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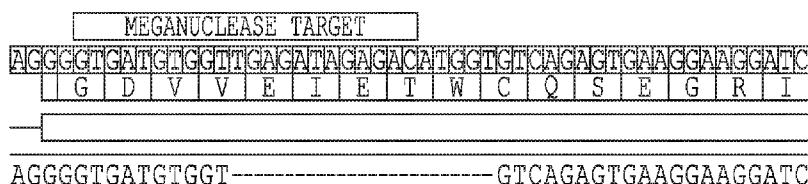


FIG. 2C

(57) Abstract: Methods are provided to mutate, in a targeted manner, the genome of a plant cell using a double stranded DNA break inducing enzyme. Also provided are plants, in particular Brassica plants that yield seeds producing oils having a reduced total saturated fatty acid content, and method for making such plants.



ENGINEERED NUCLEASES TO GENERATE MUTATIONS IN PLANTS

5 **Priority**

This application claims the benefit of priority from U.S. Provisional Patent Application Ser. No. 62/341,489, filed on May 25, 2016, which is herein incorporated by reference.

Background of the Invention

10 In recent years, diets high in saturated fats have been associated with increased levels of cholesterol and increased risk of coronary heart disease. As such, current dietary guidelines indicate that saturated fat intake should be no more than 10 percent of total calories. Based on a 2,000-calorie-a-day diet, this is about 20 grams of saturated fat a day. Oils contain saturated fats. For example canola oil typically contains about 7% to 8%
15 saturated fatty acids. A decrease in saturated fatty acid content would improve the nutritional profile of oils.

Summary of the Invention

Genes involved in plant oil synthesis, including those that regulate saturated fatty acid and oleic acid content, have been mutated by a process which involves exposing seeds to
20 chemicals or radiation in order to generate mutants with desirable traits. Unlike plants modified with engineered nucleases, in which a mutation (substitution, deletion and/or addition of one or more nucleotides) can be engineered to occur at a very specific location in the plant genome, plants developed via mutagenic processes often result in random, multiple and unspecific genetic changes. These random, multiple genetic changes all come together to
25 provide the phenotype of the mutated plant. With engineered nucleases, a very specific mutation, or set of mutations, can be generated and their effect on phenotype (e.g., oil profile) can be determined.

Provided herein is the production of mutant FatA1, FatA2, Kas2, Kas3 and/or FatB, allele(s) generated by the use of engineered nucleases, plants comprising said one or more
30 mutant alleles of FatA1, FatA2, Kas2, Kas3 and/or FatB, such as Brassica plants, and uses of such plants produce lower saturated fatty acid content. As described herein, Brassica plants containing such mutations can produce oils with reduced saturated fatty acid content. Brassica plants described herein are particularly useful for producing canola oils for certain food applications, as the plants are not genetically modified.

Provided herein are Brassica plants (e.g., *Brassica napus*, *Brassica juncea*, or *Brassica rapa* plants) and progeny thereof (e.g., seeds) that include substitution, deletion and/or insertion mutations in one or more alleles of FatA1, FatA2, Kas2, Kas3 and/or FatB via engineered nucleases, wherein each mutated allele results in the production of a FatA1, FatA2, Kas2, Kas3 and/or FatB polypeptide having reduced or no activity relative to a corresponding wild-type FatA1, FatA2, Kas2, Kas3 and/or FatB polypeptide (alternatively the substitution, deletion and/or insertion may result in no FatA1, FatA2, Kas2, Kas3 and/or FatB protein/activity being produced). A mutated allele can include a nucleic acid encoding a truncated FatA1, FatA2, Kas2, Kas3 and/or FatB polypeptide. A mutated allele can include a sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to the nucleotide sequence of the wild-type allele (e.g., SEQ ID NO: 1 for FatA1).

One embodiment provides a method to produce a plant with reduced saturated fatty acids comprising: a) contacting a plant with an engineered nuclease specific for FatA1, FatA2, Kas2, Kas3 and/or FatB gene(s); b) growing the plant from step a) and collecting the seeds from said plant; and c) selecting plants grown from the seeds of step b) with a substitution, deletion and/or insertion mutation in one or more of said genes; wherein said substitution, deletion and/or insertion mutation results in a reduced production of saturated fatty acids by said plant as compared to a control plant of identical genetic background that has not been mutated by said gene editing.

Another embodiment provides a method to produce a plant with reduced saturated fatty acids comprising: a) contacting a plant cell or tissue with an engineered nuclease specific for FatA1, FatA2, Kas2, Kas3 and/or FatB gene(s); b) generating a plant from the plant cell or tissue in step a); c) selecting plants of step b) with a substitution, deletion and/or insertion mutation in one or more of said genes; wherein said substitution, deletion and/or insertion mutation results in a reduced production of saturated fatty acids by said plant as compared to a control plant of identical genetic background that has not been mutated by said gene editing.

In one embodiment, the plant is a *Cruciferae* plant. In another embodiment, the plant is a *Brassica* plant. In another embodiment, the plant is *Brassica napus*, *Brassica juncea*, or *Brassica rapa*.

In one embodiment, the engineered nuclease is a meganuclease. In one embodiment, there is a substitution, deletion and/or insertion mutation in at least one allele of FatA1. In another embodiment, there is a substitution, deletion and/or insertion mutation in at least one allele of FatA2. In another embodiment, there is a substitution, deletion and/or insertion

mutation in at least one allele of Kas2. In one embodiment, there is a substitution, deletion and/or insertion mutation in at least one allele of Kas3. In another embodiment, there is a substitution, deletion and/or insertion mutation in at least one allele of FatB.

One embodiment provides a Brassica plant comprising a deletion in at least one allele of FatA1, FatA2, Kas2, Kas3 and/or FatB. In one embodiment, the deletion is from about 1 to about 350 base pairs in length. In another embodiment, the deletion results in a decrease in saturated fatty acid.

In one embodiment, the recognition/target sequence comprises any contiguous nucleotide (e.g., 10 or more) sequence of the FatA1 gene (SEQ ID NO: 1).

In another embodiment, provided herein is a method of producing an oil. The method includes crushing seeds produced from at least one plant described herein and extracting the oil from the crushed seeds.

One embodiment provides a method to mutate the genome of a Brassica plant cell at a target site comprising: a) inducing a double stranded DNA break at a target site, said double stranded break being induced by the introduction to said cell of a double stranded DNA break inducing (DSBI) enzyme which recognizes a recognition sequence in the vicinity of or at said target site in FatA1, FatA2, Kas2, Kas3 and/or FatB gene(s); and b) selecting a plant cell wherein said double stranded DNA break has been repaired resulting in a mutation in the genome at said target site, wherein said mutation is a substitution of at least one nucleotide, a deletion of at least one nucleotide, an insertion of at least one nucleotide or any combination thereof. In one embodiment, the plant cell is regenerated into a plant. One embodiment provides a plant cell comprising a mutation at a target site of the genome obtained by the methods provided herein. Another embodiment provides a plant, plant part, seed or propagating material thereof comprising a mutation at a target site of the genome comprising the plant cell.

One embodiment provides a method to produce a Brassica plant with reduced saturated fatty acids comprising: a) inducing a double stranded DNA break at a target site, said double stranded break being induced by the introduction to a plant cell of a double stranded DNA break inducing (DSBI) enzyme which recognizes a recognition sequence in the vicinity of or at said target site in FatA1, FatA2, Kas2, Kas3 and/or FatB gene(s); and b) selecting a plant cell wherein said double stranded DNA break has been repaired resulting in a mutation in the genome at said target site, wherein said mutation is a substitution of at least one nucleotide, a deletion of at least one nucleotide, an insertion of at least one nucleotide or any combination thereof; and c) regenerating said plant cell(s) of b) into a plant; wherein said

mutation results in reduced production of saturated fatty acids by said plant as compared to a control plant of identical genetic background that has not been mutated by said DSBI and repair.

In one embodiment, the DSBI enzyme is a single chain meganuclease or a pair of
5 meganucleases which recognizes or recognize in concert a site and induces or induce said double strand break.

In one embodiment, the plant(s) produced by the methods described herein is crossed with another plant.

One embodiment provides a plant, plant part, seed or propagating material thereof
10 comprising a modification at a target site of the genome obtained by the methods provided here.

In one embodiment, the plant is *Brassica napus*, *Brassica juncea*, or *Brassica rapa*.

In one embodiment, one or both FatA1 alleles on N3, N7, 13 and/or N17 are mutated. In another embodiment, one or both FatA1 alleles on N13 and/or N17 are mutated.
15 In one embodiment, one or both FatA1 alleles on N13 are mutated. In another embodiment, one or both FatA1 alleles on N3, N7 and/or N13 are mutated. In one embodiment, one or both FatA1 alleles on N7 are mutated. In one embodiment, the mutation is a deletion of one or more nucleotides, optionally comprising the substitution of at least one nucleotide.

In one embodiment, the plants produced by the methods described herein yield a
20 reduction of stearic acid (18:0) of about 9% to about 35% as compared to a non-mutated plant of identical genetic background. In another embodiment, the plants yield an overall reduction in total saturated fatty acids of about 5 to about 15%.

Brief Description of the Drawings

Figure 1 provides full-length wild-type sequence for FatA1 from the public *Brassica napus* sequence (Chalhoub, et al., 2014): BnaA03g47660D. (SEQ ID NO:1) An NCBI
25 accession number for a FatA1 mRNA sequence is XM_013833775.1.

Figures 2A-E provide A) a partial wild-type sequence for FatA1 (N13; SEQID NO:2); B) depicts partial sequence for a FatA1 N13 mutant in a IMC201 background (17 bp deletion in N13; SEQ IDNO:3); C) depicts the meganuclease recognition site, partial wild type FatA1
30 nucleotide sequence (SEQ ID NO:4), partial wild-type protein sequence (SEQ IDNO:5) and partial mutant sequence depicting deletion (SEQ ID NO:6); D) depicts partial sequence for a FatA1 N13 mutant in a Cargill background represented by American Type Culture Collection (ATCC) Accession No. PTA-12314, PTA-12315 and PTA-12316 (6 bp deletion in N13; SEQ IDNO:7); and E) depicts the meganuclease recognition site, partial wild type FatA nucleotide

sequence (SEQ ID NO:4), partial protein sequence (SEQ IDNO:5) and mutant sequence depicting deletion (SEQ ID NO:8).

Figures 3A-C provide A) a partial wild-type sequence for FatA1 (N7; SEQ ID NO:9); B) depicts partial sequence for a FatA1 N7 mutant in a IMC201 background (6 bp deletion in N7; SEQ IDNO:10); and C) depicts the meganuclease recognition site, partial wild type FatA1 nucleotide sequence (SEQ ID NO:11), partial wild-type protein sequence (SEQ IDNO:5) and partial mutant sequence depicting deletion (SEQ ID NO:12).

Figures 4A-C provide A) a partial wild-type sequence for FatA1 (N3; SEQ ID NO:13); B) depicts partial sequence for a FatA1 N3 mutant in a IMC201 background (24 bp deletion in N3; SEQ IDNO:14); and C) depicts the meganuclease recognition site, partial wild type FatA1 nucleotide sequence (SEQ ID NO:15), partial wild-type protein sequence (SEQ IDNO:16) and partial mutant sequence depicting deletion (SEQ ID NO:17).

Figures 5A-C provide A) a partial wild-type sequence for FatA1 (N17; SEQ ID NO:18); B) depicts partial sequence for a FatA1 N17 mutant in a Cargill background represented by American Type Culture Collection (ATCC) Accession No. PTA-12314, PTA-12315 and PTA-12316 (24 bp deletion and 1 bp change (bold and underlined A) in N17; SEQ IDNO:19); and C) depicts the meganuclease recognition site, partial wild type FatA1 nucleotide sequence (SEQ ID NO:20), partial wild-type protein sequence (SEQ IDNO:16) and partial mutant sequence depicting deletion and 1 bp change (highlighted in blue) (SEQ ID NO:21).

Detailed Description of the Invention

Methods are provided to mutate, in a targeted manner, the genome of a plant using a double stranded DNA break inducing enzyme. Also provided are plants, in particular *Brassica* plants, which yield seeds producing oils having a reduced saturated fatty acid content, and method for making such plants.

The invention provides methods to introduce a targeted mutation, including insertion, deletion, or substitution of one or more nucleotides, at a precisely localized nucleotide sequence in the genome of a plant using engineered double stranded DNA break inducing enzymes. The invention further provides a plant cell, plant part, plant or seed comprising such a mutated sequence, wherein said mutation results in a reduction of saturated fatty acid production by the plant, and methods for making such plant.

The invention is based on the observation that functional meganucleases can be engineered to specifically recognize and cleave a nucleotide sequence, such as FatA1 (SEQ ID NO: 1), in a plant cell, from which a plant can be produced. Provided herein are plants

made by the methods provided herein, such as Brassica plants including *B. napus*, *B. juncea*, and *B. rapa* species of Brassica, that yield seeds producing oils having a reduced saturated fatty acid content.

Definitions:

5 In describing and claiming the invention, the following terminology will be used in accordance with the definitions set forth below. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present
10 invention. Specific and preferred values listed below for radicals, substituents, and ranges are for illustration only; they do not exclude other defined values or other values within defined ranges for the radicals and substituents.

As used herein, the articles “a” and “an” refer to one or to more than one, i.e., to at least one, of the grammatical object of the article. By way of example, “an element” means
15 one element or more than one element.

The term “about,” as used herein, means approximately, in the region of, roughly, or around. When the term “about” is used in conjunction with a numerical range, it modifies that range by extending the boundaries above and below the numerical values set forth. In general, the term “about” is used herein to modify a numerical value above and below the
20 stated value by a variance of 20%.

As used herein, a "double stranded DNA break endonuclease" is an enzyme capable of inducing a double stranded DNA break at a particular nucleotide sequence, called the "recognition site." Homing endonucleases constitute a family of endonucleases and are sometimes also referred to as meganucleases. They may be encoded by introns, independent
25 genes or intervening sequences, and present structural and functional properties that distinguish them from the more classical restriction enzymes, usually from bacterial restriction-modification Type II systems.

A person skilled in the art would be able to either choose a double stranded DNA break inducing (“DSBI”) enzyme recognizing the selected target nucleotide sequence to
30 engineer such a DSBI endonuclease.

As used herein "located in the vicinity" refers to the site of double DNA stranded break induction, i.e. the recognition site of the DSBI enzyme, being located at a distance of 10 bp, 20 bp, 30 bp, 50 bp, 60 bp, 70 bp, 80 bp, 90 bp, 100 bp, 200, 250 bp, 500 bp, 1 kbp, 2

kbp, 3 kbp, 4 kbp, 5 kbp to 10 kbp from the target, i.e. the site in the genomic DNA which is to be mutated (the target site).

The term "heterologous" refers to the relationship between two or more nucleic acid or protein sequences that are derived from different sources. For example, a promoter is
5 heterologous with respect to an operably linked nucleic acid sequence, such as a coding sequence, if such a combination is not normally found in nature. In addition, a particular sequence may be "heterologous" with respect to a cell or organism into which it is inserted (i.e. does not naturally occur in that particular cell or organism).

The expression "operably linked" means that said elements of the chimeric gene are
10 linked to one another in such a way that their function is coordinated and allows expression of the coding sequence, i.e. they are functionally linked. By way of example, a promoter is functionally linked to another nucleotide sequence when it is capable of ensuring transcription and ultimately expression of said other nucleotide sequence.

A nullizygous organism carries two mutant or missing alleles for the same gene. The
15 mutant/missing alleles are both complete loss-of-function or 'null' alleles, so homozygous null and nullizygous are synonymous.

A gene knockout (abbreviation: KO) is a genetic technique in which both of an organism's alleles are made inoperative ("knocked out" of the organism). The term knockout, inactivated, and disrupted are used interchangeably herein to mean that the targeted site is
20 changed so that the gene expression product is eliminated or greatly reduced or the product expressed has reduced activity as compared to a control (e.g., wild type protein). Also known as knockout organisms or simply knockouts. The term also refers to the process of creating such an organism, as in "knocking out" a gene.

When an amount, concentration, or other value or parameter is given as either a range,
25 preferred range, or a list of upper preferable values and lower preferable values, this is to be understood as specifically disclosing all ranges formed from any pair of any upper range limit or preferred value and any lower range limit or preferred value, regardless of whether ranges are separately disclosed. Where a range of numerical values is recited herein, unless
30 otherwise stated, the range is intended to include the endpoints thereof, and all integers and fractions within the range. It is not intended that the scope of the invention be limited to the specific values recited when defining a range.

As used herein, "plant part" includes any plant organ or plant tissue, including but not limited to fruits, seeds, embryos, meristematic regions, callus tissue, leaves, roots, shoots, flowers, gametophytes, sporophytes, pollen, and microspores.

For the purpose of this invention, the "sequence identity" of two related nucleotide or amino acid sequences, expressed as a percentage, refers to the number of positions in the two optimally aligned sequences which have identical residues (x100) divided by the number of positions compared. A gap, i.e. a position in an alignment where a residue is present in one sequence but not in the other, is regarded as a position with non-identical residues. The optimal alignment of the two sequences is performed by the Needleman and Wunsch algorithm (Needleman and Wunsch 1970). The computer-assisted sequence alignment above, can be conveniently performed using standard software program such as GAP which is part of the Wisconsin Package Version 10.1 (Genetics Computer Group, Madison, Wis., USA) using the default scoring matrix with a gap creation penalty of 50 and a gap extension penalty of 3.

Nucleic acids can be DNA or RNA, single- or double-stranded. Nucleic acids can be synthesized chemically or produced by biological expression *in vitro* or *in vivo*. Nucleic acids can be chemically synthesized using appropriately protected ribonucleoside phosphoramidites and a conventional DNA/RNA synthesizer. DNA includes cDNA and genomic DNA.

Standard recombinant DNA and molecular cloning techniques used herein are well known in the art and are described more fully in Sambrook, J., Fritsch, E. F. and Maniatis, T. *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory: Cold Spring Harbor, N.Y. (1989); by Silhavy, T. J., Bennis, M. L. and Enquist, L. W., *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory: Cold Spring Harbor, N.Y. (1984); and by Ausubel, F. M. et al., *Current Protocols in Molecular Biology*, published by Greene Publishing Assoc. and Wiley-Interscience, Hoboken, N.J. (1987).

The terms "comprises," "comprising," and the like can have the meaning ascribed to them in U.S. Patent Law and can mean "includes," "including" and the like. As used herein, "including" or "includes" or the like means including, without limitation.

Brassica Plants

Brassica plants described herein have reduced levels of total saturated fatty acids in the seed oil as a result of reduced activity of FatA1, FatA2, Kas2, Kas3 and/or FatB. It is understood that throughout the disclosure, reference to "plant" or "plants" includes progeny, i.e., descendants of a particular plant or plant line, as well as cells or tissues from the plant. Progeny of an instant plant include seeds formed on F₁, F₂, F₃, F₄ and subsequent generation plants, or seeds formed on BC₁, BC₂, BC₃, and subsequent generation plants. Seeds produced by a plant can be grown and then selfed (or outcrossed and selfed, or doubled through

dihaploid) to obtain seeds homozygous for a mutant allele. The term "allele" or "alleles" refers to one or more alternative forms of a gene at a particular locus.

Reduced activity, including absence of detectable activity, of FatA1, FatA2, Kas2, Kas3 and/or FatB, can be achieved by mutating one or more endogenous FatA1, FatA2, Kas2, Kas3 and/or FatB allele(s) (each of these genes has one or more isoforms, for example, FatA1 has 4 isoforms, namely one on each of chromosome N3, N13, N7 and N17). An endogenous isoform/allele of FatA1, FatA2, Kas2, Kas3 and/or FatB allele can be mutated (deletion, addition and/or substitution mutation) by the use of engineered nucleases.

Genetic mutations can be introduced within, for example, regenerable plant tissue using one or more engineered nucleases. The treated population, or a subsequent generation of that population, can be screened for reduced protein activity that results from the mutation, e.g., by determining the fatty acid profile of the population and comparing it to a corresponding non-mutagenized population. Mutations can be in any portion of a gene, including coding sequence, intron sequence and regulatory elements, that render the resulting gene product non-functional or with reduced activity.

The plants on which the genetic mutations can be carried out are any plants, including those in the Brassica family, including any wild-type and mutant plant backgrounds. Such Brassica plants include, but are not limited to, IMC201 (U.S. Pat. No. 9,334,483), IMC02 (represented by American Type Culture Collection (ATCC) Accession No. PTA-6221), Westar (U.S. Pat. No. 6,342,658), 1904 (represented by American Type Culture Collection (ATCC) Accession No. PTA-11273, as well as progeny of the seed designated 1904 and represented by ATCC Accession No. PTA-11273), 2558 (represented by American Type Culture Collection (ATCC) Accession No. PTA-11274, as well as progeny of the seed designated 2558 and represented by ATCC Accession No. PTA-11274), US Pub Appln No. 2013/0081156, 95CB504 (U.S. Pat. No. 9,334,483), Cargill background (represented by American Type Culture Collection (ATCC) Accession No. PTA-12314, PTA-12315 and PTA-12316), 03LC LL and hybrid backgrounds deposited as Accession No. PTA-12314, PTA-12315 and PTA-12316, and Topas (represented by American Type Culture Collection (ATCC) Accession No. PTA-120738).

Engineered Nucleases

The use of engineered nucleases (GEEN) is a type of genetic engineering in which DNA is inserted, deleted or substituted in the genome of an organism using engineered nucleases, or "molecular scissors." These nucleases create site-specific double-strand breaks

(DSBs) at desired locations in the genome. The induced double-strand breaks are repaired resulting in targeted mutations, such as deletions.

There are currently four families of engineered nucleases being used: meganucleases, zinc finger nucleases (ZFNs), Transcription Activator-Like Effector-based Nucleases (TALEN), and the CRISPR-Cas system (Esvelt, KM. and Wang, HH. (2013). "Genome-scale engineering for systems and synthetic biology." *Mol Syst Biol* 9 (1): 641; Tan, WS. et al. (2012). "Precision editing of large animal genomes." *Adv Genet* 80: 37–97; Puchta, H. and Fauser, F. (2013). "Gene targeting in plants: 25 years later." *Int. J. Dev. Biol* 57: 629–637; Boglioli, E. and Richard, M. "Rewriting the book of life: a new era in precision genome editing" (PDF). Boston Consulting Group; Method of the Year 2011. *Nat Meth* 9 (1), 1-1; www.sciencemag.org/topic/2015-breakthrough-year).

Meganucleases, found commonly in microbial species, have the unique property of having long recognition sequences (>14bp) thus making them naturally specific (de Souza, N., Primer: genome editing with engineered nucleases. *Nat Meth* 9 (1), 27-27 (2011); Smith, J. et al., A combinatorial approach to create artificial homing endonucleases cleaving chosen sequences. *Nucleic Acids Research* 34 (22), e149 (2006)). This can be exploited to make site-specific DSB in genome editing. Meganuclease variants that recognize unique sequences have been created (Id). Also of use is the fusion of various meganucleases to create hybrid enzymes that recognize a new sequence (Chevalier, B.S. et al., Design, Activity, and Structure of a Highly Specific Artificial Endonuclease" *Molecular Cell* 10 (4), 895-905 (2002)). Yet others have altered the DNA interacting amino acids of the meganuclease to design sequence specific meganucleases in a method named rationally designed meganuclease (US Patent 8,021,867; WO2007/047859; WO2011/064736).

A well characterized megaendonuclease is I-SceI. I-SceI is a site-specific endonuclease, responsible for intron mobility in mitochondria in *Saccharomyces cerevisiae*. The enzyme is encoded by the optional intron Sc LSU.1 of the 21 S rRNA gene and initiates a double stranded DNA break at the intron insertion site generating a 4 bp staggered cut with 3'OH overhangs. The recognition site of I-SceI endonuclease extends over an 18 bp non-symmetrical sequence (Colleaux et al. 1988 *Proc. Natl. Acad. Sci. USA* 85: 6022-6026). The amino acid sequence for I-SceI and a universal code equivalent of the mitochondrial I-SceI gene have been provided by e.g. WO 96/14408. WO 96/14408 further discloses a number of variants of I-SceI protein which are still functional. PCT application PCT/EP04/013122 (incorporated herein by reference) provides synthetic nucleotide sequence variants of I-SceI which have been optimized for expression in plants.

Another well characterized designed meganuclease is based on the naturally occurring meganuclease I-CreI for use as a scaffold. I-CreI is an endonuclease found in the chloroplasts of *Chlamydomonas reinhardtii* (Thompson et al. 1992, Gene 119, 247-251).

This endonuclease is a homodimer that recognizes a pseudo-palindromic 22 bp DNA site in the 23SrRNA gene and creates a double stranded DNA break that can be used for the
5 introduction of an intron. I-CreI is a member of a group of endonucleases carrying a single LAGLIDADG (SEQ ID NO: 22) motif. LAGLIDADG (SEQ ID NO: 22) enzymes contain one or two copies of the consensus motif. Single-motif enzymes, such as I-CreI function as homodimers, whereas double-motif enzymes are monomers with two separate domains.

Accordingly, when designing meganucleases derived from an I-CreI scaffold to recognize a
10 22 bp nucleotide sequence of interest, two monomeric units are designed, each recognizing a part of the 22 bp recognition site, which are needed in concert to induce a double stranded break at the 22 bp recognition site (W02007/047859). Concerted action may be achieved by linking the two monomeric units into one single chain meganuclease, or may also be
15 achieved by promoting the formation of heterodimers, as described e.g. in W02007/047859.

A list of other DSB inducing enzymes and their respective recognition sites is provided in Table I of WO 03/004659 (pages 17 to 20) (incorporated herein by reference). These include I-See I, I-Chu I, I-Dmo I, I-Cre I, I-Csm I, PI-Fli I, Pt-Mtu I, I-Ceu I, I-See II, I-See III, HO, PI-Civ I, PI-Ctr I, PI-Aae I, PI-BSU I, PI-DhaI, PI-Dra I, PI-May I, PI-Mch I,
20 PI-Mfu I, PI-Mfl I, PI-Mga I, PI-Mgo I, PI-Min I, PI-Mka I, PI-Mle I, PI-Mma I, PI-Msh I, PI-Msm I, PI-Mth I, PI-Mtu I, PI-Mxe I, PI-Npu I, PI-Pfu I, PI-Rma I, PI-Spb I, PI-Ssp I, PI-Fae I, PI-Mja I, PI-Pho I, PI-Tag I, PI-Thy I, PI-Tko I or PI-Tsp I.

As opposed to meganucleases, the concept behind ZFNs and TALEN technology is based on a non-specific DNA cutting enzyme, which can then be linked to specific DNA
25 sequence recognizing peptides, such as zinc fingers (such methods have been described e.g. in WO 03/080809, W094/18313 or W095/09233 and in Isalan et al., 2001, Nature Biotechnology 19, 656-660; Liu et al. 1997, Proc. Natl. Acad. Sci. USA 94, 5525-5530)) and transcription activator-like effectors (TALEs; Baker, M., Gene-editing nucleases. Nat Meth 9 (1), 23-26 (2012); Christian et al., 2010, Genetics 186: 757-761, WO10/079430 and
30 WO10/146121). In these technologies, the endonuclease has a DNA recognition site and cleaving site separate from each other. Although the nuclease portions of both ZFNs and TALEN constructs have similar properties (e.g., FokI), the difference between these engineered nucleases is in their DNA recognition peptide. ZFNs rely on Cys2-His2 zinc fingers and TALEN constructs on TALEs. Both of these DNA recognizing peptide domains

have the characteristic that they are naturally found in combinations in their proteins. Cys2-His2 Zinc fingers typically happen in repeats that are 3 bp apart and are found in diverse combinations in a variety of nucleic acid interacting proteins such as transcription factors. TALEs on the other hand are found in repeats with a one-to-one recognition ratio between the amino acids and the recognized nucleotide pairs. Because both zinc fingers and TALEs happen in repeated patterns, different combinations can be tried to create a wide variety of sequence specificities (de Souza, N., Primer: genome editing with engineered nucleases. Nat Meth 9 (1), 27-27 (2011)). Zinc fingers have been more established in these terms and approaches such as modular assembly (where Zinc fingers correlated with a triplet sequence are attached in a row to cover the required sequence), OPEN (low-stringency selection of peptide domains vs. triplet nucleotides followed by high-stringency selections of peptide combination vs. the final target in bacterial systems), and bacterial one-hybrid screening of zinc finger libraries among other methods have been used to make site specific nucleases.

Another way of producing custom-made meganucleases, by selection from a library of variants, is described in W02004/067736. Custom made meganucleases with altered sequence specificity and DNA-binding affinity may also be obtained through rational design as described in W02007/047859. Such custom designed endonucleases are also referred to as a non-naturally occurring endonucleases.

The designed double stranded break inducing enzyme may comprise, but need not comprise, a nuclear localization signal (NLS), such as the NLS of SV40 large T-antigen (Raikhel, Plant Physiol. 100: 1627-1632 (1992) and references therein) (Kalderon et al. Cell 39: 499-509 (1984)). The nuclear localization signal may be located anywhere in the protein, but is conveniently located at the N-terminal end of the protein. The nuclear localization signal may replace one or more of the amino acids of the double stranded break inducing enzyme.

Conveniently, the DSBI enzyme can be provided by expression of a plant expressible recombinant gene(s) encoding such enzyme(s). To this end, a DNA region comprising a nucleotide sequence encoding, for example, a designed meganuclease or meganuclease monomeric unit can be operably linked to a plant-expressible promoter and optionally a DNA region involved in transcription termination and polyadenylation and introduced into a plant, plant part or plant cell(s). The recombinant gene(s) encoding DSBI enzyme may be introduced transiently or stably. The DSBI enzyme may also be introduced into the plant, plant part or plant cell(s) by introducing into the cell an RNA molecule which is translated into the DSBI enzyme. Alternatively, the DSBI enzyme may be introduced into the plant,

plant part or plant cell(s) directly as a protein. Methods for the introduction of DNA or RNA molecules or proteins into a plant, plant part, tissue or plant cell(s) are available to an art worker and briefly described below.

Described herein, the term "plant operative promoter" and "plant-expressible promoter" mean a promoter which is capable of driving transcription in a plant, plant tissue, plant organ, plant part, or plant cell. This includes any promoter of plant origin, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell.

Promoters that may be used in this respect are constitutive promoters, such as the promoter of the cauliflower mosaic virus (CaMV) 35S transcript (Hapster et al., 1988, Md. Gen. Genet. 212: 182-190), the CaMV 19S promoter (U.S. Pat. No. 5,352,605; WO 84/02913; Benfey et al., 1989, EMBO J. 8:2195-2202), the subterranean clover virus promoter

No 4 or No 7 (WO 96/06932), the Rubisco small subunit promoter (U.S. Pat. No. 4,962,028), the ubiquitin promoter (Holtorf et al., 1995, Plant Mol. Biol. 29:637-649), T-DNA gene promoters such as the octopine synthase (OCS) and nopaline synthase (NOS) promoters from Agrobacterium, and further promoters of genes whose constitutive expression in plants is available to the person skilled in the art.

Further promoters that may be used in this respect are tissue-specific or organ-specific promoters, such as seed-specific promoters, such as the 2S albumin promoter (Joseffson et al., 1987, J. Biol. Chem. 262:12196-12201), the phaseolin promoter (U.S. Pat. No. 5,504,200; Bustos et al., 1989, Plant Cell 1. (9):839-53), the legumine promoter (Shirsat et al., 1989, Mal. Gen. Genet. 215(2):326-331), the "unknown seed protein" (USP) promoter (Baumlein et al., 1991, Mal. Gen. Genet. 225(3):459-67), the napin promoter (U.S. Pat. No. 5,608,152; Stalberg et al., 1996, Planta 199: 515-519), the Arabidopsis oleosin promoter (WO 98/45461), the *Brassica* Bce4 promoter (WO 91/13980), and further promoters of genes whose seed-specific expression in plants is available to the person skilled in the art.

Plant Gene Editing

The use of meganucleases, ZFNs, CRISPR and TALEN, provides a novel strategy for genetic manipulation in plants and can assist in the engineering of desired plant traits by mutating endogenous genes.

Using engineered nucleases, or any method available to an art worker, various genes can be mutated (so as to create a deletion mutation/truncation, addition of one more nucleotides and/or mutating one or more nucleotides (changing its sequence/substitution) and not a mutation by insertion of foreign/non-endogenous DNA), including Fata1 (fatty acyl

thioesterase A 1; Moreno-Perez et al. 2012. Reduced expression of FatA thioesterases in Arabidopsis affects the oil content and fatty acid composition of the seeds. *Planta* 235: 629-39; Hawkins & Kridl. 1998. Characterization of acyl-ACP thioesterases of mangosteen (*Garcinia mangostana*) seed and high levels of stearate production in transgenic canola. *Plant J* 13: 743-52); FatA2 (fatty acyl thioesterase A 2; U.S. Patent No. 9,334,483); Kas3 (Dehesh et al. 2001. Overexpression of 3-ketoacyl-acyl-carrier protein synthase IIIs in plants reduces the rate of lipid synthesis. *Plant Phys* 125:1103-1114; Abbadi et al. 2000. Knockout of the regulatory site of 3-ketoacyl-ACP synthase III enhances short- and medium-chain acyl-ACP synthesis. *Plant J* 24: 1-9); Kas2 (Pidkowich et al. 2007. Modulating seed β -ketoacyl-acyl carrier protein synthase II level converts the composition of a temperate seed oil to that of a palm-like tropical oil. *PNAS* 104:4742-4747; Wu et al. 1994. A mutant of Arabidopsis deficient in the elongation of palmitic acid. *Plant Phys* 106: 143-150; Gupta et al. 2012. Transcriptional activation of Brassica napus β -ketoacyl-ACP synthase II with an engineered zinc finger protein transcription factor. *Plant Biotech J* 10:783-791); and/or FATB (acyl-acyl carrier protein thioesterases; Bonaventure, G. (2003) *Plant Cell*. April 15 (4) 1020-33; PCT/EP2008/005551; PCT/US2010/061226) of a plant, such as a *Cruciferae* plant, for example a *Brassica* plant, including a plant of the *Brassica napus*, *Brassica juncea*, or *Brassica rapa* species. In one embodiment, the plant is an oilseed crop, such as flax (*Linum* sp.), rapeseed (*Brassica* sp.), soybean (*Glycine* sp.), sunflower (*Helianthus* sp.), cotton (*Gossypium* sp.), corn (*Zea mays*), olive (*Olea* sp.), safflower (*Carthamus* sp.), cocoa (*Theobroma cacao*), peanut (*Arachis* sp.), hemp, oil palm, coconuts, groundnuts, sesame seed, castor bean, lesquerella, tallow tree, shea nuts, poppy seed, and/or jojoba seeds. Thus, provided herein are genes and plants, such as Brassica plants, that include modified alleles of, for example FatA1, FatA2, Kas2, Kas2 and/or FatB, that result in the production of the protein encoded by the gene to have reduced activity or no activity (as compared to wild type FatA1, FatA2, Kas2, Kas2 and/or FatB) or results in little to no protein product being produced.

For example, through use of a targeted/designed meganuclease and endogenous repair mechanisms, an insertion, substitution or deletion mutation can be created in any one of the genes described herein. A deletion mutation can be from 1 nucleotide to 400 plus nucleotides in length, including for example, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94,

95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114,
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133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150,
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313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330,
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367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384,
385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400 and so on (and
any range encompassing such numbers or the entire gene). Such deletions can result in little
to no expression of the gene (RNA and/or protein) and if protein is expressed from the gene,
20 it will have no or reduced activity as compared to a wild type gene.

The engineered nuclease is provided to plants or plant tissues via conventional methods (e.g., DNA coding for engineered nuclease is inserted into a plasmid (generally operably linked components comprising a promoter sequence, engineered nuclease, terminator (stop) sequence and optionally an antibiotic resistance gene)) which is then
25 introduced into the plant cells by any method available to the art, including for example into bacteria, such as *Agrobacterium tumefaciens*, but also by direct DNA transfer methods. Various methods for DNA delivery into cells/tissues (intact plant cells or partially degraded tissues or plant cells) are known in the art, and include electroporation as illustrated in U.S. Pat. No. 5,384,253; microprojectile bombardment (biolistics) as illustrated in U.S. Pat. Nos.
30 5,015,580; 5,550,318; 5,538,880; 6,160,208; 6,399,861; and 6,403,865; *Agrobacterium*-mediated transformation as illustrated in U.S. Pat. Nos. 5,635,055; 5,824,877; 5,591,616; 5,981,840; and 6,384,301; protoplast transformation as illustrated in U.S. Pat. No. 5,508,184, electroporation, chemically-assisted transformation, liposome-mediated transformation (see, e.g., A. Deshayes, et al. (1985) EMBO J. 4:2731-7.), carbon fiber, silicon carbide fiber or

aluminum borate fiber (generally termed whiskers) (see, e.g., J. Brisibe, Exp. Bot. 51 (343): 187-196 (2000); Dunwell (1999) Methods Mol. Biol. 111:375-82; and U.S. Pat. No. 5,464,765), micro-injection (see, e.g., T.J. Reich, et al. (1986) Biotechnology 4: 1001-1004) and viral-mediated transformation (see, e.g., S. B. Gelvin, (2005) Nat Biotechnol. 23: 684-5, 5 WO 90/12107, WO 03/052108 and WO 2005/098004), bombardment of plant cells with heterologous foreign DNA adhered to particles, ballistic particle acceleration, aerosol beam transformation (U.S. Patent Application No. 20010026941; U.S. Pat. No. 4,945,050; International Publication No. WO 91/00915; U.S. Patent Application No. 2002015066, WO 01/038514; all incorporated herein by reference), Led transformation, PEG transformation, 10 and various other non-particle direct-mediated methods to transfer DNA. As used herein "direct DNA transfer" is any method of DNA introduction into plant cells which does not involve the use of natural *Agrobacterium* spp. and which is capable of introducing DNA into plant cells.

It will also be clear that the terms used to describe the method such as "introduction of 15 a DNA" as well as "regeneration of a plant from the cell" do not imply that such DNA necessarily needs to be introduced by transformation techniques. Indeed, it will be immediately clear to the person skilled in the art that the DNA molecule of interest may also be introduced by breeding or crossing techniques from one plant to another. Thus, "introducing" in connection with the present application relate to the placing of genetic 20 information in a plant cell or plant by any known means. This can be effected by any method known in the art for transforming RNA or DNA into plant cells, tissues, protoplasts or whole plants or by introgressing said RNA or DNA into plants as described below.

In the case of introducing DNA into a plant, plant tissue or plant cell(s) in which the mutation is desired (e.g., canola plant or plant tissue; including, for example, several varieties 25 of the *Brassicaceae* plants, including for example, *Brassica napus*, *Brassica rapa*, *B. campestris* or *Brassica juncea* and mutated Brassica plants) via *Agrobacterium tumefaciens*, the plant, plant tissues, or plant cell(s) is exposed to the bacteria carrying the engineered nuclease. For example, the plant can be dipped in a solution comprising the bacterium or disks can be punched out from a plant leaf (or other plant tissue, such as the stems, can be 30 used) and incubated with a culture of plasmid-containing *A. tumefaciens*. The disks/plant tissue are then placed under conditions to generate callus in the presence of antibiotic. Only those plant cells/tissue that have DNA from the plasmid (the resistance gene) will have antibiotic resistance. The conditions therefore select for the plant cells/tissue by killing those that do not contain plasmid DNA. After resistant callus is selected, they are transferred to

medium that induces growth of shoots, where they grow roots, and then to soil to grow into mature plants.

Plants (offspring) are then selected for those which have a mutation in the desired gene (e.g., such as those listed above). The selection process can look for altered size in the gene of interest and/or protein activity (protein normally produced by the gene of interest), as well as antibiotic resistance (an extra piece of DNA that was included in the plasmid inserted into the bacteria that provides for resistance to a specific antibiotic) or by sequence. Those plants with reduced to no activity in the desired gene (expression of RNA and/or protein), as compared to plants that were not exposed to the engineered nuclease (with identical starting backgrounds), are of particular interest. If the bacteria inserted any foreign DNA into the plant, these plants can be further bred until such DNA is no longer part of the mutated plant. The plants can also be bred so that they are homozygous for the mutation (e.g., deletion).

Also provided is a method crossing one or more first parent plants that contain a mutant allele at one or more loci of FatA1, FatA2, FatB, Kas2, and/or Kas3 and one or more second parent plants that contain a mutant allele at a different locus of FatA1, FatA2, FatB, Kas2, and/or Kas3, wherein each mutant allele results in the production of a polypeptide having reduced activity (or no activity) relative to a corresponding wild-type (or a gene that was not mutated as described herein) FatA1, FatA2, FatB, Kas2, and/or Kas3 polypeptide (or no polypeptide is produced at all); and selecting progeny plants having mutants alleles at two or more different loci thereby obtaining a desired plant.

Plant Products

Oils obtained from such plants, such as Brassica plants (canola oil), can have low or no saturated fatty acids and an altered oleic acid content as compared to a plant that was not mutated as described herein (identical genetic background to plant prior to exposure to an engineered nuclease). Oil content in the seeds can be determined by methods known to those of skill in the art.

In another aspect, a method of producing an oil is provided. The method includes crushing seeds produced from at least one Brassica plant described herein; and extracting oil from the crushed seeds. Such oils can be used in food compositions, spray coatings for food, and/or for frying applications (such as frying food, so as to produce fried foods such as snack chips (e.g., corn or potato chips), French fries, or other quick serve foods).

The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

Examples

Example 1

Mutation of FatA1 with use of a meganuclease

5 Using a meganuclease specific for FatA1 (the expression of the desired meganuclease in a canola plant cell causes specific breaks in FatA1 DNA in the plant genome; repair of which leads to deletions, insertions and/or base pair changes), several canola plants with deletions in Fat1A were generated (ranging from 1 to 350 base pair deletions). This resulted in phenotypes with a decrease in C18:0 saturated fat production
10 from about 7% to about 38%, with a reduction in combined C18:0/C20:0/C22:0/C24:0 from about 6% to about 33%, as compared to plants with an identical genetic background to the plant prior to exposure to an engineered nuclease.

 Thus targeted mutation of Fat1A resulted in a significant and unexpected decrease in saturated fat production.

15 Example 2

FatA1 Mutation and Analysis

 In the Tables provided below, the fatty acids are referred to by the length of the carbon chain and number of double bonds within the chain. For example, C14:0 refers to myristic acid; C16:0 refers to palmitic acid; C18:0 refers to stearic acid; C18:1 refers to oleic
20 acid; C18:2 refers to linoleic acid; C18:3 refers to ALA; C20:0 refers to archidic acid; C20:1 refers to eicosenoic acid; C22:0 refers to behenic acid; C22:1 refers to erucic acid; C24:0 refers to lignoceric acid; and C24:1 refers to nervonic acid. "Total Sats" refers to the total of C14:0, C16:0, C18:0, C20:0, C22:0, and C24:0. Representative fatty acid profiles are provided for each of the specified samples.

25 Unless otherwise indicated, all percentages refer to fatty acid % based on total fatty acids (i.e., fatty acid moieties) in the oil.

 Brassica plants with lower saturated fatty acid were obtained by subjecting cells of Brassica plants to engineered meganucleases, followed by analysis of sequence (Figures 1-5) and saturated fatty acid production (Tables 1 and 2).

30 The average results of saturated fatty acid production in said mutant plant lines is presented in Tables 1 (IMC201 background) and Table 2 (Cargill background), showing mutated plant lines, prepared by the methods described herein having a reduction of saturated fatty acid 18:0 (stearic acid) of about 9% to about 34%, a reduction in 18/20/22/24 saturated fatty acids combined of about 5% to about 37%, and a reduction in total saturated fatty acids

of about 6% to about 14%. “WT” indicates average results for non-mutated (e.g., wild-type allele(s)) plants of the identical genetic background.

Table 1

Sample	% reduction					Total Sats	% reduction	Total Sats	% reduction
	C18:0	C18:0	C20:0	C22:0	C24:0	18/20/22/24	18/20/22/24		total sats
Mutant (IMC201)	1.84	23%	0.82	0.53	0.34	3.54	21%	8.02	11%
WT (IMC201)	2.39		1.04	0.65	0.38	4.46		8.97	

5 Table 2

Sample	% reduction					Total Sats	% reduction	Total Sats	% reduction
	C18:0	C18:0	C20:0	C22:0	C24:0	18/20/22/24	18/20/22/24		total sats
Mutant (Cargill)	1.08	28%	0.37	0.13	0.13	1.71	28%	5.30	10%
WT (Cargill)	1.49		0.48	0.14	0.20	2.31		5.90	

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25 All patents, patent applications, accession numbers and publications cited herein are incorporated herein by reference in their entirety.

WHAT IS CLAIMED IS:

1. A method to mutate the genome of a Brassica plant cell at a target site comprising:
 - a) inducing a double stranded DNA break at said target site, said double
5 stranded break being induced by the introduction to said cell of a double stranded
DNA break inducing (DSBI) enzyme which recognizes a recognition sequence in the
vicinity of or at said target site in FatA1, FatA2, Kas2, Kas3 and/or FatB gene(s); and
 - b) selecting a plant cell wherein said double stranded DNA break has been
10 repaired resulting in a modification in the genome at said target site, wherein said
modification is a substitution of at least one nucleotide, a deletion of at least one
nucleotide, an insertion of at least one nucleotide or any combination thereof.
2. The method of claim 1, wherein said plant cell is regenerated into a plant.
- 15 3. A plant cell comprising a mutation at a target site of the genome obtained by the
method of claim 1.
4. A plant, plant part, seed or propagating material thereof comprising a mutation at a
20 target site of the genome comprising the plant cell of claim 3.
5. A method to produce a Brassica plant with reduced saturated fatty acids comprising:
 - a) inducing a double stranded DNA break at a target site, said double stranded
break being induced by the introduction to a plant cell of a double stranded DNA
break inducing (DSBI) enzyme which recognizes a recognition sequence in the
25 vicinity of or at said target site in FatA1, FatA2, Kas2, Kas3 and/or FatB gene(s); and
 - b) selecting a plant cell wherein said double stranded DNA break has been
repaired resulting in a mutation in the genome at said target site, wherein said
mutation is a substitution of at least one nucleotide, a deletion of at least one
nucleotide, an insertion of at least one nucleotide or any combination thereof; and
30 c) regenerating said plant cell(s) of b) into a plant;
wherein said mutation results in reduced production of saturated fatty acids by
said plant as compared to a control plant of identical genetic background that has not
been mutated by said DSBI and repair.

6. The method of claim 1 or 5, wherein the DSBI enzyme is a single chain meganuclease or a pair of meganucleases which recognizes or recognize in concert a site and induces or induce said double strand break.
- 5 7. The method of any of claims 2 or 5 to 6, wherein said plant is crossed with another plant.
8. A plant, plant part, seed or propagating material thereof comprising a mutation at a target site of the genome obtained by the method of any one of claims 2 or 5 to 7.
- 10 9. The method of any one of claims 1 to 8, wherein the plant is *Brassica napus*, *Brassica juncea*, or *Brassica rapa*.
10. The method of any one of claims 1 to 8, wherein one or both FatA1 alleles on N3, N7, 13 and/or N17 are mutated.
- 15 11. The method of claim 10, wherein one or both FatA1 alleles on N13 and/or N17 are mutated.
- 20 12. The method of claim 11, wherein one or both FatA1 alleles on N13 are mutated.
13. The method of claim 10, wherein one or both FatA1 alleles on N3, N7 and/or N13 are mutated.
- 25 14. The method of claim 13, wherein one or both FatA1 alleles on N7 are mutated.
15. The method of any one of claims 10 to 14, wherein the mutation is a deletion of one or more nucleotides.
- 30 16. The method of claim 15, further comprising at least one substitution mutation.
17. The method of any one of claims 2 or 5 to 16, wherein the plant yields a reduction of stearic acid (18:0) of about 9% to about 35% as compared to a non-mutated plant of identical genetic background.

18. The method of any one of claims 2 or 5 to 16, wherein the plant yields an overall reduction in total saturated fatty acids of about 5% to about 15%.
- 5 19. A mutated Brassica plant comprising a deletion in at least one allele of FatA1, FatA2, Kas2, Kas3 and/or FatB.
20. The mutated plant of claim 19, wherein the deletion is from about 1 to about 350 base pairs in length.
- 10 21. The mutated plant of claims 19 or 20, wherein the mutation results in a decrease in the production of saturated fatty acid(s) by the mutated plant.

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ATGTCTCTCCATCTCCACTACCGGCTCTGTCAATTGTAACAGATCCCATCCTCCTTTTTAGATCTACAAATAATTAAC
TTCTCATCATCTCTCTTATGTGTGGCTTTGATTTTGTTCAGGTTGAAGAATCGAAGGGTGGAGACGAACCAATGG
AGCGATGTGGTGATGACAGAGGAAGAGGGGATTCAGTTTCTAATGGTGGACGCTCGTCACAGATCTTTTGCAGGT
TAGATTGTAGATAGTTAAACTATGTATGAATTTTATTGGTCAATATTTAAAAAAAATAACTTTTGTGTTGGTT
TGATGTATGTGAGGAGGTGCGATGTAATCAGTTTCAGAGCGTTGCATTTTCGACTGATGGGATTGCGACAACACCT
ACCATGAGGAACTGAATCTCATTTGGGTCACCTCGAGAATGCACATTGAGATCTACAGATATCCAGCTTGGTATT
GTTTTTTCATTTTTGCTCTGTATGTTTGTGACAACAAATGGATTGAATTTTTGAAAATTTTGGTTACAGGGGTGAT
GTGGTTGAGATAGAGACATGGTGTGAGAGTGAAGGAAGGATCGGGACAAGGCGTGATTGGATTCTTAAGGACAT
TGCTAACGCTGAAGTCACTGGCTGTGCTACTAGGTTTCCTTCTCATTTTTTGTCTTCTCCATTGGTTGTGCAA
TAGAATTAATTTTTCTTATGTTAAAGATATAACTTTTCAGTTACTTGGATTTATGTTAAAGATATAATTTTCATTTCCG
AGCACTTGATGTTCTGTCTTAAAGAACCCAGGTAAGGAAGGAACTTTGTGTCCAGGTCAATGCAATGCTTGCTGGTCA
ATCATATCGTTATATTCATGAAATGCCACTACTATGTTTTATGTATATCTTTGTAGATTAGCATTTCCTGTGGAGGA
AAATAACAGAAGCTTGAAGAAAATCCCCACACTCGAAGATCTAGCTAAGTACTCAATCATTGGACTAAAGGTATAA
AATAGAAAAATAATATTCTTTGTAGGAATCAACATTCCTAGAGGACTTTATAATCATGTTTCTTTGCAGCCAAGACG
AGCTGATCTCGACATGAACCATCATGTCAATAATTTACCTATATTGGATGGATTCTTGAGGTTAGTGTATCATCA
GGTTCTTTTTAAAATAATAACTTCAGTAATCACCATATGACTTTGTTTTCTGATATTGTCAGAGCATACTCAAGAGAT
TGTAGACACGCATGAACTTTGGATTACAGACGAGAATGTCAGCAAGACGATGTGGTGGATTCACTCACCACCTCA
AAGAATGGCTCTGCAACATCAGGCACACAAAGCCACAACGATAGCCAGTTCTTATCTGGAGATGGTCAGGAGATC
AACTGTGGGACAACCCTGTGGAGAAAGAAGCCCTCCAGATAGACAATCCCTAAGCCATTACGAGTCAAGGACCAA
TCATTTTCACATAAACCTCTTTGCTTATTTGATTAAACAAGTTACATGACTGATAACAGATTCTGCCTATTACAAAGT
CTCATAAATTTCAAATAATGTGAGTAAATAAATAGAAAACAGAGAATTGG (SEQ ID NO:1)

FIG. 1

GGATAAATGTCCTTCTCCATCTCCTGTTCCCATATAAGAAAACCTGGTTTGAGTCCTCTGCGGGCGGGCTGTATCTGCT
 GATCAAGAAAAGTGTGATTGAGCAGAACAAAGGTTTGGACACACTCGCGGGTCGGCTCCGGTTGGGTAGCTTGAC
 GGAGGATGGTTTATCGTATAAAGAGAAGTTCATAGTCAGATCCCACGAAGTGCAGAGTAACAAAACCGCTACGGT
 CCAAACCATTGCCAATCTTTG CAGGTTAGATTGTAGTTTGTAAAACCTATGTATGAATCTTGATTGGTCAATATTT
 TAAAAATAAGAATTTTATTTTGTGGTTTGATGTATTTAGGAGGTGGGATGTAATCAGTTTCAGAGCGTTGGATTTT
 CGACTGATGGGTTTGCGACAACACCTACCATGAGGAACTGAATCTCATTGGGTCACTTCGAGAATGCACATTGG
 GATTTACAAATATCCAGCTTGGTATTTTTTTCTTCTGCTGTGTATGTTTTGATGACACAACAAATGAGCAGAGATTTT
 GAAATTTTTGGTTACAGGGGTGATGTGGTTGAGATAGAGACATGGTGTGAGAGTGAAGGAAGGATCGGGACAAG
 CGATGATTGGATTCTTAAGGATGTTGCTAACGGTGAAGTCACTGGCCGTACTACTAGGTTTCCCTCTCATCA (SEQ
 ID NO:2)

FIG. 2A

GGATAAATGTCCTTCTCCATCTCCTGTTCCCATATAAGAAAACCTGGTTTGAGTCCTCTGCGGGCGGGCTGTATCTGCT
 GATCAAGAAAAGTGTGATTGAGCAGAACAAAGGTTTGGACACACTCGCGGGTCGGCTCCGGTTGGGTAGCTTGAC
 GGAGGATGGTTTATCGTATAAAGAGAAGTTCATAGTCAGATCCCACGAAGTGCAGAGTAACAAAACCGCTACGGT
 CCAAACCATTGCCAATCTTTG CAGGTTAGATTGTAGTTTGTAAAACCTATGTATGAATCTTGATTGGTCAATATTT
 TAAAAATAAGAATTTTATTTTGTGGTTTGATGTATTTAGGAGGTGGGATGTAATCAGTTTCAGAGCGTTGGATTTT
 CGACTGATGGGTTTGCGACAACACCTACCATGAGGAACTGAATCTCATTGGGTCACTTCGAGAATGCACATTGG
 GATTTACAAATATCCAGCTTGGTATTTTTTTCTTCTGCTGTGTATGTTTTGATGACACAACAAATGAGCAGAGATTTT
 GAAATTTTTGGTTACAGGGGTGATGTGGT-----
 GTCAGAGTGAAGGAAGGATCGGGACAAGGCATGATTGGATTCTTAAGGATGTTGCTAACGGTGAAGTCACTGGC
 CGTACTACTAGGTTTCCCTCTCATCA (SEQ ID NO:3)

FIG. 2B

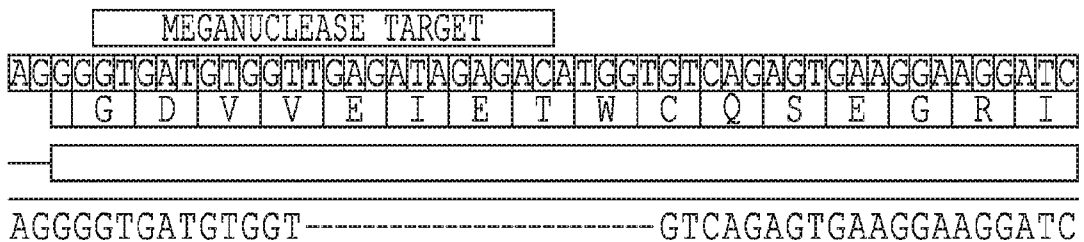


FIG. 2C

GGATAAATGTCCTTCTCCATCTCCTGTTCCCATATAAGAAAACCTGGTTTGAGTCCTCTGCCGGGCGGCTGTATCTGCT
 GATCAAGAAAGTGTGATTTCGAGCAGAACAAGGTTTGGACACACTCGCGGGTCCGGTCCGGTTGGGTAGCTTGAC
 GGAGGATGGTTTATCGTATAAAGAGAAGTTCATAGTCAGATCCCACGAAAGTGCAGAGTAACAAAACCGCTACGGT
 CCAAACCATTGCCAATCTTTTGCAGGTTAGATTGTAGTTTGTAAAACCTATGTATGAATCTTGATTGGTCAATATTT
 TAAAAATAAGAATTTTATTTTGTGGTTTGATGTATTTAGGAGGTGGGATGTAATCAGTTTCAGAGCGTTGGATTTT
 CGACTGATGGGTTTGCACAAACACCTACCATGAGGAAACTGAATCTCATTGGGTCACTTCGAGAATGCACATTGA
 GATTTACAAATATCCAGCTTGGTATTTTTTTTTGCTGTGTATGTTTTGATGACACAACAAATGAGCAGAGATTTTG
 AAATTTTGGTATAGGGGTGATGTGGTTGAGA-----
 CATGGTGTGAGAGTGAAGGAAGGATCGGGACAAGGCGTGATTGGATTCTTAAGGATCTTGCTAACGGTGAAGTC
 ACTGGCCGTACTACTAGGTTTCCCTCTCATCA (SEQ ID NO:7)

FIG. 2D

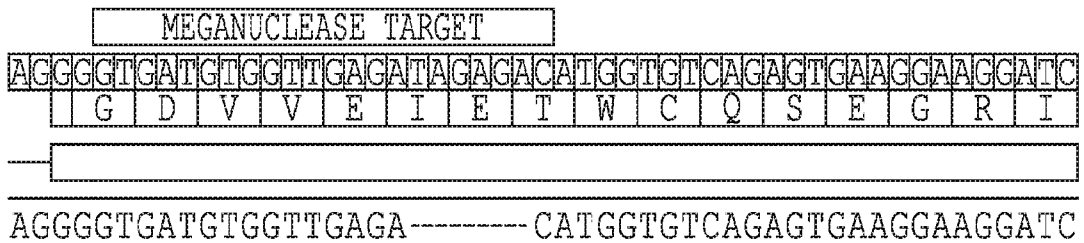


FIG. 2E

TCAATCTTGATTGGTGGAAATTTGTAAGACAAGAACTTTGTTGGTTGGTTGATGTGTATATTATAGGAGGTGGGAT
 GTAATCATGCCGAGAGCGTTGGATTCTCGACTGATGGGTTTGCACAAACACCGACAATGAGGAAACTGCATCTCA
 TTTGGGTCACCTGCGAGAATGCATATAGAGATCTACAAGTACCCTGCTTGGTATTTGGTTTCTGCTTCGTTTCTTTTA
 TCTATGTGTCTCTGTTTTGATGACAACCTAATGAGAGGAATCTTTGGTTACAGGGGTGATGTGGTTGAGATAGAG
 ACATGGTGTGAGAGTGAAGGAAGGATCGGGACTAGGCGTGATTGGATTCTTAAGGATGTTGCTACGGGTGAAGT
 CACTGGCCGTGCTACAAGGTTTCCTTTTCATCATTTTTTTTAGCTTCTGGATTGGTTTGGACCTTATGTTCCGTAT
 TTAATGGTATTGTCGTGATTTGTTGTTTGAC (SEQ ID NO:9)

FIG. 3A

TCAATCTTGATTGGTGGAAATTTGTAAGACAAGAACTTTGTTGGTTGGTTGATGTGTATATTATAGGAGGTGGGAT
 GTAATCATGCCGAGAGCGTTGGATTCTCGACTGATGGGTTTGCACAAACACCGACAATGAGGAAACTGCATCTCA
 TTTGGGTCACCTGCGAGAATGCATATAGAGATCTACAAGTACCCTGCTTGGTATTTGGTTTCTGCTTCGTTTCTTTTA
 TCTATGTGTCTCTGTTTTGATGACAACCTAATGAGAGGAATCTTTGGTTACAGGGGTGATGTGGTTGAGA-----
 CATGGTGTGAGAGTGAAGGAAGGATCGGGACTAGGCGTGATTGGATTCTTAAGGATGTTGCTACGGGTGAAGTC
 ACTGGCCGTGCTACAAGGTTTCCTTTTCATCATTTTTTTTAGCTTCTGGATTGGTTTGGACCTTATGTTCCGTATT
 TAATGGTATTGTCGTGATTTGTTGTTTGAC (SEQ ID NO: 10)

FIG. 3B

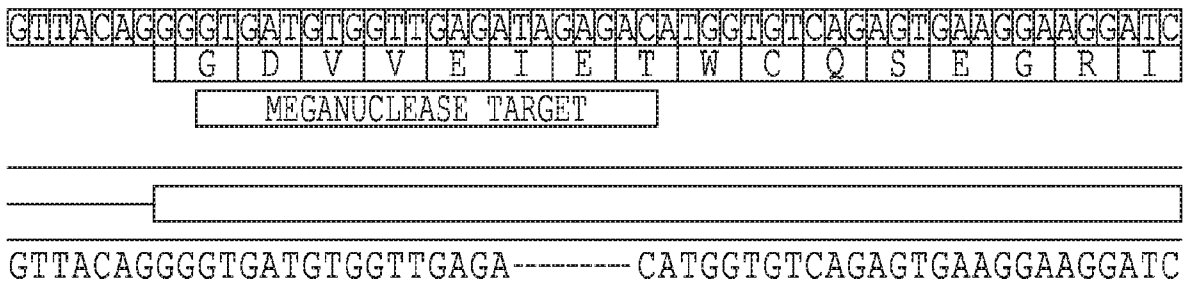


FIG. 3C

GATTTTCGACTGATGGGTTTGCAACAACACCTACCATGAGGAACTGAATCTCATTGGGGTCACTTCGAGAATGCA
 CATTGAGATTTACAAATATCCAGCTTGGTATTTTTTTTTGCTGTGTATGTTTTGATGACACAACAAATGAGCAGAG
 ATTTTGAAATTTGGTATAGGGGTGATGTGGTTGAGATAGAGACATGGTGTGAGAGTGAAGGAAGGATCGGGAC
 AAGGCGTGATTGGATTCTTAAGGATCTTGCTAACGGTGAAGTCACTGGCCGTGCTACTAGGTTCCCTCTCATCATT
 GTTAGCTTTCTCCATTGGTTGTGCAATGGAATTAATTTTCTTATGTTAAAGATATAATTTTCAGTTACTTGGATT
 ATGGGACTGTCATGATTTGTTGTACCTATGTTTGTGTTACTGTTTCAGCAAGTGGGTGATGATGAACCAAGACACA
 AGACGGCTACAGAAAGTTTCTGATGATATCCGGGACGAGCACTTGATT (SEQ ID NO:13)

FIG. 4A

GATTTTCGACTGATGGGTTTGCAACAACACCTACCATGAGGAACTGAATCTCATTGGGGTCACTTCGAGAATGCA
 CATTGAGATTTACAAATATCCAGCTTGGTATTTTTTTTTGCTGTGTATGTTTTGATGACACAACAAATGAGCAGAG
 ATTTTGAAATTTGGTATAGGGGTGATGTGGTTGA-----
 AGGAAGGATCGGGACAAGGCGTGATTGGATTCTTAAGGATCTTGCTAACGGTGAAGTCACTGGCCGTGCTACTAG
 GTTCCCTCTCATCATTGTTAGCTTTCTCCATTGGTTGTGCAATGGAATTAATTTTCTTATGTTAAAGATATAATTT
 TCAGTTACTTGGATTTATGGGACTGTCATGATTTGTTGTACCTATGTTTGTGTTACTGTTTCAGCAAGTGGGTGATG
 ATGAACCAAGACACAAGACGGCTACAGAAAGTTTCTGATGATATCCGGGACGAGCACTTGATT (SEQ ID NO:14)

FIG. 4B

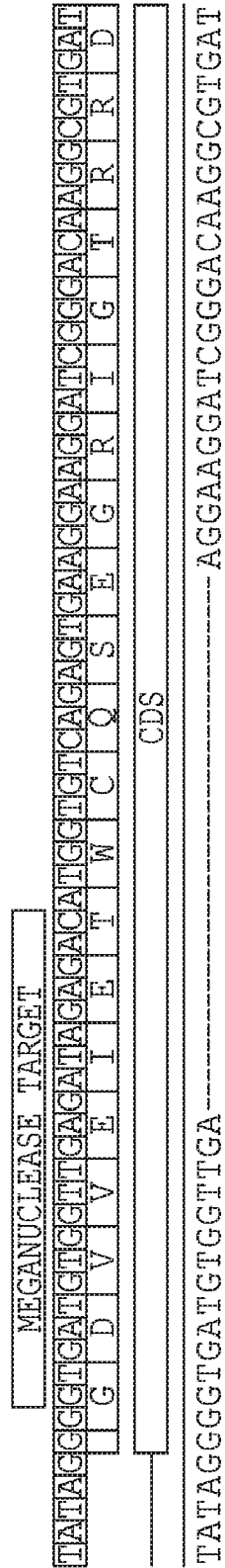


FIG. 4C

TATGAATGGAAAAAAGTATCAATCTTTGTAATTATGAATCTTGATTGGTCAATTGTGAAAGACAAGA AACTTTGTTG
 GTTGATTGATGTGTATATAGGAGGTGGGATGTAATCATGCTCAGAGCGTAGGATTCTCGACTGATGGGTTTGCGA
 CAACACCTACCATGAGGAAATTGCATCTCATTTGGGTCCTGCCAGAATGCACATTGAGATCTACAAGTACCCTGC
 TTGGTATTGGTTTCTGCTTCATCTGTCTATCTATCTAGATGTGTCTCTGTTTTGATGACAACCTAACGAGGAATCTTC
 GGTTTACAGGGGTGATGTGGTTGAGATAGAGACATGGTGTGAGAGTGAAGGAAGGATCGGGACTAGGCGTGATT
 GGATTCTTAAGGATGTTGCTACCGGTGAAGTCACTGGCCGTGCTACAAGGTTTCCTTTTCATCATTTTTTAGCTTCC
 GGGATTGGTTTGGGACCTTAATGTTCCGATTTTTATGGTGCTGTCTGATTGTTGTTTG (SEQ ID NO:18)

FIG. 5A

TATGAATGGAAAAAAGTATCAATCTTTGTAATTATGAATCTTGATTGGTCAATTGTGAAAGACAAGA AACTTTGTTG
 GTTGATTGATGTGTATATAGGAGGTGGGATGTAATCATGCTCAGAGCGTAGGATTCTCGACTGATGGGTTTGCGA
 CAACACCTACCATGAGGAAATTGCATCTCATTTGGGTCCTGCCAGAATGCACATTGAGATCTACAAGTACCCTGC
 TTGGTATTGGTTTCTGCTTCATCTGTCTATCTATCTAGATGTGTCTCTGTTTTGATGACAACCTAACGAGGAATCTTC
 GGTTTACAGGGGTGATGTGGTTGA-----
 AGGAAGGATCAGGACTAGGCGTGATTGGATTCTTAAGGATGTTGCTACCGGTGAAGTCACTGGCCGTGCTACAAG
 GTTTCCTTTTCATCATTTTTTAGCTTCCGGGATTGGTTTGGGACCTTAATGTTCCGATTTTTATGGTGCTGTCTGAT
 TTGTTGTTTG (SEQ ID NO 19)

FIG. 5B

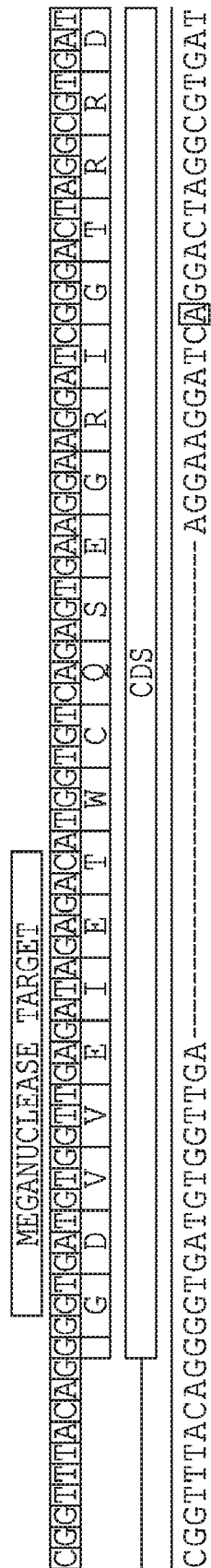


FIG. 5C

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2017/034541

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12N15/82
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED
Minimum documentation searched (classification system followed by classification symbols)
C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, BIOSIS, Sequence Search, EMBASE, WPI Data

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Further documents are listed in the continuation of Box C. See patent family annex.

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"P" document published prior to the international filing date but later than the priority date claimed	"&" document member of the same patent family

Date of the actual completion of the international search 27 July 2017	Date of mailing of the international search report 07/08/2017
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Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Authorized officer Kania, Thomas
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International application No
PCT/US2017/034541

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