgaacact atattattaa actccctagg gaaagagcca 1140

atcttttgta caactcaaag cagcaagtaa aaaataagta atctacacct atcgactatc 1200

cttctagcta ttcctc 1216

<210> SEQ ID NO 26
<211> LENGTH: 893
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 26

gaactcctct tgtgattaaa tcttctagcc atgatctgtc tttacacgtt ggctccttca 60

tgagctctct agtatgcaag catttgtttc cattttaatt ctttggttca ctatctgtgg 120

gcatgggaca ttgtgattca atagggcctc attctttgcc atccaaatgt ggtatattag 180

cgctgcggct tctgctcata tgggttccct gctaacccat ccatttgttc gtctcactat 240

cctagttcag aacccctcga tggttttatt ttttatcctt atttttagca attggaggtt 300

ctcttctaag ctagcttttg aaaaaccgct ctcgaaagat aaagatcatt agtttcattc 360

tcccttccac atagtaggca gacttcgtct tggcatatcc ccattcagta taatcgatct 420

cttgttaata gtctcccctg tgcatagtta aacaacaaat gaggctgtgc tttggaacat 480

ttactctatt ccatacacct ctccaagtgg tccataggcc tccttctccc tttgtccaag 540

tgcagcaact tctgattgtg tatttgcctg aacttgtgag ccagccattg tgtacatagc 600

ctggagcaaa cactgttttc actctgcaaa tcattttcca gtaccagcag atattaatgg 660

agggtctata ttcccaccag ttgtcaccct ttaagtaaag tggttcaccc atgtaaccca 720

aaggttatca gcttttcttg ctttgttcca tacttatttc gctactgctg cttcattcca 780

agatacagtc tctcacccct aaacttccgt ctttctttgt tctacaaatc atatcccaat 840

atatatagga ggtagttagc ctgtgttaac atttccactc catataaagt tcc 893

<210> SEQ ID NO 27
<211> LENGTH: 1622
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 27

cgttgataaa cactagaaga gaatatgtga atggttcatg cacataaaat agattttaca 60

tatgaagttg tcctcattat ttgtatttgt gatgatgcag gacatgtctg aagaaaacta 120

tacaatcatg ttaatctcag tggttgttat aacaggagtt gtatcacctc ttgttaaggt 180

tctatatgac ccttcaagta agtacattgc ctacaagagg aggacaataa tgcatagcag 240

agaaaaagat gaatttcgta tacttgcttg tatacacagc caagaaaatg ttcgcgcagt 300

catcagttta cttcaagtct cgaatcctac aaaagaaagt tgtattaatc tagtagttct 360

tcatcttact aagctaacgg gccgtgcctc ctcagttctc atagcccatc aaaagcgtga 420

caggccatca acaaatccaa cacaatctga aagaatcttc aatattttcg aaaaacttga 480

gcaacaaaac agtgacctca ttatggtaca ttgctacaaa ggagtctcac catatgtaac 540

aatgcacaat gatgtttgtt cccttgcttt agaaaagaga acaactctta tcattgtccc 600

ttttcacaag cattggatgt gtgagaaaag aatcgaaaca tcctatgcat atcgacatct 660

aaacaagaat gtacttgaga aatctccttg ttcagtcggg atactgattg atcgaggcaa 720

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caaaaaaaat ctcgttatgc aatcacagta ccatcattat atagagtcgt ggtactattt 780

tttggcggag cagatgatcg cgaagctttg tcatatgcag aaagaatgtc caaacatcct 840

agtgtgaaaa tgacattcat acgtttcacc agatcaggta atgcatttga aaatgttgtt 900

ggtggatcgg agagaagtaa ggttcttgat tcacaaatct tgaatgaatt caatctccaa 960

taccttcatt cagaacaagt ttcttatcaa gaagcagagg tgaaaagagg cgcggacgtg 1020

ttagaagtta ttaaatcttt gggacgtttt tatgatcttg ttatggttgg taaacgtcac 1080

gtagactcac caatattgtt gcaattgaca aagaggactg atgaggatgg tgaattaggg 1140

attgtaggag gcattcttgt cgcctcagat tttgaaagtg agacttcagt tttggtggtg 1200

cagcaacaaa ccagattatg gggacttcat gatcctgaag agtctacaca tttgagaagg 1260

ataaactaat tatagttgta tagacgtatg tcgctctgac tcaatcaaaa atgtcaatgg 1320

atgtgtgtta catcctgaag tagtctacac atttgagaag gataaactaa taattgtagt 1380

tgtatagaca tgttgctctg actcatcaaa aatatcaacg agtacgtgtt agatcttgaa 1440

gagtcttaac acatttgaga aggatcaact tatagttgta tagacctata tcgctcgaac 1500

acttcaaaaa atgttgatgg tgcgtgcaag accttccaaa agaagtgctt ttttcgagaa 1560

tctaacacag gtgctgcact atagtgtcac ctaaatcgta tacgatttag gtgacactat 1620

ag 1622

<210> SEQ ID NO 28
<211> LENGTH: 393
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 28

atcttgttca cttatgagga catctgtcac aggctacatg attaaagttg gtaattcttt 60

ggtctcatga aaagcaaaga agaaaactac atttttaagt agttcagctt aagctgaata 120

cagaagcctt gcttgtactg tgtcagagtt agtatggtta cttagaatac tgaaagaagt 180

aaatgctgaa gttcagttac cagttcaagt ttatagtgac aacaaggttg ttattcaaat 240

tgcagtcaat ccagtgttat catgaaagga acaaaccata ttgaaattga ttgtcatttc 300

acaagagaaa aattgcaaca aggcatgatc aaagttaact atcattctac tcaagaacaa 360

ccagttgatg tgttgacaaa aggcttatct aga 393

<210> SEQ ID NO 29
<211> LENGTH: 733
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 29

gcaagagtta tcacttaaag gaaagaactt gataggcaga aagccaagtt tcacaagcta 60

gattttctgc actaactctg attttgaaat cttgtactac ttttaagtat cgattacaag 120

cacgacatgt tcattagctt cctacttgtt tatcgtaatt atcaaaactt gatttagatg 180

gagtcttggg acagacttta ttgtgataaa aagttgcaga ctttttgtga gagatgtagt 240

tacaacgata gctactgatt gactcgtgaa aaataattga actggatgct ccaatgggac 300

gacctagcca atgatcgagt tggagtatag accttggaac caagattcta attccagtag 360

aggtgataca aagtgaaatt ttcccatcta cctgggcata gttagctgat atcttttctg 420

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gtgggaggta acaagtacac ttaagttagt tgaggagtgc gtgaccttcc cgctagctca 480

ggagtgtgca agcttccacg aataccatga tatctttaaa aggaggagtt gatatggtta 540

caggctcttc caagtcttgc ttcttataca ttttgtacgt gcaaacaagt tgctgaaggg 600

tagatttgat tacaaaaaag ctatttacga caaagatatt gctgtcatgt acttgtacat 660

tgtatttctc tttgttttat tattctttgc tagccgaaca aatttgcttt actctgtgat 720

ttgcagtggt gat 733

<210> SEQ ID NO 30
<211> LENGTH: 730
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 30

gcaaagaact gcagaattta ctcccacact aactgaccat aattacactt caatgtatac 60

atatttgcaa ctttgtcatc atctctacat tctctttttc cgctacgcca gctggccttt 120

ttataggttt tccaccctaa gatcttggtt tggtaaatgt atttttttatt gagcatcgtt 180

tcaaagatta gaatcttaga aaaggaaaag cagccataag ggacgtgaaa tttgggtaac 240

agcttaatta ggctaaacgc ttactacaac aacaacaaca acataccaag tgtaatccca 300

gtattgataa agaaacccag acgataacat aatatgtacc tggaaatgca aatcacagta 360

ttgatacacc atcataagat attgacgaac acattatagt atagtacaac tgtgacaaat 420

ttaaacctag taaaatttgt tgtgggaact caaacaattt ggattcaaga agaaaccaag 480

gaactagata atttgtagaa tttttaggac caaagaaaaa aaaggtgttt ttaaaaaaat 540

catttctttg atttctttga atcttctcct attttccttt tgcttcttct cgagatgctg 600

aagtgatctt ctctgttaaa gtcacaaaat gtgtttaata aaaggttggt gaaatacata 660

tagagctccg taaacttggc aacaattttc acttgaatac ctctacttga ggcttgtacc 720

tattagatac 730

<210> SEQ ID NO 31
<211> LENGTH: 430
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (45)..(45)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 31

tttattaaca cattttgtga ctttaacaga gaagatcant tcagnatctc cagtagaagc 60

aaaaggaaaa taggagaaga ttcaaagaaa tcaaagaaat gatttttttta aaaacacctt 120

ttttttcttt ggtcctaaaa agtctacaaa ttatctagtt ccttggtttc ttcttgaatc 180

caaattgttt gagttcccac aacaaatttt actaggttta aatttgtcac agttgtacta 240

tactataatg tgttcgtcaa tatcttatga tggtgtatca atactgtgat ttgcatttcc 300

aggtacatat tatgttatcg tctgggtttc tttatcaata ctgggattac acttggtatg 360

ttgttgttgt tgttgtagta agcgtttagc ctaattaagc tgttacccaa atttcacgtc 420

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ccttatggct 430

<210> SEQ ID NO 32
<211> LENGTH: 1887
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 32

tatagtgcag caggaatact tttgaatcag agaaagtatg tgttggaact tatatctaag 60

ttaggtttga gtgggtcaaa acctgctccc acacctttgg aacttaatca caagctcacc 120

acaatggagt atgatgagat tacagataat actgctggag atgaactatt gagtgatgta 180

agttcatatc aaaagttgat tggaaagttg ttgtatgtta ccatcacaag gcctgatatc 240

agcttctcag tgcaaaccct gagtcagttc atgcagcaac ccaagaaatc acattgggaa 300

gctgcactca gaactgtaag atacctgaaa aatgcaccag gtcaaggaat ccttatgaaa 360

tctggtcata ctcaacaact tacatgttgg tgtgactctg actgggcagc atgtccaaac 420

accagaaagt cggttactgg ttttgcagtg aaatttggag agtccttgat ttcttggaat 480

caaagaagca acaaactgtc ttaaggagct cagagtatag aagccttgca gcagcagtag 540

cagagttgac atggttgcaa ggattatttc aggagctgga tgttcacatt gacaaaccta 600

ttgcagtctt cagtgatagt aaatctgcca gattgcagag aatcccatat ttcacgaaag 660

aacaaagcac atcgagatcg attgccattt tatcagagac gagattaaag aaggagtggt 720

taaggctgtc tatgtgaata cgaaggaaca agaagctgac ttgctgacta aggccttgac 780

tacttctcaa cacatgcatt tacttggcaa gcttggagtg ttcaacattt tggaccctcc 840

agcttgaggg ggagtattaa agtcaattag agtcagttag ataggtgctt agctgaagtt 900

agttgcggtt gttagtggta gttgaagttt gttagtagtg gaagttgtta gccagctgtc 960

atgtccagct gtcaatgatt aagttagtgg ggcaacaatg agggaagtta ctagaagctt 1020

atgagcttgt gtatatatat tctattccag attgaataat caattaattt cattaccaca 1080

aaatatcttc tttctcaatt cctatcataa actagcaatt ctgtcacttg atgttgcttc 1140

agttttgggt atgggattca ctggatactg gtgttttcga tttgaaatca tctattccat 1200

aatgatgact catagactga tagtacagtc tattggcccc tgttagagtt tatgacccgg 1260

attttgttga tccggccctg aaaagttcac ggtgcgatcc atgtttgtgc tttttgtggg 1320

gtctgtggtg gtgatgtttg tgagcttagg atttatttgt atgcacgtat tatataagtg 1380

catttagtgg gctatttcga gcagttttca catacacgta attgagacta tcgtctccac 1440

cttgtattcc tcttcttcat agtgaatttc ctctctctgc ccgtggtttt tcccatggag 1500

ggtttccacg taaatatgtg tgttcttctt gtttttattt tgcttgtggt attgcctatt 1560

ctgtccgatc ataacaactc caaatatatt tgttcaaaac tggaaggatg gtcgaaggag 1620

tatggagagt ttttcgagcc ttgtgcatac ttagtcgaac gaacttccaa gagatgttct 1680

ttggtgagaa attgttaatt ttcttgaaca cctgaaatga aacaactacg agaaaatgga 1740

ttggcaaaca ctattgtttg acgaattgca tcacgtgttg ctgacagaag acaaaaggat 1800

caatttgata ataaatatga ccggtatgtt gggtcctaac aacaacaatt ggattgatct 1860

tttgctaatt gaggagtttc acacgtc 1887

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<210> SEQ ID NO 33
<211> LENGTH: 1024
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 33

gaactcaata gcccttcttt tattccagct ctaacgggac cttcacattt tctttcgtac 60

aattgcacca ccttctcttc aacagagaaa gaagccagtg ttctgatact tccaactgct 120

tcactagcaa cttgactcgc atcctcgtat agtttctaca agaaaatctt acttaaataa 180

gcactgttag agtgtgtgcc ctactaattt taatatttta ctctactggt ttcctatctg 240

tgcaacaagt cagtaaacgt ggttcacata attaaaagct gaacacagtg tttttaagtg 300

aaaaacaccc ggctcaagaa aggtgtaaag gctcaagaaa agtgtaaaaa accacgacct 360

atacctctac agtatttaaa cccctactta ctataactct tgagcctcaa caatcaacaa 420

tattacaaga ctttttgtaa aactaggaat taaaacttcc aactcctata ctacaaaaac 480

acaaatcttc ccaagtcttc gagttcctta acttgaagct cctaactcag tttatagatt 540

actgagacta gaacaatgac tcattacaac tcaaagaacc tatctactac aaacagtcta 600

agactttgct aactaaagga ccaggttctt cttcaagtaa gtgaactgtt ttgctgattg 660

ttgattatct tatcagtgca tgagtgaatg ctttgaaagt tgtttcttcc atttaagcca 720

acacctgatg tatatttcta tcctcactag gactcccagt tagtttcact cattctttac 780

tgccttctct ccctcttgtt gtttgaatag gactcttctt gattatctca taatttctgc 840

aagacttctt attcgaccga acttcttcaa gatttcttat tcaactcaac ttctgcaaga 900

cttcttgttc aaaccaaact tcttcaagat ttcttgttca actcagcttc tgcaagactt 960

cttgttgtga taagtgttat ccactcccat tttgcacgca gattcagttt ttcaataact 1020

tgcc 1024

<210> SEQ ID NO 34
<211> LENGTH: 782
<212> TYPE: DNA
<213> ORGANISM: Capsicum annuum

<400> SEQUENCE: 34

cacaatgctt agcagttccg ctgtttctct ctaattgtat ccgttcaaaa atacaagctt 60

gtgacagatg aatcttagac tctctgacta cttgtaattc tatctacaat ttagccatct 120

ttctctatca tttgcttttg aaatggagtg acatgaacaa tgaggattca ttcattcagt 180

cgatctccac ttgctttgca ttgaggagtt ttttctctat catttgcttg agagttcaag 240

tgtctgggat ggacaatgtg gtcgttaaca ttgcctcttc tcatccaggt ttgttctttt 300

gcttcttaac tgaggggtat ttcttggttc cggagaatct ttttttggt aactaacata 360

ttcattttat taccaaagta atattacaaa tcaactacca gcctgatgac acaacctggt 420

agactcaaag aagaacccta ctgatcagac taataataat gaggatagta gtttagatca 480

ttgatcacag ctgctaactt atgcctaaca gtagcaatac aaataacatc ctgaaatact 540

agcctaacca ctttctccgg tgtagtactg attgtcctga caatcctaca attcctatca 600

tgccatatat ggtaaacgca tgcagcagta ccatcctgaa tatgtgttga ggctgatcga 660

cctttgacat tgttctcaat ccactcaagt tcactggacc aagccaaagc aatcctttga 720

atctttatcc agccgagcaa agcattccca cagtttagca gcatagctac acctaaagaa 780

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ct 782

<210> SEQ ID NO 35
<211> LENGTH: 1641
<212> TYPE: DNA
<213> ORGANISM: Capsicum baccatum

<400> SEQUENCE: 35

gaaatttgtt cttcttcttt cccttccttt tttgttttgg attttcctca ttgcaagtag 60

aaatgtctct aacggctatg gttttaatag ttcatccgag aagagagtta ctgctgttgc 120

catcagtaat gacggtcgtt ttgtagcttt cgcggataaa tttggtgtaa tttatgcagt 180

tgaaatagaa ggttatcatg aaaatcaaac tctgcccgat aagaaggcag tcccgattct 240

tgcccactat tgcagcatca ttactagtct ggtatgtttc tttcctttcc tcttcatgtg 300

aatttgcttt agttttcgat gagtcaattt ttgtatccta tatatatgag ggttagcagt 360

ttactcagat attgttacga tactcatgat ctatgttgct cgaactcttt aaaaatgcta 420

ttaggtgcat gtcggattct tcaaaagtag ggcatttttg gaggatccga cacgagtatg 480

gcaacatttt tggtgagtcg gagcaactta gctcatgatt ggtccttgta agcagttttc 540

tacggaaatt gtgttttcat atacactgtt ctggcaatgg cattcatcgc tcgactcttc 600

tacacaaata ttatggataa tgatctactg tctcgatgca catctcttgc acaatttgtt 660

gcaagcgttg tccatcctgc cagtcaagta taaagcgtta tctttctggt gactagacca 720

tgatactctt atcgtctatg attacttcat ataagattaa gtttagcgta ttcctagctc 780

gccatatcac ataacacttt ctctaccaaa ttagtttgat tccataatca aggcctcttg 840

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What is claimed is:

1. A *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm, wherein said plant comprises a chromosomal segment on chromosome 6 that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment.

2. The plant of claim **1**, wherein the chromosomal segment is further defined as:

(a) flanked by Marker M29 (SEQ ID NO: 29) and a marker selected from the group consisting of Marker M14 (SEQ ID NO: 14), Marker M15 (SEQ ID NO: 15), Marker M16 (SEQ ID NO: 16), and Marker M17 (SEQ ID NO: 17) in said plant; or

(b) located between 26,405 bp and 213,924,156 bp on chromosome 6 of public pepper genome sequence Pepper CM334 v.1.55.

3. The plant of claim **2**, wherein said chromosomal segment comprises a marker locus selected from the group consisting of Marker M18 (SEQ ID NO: 18), Marker M19 (SEQ ID NO: 19), Marker M20 (SEQ ID NO: 20), Marker M21 (SEQ ID NO: 21), Marker M22 (SEQ ID NO: 22), Marker M23 (SEQ ID NO: 23), Marker M24 (SEQ ID NO: 24), Marker M25 (SEQ ID NO: 25), Marker M26 (SEQ ID NO: 26), Marker M27 (SEQ ID NO: 27), and Marker M28 (SEQ ID NO: 28) on chromosome 6.

4. The plant of claim **1**, wherein said chromosomal segment comprises:

(a) the haplotype of variety Ganti, wherein a representative sample of seed of said variety has been deposited under NCIMB accession number 43055; or

(b) the haplotype of variety Flame Fountain, wherein a representative sample of seed of said variety has been deposited under NCIMB accession number 43054.

5. A seed that produces the plant of claim **1**.

6. A plant part of the plant of claim **1**.

7. The plant part of claim **6**, wherein the plant part is a cell, a seed, a root, a stem, a leaf, a flower, a fruit, or pollen.

8. The plant of claim **1**, wherein the plant is a sweet pepper variety.

9. The plant of claim **1**, wherein the plant has a blocky type fruit shape.

10. The plant of claim **1**, wherein said plant further comprises a chromosomal segment from *Capsicum baccatum* on chromosome 6 that confers uniform female fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment, wherein said chromosomal segment from *Capsicum baccatum* is flanked by Marker A12 (SEQ ID NO: 35) and Marker A35 (SEQ ID NO: 36) in said plant.

11. A method for producing a *Capsicum annuum* plant that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm, comprising introgressing into said plant a chromosomal segment on chromosome 6 that confers male fertility in a male sterile *Capsicum annuum* plant comprising a *Capsicum baccatum* cytoplasm relative to a plant lacking said chromosomal segment.

12. The method of claim **11**, wherein said introgressing comprises:

a) crossing a plant comprising said chromosomal segment with itself or with a second *Capsicum annuum* plant of a different genotype to produce one or more progeny plants; and

b) selecting a progeny plant comprising said chromosomal segment.

13. The method of claim **12**, wherein selecting a progeny plant comprises detecting at least one allele on chromosome 6 flanked by Marker M29 (SEQ ID NO: 29) and a marker selected from the group consisting of Marker M14 (SEQ ID NO: 14), Marker M15 (SEQ ID NO: 15), Marker M16 (SEQ ID NO: 16), and Marker M17 (SEQ ID NO: 17).

14. The method of claim **12**, wherein the progeny plant is an F_2-F_6 progeny plant.

15. The method of claim **12**, wherein said crossing comprises backcrossing.

16. The method of claim **15**, wherein said backcrossing comprises from 2-7 generations of backcrosses.

17. A *Capsicum annuum* plant produced by the method of claim **11**.

18. A method of producing food or feed comprising obtaining a plant according to claim **1** or **17**, or a part thereof, and producing said food or feed from said plant or part thereof.

19. A *Capsicum annuum* plant obtainable by a method comprising the step of introgressing into a plant a male fertility restoration locus allele for *Baccatum* cytoplasmic male sterility, wherein said male fertility restoration locus allele is defined as located in a chromosomal segment on chromosome 6 flanked by Marker M29 (SEQ ID NO: 29) and a marker selected from the group consisting of Marker M14 (SEQ ID NO: 14), Marker M15 (SEQ ID NO: 15), Marker M16 (SEQ ID NO: 16), and Marker M17 (SEQ ID NO: 17).

20. The *Capsicum annuum* plant of claim **19**, wherein said introgressing comprises backcrossing or marker-assisted selection.

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