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(54) **Titre** : GENE CAPABLE D'AMELIORER LA PRODUCTIVITE D'UNE SUBSTANCE DANS UNE SEMENCE, ET SON PROCEDE D'UTILISATION

(54) **Title**: GENE CAPABLE OF IMPROVING MATERIAL PRODUCTIVITY IN SEED AND METHOD FOR USE THEREOF

(57) **Abrégé/Abstract**:

An object of the present inventioin is to search for a gene having a novel function that can cause an increase or decrease in material productivity, and particularly, fat and oil content. In the present invention, a chimeric protein obtained by fusing a transcription factor consisting of a protein comprising an amino acid sequence shown in any of the even-numbered SEQ ID NOS: 1 to 158 and a functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor is expressed in a plant.

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ABSTRACT

An object of the present inventioin is to search for a gene having a novel function that can cause an increase or decrease in material productivity, and particularly, fat and oil content. In the present invention, a chimeric protein obtained by fusing a transcription factor consisting of a protein comprising an amino acid sequence shown in any of the even-numbered SEQ ID NOS: 1 to 158 and a functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor is expressed in a plant.

GENE CAPABLE OF IMPROVING MATERIAL PRODUCTIVITY IN SEED AND METHOD FOR USE THEREOF

This application is a divisional application of co-pending application Serial No. 2,764,589, filed June 4, 2010.

Technical Field

Background Art

[0001] Plants are cultivated for the purpose of using some tissues thereof (e.g., seeds, roots, leaves, or stems) or for the purpose of producing various substances (materials), such as fats and oils. Examples of fats and oils produced from plants that have been heretofore known include soybean oil, sesame oil, olive oil, coconut oil, rice oil, cottonseed oil, sunflower oil, corn oil, safflower oil, palm oil, and rapeseed oil. Such fats and oils are extensively used for household and industrial applications. Also, fats and oils produced from plants are used as raw materials for biodiesel fuel or bioplastic, and the applicability thereof is increasing for alternative energy to petroleum.

[0002] Under such circumstances, it is necessary to improve productivity per unit area of cultivated acreage in order to succeed in the industrial production of fats and oils using plants. Here, assuming that the number of cultivated plant individuals per unit area of cultivated acreage is stable, it can be understood that the fat and oil production per plant individual needs to be improved. When fats and oils are collected from seeds obtained from plants, it is expected that the fat and oil production per plant individual can be improved by techniques for improving the seed yield per plant individual, techniques for improving the fat and oil content in seeds, and similar techniques.

[0003] Techniques for improving the fat and oil production in plant seeds are roughly divided into the improvement of cultivation and the development of varieties with increased fat and oil productivity. Methods for developing varieties with increased fat and oil productivity are roughly divided into conventional breeding methods mainly involving crossing technology and molecular breeding methods comprising gene recombination. The following are known techniques for increasing fat and oil productivity via gene recombination: (A): a technique for modifying a system for synthesizing triacylglycerol (TAG) contained in seeds as a main component of plant fat and oil; and (B): a technique for modifying various regulatory genes that regulate plant morphogenesis or metabolism and expression of genes involved plant morphogenesis or metabolism.

[0004] Regarding technique (A), the following methods can be used as a method for increasing the amount of TAG syntheseized using, as a starting material, a sugar produced via photosynthesis: (1): a method for increasing activity of synthesizing fatty acid or glycerol that is a constitutive component of TAG from a sugar; (2): a method for enhancing a reaction of synthesizing TAG from glycerol and fatty acid. In relation to the above technique, the following have been reported as gene engineering techniques. In one example of method (1), the fat and oil content in seeds was reportedly improved by 5% by causing *Arabidopsis thaliana* cytoplasm acetyl-coenzyme A carboxylase (ACCase) to be overexpressed in rapeseed plastids (Non-Patent Document 1). In one example of (2), a technique for increasing fat and oil productivity by causing overexpression of DGAT (diacylglycerol acyltransferase) capable of transfering an acyl group at the sn-3 position of diacylglycerol (Non-Patent Document 2) was reportedly developed. Regarding the technique of Non-Patent Document 2, fat and oil content and seed weight were reported to have increased with an increase in

DGAT expression level, which might cause an increase in the number of seeds per plant individual. By the use of this method, the fat and oil content in seeds of *Arabidopsis thaliana* was found to have increased by 46%, and the fat and oil amount per plant individual was found to have increased by up to approximately 125%.

[0005] Meanwhile, one possible example of technique (B) is a method for regulating the expression of a transcription factor gene involved in the regulation of expression of a biosynthetic enzyme gene. Patent Document 1 discloses such method. According to the technique used in Patent Document 1, a recombinant plant in which a transcription factor is exhaustively overexpressed or knocked out is prepared, followed by selection of a gene that causes an increase in the fat and oil content in seeds. Patent Document 1 describes that the fat and oil content in seeds was found to have increased by 23% as a result of overexpression of the ERF subfamily B-4 transcription factor gene. However, Patent Document 1 does not describe an increase or decrease in the fat and oil content per plant individual. Non-Patent Document 3 describes that the fat and oil content in seeds can be improved by causing the overexpression of WRINKLED1, which is a transcription factor having an AP2/EREB domain.

[0006] Meanwhile, when a hydrocarbon component such as cellulose contained in a plant is glycosylated and then alcohol is produced via fermentation, it can be predicted that fat and oil components contained in a plant become impurities and thus cause reduction of glycosylation efficiency in the glycosylation step. Therefore, if the fat and oil content can be reduced, the glycosylation efficiency in the glycosylation step can be improved. As a result, improvement of alcohol productivity can be expected. For example, Non-Patent Document 3 discloses that seeds of a WRI1/ASML1 (AP2 family transcription factor; AGI-code:AT3g54320)-deficient strain become wrinkled, resulting in reduction of the fat and oil content. In addition, Patent Document 2 discloses that overexpression of AT3g23250 (MYB15) resulted in a 13% decrease in the fat and oil content in seeds, overexpression of AT1g04550 (IAA12) resulted in a 12% decrease in the same, and overexpression of AT1g66390 (MYB90) resulted in a 16% decrease in the same.

[0007] In spite of the development of the above molecular breeding methods for the improvement of a variety of traits, there are still no practically available techniques to increase or decrease fat and oil productivity.

[0008] As reasons for the above, it is considered that truly excellent genes remain undiscovered, and that new recombinant varieties that have been confirmed to have desirable effects in the test phase cannot exhibit expected effects upon practical use in differerent natural environments. In addition, a number of genes are involved in the expression of quantitative traits such as productivity of a desired material in different steps in the regulation system, the metabolizing system, and other systems. Thus, it has been difficult to discover or develop truly excellent and useful genes capable of improving quantitative traits. In order to solve such problems, an object of the present invention is to find a novel gene exhibiting remarkably high effects. Another object of the present invention is to develop a gene capable of exerting effects in a pracitcal environment to an extent comparable to the effects exereted in the test phase.

Citation List

Patent Literature

[0009]

Patent Document 1: WO01/36597

Patent Document 2: WO01/35727

Non-Patent Literature

[0010]

Non-Patent Document 1: Plant Physiology (1997) Vol. 11, pp. 75-81

Non-Patent Document 2: Plant Physiology (2001), Vol. 126, pp. 861-874

Non-Patent Document 3: Plant J. (2004) 40, 575-585

Summary of Invention

Technical Problem

[0011] In view of the above circumstances, an object of the present invention is to provide a technique for searching for a gene having a novel function that can cause an increase or decrease in material productivity so as to improve such feature of a plant.

Solution to Problem

[0012] As a result of intensive studies to achive the above objects, the present inventors found that it is possible to improve various quantitative traits and particularly to increase or decrease material productivity via induction of expression of a chimeric protein obtained by fusing a particular transcription factor and a functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor (hereinafter sometimes referred to as a "repressor domain"). This has led to the completion of the present invention.

[0013] The plant of the present invention is obtained by inducing expression of a chimeric protein obtained by fusing a transcription factor consisting of any one of the following proteins (a) to (c) and a functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor.

[0014]

(a) A protein comprising an amino acid sequence shown in any of the even-numbered SEQ ID NOS: 1 to 158

(b) A protein having transactivation activity and comprising an amino acid sequence that has a deletion, a substitution, an addition, or an insertion of one or a plurality of amino acids with respect to an amino acid sequence shown in any of the even-numbered SEQ ID NOS: 1 to 158.

(c) A protein having transactivation activity encoded by a polynucleotide that hybridizes under stringent conditions to a polynucleotide consisting of a nucleotide sequence complementary to a nucleotide sequence shown in any of the odd-numbered SEQ ID NOS: 1 to 158.

Preferably, the fusion of a functional peptide with a predetermined transcription factor causes repression of transcriptional regulatory activity, and particularly, transactivation activity, of the transcription factor in the plant of the present invention. Examples of the above functional peptide used herein include peptides expressed by the following formulae (1) to (8).

[0015]

(1) X1-Leu-Asp-Leu-X2-Leu-X3

(where X1 denotes a set of 0 to 10 amino acid residues, X2 denotes Asn or Glu, and X3 denotes a set of at least 6 amino acid residues.)

(2) Y1-Phe-Asp-Leu-Asn-Y2-Y3

(where Y1 denotes a set of 0 to 10 amino acid residues, Y2 denotes Phe or Ile, and Y3 denotes a set of at least 6 amino acid residues.)

(3) Z1-Asp-Leu-Z2-Leu-Arg-Leu-Z3

(where Z1 denotes Leu, Asp-Leu, or Leu-Asp-Leu, Z2 denotes Glu, Gln, or Asp, and Z3 denotes a set of 0 to 10 amino acid residues.)

(4) Asp-Leu-Z4-Leu-Arg-Leu

(where Z4 denotes Glu, Gln, or Asp.)

(5) α1-Leu-β1-Leu-γ1-Leu

(6) α1-Leu-β1-Leu-γ2-Leu

(7) α1-Leu-β2-Leu-Arg-Leu

(8) α2-Leu-β1-Leu-Arg-Leu

(where α1 denotes Asp, Asn, Glu, Gln, Thr, or Ser, α2 denotes Asn, Glu, Gln, Thr, or Ser, β1 denotes Asp, Gln, Asn, Arg, Glu, Thr, Ser, or His, β2 denotes Asn, Arg, Thr, Ser, or His, γ1 denotes Arg, Gln, Asn, Thr, Ser, His, Lys, or Asp, and γ2 denotes Gln, Asn, Thr, Ser, His, Lys, or Asp in formulae (5) to (8).)

In addition, the plant of the present invention is characeterized by significant improvement or reduction of material productivity per plant individual and particularly productivity of fat and oil contained in seeds. A specific tissue used in the present invention can be seed tissue. Here, the expression "significant improvement or reduction" indicates that the plant of the present invention allows an increase or decrease in the material productivity associated with a statistically significant difference when compared in terms of material productivity with a plant in which the above chimeric protein is not expressed.

[0016] Meanwhile, according to the present invention, the above chimeric protein, the gene encoding the chimeric protein, an expression vector comprising the gene, and a transformant comprising the gene can be provided.

[0017] This description includes part or all of the contents as disclosed in the description and/or drawings of Japanese Patent Application No. 2009-135321, which is a priority document of the present application.

Advantageous Effects of Invention

[0018] The material productivity per plant individual (and particularly the fat and oil content in seeds) is improved or reduced in the plant of the present invention. Therefore, the use of the plant of the present invention enables improvement of productivity of plant-derived fats and oils. Alternatively, for example, bioalcohol or the like can be produced with good efficiency using the plant of the present invention in which fats and oils contained as impurities can be reduced.

Description of Embodiments

[0019] The present invention will be described in detail as follows.

[0020] The plant of the present invention is a plant in which a chimeric protein obtained by fusing a predetermined transcription factor and a functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor is expressed. The plant of the present invention is found to exhibit significant improvement or reduction of the material productivity per plant individual (and particularly the fat and oil content in seeds) when compared with a wild-type plant. Specifically, the plant of the present invention is produced by causing a transcription factor to be expressed in the form of a chimeric protein with the functional peptide in a desired plant so as to significantly improve or reduce the material productivity of the desired plant.

[0021] In particular, preferably, the transactivation activity of a transcription factor is repressed in the plant of the present invention by fusing the factor with the above functional peptide. In other words, when a chimeric protein obtained by fusing a transcription factor with the functional peptide is expressed in the plant of the present invention, this preferably results in expression of transcription repression effects originally imparted to the functional peptide as a dominant trait.

[0022] Here, the term "material productivity per plant individual" refers to the content of an individual substance (material) produced per unit volume of a plant. Such substance is not particularly limited. It may be a substance originally produced by a plant. Alternatively, it may be a substance that is not originally produced in a plant but can be produced in the plant via genetic engineering or the like.

[0023] In particular, if the content of a desired product per tissue increases, purification cost or transport cost can be reduced. Thus, such plant is highly industrially applicable. A particularly desired product may be lignocellulose, which accounts for the substantially total weight of a plant. It may be a plant oil industrially available as a seed oil. A plant oil may be composed of simple lipid in the form of ester of fatty acid and alcohol or of complex lipid containing phosphorus, sugar, nitrogen, and other components. It may be fatty acid itself. Examples of alcohol that can be used for simple lipid include higher alcohol with a large molecular weight and polyalcohol such as glycerol (glycerine). Examples of fatty acid that can be used for simple lipid include saturated fatty acid, unsaturated fatty acid, and specialty fatty acid containing a hydroxyl group or an epoxy group. Examples of simple lipid that can be used in the form of ester of glycerol and fatty acid include monoacylglycerol, diacylglycerol, and triacylglycerol.

[0024] Meanwhile, certain substances contained in plants becomes impurities depending on the use of the plants. Therefore, if productivity of such a certain substance in a plant decreases, the impurity content decreases. Such plant is highly industrially applicable. For example, in the case of glycosylation of lignocellulose contained in a plant, fat and oil components contained in the plant might become impurities and thus negatively influence glycosylation efficiency. Therefore, if the fat and oil productivity decreases, the efficiency of the glycosylation step in the process of producing bioalcohol or the like using a plant can be improved.

[0025] Fats and oils are described below as examples of target substances for productivity improvement or reduction. However, the technical scope of the present invention is not limited thereto. The present invention can be applied to substances other than fat and oil that are produced by plants.

[0026] Plants used herein are not particularly limited, and thus any plant can be used as a target plant. Particularly preferably, a plant conventioinally used for production of fat and oil is used. Examples of an available target plant include soybean, sesame, olive oil, coconut, rice, cotton, sunflower, corn, sugarcane, Jatropha, palm, tobacco, safflower, and rapeseed. Also, *Arabidopsis thaliana*, which has been widely used as an biological model for plant gene analysis and for which gene expression analysis methods have been established, can be used as a target plant.

[0027] In addition, transcription repression activity of a chimeric protein comprising a transcription factor is activity of recognizing a cis sequence that is recognized by the transcription factor or a cis sequence of a different transcription factor that is analogous to such a cis sequence so as to actively repress the expression of downstream genes. Thus, such chimeric protein can also be called a "transcriptional repressor." A method for causing a chimeric protein comprising a transcription factor to have transcription repression activity is not particularly limited. However, in particular, the most preferable method may be a method for constructing a chimeric protein (fusion protein) by adding a repressor domain sequence or an SRDX sequence thereto.

[0028] In the above method, as a repressor domain sequence, a variety of amino acid sequences discovered by the present inventors, each of which constitutes a peptide capable of converting an arbitrary transcription factor into a transcriptional repressor, can be used. For example, the following can be referred to for a method using a repressor domain sequence: JP Patent Publication (Kokai) No. 2001-269177 A; JP Patent Publication (Kokai) No. 2001-269178 A; JP Patent Publication (Kokai) No. 2001-292776 A; JP Patent Publication (Kokai) No. 2001-292777 A; JP Patent Publication (Kokai) No. 2001-269176 A; JP Patent Publication (Kokai) No. 2001-269179 A; WO03/055903; Ohta, M., Matsui, K., Hiratsu, K., Shinshi, H. and Ohme-Takagi, M., The Plant Cell, Vol. 13, 1959-1968, August, 2001; and Hiratsu, K., Ohta, M., Matsui, K., or Ohme-Takagi, M., FEBS Letters 514(2002) 351-354. A repressor domain sequence can be excised from a Class II ERF (Ethylene Responsive Element Binding Factor) protein or a plant zinc finger protein (zinc finger protein such as *Arabidopsis thaliana* SUPERMAN protein). The sequence has a very simple structure.

[0029] Examples of a transcription factor constituting a chimeric protein to be expressed include transcription factors specified by AGI codes for *Arabidopsis thaliana* listed in tables 1 and 2. In addition, any transcription factor listed in table 1 causes a significant increase in fat and oil content in seeds when a chimeric protein comprising the transcription factor and a repressor domain is expressed in a plant. Meanwhile, any transcription factor listed in table 2 causes a significant decrease in fat and oil content in seeds when a chimeric protein comprising the transcription factor and a repressor domain is expressed in a plant.

[Table 1]

AGI code	Nucleotide sequence	Amino acid sequence
At5g47230	SEQ ID NO 1	SEQ ID NO 2
At1g22985	SEQ ID NO 3	SEQ ID NO 4
At1g80580	SEQ ID NO 5	SEQ ID NO 6
At1g25470	SEQ ID NO 7	SEQ ID NO 8
At1g67260	SEQ ID NO 9	SEQ ID NO 10
At4g36160	SEQ ID NO 11	SEQ ID NO 12
At5g64750	SEQ ID NO 13	SEQ ID NO 14
At4g01550	SEQ ID NO 15	SEQ ID NO 16
At1g24260	SEQ ID NO 17	SEQ ID NO 18
At5g09330	SEQ ID NO 19	SEQ ID NO 20
At2g31230	SEQ ID NO 21	SEQ ID NO 22

[Table 2]

AG code	Nucleotide sequence	Amino acid sequence
At2g30470	SEQ ID NO 23	SEQ ID NO 24
At2g17040	SEQ ID NO 25	SEQ ID NO 26
At5g07690	SEQ ID NO 27	SEQ ID NO 28
At3g15500	SEQ ID NO 29	SEQ ID NO 30
At2g30420	SEQ ID NO 31	SEQ ID NO 32
At3g09600	SEQ ID NO 33	SEQ ID NO 34
At1g36060	SEQ ID NO 35	SEQ ID NO 36
At1g01250	SEQ ID NO 37	SEQ ID NO 38
At1g25580	SEQ ID NO 39	SEQ ID NO 40
At3g20770	SEQ ID NO 41	SEQ ID NO 42
At1g12890	SEQ ID NO 43	SEQ ID NO 44
At2g18060	SEQ ID NO 45	SEQ ID NO 46
At4g18390	SEQ ID NO 47	SEQ ID NO 48
At5g08070	SEQ ID NO 49	SEQ ID NO 50
At1g76580	SEQ ID NO 51	SEQ ID NO 52
At4g28140	SEQ ID NO 53	SEQ ID NO 54
At5g60970	SEQ ID NO 55	SEQ ID NO 56
At2g42830	SEQ ID NO 57	SEQ ID NO 58
At1g30210	SEQ ID NO 59	SEQ ID NO 60
At1g71450	SEQ ID NO 61	SEQ ID NO 62
At1g09540	SEQ ID NO 63	SEQ ID NO 64
At3g10490	SEQ ID NO 65	SEQ ID NO 66
At1g62700	SEQ ID NO 67	SEQ ID NO 68
At1g49120	SEQ ID NO 69	SEQ ID NO 70
At1g44830	SEQ ID NO 71	SEQ ID NO 72
At1g30810	SEQ ID NO 73	SEQ ID NO 74
At1g74840	SEQ ID NO 75	SEQ ID NO 76
At5g18830	SEQ ID NO 77	SEQ ID NO 78
At1g72360	SEQ ID NO 79	SEQ ID NO 80
At1g32770	SEQ ID NO 81	SEQ ID NO 82
At5g14000	SEQ ID NO 83	SEQ ID NO 84
At2g23290	SEQ ID NO 85	SEQ ID NO 86
At2g02450	SEQ ID NO 87	SEQ ID NO 88
At1g27360	SEQ ID NO 89	SEQ ID NO 90
At1g33760	SEQ ID NO 91	SEQ ID NO 92
At3g27920	SEQ ID NO 93	SEQ ID NO 94
At3g18550	SEQ ID NO 95	SEQ ID NO 96
At1g52880	SEQ ID NO 97	SEQ ID NO 98
At5g07310	SEQ ID NO 99	SEQ ID NO 100
At4g26150	SEQ ID NO 101	SEQ ID NO 102
At1g19490	SEQ ID NO 103	SEQ ID NO 104
At1g52150	SEQ ID NO 105	SEQ ID NO 106
At3g04060	SEQ ID NO 107	SEQ ID NO 108
At4g32800	SEQ ID NO 109	SEQ ID NO 110
At5g66300	SEQ ID NO 111	SEQ ID NO 112
At5g13180	SEQ ID NO 113	SEQ ID NO 114
At1g71692	SEQ ID NO 115	SEQ ID NO 116
At1g27730	SEQ ID NO 117	SEQ ID NO 118
At3g49850	SEQ ID NO 119	SEQ ID NO 120
At3g02150	SEQ ID NO 121	SEQ ID NO 122
At5g47220	SEQ ID NO 123	SEQ ID NO 124
At5g43270	SEQ ID NO 125	SEQ ID NO 126
At5g52020	SEQ ID NO 127	SEQ ID NO 128
At1g69490	SEQ ID NO 129	SEQ ID NO 130
At4g38620	SEQ ID NO 131	SEQ ID NO 132
At2g45650	SEQ ID NO 133	SEQ ID NO 134
At5g02460	SEQ ID NO 135	SEQ ID NO 136
At1g12260	SEQ ID NO 137	SEQ ID NO 138
At5g13330	SEQ ID NO 139	SEQ ID NO 140
At4g01060	SEQ ID NO 141	SEQ ID NO 142
At2g46590	SEQ ID NO 143	SEQ ID NO 144
At1g69120	SEQ ID NO 145	SEQ ID NO 146
At1g77450	SEQ ID NO 147	SEQ ID NO 148
At2g23760	SEQ ID NO 149	SEQ ID NO 150
At2g02070	SEQ ID NO 151	SEQ ID NO 152
At1g22640	SEQ ID NO 153	SEQ ID NO 154
At5g22380	SEQ ID NO 155	SEQ ID NO 156
At5g62380	SEQ ID NO 157	SEQ ID NO 158

[0030] In addition, examples of a transcription factor constituting a chimeric protein are not limited to amino acid sequences (shown in the even-numbered SEQ ID NOS: 1 to 158) listed in tables 1 and 2. Also, it is possible to use a transcription factor having transactivation activity and comprising an amino acid sequence that has a deletion, a substitution, an addition, or an insertion of one or a plurality of amino acid sequences with respect to any of the amino acid sequences. Here, the term "a plurality of amino acids" refers to 1 to 20, preferably 1 to 10, more preferably 1 to 7, further preferably 1 to 5, and particularly preferably 1 to 3 amino acids, for example. In addition, amino acid deletion, substitution, or addition can be performed by modifying a nucleotide sequence encoding any of the above transcription factors by a technique known in the art. Mutation can be introduced into a nucleotide sequence by a known technique such as the Kunkel method or the Gapped duplex method or a method based thereon. For example, mutation is introduced with a mutagenesis kit using site-directed mutagenesis (e.g., Mutant-K or Mutant-G (both are trade names of Takara Bio)) or the like, or a LA PCR *in vitro* Mutagenesis series kit (trade name, Takara Bio). Also, a mutagenesis method may be: a method using a chemical mutation agent represented by EMS (ethyl methanesulfonate), 5-bromouracil, 2-aminopurine, hydroxylamine, N-methyl-N'-nitro-N nitrosoguanidine, or other carcinogenic compounds; or a method that involves radiation treatment or ultraviolet [UV] treatment typically using X-rays, alpha rays, beta rays, gamma rays, an ion beam, or the like.

[0031] Further, examples of a transcription factor constituting a chimeric protein are not limited to *Arabidopsis thaliana* transcription factors listed in tables 1 and 2. Examples of such transcription factor can include transcription factors that function in a similar manner in non-*Arabidopsis thaliana* plants (e.g., the aforementioned plants) (hereinafter referred to as homologous transcription factors). These homologous transcription factors can be searched for using the genomic information of a search target plant based on amino acid sequences listed in tables 1 and 2 or the nucleotide sequences of individual genes if the plant genomic information has been elucidated. Homologous transcription factors can be identified by searching for amino acid sequences having, for example, 70% or higer, preferably 80% or higher, more preferably 90% or higher, and most preferably 95% or higher homology to the amino acid sequences listed in tables 1 and 2. Here, the value of homology refers to a value that can be found based on default setting using a computer equipped with a BLAST algorithm and a database containing gene sequence information.

[0032] In addition, a homologous gene can be identified by, when the plant genome information remains unclarified, extracting the genome from a target plant or constructing a cDNA library for a target plant and then isolating a genomic region or cDNA hybridizing under stringent conditions to at least a portion of the gene encoding any one of the transcription factors listed in tables 1 and 2. Here, the term "stringent conditions" refers to conditions under which namely a specific hybrid is formed, but a non-specific hybrid is never formed. For example, such conditions comprise hybridization at 45°C with 6 x SSC (sodium chloride/sodium citrate), followed by washing at 50°C to 65°C with 0.2-1 x SSC and 0.1% SDS. Alternatively, such conditions comprise hybridization at 65°C to 70°C with 1 x SSC, followed by washing at 65°C to 70°C with 0.3 x SSC. Hybridization can be performed by a conventionally known method such as a method described in J. Sambrook et al. Molecular Cloning, A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory (1989).

[0033] A feature of causing the fat and oil production in seeds to vary significantly (to be improved or reduced significantly) is imparted to the plant of the present invention by causing expression of the aforementioned chimeric protein comprising a transcription factor and a functional peptide in a plant. In particular, a feature of causing the fat and oil production in seeds to vary significantly (to be improved or reduced significantly) is imparted to the plant of the present invention by causing expression of a chimeric protein comprising a transcription factor of interest having repressed transactivation activity, further causing expression of transcription repression activity through recognition of a cis sequence homologous to a cis sequence recognized by the transcription factor of interest, or altering the specific affinity of the transcription factor of interest to that of another factor, nucleic acid, lipid, or carbohydrate. In the plant of the present invention, it is possible to create a chimeric protein by modifying an endogenous transcription factor. Alternatively, it is also possible to introduce a gene encoding a chimeric protein into the plant so as to cause the gene to be expressed therein.

[0034] For instance, it is preferable to use a method wherein a gene encoding a chimeric protein (fusion protein) obtained by fusing the aforementioned transcription factor and a functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor is introduced into a target plant to cause the chimeric protein (fusion protein) to be expressed in the plant.

[0035] The expression "transcription factor having repressed transactivation activity" used herein is not particularly limited. Such transcription factor has significantly lower transactivation activity than the original transcription factor. In addition, a "functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor" (sometimes referred to as a "transcription repressor converting peptide") is defined as a peptide having the function of causing an arbitrary transcription factor to have significantly lower transactivation activity than the original transcription factor when the peptide is fused with the transcription factor to create a chimeric protein. Such "functional peptide capable of converting an arbitrary transcription factor into a transcriptional repressor" is not particularly limited. However, it is particularly preferable for the functional peptide to consist of an amino acid sequence known as a repressor domain sequence or an SRDX sequence. Examples of such transcription repressor converting peptide are described in detail in JP Patent Publication (Kokai) No. 2005-204657 A. Any example disclosed in such document can be used.

[0036] For example, a transcription repressor converting peptide consists of an amino acid sequence expressed by any one of the following formulae (1) to (8).

[0037]

(1) X1-Leu-Asp-Leu-X2-Leu-X3

(where X1 denotes a set of 0 to 10 amino acid residues, X2 denotes Asn or Glu, and X3 denotes a set of at least 6 amino acid residues.)

(2) Y1-Phe-Asp-Leu-Asn-Y2-Y3

(where Y1 denotes a set of 0 to 10 amino acid residues, Y2 denotes Phe or Ile, and Y3 denotes a set of at least 6 amino acid residues.)

(3) Z1-Asp-Leu-Z2-Leu-Arg-Leu-Z3

(where Z1 denotes Leu, Asp-Leu, or Leu-Asp-Leu, Z2 denotes Glu, Gln, or Asp, and Z3 denotes a set of 0 to 10 amino acid residues.)

(4) Asp-Leu-Z4-Leu-Arg-Leu

(where Z4 denotes Glu, Gln, or Asp.)

(5) $\alpha1$-Leu-$\beta1$-Leu-$\gamma1$-Leu

(6) $\alpha1$-Leu-$\beta1$-Leu-$\gamma2$-Leu

(7) $\alpha1$-Leu-$\beta2$-Leu-Arg-Leu

(8) $\alpha2$-Leu-$\beta1$-Leu-Arg-Leu

(where $\alpha1$ denotes Asp, Asn, Glu, Gln, Thr, or Ser, $\alpha2$ denotes Asn, Glu, Gln, Thr, or Ser, $\beta1$ denotes Asp, Gln, Asn, Arg, Glu, Thr, Ser, or His, $\beta2$ denotes Asn, Arg, Thr, Ser, or His, $\gamma1$ denotes Arg, Gln, Asn, Thr, Ser, His, Lys, or Asp, and $\gamma2$ denotes Gln, Asn, Thr, Ser, His, Lys, or Asp in formulae (5) to (8).)

Transcription repressor converting peptide of formula (1)

The number of amino acid residues in the set denoted by "X1" may be 0 to 10 for the transcription repressor converting peptide of formula (1). In addition, types of specific amino acids corresponding to amino acid residues in the set denoted by X1 are not particularly limited. Any amino acid can be used. In view of ease of synthesis of the transcription repressor converting peptide of formula (1), it is preferable to minimize the length of the set of amino acid residues denoted by X1. Specifically, the number of amino acid residues in the set denoted by X1 is preferably not more than 5.

[0038] Similarly, the number of amino acid residues in the set denoted by X3 may be at least 6 for the transcription repressor converting peptide of formula (1). In addition, types of specific amino acids corresponding to amino acid residues in the set denoted by X3 are not particularly limited, and thus any amino acid may be used.

[0039]

Transcription repressor converting peptide of formula (2)

As in the case of X1 for the transcription repressor converting peptide of formula (1), the number of amino acid residues in the set denoted by Y1 for the transcription repressor converting peptide of formula (2) may be 0 to 10. In addition, types of specific amino acids corresponding to amino acid residues in the set denoted by Y1 are not particularly limited, and thus any amino acid may be used. The number of specific amino acid residues in the set denoted by Y1 is preferably not more than 5.

[0040] Similarly, as in the case of X3 for the transcription repressor converting peptide of formula (1), the number of amino acid residues in the set denoted by Y3 for the transcription repressor converting peptide of formula (2) may be at least 6. In addition, types of specific amino acids corresponding to amino acid residues in the set denoted by Y3 are not particularly limited, and thus any amino acid may be used.

[0041]

Transcription repressor converting peptide of formula (3)

For the transcription repressor converting peptide of formula (3), the set of amino acid residues denoted by Z1 contains 1 to 3 "Leu" amio acids. When it contains a single amino acid, Z1 denotes Leu. When it contains two amino acids, Z1 denotes Asp-Leu. When it contains 3 amino acids, Z1 denotes Leu-Asp-Leu.

[0042] Meanwhile, for the transcription repressor converting peptide of formula (3), the number of amino acid residues in the set denoted by Z3 may be 0 to 10. In addition, types of specific amino acids corresponding to amino acid residues in the set denoted by Z3 are not particularly limited, and thus any amino acid may be used. Specifically, the number of amino acid residues in the set denoted by Z3 is preferably not more than 5. Specific examples of an amino acid residue in the set denoted by Z3 include, but are not limited to, Gly, Gly-Phe-Phe, Gly-Phe-Ala, Gly-Tyr-Tyr, and Ala-Ala-Ala.

[0043] In addition, the number of amino acid residues consisting of a transcription repressor converting peptide as a whole of formula (3) is not particularly limited. However, in view of ease of synthesis, it is preferably not more than 20 amino acids.

[0044]

Transcription repressor converting peptide of formula (4)

The transcription repressor converting peptide of formula (4) is a hexamer (6mer) consisting of 6 amino acid residues. In addition, if the amino acid residue denoted by Z4 in the transcription repressor converting peptide of formula (4) is Glu, the amino acid sequence of the peptide corresponds to a region ranging from position 196 to position 201 of the amino acid sequence of the *Arabidopsis thaliana* SUPERMAN protein (SUP protein).

[0045] A chimeric protein (fusion protein) is created through fusion of any of the different transcription repressor converting peptides described above and any of the transcription factors described above so as to modify characteristics of the transcription factor. Specifically, a chimeric protein (fusion protein) is created through fusion of the transcription factor and the transcription repressor converting peptide, making it possible to modify the transcription factor into a transcriptional repressor or a negative transcriptional coactivator. In addition, it is possible to further convert a non-dominant transcriptional repressor into a dominant transcriptional repressor.

[0046] In addition, a chimeric protein (fusion protein) can be produced by obtaining a fusion gene of a polynucleotide encoding any transcription repressor converting peptide described above and a gene encoding a transcription factor. Specifically, a fusion gene is constructed by linking a polynucleotide encoding the transcription repressor converting peptide (hereinafter refferred to as a "transcription repressor converting polynucleotide") and the gene encoding a transcription factor. The fusion gene is introduced into plant cells, thereby allowing production of a chimeric protein (fusion protein). The specific nucleotide sequence of the transcription repressor converting polynucleotide is not particularly limited. It is only necessary for the transcription repressor converting polynucleotide to comprise a nucleotide sequence corresponding to the amino acid sequence of the transcription repressor converting peptide in accordance with the genetic code of the peptide. In addition, if necessary, the transcription repressor converting polynucleotide may have a nucleotide sequence that serves as a linking site via which the transcription repressor converting polynucleotide is linked to a transcription factor gene. Further, if the amino acid reading frame of the transcription repressor converting polynucleotide does not match the reading frame of the transcription factor gene, the transcription repressor converting polynucleotide can comprise an additional nucleotide sequence that allows matching of both reading frames. Furthermore, the transcription repressor converting polynucleotide may comprise a variety of additional polypeptides such as a polypeptide having a linker function to link a transcription factor and a transcription repressor converting peptide and a polypeptide such as His, Myc, or Flag used for epitope labeling of a chimeric protein (fusion protein). Moreover, if necessary, the chimeric protein (fusion protein) may have a construct such as a sugar chain, an isoprenoid group, or the like as well as such polypeptide.

[0047] A method for producing a plant is not particularly limited as long as it comprises a step of producing the above chimeric protein comprising a transcription factor and a transcription repressor converting peptide in a plant. However, for example, a production method comprising steps such as an expression vector construction step, a transformation step, and a selection step can be used. Each step is specifically described below.

[0048]

Expression vector construction step

The expression vector construction step is not particularly limited as long as it includes a step of constructing a recombinant expression vector containing the gene encoding a transcription factor, a transcription repressor converting polynucleotide, and a promoter. As a vector serving as a mother body for a recombinant expression vector, various conventionally known vectors can be used. For example, plasmids, phages, cosmids, or the like can be used and such vector can be appropriately selected depending on plant cells into which it is introduced and introduction methods. Specific examples of such vector include pBR322, pBR325, pUC19, pUC119, pBluescript, pBluescriptSK, and pBI vectors. Particularly, when a method for introduction of a vector into a plant uses Agrobacterium, a pBI binary vector is preferably used. Specific examples of such pBI binary vector include pBIG, pBIN19, pBI101, pBI121, and pBI221.

[0049] A promoter used herein is not particularly limited as long as it can cause gene expression in plants. Any known promoter can be appropriately used. Examples of such promoter include a cauliflower mosaic virus 35S promoter (CaMV35S), various actin gene promoters, various ubiquitin gene promoters, a nopaline synthase gene promoter, a tobacco PR1a gene promoter, a tomato ribulose1,5-bisphosphate carboxylase·oxidase small subunit gene promoter, a napin gene promoter, and an oleosin gene promoter. Of these, a cauliflower mosaic virus 35S promoter, an actin gene promoter, or a ubiquitin gene promoter can be more preferably used. The use of each of the above promoters enables strong expression of any gene when it is introduced into plant cells. The specific structure of a recombinant expression vector itself is not particularly limited as long as the promoter is linked to a fusion gene obtained by linking a gene encoding a transcription factor or a transcriptional coactivator and a transcription repressor converting polynucleotide so as to cause expression of the gene and introduced into the vector.

[0050] In addition, a recombinant expression vector may further contain other DNA segments, in addition to a promoter and the fusion gene. Such other DNA segments are not particularly limited and examples thereof include a terminator, a selection marker, an enhancer, and a nucleotide sequence for enhancing translation efficiency. Also, the above recombinant expression vector may further have a T-DNA region. A T-DNA region can enhance efficiency for gene introduction particularly when the above recombinant expression vector is introduced into a plant using Agrobacterium.

[0051] A transcription terminator is not particularly limited as long as it has functions as a transcription termination site and may be any known transcription terminator. For example, specifically, a transcription termination region (Nos terminator) of a nopaline synthase gene, a transcription termination region (CaMV35S terminator) of cauliflower mosaic virus 35S, or the like can be preferably used. Of them, the Nos terminator can be more preferably used. In the case of the above recombinant vector, a phenomenon such that an unnecessarily long transcript is synthesized and that a strong promoter decreases the number of copies of a plasmid after introduction into plant cells can be prevented by arranging a transcription terminator at an appropriate position.

[0052] As a transformant selection marker, a drug resistance gene can be used, for example. Specific examples of such drug resistance gene include drug resistance genes against hygromycin, bleomycin, kanamycin, gentamicin, chloramphenicol, and the like. Transformed plants can be easily selected by selecting plants that can grow in medium containing the above antibiotics.

[0053] An example of a nucleotide sequence for increasing translation efficiency is an omega sequence from tobacco mosaic virus. This omega sequence is arranged in an untranslated region (5'UTR) of a promoter, so that the translation efficiency of the fusion gene can be increased. As such, the recombinant expression vector can contain various DNA segments depending on purposes.

[0054] A method for constructing a recombinant expression vector is not particularly limited. To an appropriately selected vector serving as a mother body, the above promoter, a gene encoding a transcription factor, a transcription repressor converting polynucleotide, and, if necessary, the above other DNA segments may be introduced in a predetermined order. For example, a gene encoding a transcription factor and a transcription repressor converting polynucleotide are linked to construct a fusion gene, and then the fusion gene and the promoter (e.g., a transcription terminator according to need) are then linked to construct an expression cassette and then the cassette may be introduced into a vector.

[0055] In construction of a chimeric gene (fusion gene) and an expression cassette, for example, cleavage sites of DNA segments are prepared to have protruding ends complementary to each other and then performing a reaction with a ligation enzyme, making it possible to specify the order of the DNA segments. In addition, when an expression cassette contains a terminator, DNA segments may be arranged in the following order from upstream: a promoter, the chimeric gene, and a terminator. Also, reagents for construction of an expression vector (that is, types of restriction enzymes, ligation enzymes, and the like) are also not particularly limited. Hence, commercially available reagents can be appropriately selected and used.

[0056] Also, a method for replicating (a method for producing) the above expression vector is not particularly limited and conventionally known replication methods can be used herein. In general, such expression vector may be replicated within *Escherichia coli* as a host. At this time, preferred types of *Escherichia coli* may be selected depending on the types of vector.

[0057]

Transformation step

The transformation step carried out in the present invention is a step of introducing the fusion gene into plant cells using the above recombinant expression vector so as to cause the expression of the gene. A method for introducing such gene into plant cells (transformation method) using a recombinant expression vector is not particularly limited. Conventionally known appropriate introduction methods can be used depending on plant cells. Specifically, a method using Agrobacterium or a method that involves direct introduction into plant cells can be used, for example. As a method using Agrobacterium, a method described in the following can be employed, for example: Bechtold, E., Ellis, J. and Pelletier, G. (1993), In Planta

Agrobacterium-mediated gene transfer by infiltration of adult Arabidopsis plants. C. R. Acad. Sci. Paris Sci. Vie, 316, 1194-1199; or Zyprian E, Kado Cl, Agrobacterium-mediated plant transformation by novel mini-T vectors in conjunction with a high-copy vir region helper plasmid, Plant Molecular Biology, 1990, 15(2), 245-256.

[0058] As a method for directly introducing DNA comprising a recombinant expression vector and a target gene into plant cells, microinjection, electroporation, a polyethylene glycol method, a particle gun method, protoplast fusion, a calcium phosphate method, or the like can be employed.

[0059] Also, when a method for directly introducing DNA into plant cells is employed, DNA that can be used herein contains transcriptional units required for the expression of a target gene, such as a promoter and a transcription terminator, and a target gene. Vector functions are not essential in such case. Moreover, a DNA that contains a protein coding region alone of a target gene having no transcriptional unit may be used herein, as long as it is integrated into a host's transcriptional unit and then the target gene can be expressed.

[0060] Examples of plant cells into which DNA comprising the above recombinant expression vector and a target gene or DNA containing no expression vector but a target gene DNA is introduced include cells of each tissue of plant organs such as flowers, leaves, and roots, calluses, and suspension-cultured cells. At this time, according to the plant production method of the present invention, an appropriate expression vector may be constructed as the above recombinant expression vector according to the type of plant to be produced or a versatile expression vector may be constructed in advance and then introduced into plant cells. That is to say, the plant production method of the present invention may or may not comprise a step of constructing a DNA for transformation using the recombinant expression vector.

[0061]

Other steps and methods

The plant production method of the present invention needs to comprise at least the transformation step, and the method may further comprise a step of constructing the DNA for transformation using the recombinant expression vector. The method may further comprise other steps. Specifically, for example, a step of selecting an appropriate transformant from among transformed plants can be employed.

[0062] A selection method is not particularly limited. For example, selection may be carried based on drug resistance such as hygromycin resistance. Alternatively, selection may be carried out based on the fat and oil content in seeds collected from cultivated transformants (plants). For example, a method comprising collecting plant seeds, determining the fat and oil content in the seeds according to a standard method, and comparing the fat and oil content with the fat and oil content in non-transformed plant seeds can be employed in a case in which selection is carrried out based on the fat and oil content (see the Examples described below).

[0063] According to the plant production method of the present invention, the fusion gene is introduced into a plant. This makes it possible to obtain an offspring plant having a significantly improved fat and oil content in comparison with the plant via sexual reproduction or asexual reproduction. Also, plant cells or reproductive materials, such as seeds, fruits, stocks, calluses, tubers, cut ears, or lumps, may be obtained from the plant or an offspring plant thereof. The plant can be mass-produced therefrom based on such materials. Therefore, the plant production method of the present invention may comprise a reproduction step (mass production step) for reproducing a selected plant.

[0064] In addition, the plant of the present invention may include a matter comprising at least any one of an adult plant, plant cells, plant tissue, callus, and seeds. That is, according to the present invention, any matter in a state that allows it to eventually grow to become a plant can be regarded as a plant. In addition, plant cells include plant cells in various forms. Examples of such plant cells include suspension-cultured cells, protoplasts, and leaf sections. As a result of proliferation/differentiation of such plant cells, a plant can be obtained. In addition, a plant can be reproduced from plant cells by a conventionally known method depending on the types of plant cells. Therefore, the plant production method of the present invention may comprise a regeneration step of regenerating a plant from plant cells or the like.

[0065] In addition, the plant production method of the present invention is not limited to a method of transformation using a recombinant expression vector. A different method may be used. Specifically, for example, the chimeric protein (fusion protein) itself can be administered to a plant. In this case, the chimeric protein (fusion protein) can be administered to a young plant such that the fat and oil content can be improved at a part of a plant that is eventually used. In addition, a method of administration of a chimeric protein (fusion protein) is not particularly limited, and a different known method can be used.

[0066] As described above, according to the present invention, it becomes possible to provide a plant for which the material productivity has been caused to vary (to be improved or reduced) relative to the material productivity of a wild-type plant by inducing expression of a chimeric protein comprising a predetermined transcription factor and any functional peptide described above. When the chimeric protein is expressed in a plant, it might cause reppression of transactivation activity of a target transcription factor or it might cause exhibition of transcription repression effects upon a sequence homologous to a cis sequence recognized by a target transcription factor. Further, in some cases, such chimeric protein functions to change the specific affinity of another factor, DNA, RNA, lipid, or carbohydrate having affinity to a target transcription factor or transcriptional coactivator. Alternatively, in some cases, it functions to cause a substance having no affinity to a target transcription factor to have improved affinity thereto. The following factors can be expressed in a similar manner in the plant of the present invention: a transcription factor that constitutes a chimeric protein; a transcription factor capable of recognizing a cis sequence homologous to a cis sequence recognized by the transcription factor; a transcription factor homologous to a transcription factor that constitutes a chimeric protein; other factors each having affinity to a transcription factor that constitutes a chimeric protein; and the like. However, the above effects of a chimeric protein allow suppression of gene expression to be controlled in a dominant-negative manner. Accordingly, the expression levels of gene groups involved in plant growth and the expression levels of gene groups involved in fat and oil production in seeds and/or gene groups involved in decomposition of produced fats and oils would vary in the plant of the present invention. This is thought to cause significant variation in fat and oil content.

[0067] Here, significant variation in the fat and oil content exists in a case in which the plant of the present invention exhibits an improvement of fat and oil content over a wild-type plant while the single seed mass remains stable, a case in which the plant of the present invention is found to exhibit improvement of fat and oil content with a significantly higher or lower level of single seed mass than that of a wild-type plant, or a case in which the plant of the present invention is found to exhibit improvement or reduction of fat and oil content in seeds when compared with a wild-type plant. In any case, it corresponds to a variation in the content of fat and oil produced by a single individual plant.

[0068] More specifically, if a chimeric protein comprising any transcription factor listed in table 1 is expressed in a plant, the fat and oil content in the plant would be improved. Among the plants of the present invention, a plant confirmed to have increased fat and oil content can be used for a method for producing plant-derived fats and oils. For example, fat and oil can be produced by cultivating the plant of the present invention, taking seeds therefrom, and collecting fat and oil components from the obtained seeds. In particular, it can be said that the fat and oil production method using the plant of the present invention is a method whereby high fat and oil content in a single plant indiviual can be achieved, resulting in excellent productivity. In other words, assuming that the number of cultivated plant individuals per unit area of cultivated acreage is stable, the amount of fat and oil produced per unit area of cultivated acreage can be remarkabley improved with the use of the plant of the present invention. Therefore, cost necessary for fat and oil production can be significantly reduced with the use of the plant of the present invention.

[0069] Further, it can be said that the method for producing fat and oil using a plant of the present invention is a method excellent in terms of productivity. This is because high fat and oil contents per unit weight can be achieved thereby. In addition, fats and oils produced by the method for producing fat and oil using a plant of the present invention are not particularly limited. Examples of such fats and oils include plant-derived fats and oils such as soybean oil, sesame oil, olive oil, coconut oil, rice oil, cottonseed oil, sunflower oil, corn oil, safflower oil, and rapeseed oil. In addition, produced fat and oil can be extensively used for household and industrial applications. Also, such fat and oil can be used as raw materials for biodiesel fuel. That is, the above fats and oils used for household and industrial applications, biodiesel fuel, and the like can be produced at low cost with the use of the plant of the present invention.

[0070] Meanwhile, when a chimeric protein comprising any transcription factor listed in table 2 is expressed in a plant, the fat and oil content in the plant decreases. The plant of the present invention in which the fat and oil content is reduced can be used for a method for producing bioalcohol using lignocellulose contained in plants. That is, bioalcohol can be produced with excellent glycosylation efficiency and low impurity contents because the contents of fat and oil components that become impurities in a step of glycosylation of lignocellulose are low in such plant.

[0071]

Concerning At5g22380

As described above, when a chimeric protein comprising a repressor domain and any transcription factor listed in table 1 is expressed in a plant, the fat and oil content in seeds is significantly improved. When a chimeric protein comprising a repressor domain and any transcription factor listed in table 2 is expressed in a plant, the fat and oil content in seeds is significantly reduced. Therefore, if any transcription factor listed in table 1 that is originally not fused with a repressor domain is introduced as is into a plant, it is highly probable that the fat and oil content in seeds will be significantly reduced. In addition, if any transcription factor listed in table 2 that is originally not fused with a repressor domain is introduced as is into a plant, it is highly probable that the fat and oil content in seeds will be significantly improved. Here, each transcription factor can be obtained by techniques described in the above paragraphs about "the expression vector construction step," "the transformation step," and "the other step or method."

[0072] In particular, as demonstrated in the Examples below, when a chimeric protein comprising At5g22380, which is one of the transcription factors listed in table 2, and a repressor domain is expressed in a plant, the fat and oil content in seeds is significantly reduced. However, when At5g22380 (used as a transcription factor that is originally not fused with a repressor domain in a plant) is expressed as is in a plant, it exhibits a characteristic feature of causing the fat and oil content in seeds to be significantly improved. That is, productivity of fat and oil in seeds can be improved by causing At5g22380 to be expressed in a plant as an *Arabidopsis-thaliana*-derived transcription factor.

[0073] In order to cause a transcription factor (At5g22380) to be expressed in a plant, techniques described in the above paragraphs about "the expression vector construction step," "the transformation step," and "the other step or method" can be employed. In addition, a transcription factor that is expressed to improve the fat and oil content in seeds is not limited to an *Arabidopsis-thaliana*-derived transcription factor (At5g22380). It may be a homologous transcription factor defined as above. These homologous transcription factors can be searched for using the genomic information of a search target plant based on the amino acid sequence of At5g22380 shown in SEQ ID NO: 156 or the nucleotide sequence of the At5g22380 gene shown in SEQ ID NO: 155. Homologous transcription factors can be identified by searching for amino acid sequences having, for example, 70% or higer, preferably 80% or higher, more preferably 90% or higher, and most preferably 95% or higher homology to the amino acid sequence shown in SEQ ID NO:156. Here, the value of homology refers to a value that can be found based on default setting using a computer equipped with a BLAST algorithm and a database containing gene sequence information.

[0074] In addition, a homologous gene can be identified by, when the plant genome information remains unclarified, extracting the genome from a target plant or constructing a cDNA library for a target plant and then isolating a genomic region or cDNA hybridizing under stringent conditions to at least a portion of the gene comprising the nucleotide sequence shown in SEQ ID NO: 155. Here, the term "stringent conditions" is defined as the same as the above conditions.

[Example]

[0075] The present invention is hereafter described in greater detail with reference to the following examples, although the technical scope of the present invention is not limited thereto.

[0076]

[Example 1]

Transcription factor gene amplification

Each of the following transcription factors was subjected to PCR amplification of a coding region DNA fragment excluding a termination codon using the *Arabidopsis thaliana* cDNA library and primers described below: At1g01010, At1g01250, At1g09540, At1g10200, At1g12260, At1g12890, At1g12980, At1g14510, At1g15360, At1g17520, At1g18330, At1g18570, At1g19490, At1g22640, At1g22985, At1g24260, At1g24590, At1g25470, At1g25580, At1g27360, At1g27370, At1g27730, At1g28160, At1g28520, At1g30210, At1g30810, At1g32770, At1g33760, At1g34190, At1g36060, At1g43160, At1g43640, At1g44830, At1g49120, At1g52150, At1g52880, At1g52890, At1g53230, At1g56010, At1g56650, At1g60240, At1g61110, At1g62700, At1g63040, At1g63910, At1g64380, At1g67260, At1g67780, At1g68800, At1g69120, At1g69490, At1g71030, At1g71450, At1g71692, At1g72360, At1g72570, At1g74840, At1g74930, At1g76580, At1g77200, At1g77450, At1g78080, At1g79180, At1g80580, At2g02070, At2g02450, At2g17040, At2g18060, At2g22200, At2g23290, At2g23760, At2g26060, At2g28550, At2g30420, At2g30470, At2g31230, At2g33480, At2g33710, At2g35700, At2g40220, At2g41710, At2g42400, At2g42830, At2g44840, At2g44940, At2g45650, At2g45680, At2g46310, At2g46590, At2g47520, At3g01530, At3g02150, At3g02310, At3g04060, At3g04070, At3g04420, At3g05760, At3g09600, At3g10490, At3g11280, At3g14230, At3g15500, At3g15510, At3g18550, At3g20770, At3g23220, At3g23230, At3g23240, At3g25890, At3g27920, At3g28910, At3g29035, At3g45150, At3g49850, At3g54320, At3g61910, At4g01060, At4g01550, At4g18390, At4g18450, At4g23750, At4g26150, At4g27950, At4g28140, At4g28530, At4g31060, At4g31270, At4g32800, At4g34410, At4g35580, At4g36160, At4g37750, At4g38620, At4g39780, At5g02460, At5g06100, At5g07310, At5g07580, At5g07680, At5g07690, At5g08070, At5g08790, At5g09330, At5g13180, At5g13330, At5g13910, At5g14000, At5g18270, At5g18560, At5g18830, At5g22290, At5g22380, At5g23260, At5g24520, At5g24590, At5g25190, At5g25390, At5g25810, At5g35550, At5g39610, At5g40330, At5g41030, At5g43270, At5g47220, At5g47230, At5g47390, At5g51190, At5g52020, At5g53290, At5g54230, At5g58900, At5g60970, At5g61600, At5g62380, At5g64530, At5g64750, At5g66300, At5g67000, At5g67300 and At5g67580. Note that a DNA fragment of a region including a termination codon was amplified for At5g22380. PCR was carried out under conditions of 94°C for 1 minute, 47°C for 2 minutes, and elongation reaction at 74°C for 1 minute for 25 cycles. Next, each PCR product was isolated by agarose gel electrophoresis and collected.

[Table 3]

AG code	Fowerd primer	Nucleotide sequence	Reverse primer	Nucleotide sequence
At 1g01010	GATGGAGGATCAAGTTGGGTTTGGG	SEQ ID NO 159	ACCAACAAGAATGATCCAACTAATG	SEQ ID NO 160
At 1g01250	ATGTCACCACAGAGAATGAAGC	SEQ ID NO 161	CAGACACGCCATGAACTGATAC	SEQ ID NO 162
At 1g09540	GATGGGGAGACATTCTTGCTGTTACAAACA	SEQ ID NO 163	AAGGGACTGACCAAAAGAGACGGCCATTCT	SEQ ID NO 164
At 1g10200	GGGATGGCGTTCGCAGGAACAACCCAGAAATG	SEQ ID NO 165	AGCAGCGACGACTTTGTCCTTGGCG	SEQ ID NO 166
At 1g12260	GATGAATTCATTTTCCCACGTCCCTCCGGG	SEQ ID NO 167	CTTCCATAGATCAATCTGACAACTCGAAGA	SEQ ID NO 168
At 1g12890	ATGTTGAAATCAAGTAACAAGAG	SEQ ID NO 169	CATAAGAAACTGTGGAGCATC	SEQ ID NO 170
At 1g12980	AATGGAAAAAGCCTTGAGAAACTTC	SEQ ID NO 171	TCCCCACGATCTTCGGCAAGTACA	SEQ ID NO 172
At 1g14510	ATGGAAGGAATTCAGCATCC	SEQ ID NO 173	GGCTTTCATTTTCTTGCTGG	SEQ ID NO 174
At 1g15360	ATGGTACAGACGAAGAAGTTCAG	SEQ ID NO 175	GTTTGTATTGAGAAGCTCCTCTATC	SEQ ID NO 176
At 1g17520	GATGGGAAATCAGAAGCTCAAATGGACGGC	SEQ ID NO 177	ATTCAAGTACATAATCTTTCCCTGACTACA	SEQ ID NO 178
At 1g18330	GATGGCCGCTGAGGATCGAAGTGAGGAACT	SEQ ID NO 179	GCATATACGTGCTCTTTGGCTTTTCTTTTC	SEQ ID NO 180
At 1g18570	GATGGTGCGGACACCGTGTTGCAAAGCTGA	SEQ ID NO 181	TCCAAAATAGTTATCAATTTCGTCAAACAA	SEQ ID NO 182
At 1g19490	GATGGAGTTGGAGCCTATATCATCGAGTTG	SEQ ID NO 183	TCCGACCTGCATCCGACATTGACGGCCATG	SEQ ID NO 184
At 1g22640	GATGGGAAGATCACCATGCTGCGAGAAAGC	SEQ ID NO 185	ATGAGTTCTAACATCAGAAACCCGACAATT	SEQ ID NO 186
At 1g22985	ATGAAACGAATTGTTCGAATTTCATTC	SEQ ID NO 187	AACAACTTCTTCAGAAGCACCAC	SEQ ID NO 188
At 1g24260	GATGGGAAGAGGGAGAGTAGAATTGAAGAG	SEQ ID NO 189	AATAGAGTTGGTGTCATAAGGTAACCAACC	SEQ ID NO 190
At 1g24590	ATGGAAGAAGCAATCATGAGAC	SEQ ID NO 191	ATAATCATCATGAAAGCAATACTG	SEQ ID NO 192
At 1g25470	ATGTCGGCTGTGTCTGAATCG	SEQ ID NO 193	AACCAAACCGAGAGGCGGTG	SEQ ID NO 194
At 1g25580	GATGGCTGGGCGATCATGGCTGATC	SEQ ID NO 195	CAGCAGCGTGGCAGTGTGTTGCC	SEQ ID NO 196
At 1g27360	GATGGACTGCAACATGGTATCTTCGTCCCA	SEQ ID NO 197	TTTTGGTACAACATCATATGAACAGAGTAG	SEQ ID NO 198
At 1g27370	GATGGACTGCAACATGGTATCTTCGTTCCC	SEQ ID NO 199	GATGAAATGACTAGGGAAAGTGCCAAATAT	SEQ ID NO 200
At 1g27730	GATGGCGCTCGAGGCTCTTACATCACCAAG	SEQ ID NO 201	AAGTTGAAGTTTGACCGGAAAGTCAAACCG	SEQ ID NO 202
At 1g28160	ATGGAGTTCAATGGTAATTTGAATG	SEQ ID NO 203	TTGGTAGAAGAATGTGGAGGG	SEQ ID NO 204
At 1g28520	GATGACGGGGAAGCGATCAAAGAC	SEQ ID NO 205	GGGGATATAATAGTCGCTTAGATTTC	SEQ ID NO 206
At 1g30210	ATGGAGGTTGACGAAGACATTG	SEQ ID NO 207	TCTCCTTTCCTTTGCCTTGTC	SEQ ID NO 208
At 1g30810	GATGGAAAATCCTCCATTAGAATCTGAGAT	SEQ ID NO 209	CATCAAATCTACTCCGAAAAGTTTTCCTTT	SEQ ID NO 210
At 1g32770	GATGGCTGATAATAAGGTCAATCTTTCGAT	SEQ ID NO 211	TACAGATAAATGAAGAAGTGGGTCTAAAGA	SEQ ID NO 212
At 1g33760	ATGGAAAACACTTACGTTGGCC	SEQ ID NO 213	ATTATTAGAATTCCATATGGACTG	SEQ ID NO 214
At 1g34190	GATGGCGGATTCTTCACCCGATTCG	SEQ ID NO 215	GTCTTTCAAGAGAAGACTTCTACC	SEQ ID NO 216
At 1g36060	ATGGCGGATCTCTTCGGTGG	SEQ ID NO 217	CGATAAAATTGAAGCCCAATCTATC	SEQ ID NO 218
At 1g43160	ATGGTGTCTATGCTGACTAATG	SEQ ID NO 219	ACCAAAAGAGGAGTAATTGTATTG	SEQ ID NO 220
At 1g43640	GATGTCGTTTCTGAGTATTGTTCGTGATGT	SEQ ID NO 221	TTCACATGCCAATTTAGTATCAAAGGTGCT	SEQ ID NO 222
At 1g44830	ATGGTGAAAACACTTCAAAAGACAC	SEQ ID NO 223	GCAGAAGTTCCATAATCTGATATC	SEQ ID NO 224
At 1g49120	ATGATCAGTTTCAGAGAAGAGAAC	SEQ ID NO 225	TAAAAACTTATCGATCCAATCAGTAG	SEQ ID NO 226
At 1g52150	GATGGCAATGTCTTGCAAGGATGGTAAGTT	SEQ ID NO 227	CACAAAGGACCAATTGATGAACACAAAGCA	SEQ ID NO 228
At 1g52880	GATGGAGAGTACAGATTCTTCCGGTGGTCC	SEQ ID NO 229	AGAATACCAATTCAAACCAGGCAATTGGTA	SEQ ID NO 230
At 1g52890	GATGGGTATCCAAGAAACTGACCCGTTAAC	SEQ ID NO 231	CATAAACCCAAACCCACCAACTTGCCCCGA	SEQ ID NO 232
At 1g53230	GATGAAGAGAGATCATCATCATCATCATCA	SEQ ID NO 233	ATGGCGAGAATCGGATGAAGC	SEQ ID NO 234
At 1g56010	GATGGAGACGGAAGAAGAGATGAAG	SEQ ID NO 235	GCAATTCCAAACAGTGCTTGGAATAC	SEQ ID NO 236
At 1g56650	GGGATGGAGGGTTCGTCCAAAGGGCTGCGAAAAGC	SEQ ID NO 237	ATCAAATTTCACAGTCTCTCCATCGAAAAGACTCC	SEQ ID NO 238
At 1g60240	GATGAAGTCAAGACGTGAACAATCAATCGA	SEQ ID NO 239	TTTATAGTAACCTCGAATGTGCTGGGCCAA	SEQ ID NO 240
At 1g61110	GATGGAAAACATGGGGGATTCGAGCATAG	SEQ ID NO 241	TGAGTGCCAGTTCATGTTAGGAAGCTG	SEQ ID NO 242
At 1g62700	GATGAATTCGTTTTCACAAGTACCTCCTGG	SEQ ID NO 243	GAGATCAATCTGACAACTTGAAGAAGTAGA	SEQ ID NO 244
At 1g63040	ATGGCTGACCCTAACAATCCTATC	SEQ ID NO 245	ATAGCTCCACAAGCTCTCTCC	SEQ ID NO 246
At 1g63910	GATGGGTCATCACTCATGCTGCAACCAGCA	SEQ ID NO 247	AAACGAAGAAGGGAAAGAAGAAGATAAGGC	SEQ ID NO 248
At 1g64380	ATGGAAGAAAGCAATGATATTTTTC	SEQ ID NO 249	ATTGGCAAGAACTTCCCAAATCAG	SEQ ID NO 250
At 1g67260	ATGTCGTCTTCCACCAATGAC	SEQ ID NO 251	GTTTACAAAAGAGTCTTGAATCC	SEQ ID NO 252
At 1g67780	GATGGCTATTGAGGGTGAGAAAGAGAAACC	SEQ ID NO 253	TGCTACCACATTTGTGTTCTTCAATGTTTG	SEQ ID NO 254
At 1g68800	ATGTTTCCTTCTTTCATTACTCAC	SEQ ID NO 255	ATTAGGGTTTTTAGTTAACACATTG	SEQ ID NO 256
At 1g69120	GATGGGAAGGGGTAGGGTTCAATTGAAGAG	SEQ ID NO 257	TGCGGCGAAGCAGCCAAGGTTGCAGTTGTA	SEQ ID NO 258
At 1g69490	GATGGAAGTAACTTCCCAATCTACCCTCCC	SEQ ID NO 259	AAACTTAAACATCGCTTGACGATGATGGTT	SEQ ID NO 260
At 1g71030	GATGAACAAAACCCGCCTTCGTGCTCTCTC	SEQ ID NO 261	TCGGAATAGAAGAAGCGTTTCTTGACCTGT	SEQ ID NO 262
At 1g71450	ATGGCTGGTCTTAGGAATTCCG	SEQ ID NO 263	AGGGTCCCAAAGAAAGTCACTC	SEQ ID NO 264
At 1g71692	GATGGCTCGTGGAAAGATTCAGCTTAAGAG	SEQ ID NO 265	GAACTGAAATATTTCACTTGGCATTGTTAG	SEQ ID NO 266

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At 1g72360	ATGTGCGGAGGAGCTGTAATTTC	SEQ ID NO 267	GGACCATAGACCCATGTCATTG	SEQ ID NO 268
At 1g72570	ATGAAGAAATGGTTGGGATTTTCATTG	SEQ ID NO 269	GTGGCCGGCGCCAGAGCTGGTG	SEQ ID NO 270
At 1g74840	GATGGCCGACGGTAGTACTAGTTCTTCGGA	SEQ ID NO 271	AGCGACTCCAATCGTGTTGAATGCTGGATG	SEQ ID NO 272
At 1g74930	ATGGTGAAGCAAGCGATGAAGG	SEQ ID NO 273	AAAATCCCAAAGAATCAAAGATTC	SEQ ID NO 274
At 1g76580	GATGGATGTTATGGCTTTGTTAACAGCTTT	SEQ ID NO 275	ACTCTTTGCAAATCGTGGCATTGGCTCAAT	SEQ ID NO 276
At 1g77200	ATGACCGAGTCATCCATTATCTC	SEQ ID NO 277	AGGAAAAAGGGGGCCAAAATTG	SEQ ID NO 278
At 1g77450	GATGATGAAATCTGGGGCTGATTTGC	SEQ ID NO 279	GAAAGTTCCCTGCCTAACCACAAGTGG	SEQ ID NO 280
At 1g78080	GATGGCAGCTGCTATGAATTTGTAC	SEQ ID NO 281	AGCTAGAATCGAATCCCAATCG	SEQ ID NO 282
At 1g79180	GATGGGGAAGGGAAGAGCACCTTGTTGTGA	SEQ ID NO 283	ATGTATCATGAGCTCGTAGTTCTTCAAGAG	SEQ ID NO 284
At 1g80580	ATGGAAAACAGCTACACCGTTG	SEQ ID NO 285	CTTCCTAGACAACAACCCTAAAC	SEQ ID NO 286
At 2g02070	GATGGCTGCTTCTTCATCCTCCGCTGCTTC	SEQ ID NO 287	GAAACTCGCATGATGGATTCCATAAGGTGG	SEQ ID NO 288
At 2g02450	GATGGCGGCGATAGGAGAGAAAG	SEQ ID NO 289	CTTAAAAGGAATATTAGTATAGTG	SEQ ID NO 290
At 2g17040	GATGGTTTACGGTAAGAGATCGAG	SEQ ID NO 291	CCAATATATGTTAACTATTGGTG	SEQ ID NO 292
At 2g18060	GATGGAGCCAATGGAATCTTGTAGCGTTCC	SEQ ID NO 293	ATTATCAAATACGCAAATCCCAATATCATA	SEQ ID NO 294
At 2g22200	ATGGAAACTGCTTCTCTTTCTTTC	SEQ ID NO 295	AGAATTGGCCAGTTTACTAATTGC	SEQ ID NO 296
At 2g23290	GATGTCTGGTTCGACCCCGGAAAGAAATGGA	SEQ ID NO 297	CTCGATCCTACCTAATCCAATAAACTCTCT	SEQ ID NO 298
At 2g23760	GATGGGTTTAGCTACTACAACTTCTTCTAT	SEQ ID NO 299	AAAATCTCCAAAGTCTCTAACGGAGAAAGA	SEQ ID NO 300
At 2g26060	GATGGATTTGATGGAGAAGAACTTGGAGTT	SEQ ID NO 301	CGGTTTAGTTGCAAGCTGCCAAATCTTGAC	SEQ ID NO 302
At 2g28550	GATGTTGGATCTTAACCTCAACGC	SEQ ID NO 303	AGGGTGTGGATAAAAGTAACCAC	SEQ ID NO 304
At 2g30420	GATGGATAATACCAACCGTCTTCGTCTTCG	SEQ ID NO 305	CAATTTTAGATTTTCTTGGAGATTAAGAGG	SEQ ID NO 306
At 2g30470	GATGTTTGAAGTCAAAATGGGGTCAAAGAT	SEQ ID NO 307	GCTTGAAACTCTCGGCTCTTCACGAACATT	SEQ ID NO 308
At 2g31230	ATGTATTCATCTCCAAGTTCTTGG	SEQ ID NO 309	ACATGAGCTCATAAGAAGTTGTTC	SEQ ID NO 310
At 2g33480	GATGGAGAAGAGGAGCTCTATTAAAAACAG	SEQ ID NO 311	TAGAAACAAACAAAACTTATTTTCCCGATA	SEQ ID NO 312
At 2g33710	ATGCATAGCGGGAAGAGACCTC	SEQ ID NO 313	TTTTCGTCGTTTGTGGATACTAATG	SEQ ID NO 314
At 2g35700	ATGGAACGTGACGACTGCCGG	SEQ ID NO 315	GTAACTTTGAGAGAGGAAGGGTTC	SEQ ID NO 316
At 2g40220	ATGGACCCTTTAGCTTCCCAAC	SEQ ID NO 317	ATAGAATTCCCCCAAGATGGGATC	SEQ ID NO 318
At 2g41710	GATGGCGTCGGTGTCGTCGTC	SEQ ID NO 319	TTTCTCTTGTGGGAGGTAGCTG	SEQ ID NO 320
At 2g42400	GATGAAGAGAACACATTTGGCAAGTTTTAG	SEQ ID NO 321	GAGGTAGCCTAGTCGAAGCTCCAAATCAAG	SEQ ID NO 322
At 2g42830	GATGGAGGGTGGTGCGAGTAATGAAGTAGC	SEQ ID NO 323	AACAAGTTGCAGAGGTGGTTGGTCTTGGTT	SEQ ID NO 324
At 2g44840	ATGAGCTCATCTGATTCCGTTAATAAC	SEQ ID NO 325	TATCCGATTATCAGAATAAGAACATTC	SEQ ID NO 326
At 2g44940	ATGGCAAGACAAATCAACATAGAG	SEQ ID NO 327	TTCAGATAGAAAAAACGGCTCTTC	SEQ ID NO 328
At 2g45650	GATGGGAAGAGGGAGAGTGGAGATGAAGAG	SEQ ID NO 329	AAGAACCCAACCTTGGACGAAATTAGTCTC	SEQ ID NO 330
At 2g45680	ATGGCGACAATTCAGAAGCTTG	SEQ ID NO 331	GTGGTTCGATGACCGTGCTG	SEQ ID NO 332
At 2g46310	ATGAAAAGCCGAGTGAGAAAATC	SEQ ID NO 333	TTACTTATCCAACAAATGATCTTGG	SEQ ID NO 334
At 2g46590	GATGATGAACGTTAAACCAATGGAGCAGAT	SEQ ID NO 335	CCATGAAGATCCTCCTCCTGTAGTACTGAA	SEQ ID NO 336
At 2g47520	ATGTGTGGGGGAGCTATCATTTC	SEQ ID NO 337	ATTGGAGTCTTGATAGCTCC	SEQ ID NO 338
At 3g01530	GATGGAGACGACGATGAAGAAGAAAGGGAG	SEQ ID NO 339	AATCACATGGTGGTCACCATTAAGCAAGTG	SEQ ID NO 340
At 3g02150	ATGAATATCGTCTCTTGGAAAGATG	SEQ ID NO 341	ATTGGTGGAGAGTTTTCCAAGCCGAGGTGGC	SEQ ID NO 342
At 3g02310	GATGGGAAGAGGAAGAGTAGAGCTCAAGAG	SEQ ID NO 343	CAGCATCCAGCCAGGGATGTAGCCGTTTCC	SEQ ID NO 344
At 3g04060	GATGGTGGAAGAAGGCGGCGTAG	SEQ ID NO 345	GCTAGTATATAAATCTTCCCAGAAG	SEQ ID NO 346
At 3g04070	GATGATAAGCAAGGATCCAAGATCGAGTTT	SEQ ID NO 347	GCCTTGATATTGAAGGTGAGAACTCATCAT	SEQ ID NO 348
At 3g04420	GATGGAGAATCCGGTGGGTTTAAG	SEQ ID NO 349	TGTTCTTGAGATAGAAGAACATTGG	SEQ ID NO 350
At 3g05760	GATGGCTTCGAGCAACACGACTACTGGGGT	SEQ ID NO 351	TGATTTTTTTGAAGATCCAAAGCCCCCAAA	SEQ ID NO 352
At 3g09600	GATGAGCTCGTCGCCGTCAAGAAATCCAAC	SEQ ID NO 353	TGCTGATTTGTCGCTTGTTGAGTTCTTGAC	SEQ ID NO 354
At 3g10490	GATGGGTCGCGAATCTGTGGCTGTTG	SEQ ID NO 355	TTGTCCATTAGCATTGTTCTTCTTG	SEQ ID NO 356
At 3g11280	GATGGAGACTCTGCATCCATTCTCTCACCT	SEQ ID NO 357	AGCTCCGGCACTGAAGACATTTTCTCCGGC	SEQ ID NO 358
At 3g14230	ATGTGTGGAGGAGCTATAATCTC	SEQ ID NO 359	AAAGTCTCCTTCCAGCATGAAATTG	SEQ ID NO 360
At 3g15500	GATGGGTCTCCAAGAGCTTGACCCGTTAGC	SEQ ID NO 361	AATAAACCCGAACCCACTAGATTGTTGACC	SEQ ID NO 362
At 3g15510	GATGGAGAGCACCGATTCTTCCGGTGGTCC	SEQ ID NO 363	AGAAGAGTACCAATTTAAACCGGGTAATTG	SEQ ID NO 364
At 3g18550	ATGAACAACAACATTTTCAGTACTAC	SEQ ID NO 365	ACTGTGTATAGCTTTAGATAAAACC	SEQ ID NO 366
At 3g20770	GATGATGTTTAATGAGATGGGAATGTGTGG	SEQ ID NO 367	GAACCATATGGATACATCTTGCTGCTTCTG	SEQ ID NO 368
At 3g23220	ATGAAATACAGAGGCGTACGAAAG	SEQ ID NO 369	GCGGTTTGCGTCGTTACAATTG	SEQ ID NO 370
At 3g23230	ATGGAGAGCTCAAACAGGAGC	SEQ ID NO 371	TCTCTTCCTTTCTTCTGAATCAAG	SEQ ID NO 372
At 3g23240	CATGGATCCATTTTTAATTCAGTCC	SEQ ID NO 373	CCAAGTCCCACTATTTTCAGAAG	SEQ ID NO 374
At 3g25890	ATGGCTGAACGAAAGAAACGC	SEQ ID NO 375	TGGGCACGCGATATTAAGAGG	SEQ ID NO 376

[0078]

At 3g27920	GATGAGAATAAGGAGAAGAGATGAAAAAGA	SEQ I D NO 377	AAGGCAGTACTCAACATCACCAGAAGCAAA	SEQ I D NO 378
At 3g28910	GATGGTGAGGCCTCCTTGTTGTGACAAAGG	SEQ I D NO 379	GAAGAAATTAGTGTTTTCATCCAATAGAAT	SEQ I D NO 380
At 3g29035	GATGGATTACAAGGTATCAAGAAG	SEQ I D NO 381	GAATTTCCAAACGCAATCAAGATTC	SEQ I D NO 382
At 3g45150	ATGGATTCGAAAAATGGAATTAAC	SEQ I D NO 383	AACTGTGGTTGTGGCTGTTGTTG	SEQ I D NO 384
At 3g49850	GATGGGAGCTCCAAAGCTGAAGTGGACACC	SEQ I D NO 385	CCGAGTTTGGCTATGCATTCTATACTTCAC	SEQ I D NO 386
At 3g54320	ATGAAGAAGCGGCTTAACCACTTC	SEQ I D NO 387	GACCAAATAGTTACAAGAAACCGAG	SEQ I D NO 388
At 3g61910	GATGAACATATCAGTAAACGGACAGTCACA	SEQ I D NO 389	TCCACTACCGTTCAACAAGTGGCATGTCGT	SEQ I D NO 390
At 4g01060	GATGGATAACCATCGCAGGACTAAGCAACC	SEQ I D NO 391	ATTTTTCATGACCCAAAACCTCTCAATTTC	SEQ I D NO 392
At 4g01550	GATGGTGAAAGATCTGGTTGGG	SEQ I D NO 393	TCTCTCGGCGATCAAACTTCATCGC	SEQ I D NO 394
At 4g18390	ATGATTGGAGATCTAATGAAG	SEQ I D NO 395	GTTCTTGCCTTTACCCTTATG	SEQ I D NO 396
At 4g18450	ATGGCTTTTGGCAATATCCAAG	SEQ I D NO 397	AAAAGAAGATAATAACGTCTCC	SEQ I D NO 398
At 4g23750	ATGGAAGCGGAGAAGAAAATGG	SEQ I D NO 399	AACAGCTAAAAGAGGATCCGAC	SEQ I D NO 400
At 4g26150	GATGGGTTCCAATTTTCATTACACAATAGA	SEQ I D NO 401	CCCGTGAACCATTCCGTGCGATAGAGCCAT	SEQ I D NO 402
At 4g27950	ATGATGATGGATGAGTTTATGGATC	SEQ I D NO 403	CACAAGTAAGAGATCGGATATC	SEQ I D NO 404
At 4g28140	ATGGACTTTGACGAGGAGCTAAATC	SEQ I D NO 405	AAAGAAAGGCCTCATAGGACAAG	SEQ I D NO 406
At 4g28530	GATGGGTTTGAAAGATATTGGGTCC	SEQ I D NO 407	TTGGAAAGCGAGGATATTTTCGGTC	SEQ I D NO 408
At 4g31060	ATGCCACCCTCTCCTCCTAAATC	SEQ I D NO 409	GTTTATCCAATCAATGTCCATCATG	SEQ I D NO 410
At 4g31270	GATGGAGGAAGGAACTTCAGGTTCACGGAG	SEQ I D NO 411	CTCGATTTCTTGTGGAACTTCATGAAGCCT	SEQ I D NO 412
At 4g32800	ATGGCGGATTCGTCTTCCGAC	SEQ I D NO 413	GGGAAAATGTTTCCAAGATTCG	SEQ I D NO 414
At 4g34410	ATGCATTATCCTAACAACAGAACC	SEQ I D NO 415	CTGGAACATATCAGCAATTGTATTTC	SEQ I D NO 416
At 4g35580	GATGCTGCAGTCTGCAGCACCAGAG	SEQ I D NO 417	TGAACTCACCAGTGTCCTCCATATAC	SEQ I D NO 418
At 4g36160	GATGGAATCGGTGGATCAATCATGTAGTGT	SEQ I D NO 419	AACATGTAAATCCCTATATAAGTCATAGTC	SEQ I D NO 420
At 4g37750	ATGAAGTCTTTTTGTGATAATGATG	SEQ I D NO 421	AGAATCAGCCCAAGCAGCGAAAACCGG	SEQ I D NO 422
At 4g38620	GATGGGAAGGTCACCGTGCTGTGAGAAAGC	SEQ I D NO 423	TTTCATCTCCAAGCTTCGAAAGCCCAAAAG	SEQ I D NO 424
At 4g39780	ATGGCAGCCATAGATATGTTCAATAGC	SEQ I D NO 425	AGATTCGGACAATTTGCTAATCGC	SEQ I D NO 426
At 5g02460	GATGGTTTTTTCTTCATTTCCTACTTATCC	SEQ I D NO 427	TATATTGCTAGTAGAAGAAGAACTGAAATT	SEQ I D NO 428
At 5g06100	GATGAGTTACACGAGCACTGACAGTGACCA	SEQ I D NO 429	ACAAACTATTTCAAGTGATGGTAAGGTGAA	SEQ I D NO 430
At 5g07310	ATGGCGAATTCAGGAAATTATGG	SEQ I D NO 431	AAAACCAGAATTAGGAGGTGAAG	SEQ I D NO 432
At 5g07580	ATGGCGAGTTTTGAGGAAAGC	SEQ I D NO 433	AAATGCATCACAGGAAGATGAAG	SEQ I D NO 434
At 5g07680	GATGGATTTGCCTCCTGGTTTTAG	SEQ I D NO 435	GTAATTCCAGAAAGGTTCAAGATC	SEQ I D NO 436
At 5g07690	GATGTCAAGAAAGCCATGTTGTGTGGGAGA	SEQ I D NO 437	TATGAAGTTCTTGTCGTCGTAATCTTGGCT	SEQ I D NO 438
At 5g08070	ATGGGAATAAAAAAAGAAGATCAG	SEQ I D NO 439	CTCGATATGGTCTGGTTGTGAG	SEQ I D NO 440
At 5g08790	GATGAAGTCGGAGCTAAATTTACCAGCTGG	SEQ I D NO 441	CCCCTGTGGAGCAAAACTCCAATTCAAGAA	SEQ I D NO 442
At 5g09330	GATGGGGAAAACTCAACTCGCTCCTGGATT	SEQ I D NO 443	CATTTTTGGTCTATGTCTCATGGAAGCAGA	SEQ I D NO 444
At 5g13180	GATGGATAATGTCAAACTTGTTAAGAATGG	SEQ I D NO 445	TCTGAAACTATTGCAACTACTGGTCTCTTC	SEQ I D NO 446
At 5g13330	ATGGTCTCCGCTCTCAGCCG	SEQ I D NO 447	TTCTCTTGGGTAGTTATAATAATTG	SEQ I D NO 448
At 5g13910	ATGAACACAACATCATCAAAGAGC	SEQ I D NO 449	GGAGCCAAAGTAGTTGAAACCTTG	SEQ I D NO 450
At 5g14000	GATGGAGGTGGAGAAGAGGATTGTAG	SEQ I D NO 451	CTCATCAGCTGAGGTAGGAGGAG	SEQ I D NO 452
At 5g18270	GATGGCGGTTGTGGTTGAAGAAGG	SEQ I D NO 453	GAAGTCCCACAAGTCCCCCCTC	SEQ I D NO 454
At 5g18560	ATGGGTTTTGCTCTGATCCACC	SEQ I D NO 455	AAAGACTGAGTAGAAGCCTGTAG	SEQ I D NO 456
At 5g18830	GATGTCTTCTCTGTCGCAATCGCCACCACC	SEQ I D NO 457	AATTTTGTGTACCAATCTCATTCGGATTGC	SEQ I D NO 458
At 5g22290	GATGGACACGAAGGCGGTTGGAGTTTC	SEQ I D NO 459	TTCTAGATAAAACAACATTGCTATC	SEQ I D NO 460
At 5g22380	GATGGCCGATGAGGTCACAATCGGGTTTCG	SEQ I D NO 461	AGGCCAAGTCAGCTGTTCCCAGTCCCACAT	SEQ I D NO 462
At 5g23260	GATGGGTAGAGGGAAGATAGAGATAAAGAA	SEQ I D NO 463	ATCATTCTGGGCCGTTGGATCGTTTTGAAG	SEQ I D NO 464
At 5g24520	GATGGATAATTCAGCTCCAGATTCGTTATC	SEQ I D NO 465	AACTCTAAGGAGCTGCATTTTGTTAGCAAA	SEQ I D NO 466
At 5g24590	GATGAAAGAAGACATGGAAGTACTATC	SEQ I D NO 467	TGCGACTAGACTGCAGACCGACATC	SEQ I D NO 468
At 5g25190	ATGGCACGACCACAACAACGC	SEQ I D NO 469	CAGCGTCTGAGTTGGTAAAACAG	SEQ I D NO 470
At 5g25390	ATGGTACATTCGAAGAAGTTCCG	SEQ I D NO 471	GACCTGTGCAATGGATCCAG	SEQ I D NO 472
At 5g25810	ATGATAGCTTCAGAGAGTACCAAG	SEQ I D NO 473	ATAATTATACAGTCCTTGAAGATCCC	SEQ I D NO 474
At 5g35550	GATGGGAAAGAGAGCAACTACTAGTGTGAG	SEQ I D NO 475	ACAAGTGAAGTCTCGGAGCCAATCTTCATC	SEQ I D NO 476
At 5g39610	GATGGATTACGAGGCATCAAGAATC	SEQ I D NO 477	GAAATTCCAAACGCAATCCAATTC	SEQ I D NO 478
At 5g40330	ATGAGAATGACAAGAGATGGAAAAG	SEQ I D NO 479	AAGGCAATACCCATTAGTAAAATCCATCATAG	SEQ I D NO 480
At 5g41030	ATGGTCATGGAGCCCAAGAAG	SEQ I D NO 481	TGAACCATTTTCCTCTGCACTC	SEQ I D NO 482
At 5g43270	GATGGAGTGTAATGCAAAGCCACCGTTTCA	SEQ I D NO 483	GTTATAAAACTGGTTCAAGCTGAAGTAGTT	SEQ I D NO 484
At 5g47220	GATGTACGGACAGTGCAATATAGAATCCG	SEQ I D NO 485	TGAAACCAATAACTCATCAACACGTGT	SEQ I D NO 486

[0079]

At 5g47230	GGGGATGGCGACTCCTAACGAAGT	SEQ I D NO 487	AACAACGGTCAACTGGGAATAACCAAACG	SEQ I D NO 488
At 5g47390	GATGACTCGTCGATGTTCTCACTGCAATCA	SEQ I D NO 489	TAAAGCGTGTATCACGCTTTTGATGTCTGA	SEQ I D NO 490
At 5g51190	ATGGCTTCTTCACATCAACAACAG	SEQ I D NO 491	AGTAACTACGAGTTGAGAGTGTC	SEQ I D NO 492
At 5g52020	ATGTCGAATAATAATAATTCTCCGAC	SEQ I D NO 493	TTTATAACTCCAAAGATTATCTCCTTC	SEQ I D NO 494
At 5g53290	ATGGACGAATATATTGATTTCCGAC	SEQ I D NO 495	AGCAACTAATAGATCTGATATCAATG	SEQ I D NO 496
At 5g54230	GATGGGAAAATCTTCAAGCTCGGAGGAAAG	SEQ I D NO 497	TGATAGATTCAAAGCATTATTATTATGATC	SEQ I D NO 498
At 5g58900	GATGGAGGTTATGAGACCGTCGACGTCACA	SEQ I D NO 499	TAGTTGAAACATTGTGTTTTGGGCGTCATA	SEQ I D NO 500
At 5g60970	ATGAGATCAGGAGAATGTGATG	SEQ I D NO 501	AGAATCTGATTCATTATCGCTAC	SEQ I D NO 502
At 5g61600	ATGGCAACTAAACAAGAAGCTTTAG	SEQ I D NO 503	AGTGACGGAGATAACGGAAAAG	SEQ I D NO 504
At 5g62380	GATGGAAAGTCTCGCACACATTCCTCCCCGG	SEQ I D NO 505	CGTGTGTGTATTTTGAGCCCAAGAGTAGAA	SEQ I D NO 506
At 5g64530	GATGAATCTACCACCGGGATTTAGG	SEQ I D NO 507	CGGTAAGCTTACTTCGTCAAGATC	SEQ I D NO 508
At 5g64750	ATGTGTGTCTTAAAAGTGGCAAATC	SEQ I D NO 509	GGAGGATGGACTATTATTGTAG	SEQ I D NO 510
At 5g66300	GATGATGAAGGTTGATCAAGATTATTCGTG	SEQ I D NO 511	GTCTTCTCCACTCATCAAAAATTGAGACGC	SEQ I D NO 512
At 5g67000	ATGGATAATTCAGAAAATGTTC	SEQ I D NO 513	TCTCCACCGCCGTTTAATTC	SEQ I D NO 514
At 5g67300	GATGGCTGATAGGATCAAAGGTCCATGGAG	SEQ I D NO 515	CTCGATTCTCCCAACTCCAATTTGACTCAT	SEQ I D NO 516
At 5g67580	GATGGGTGCACCAAAGCAGAAGTGGACACC	SEQ I D NO 517	CCAAGGATGATTACGGATCCTGAACTTCAA	SEQ I D NO 518

[0080]

Production of improved transcription factors

In order to add a repressor domain sequence to the 3' terminal of a transcription factor gene encoded by the above DNA fragment, p35SSXG, which is a vector having an SmaI site and a repressor domain sequence (amino acid sequence: GLDLDLELRLGFA (SEQ ID NO: 519)) downstream of a CaMV35S promoter, was used. In order to link a transcription factor gene sequence and a repressor domain sequence, p35SSXG was cleaved with SmaI. Each PCR amplification fragment encoding the relevant transcription factor obtained above was separataely inserted at the cleavage site. Thus, 180 types vectors (each denoted by p35SSXG(TFs)) were produced. Here, each vector is denoted by p35SSXG(TFs), provided that "TFs" represents the AGI code for each transcription factor. For example, a vector having the transcription factor specified by At3g04070 is denoted by p35SSXG(At3g04070). Also, in the descriptions below, "TFs" is used in a similar manner to denote vectors and the like.

[0081]

Construction of improved transcription factor expression vectors pBCKH was used as a binary vector for gene introduction into plants with Agrobacterium. This vector was obtained by incorporating a casset of the Gateway vector conversion system (Invitrogen) into the HindIII site of pBIG(Hygr) (Nucleic Acids Res. 18,203 (1990)). In order to incorporate an improved transcription factor gene sequence into the vector, 180 types of p35SSXG(TFs) were each separately mixed with the vector, followed by a recombination reaction using GATEWAY LR clonase (Invitrogen). Thus, 180 types of vectors (each denoted by pBCKH-p35SSXG(TFs)) were produced.

[0082]

Introduction of improved transcription factor gene expression vectors into plants

Arabidopsis thaliana (Columbia (Col-0)) was used as a plant for introduction of an improved transcription factor. Gene introduction was carried out in accordance with "Transformation of Arabidopsis thaliana by vacuum infiltration". Note that each plant was infected only by immersing it in an *Agrobacterium* bacterial liquid without conducting depressurization treatment. Specifically, an improved transcription factor expression vector (pBCKH-p35SSXG(TFs)) was introduced into the soil bacterium (*Agrobacterium tumefaciens*) strain (GV3101 (C58C1Rifr) pMP90 (Gmr), Koncz and Schell 1986)) by electroporation. For each vector, gene-transfected bacterial cells were cultured in 1 liter of a YEP medium containing antibioitics (kanamycin (Km): 50 μg/ml; gentamicin (Gm): 25 μg/ml; and rifampicin (Rif): 50 μg/ml)) until OD600 became 1. Subsequantly, bacterial cells were recovered from each culture solution and suspended in 1 liter of an infection medium (an infiltration medium containing 2.2 g of an MS salt, 1X B5 vitamins, 50 g of sucrose, 0.5 g of MES, 0.044 μM of benzylaminopurine, and 400 μl of Silwet per litter (pH 5.7)).

[0083] *Arabidopsis thaliana* plants cultivated for 14 days were immersed in each solution for 1 minute for infection. Thereafter, the plants were continuously cultivated to result in seed setting. The collected seeds (T1 seeds) were sterilized in a solution containing 50% bleech and 0.02% Triton X-100 for 7 minutes, rinsed 3 times with sterilized water, and seeded on a sterilized hygromycin selection medium (containing a 4.3 g/l MS salt, 0.5% sucrose, 0.5 g/l MES (pH 5.7), 0.8% agar, 30 mg/l hygromycin, and 250 mg/l vancomycin). Five to ten lines of the transformed plants (T1 plants) growing on the hygromycin plate were selected for each improved transcription gene and transplanted into pots (each with a diameter of 50 mm) containing vermiculite mixed soil. Then, the plants were cultivated under conditions of 22°C for 16 hours in the light and 8 hours in the dark at a light intensity ranging from about 60 to 80 μE/cm^2. Thus, seeds (T2 seeds) were obtained.

[0084]

Analysis of T2 seeds

T2 seeds from 5 to 10 lines of transformants prepared via transfecion with 180 types of TFs-SRDXs were analyzed for fat and oil content. *Arabidopsis thaliana* seeds (2 to 10 mg each) were subjected to quantitative analysis of fats and oils using MARAN-23 (ResonanceInsturuments Ltd., UK) H-NMR and analysis software (RI-NMR Ver. 2.0). Olive oil was used as a fat and oil reference substance to create a calibration curve for determination of the fat and oil content in seeds (% by weight).

[0085] Tables 4 to 6 summarize the analysis results of the fat and oil content in T2 seeds for the transformants obtained via transfection with the relevant TFs-SRDX genes.

[Table 4]

AGI code	Genes	Fat and oil content (average)	Standard deviation	P value (t-test)
WT(Col-0)	WT(Col-0)	34.9%	3.8%	
At1g56650	At1g56650-SRDX	41.3%	4.7%	0.00%
At5g47230	At5g47230-SRDX	40.5%	1.5%	0.00%
At1g22985	At1g22985-SRDX	39.3%	3.1%	0.05%
At1g80580	At1g80580-SRDX	39.1%	3.3%	0.14%
At1g25470	At1g25470-SRDX	39.0%	2.6%	0.04%
At1g67260	At1g67260-SRDX	38.7%	3.4%	0.39%
At5g24520	At5g24520-SRDX	38.3%	2.4%	0.15%
At1g71030	At1g71030-SRDX	38.3%	3.3%	0.57%
At4g36160	At4g36160-SRDX	37.9%	3.0%	1.34%
At3g15510	At3g15510-SRDX	37.9%	3.3%	2.11%
At5g64750	At5g64750-SRDX	37.1%	2.1%	2.03%
At5g07580	At5g07580-SRDX	37.1%	3.8%	11.48%
At5g61600	At5g61600-SRDX	37.0%	3.7%	13.06%
At1g74930	At1g74930-SRDX	37.0%	2.7%	5.61%
At2g31230	At2g31230-SRDX	36.7%	1.1%	1.81%
At4g01550	At4g01550-SRDX	36.7%	1.0%	1.97%
At1g68800	At1g68800-SRDX	36.6%	2.8%	12.64%
At5g51190	At5g51190-SRDX	36.6%	4.6%	29.97%
At5g47390	At5g47390-SRDX	36.5%	3.3%	18.20%
At1g24260	At1g24260-SRDX	36.5%	1.4%	4.63%
At5g09330	At5g09330-SRDX	36.5%	1.4%	4.97%
At5g40330	At5g40330-SRDX	36.5%	5.8%	41.64%
At3g04420	At3g04420-SRDX	36.4%	1.4%	5.24%
At3g23240	At3g23240-SRDX	36.3%	4.7%	37.70%
At5g18560	At5g18560-SRDX	36.3%	3.2%	24.67%
At3g23220	At3g23220-SRDX	36.3%	1.9%	13.44%
At1g10200	At1g10200-SRDX	36.1%	1.2%	16.57%
At5g25810	At5g25810-SRDX	36.0%	1.4%	16.19%
At5g24590	At5g24590-SRDX	35.9%	1.9%	23.99%
At1g15360	At1g15360-SRDX	35.8%	5.0%	60.12%
At4g31270	At4g31270-SRDX	35.8%	2.1%	33.95%
At3g11280	At3g11280-SRDX	35.7%	3.2%	48.17%
At2g40220	At2g40220-SRDX	35.7%	1.8%	32.94%
At2g46310	At2g46310-SRDX	35.6%	1.8%	39.17%
At1g72570	At1g72570-SRDX	35.6%	1.6%	37.63%
At2g44840	At2g44840-SRDX	35.6%	1.8%	43.45%
At3g45150	At3g45150-SRDX	35.5%	5.7%	75.03%
At5g67300	At5g67300-SRDX	35.4%	2.6%	59.92%
At3g14230	At3g14230-SRDX	35.4%	2.8%	63.53%
At4g27950	At4g27950-SRDX	35.3%	2.1%	65.97%
At5g25190	At5g25190-SRDX	35.3%	3.7%	77.19%
At2g42400	At2g42400-SRDX	35.3%	1.7%	64.86%
At5g06100	At5g06100-SRDX	35.2%	1.1%	68.48%
At5g67000	At5g67000-SRDX	35.2%	1.7%	72.40%
At5g64530	At5g64530-SRDX	35.2%	1.4%	70.59%
At3g05760	At3g05760-SRDX	35.1%	4.8%	89.74%
At1g63910	At1g63910-SRDX	35.1%	2.4%	82.95%
At5g35550	At5g35550-SRDX	35.0%	1.7%	86.61%
At3g61910	At3g61910-SRDX	35.0%	5.6%	94.10%
At4g37750	At4g37750-SRDX	34.8%	2.4%	98.10%
At1g24590	At1g24590-SRDX	34.8%	3.4%	96.18%
At5g23260	At5g23260-SRDX	34.8%	1.6%	94.23%
At1g78080	At1g78080-SRDX	34.8%	1.1%	92.81%
At2g22200	At2g22200-SRDX	34.8%	3.1%	92.51%
At5g08790	At5g08790-SRDX	34.7%	2.2%	89.22%
At1g43640	At1g43640-SRDX	34.7%	1.8%	86.52%
At1g79180	At1g79180-SRDX	34.7%	2.1%	84.04%
At5g25390	At5g25390-SRDX	34.7%	1.7%	81.22%
At2g28550	At2g28550-SRDX	34.6%	2.6%	82.85%
At4g39780	At4g39780-SRDX	34.6%	2.1%	79.62%
At5g39610	At5g39610-SRDX	34.5%	3.6%	80.18%

[Table 5]

AGI code	Genes	Fat and oil content (average)	Standard deviation	P value (t-test)
At4g23750	At4g23750-SRDX	34.5%	3.3%	77.60%
At4g35580	At4g35580-SRDX	34.5%	2.4%	67.37%
At2g33480	At2g33480-SRDX	34.4%	2.2%	64.16%
At3g02310	At3g02310-SRDX	34.4%	1.9%	57.72%
At4g34410	At4g34410-SRDX	34.3%	4.2%	71.90%
At5g58900	At5g58900-SRDX	34.3%	2.8%	59.57%
At5g53290	At5g53290-SRDX	34.2%	2.9%	52.74%
At1g01010	At1g01010-SRDX	34.1%	1.3%	34.04%
At3g25890	At3g25890-SRDX	34.1%	2.2%	43.34%
At1g67780	At1g67780-SRDX	34.1%	2.8%	48.95%
At1g63040	At1g63040-SRDX	34.1%	2.0%	38.51%
At1g52890	At1g52890-SRDX	34.0%	1.7%	29.38%
At4g31060	At4g31060-SRDX	33.9%	2.9%	40.19%
At1g53230	At1g53230-SRDX	33.9%	3.0%	40.84%
At1g27370	At1g27370-SRDX	33.9%	2.8%	37.54%
At1g12980	At1g12980-SRDX	33.9%	2.2%	29.35%
At5g67580	At5g67580-SRDX	33.9%	3.4%	42.60%
At1g17520	At1g17520-SRDX	33.8%	2.8%	34.90%
At2g33710	At2g33710-SRDX	33.8%	1.9%	23.88%
At3g28910	At3g28910-SRDX	33.8%	5.2%	54.42%
At2g26060	At2g26060-SRDX	33.8%	1.5%	17.87%
At1g77200	At1g77200-SRDX	33.7%	2.3%	25.47%
At3g23230	At3g23230-SRDX	33.7%	4.6%	47.57%
At1g64380	At1g64380-SRDX	33.6%	3.6%	34.06%
At1g43160	At1g43160-SRDX	33.6%	2.1%	17.39%
At1g28160	At1g28160-SRDX	33.6%	3.1%	27.37%
At2g35700	At2g35700-SRDX	33.5%	2.0%	14.13%
At3g29035	At3g29035-SRDX	33.5%	1.6%	10.20%
At2g44940	At2g44940-SRDX	33.5%	2.2%	15.44%
At1g14510	At1g14510-SRDX	33.5%	3.6%	29.60%
At1g56010	At1g56010-SRDX	33.4%	5.4%	43.55%
At5g41030	At5g41030-SRDX	33.4%	3.4%	25.95%
At2g41710	At2g41710-SRDX	33.4%	3.0%	20.11%
At1g34190	At1g34190-SRDX	33.3%	2.8%	15.19%
At1g61110	At1g61110-SRDX	33.3%	2.5%	12.63%
At2g45680	At2g45680-SRDX	33.2%	3.0%	16.92%
At1g28520	At1g28520-SRDX	33.2%	2.3%	9.64%
At5g13910	At5g13910-SRDX	33.2%	3.4%	18.79%
At3g01530	At3g01530-SRDX	33.2%	4.1%	24.65%
At5g22290	At5g22290-SRDX	33.1%	2.4%	7.40%
At5g18270	At5g18270-SRDX	33.0%	3.0%	11.81%
At2g30470	At2g30470-SRDX	33.0%	1.8%	3.80%
At1g18570	At1g18570-SRDX	33.0%	2.6%	8.10%
At5g07680	At5g07680-SRDX	33.0%	2.7%	8.13%
At2g17040	At2g17040-SRDX	33.0%	1.8%	3.26%
At5g07690	At5g07690-SRDX	32.9%	2.2%	4.47%
At3g54320	At3g54320-SRDX	32.9%	2.3%	5.12%
At3g15500	At3g15500-SRDX	32.9%	1.9%	2.97%
At2g30420	At2g30420-SRDX	32.9%	1.4%	1.51%
At3g09600	At3g09600-SRDX	32.8%	1.6%	1.71%
At1g36060	At1g36060-SRDX	32.8%	2.2%	3.25%
At1g01250	At1g01250-SRDX	32.7%	1.7%	1.53%
At1g25580	At1g25580-SRDX	32.7%	2.1%	2.46%
At5g54230	At5g54230-SRDX	32.7%	3.0%	6.49%
At3g20770	At3g20770-SRDX	32.7%	2.4%	3.36%
At1g12890	At1g12890-SRDX	32.7%	2.0%	2.03%
At1g60240	At1g60240-SRDX	32.6%	4.5%	15.84%

[Table 6]

AGI code	Genes	Fat and oil content (average)	Standard deviation	P value (t-test)
At4g28530	At4g28530-SRDX	32.5%	3.5%	7.11%
At4g18450	At4g18450-SRDX	32.4%	4.3%	8.56%
At2g47520	At2g47520-SRDX	32.4%	3.3%	5.10%
At2g18060	At2g18060-SRDX	32.4%	1.8%	0.61%
At4g18390	At4g18390-SRDX	32.3%	2.1%	1.03%
At5g08070	At5g08070-SRDX	32.3%	1.9%	0.59%
At1g76580	At1g76580-SRDX	32.2%	2.2%	0.84%
At4g28140	At4g28140-SRDX	32.2%	2.9%	2.15%
At5g60970	At5g60970-SRDX	32.1%	2.2%	0.69%
At2g42830	At2g42830-SRDX	32.1%	3.2%	2.52%
At1g30210	At1g30210-SRDX	32.1%	2.8%	1.61%
At1g71450	At1g71450-SRDX	32.1%	2.4%	0.89%
At1g09540	At1g09540-SRDX	32.1%	1.8%	0.26%
At3g10490	At3g10490-SRDX	32.0%	2.5%	0.72%
At1g62700	At1g62700-SRDX	32.0%	1.9%	0.21%
At1g49120	At1g49120-SRDX	31.9%	2.3%	0.44%
At1g44830	At1g44830-SRDX	31.9%	3.2%	1.84%
At1g30810	At1g30810-SRDX	31.8%	2.2%	0.31%
At1g74840	At1g74840-SRDX	31.8%	3.2%	1.35%
At5g18830	At5g18830-SRDX	31.8%	1.8%	0.09%
At1g72360	At1g72360-SRDX	31.4%	2.0%	0.04%
At1g32770	At1g32770-SRDX	31.3%	1.9%	0.03%
At5g14000	At5g14000-SRDX	31.3%	2.1%	0.05%
At2g23290	At2g23290-SRDX	31.3%	2.8%	0.21%
At2g02450	At2g02450-SRDX	31.1%	2.3%	0.04%
At1g27360	At1g27360-SRDX	31.0%	2.3%	0.03%
At1g33760	At1g33760-SRDX	31.0%	2.1%	0.02%
At3g27920	At3g27920-SRDX	30.9%	2.1%	0.01%
At3g18550	At3g18550-SRDX	30.8%	2.9%	0.08%
At1g52880	At1g52880-SRDX	30.8%	3.4%	0.23%
At5g07310	At5g07310-SRDX	30.7%	2.3%	0.01%
At4g26150	At4g26150-SRDX	30.6%	2.0%	0.00%
At1g19490	At1g19490-SRDX	30.6%	2.3%	0.01%
At1g52150	At1g52150-SRDX	30.6%	1.5%	0.00%
At3g04060	At3g04060-SRDX	30.5%	3.1%	0.07%
At4g32800	At4g32800-SRDX	30.5%	2.8%	0.03%
At5g66300	At5g66300-SRDX	30.5%	2.1%	0.00%
At5g13180	At5g13180-SRDX	30.5%	5.5%	2.41%
At1g71692	At1g71692-SRDX	30.5%	2.9%	0.03%
At1g27730	At1g27730-SRDX	30.4%	1.4%	0.00%
At3g49850	At3g49850-SRDX	30.1%	1.3%	0.00%
At3g02150	At3g02150-SRDX	30.1%	2.8%	0.02%
At5g47220	At5g47220-SRDX	30.0%	4.9%	0.60%
At5g43270	At5g43270-SRDX	29.7%	2.1%	0.00%
At5g52020	At5g52020-SRDX	29.7%	2.1%	0.00%
At1g69490	At1g69490-SRDX	29.6%	4.8%	0.28%
At4g38620	At4g38620-SRDX	29.4%	4.1%	0.05%
At2g45650	At2g45650-SRDX	29.2%	1.3%	0.00%
At5g02460	At5g02460-SRDX	29.0%	1.6%	0.00%
At1g12260	At1g12260-SRDX	28.9%	2.9%	0.00%
At5g13330	At5g13330-SRDX	28.7%	3.6%	0.00%
At4g01060	At4g01060-SRDX	28.5%	3.0%	0.00%
At2g46590	At2g46590-SRDX	28.5%	2.4%	0.00%
At1g69120	At1g69120-SRDX	28.3%	3.2%	0.00%
At1g77450	At1g77450-SRDX	28.1%	6.1%	0.17%
At2g23760	At2g23760-SRDX	28.0%	2.4%	0.00%
At2g02070	At2g02070-SRDX	27.9%	2.4%	0.00%
At1g22640	At1g22640-SRDX	27.8%	2.2%	0.00%
At1g18330	At1g18330-SRDX	27.6%	4.0%	0.00%
At5g22380	At5g22380-SRDX	27.5%	5.1%	0.01%
At5g62380	At5g62380-SRDX	26.0%	3.7%	0.00%
At3g04070	At3g04070-SRDX	25.2%	3.5%	0.00%

[0086] The fat and oil content in fructified seeds was found to be 34.9 ± 3.8% for 33 untransfected control WT(Col-0) individuals.

Meanwhile, the average fat and oil content in T2 seeds was found to be 25.2% to 41.3% for the transformants each overexpressing a chimeric protein comprising a different one of the 180 types of transcription factors fused with SRDX. For a comparison of the obtained average value with the average fat and oil content for the wild-type strain, a t-test was performed. Accordingly, T2 seeds expressing chimeric proteins from 15 lines (accounting for 8.3% of the analyzed transcription factors) were found to exhibit a significant increase in the fat and oil content ($P < 0.05$). Meanwhile, T2 seeds expressing chimeric proteins from 70 lines (accounding for 38.9% of the analyzed transcription factors) were found to exhibit a significant decrease in fat and oil content ($P < 0.05$). That is, expression of approximately 47.2% of chimeric proteins caused an increase or decrease in fat and oil content. In other words, about more than half of the transcription factors (e.g., At5g40330, At4g23750, and At5g18270) examined herein substantially do not influence the fat and oil content in seeds even when a chimeric protein comprising such a transcription factor and a repressor domain is expressed.

[0087] In this Example, each of the following 11 types of transcription factors was newly identified as a transcription factor capable of functioning to improve the fat and oil content in seeds when a chimeric protein comprising the transcription factor fused with a repressor domain was expressed: At5g47230, At1g22985, At1g80580, At1g25470, At1g67260, At4g36160, At5g64750, At4g01550, At1g24260, At5g09330, and At2g31230. Also in this Example, each of the following 68 types of transcription factors was newly identified as a transcription factor capable of functioning to reduce the fat and oil content in seeds when a chimeric protein comprising the transcription factor fused with a repressor domain was expressed: At2g17040, At5g07690, At3g15500, At2g30420, At3g09600, At1g36060, At1g01250, At1g25580, At3g20770, At1g12890, At2g18060, At4g18390, At5g08070, At1g76580, At4g28140, At5g60970, At2g42830, At1g30210, At1g71450, At1g09540, At3g10490, At1g62700, At1g49120, At1g44830, At1g30810, At1g74840, At5g18830, At1g72360, At1g32770, At5g14000, At2g23290, At2g02450, At1g27360, At1g33760, At3g27920, At3g18550, At1g52880, At5g07310, At4g26150, At1g19490, At1g52150, At3g04060, At4g32800, At5g66300, At5g13180, At1g71692, At1g27730, At3g49850, At3g02150, At5g47220, At5g43270, At5g52020, At1g69490, At4g38620, At2g45650, At5g02460, At1g12260, At5g13330, At4g01060, At2g46590, At1g69120, At1g77450, At2g23760, At2g02070, At1g22640, At5g22380, and At5g62380.

[0088] As described above, the Examples revealed that the fat and oil contents in seeds can be significantly modified by causing expression of a particular transcription factor fused with a repressor domain.

[0089]

Production of a At5g22380-expressing strain and analysis of fat and oil content

As described above, a DNA fragment of At5g22380 was amplified such that the fragment contained a termination codon. Then, the DNA fragment was ligated downstream of a 35S promoter in the manner described above and the ligation product was introduced into *Arabidopsis thaliana*. Specifically, an *Arabidopsis thaliana* transformant capable of expressing At5g22380 (which was in its original state and thus was not fused with SRDX) under the regulation of a constitutive expression promoter was produced for experimentation. The produced *Arabidopsis thaliana* transformant was subjected to determination of the fat and oil content in T2 seeds in the manner described above. Accordingly, the fat and oil content in T2 seeds was found to be 37.6 ± 1.8% for plant individuals expressing At5g22380. Meanwhile, the fat and oil content was found to be 36.3 ± 0.4% for the wild-type strain that had been cultivated in the same period. As a result of a t-test, a significant increase in the fat and oil content was confirmed ($P < 0.05$). The fat and oil content of the line with the highest fat and oil content was found to be 40.0%, which was 10.3% greater than that of the wild-type strain.

[0090] The above experimental results revealed that a transcription factor expressed in a state of being fused with a repressor domain can significantly reduce the fat and oil content in seeds. This strongly suggested that the fat and oil content in seeds can be significantly improved when such transcription factor, which is originally not fused with a repressor domain, is expressed as is (that is to say, expressed under expression regulation by a constitutive expression promoter). Also, the above experimental results revealed that a transcription factor expressed in a state of being fused with a repressor domain can significantly improve the fat and oil content in seeds. This strongly suggested that the fat and oil content in seeds can be significantly reduced when such transcription factor, which is originally not fused with a repressor domain, is expressed as is (that is to say, expressed under expression regulation by a constitutive expression promoter).

CLAIMS:

1. A method for improving a productivity of fats and oils in seeds by introducing a fusion gene encoding a chimeric protein obtained by fusing a transcription factor consisting of any one of the following proteins (a) to (b) and a functional peptide for converting an arbitrary transcription factor into a transcriptional repressor in a plant:

(a) a protein comprising any amino acid listed in the following table

AGI code	Nucleotide sequence	Amino acid sequence
At1g80580	SEQ ID NO: 5	SEQ ID NO: 6

; and

(b) a protein having transactivation activity encoded by a polynucleotide that hybridizes under stringent conditions to a polynucleotide consisting of a nucleotide sequence complementary to any nucleotide sequence listed in the above table, said stringent conditions comprising the steps of hybridization with 6 x SSC (sodium chloride/sodium citrate), washing at 50°C to 60°C with 0.2 to 1 x SSC and 0.1% SDS,

wherein the functional peptide has an amino acid sequence of any one of the following formulae (1) to (8):

(1) X1-Leu-Asp-Leu-X2-Leu-X3 (where X1 denotes a set of 0 to 10 amino acid residues, X2 denotes Asn or Glu, and X3 denotes a set of at least 6 amino acid residues);

(2) Y1-Phe-Asp-Leu-Asn-Y2-Y3 (where Y1 denotes a set of 0 to 10 amino acid residues, Y2 denotes Phe or Ile, and Y3 denotes a set of at least 6 amino acid residues);

(3) Z1-Asp-Leu-Z2-Leu-Arg-Leu-Z3 (where Z1 denotes Leu, Asp-Leu, or Leu-Asp-Leu, Z2 denotes Glu, Gln, or Asp, and Z3 denotes a set of 0 to 10 amino acid residues);

(4) Asp-Leu-Z4-Leu-Arg-Leu (where Z4 denotes Glu, Gln, or Asp);

(5) α1-Leu-β1-Leu-γ1-Leu;

(6) α1-Leu-β1-Leu-γ2-Leu;

(7) α1-Leu-β2-Leu-Arg-Leu; and

(8) α2-Leu-β1-Leu-Arg-Leu,

wherein α1 denotes Asp, Asn, Glu, Gln, Thr, or Ser, α2 denotes Asn, Glu, Gln, Thr, or Ser, β1 denotes Asp, Gln, Asn, Arg, Glu, Thr, Ser, or His, β2 denotes Asn, Arg, Thr, Ser, or His, $\gamma1$ denotes Arg, Gln, Asn, Thr, Ser, His, Lys, or Asp, and $\gamma2$ denotes Gln, Asn, Thr, Ser, His, Lys, or Asp in formulae (5) to (8).

2. The method according to claim 1, wherein the chimeric protein has transcriptional repressor activity.

3. The method according to claim 1, wherein the plant is an angiosperm.

4. The method according to claim 1, wherein the plant is a dicotyledon.

5. The method according to claim 1, wherein the plant is a cruciferous plant.

6. The method according to claim 1, wherein the plant is *Arabidopsis thaliana.*