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(54) DELTA 6 DESATURASES FROM PRIMULACEAE, EXPRESSING PLANTS AND PUFA-CONTAINING OILS

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(56) References Cited
FOREIGN PATENT DOCUMENTS
WO WO-96/21022 A1 1996
WO WO-99/64614 1999

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(57) ABSTRACT
The present invention relates to an improved method for the specific production of unsaturated ω-3 fatty acids and a method for the production of triglycerides having an increased content of unsaturated fatty acids, in particular ω-3 fatty acids having more than three double bonds. The invention relates to the production of a transgenic organism, preferably a transgenic plant or a transgenic microorganism, having an increased content of fatty acids, oils or lipids having Δ6 double bonds due to the expression of a Δ6-desaturase from Primulaceae. The invention additionally relates to expression cassettes containing a nucleic acid sequence, a vector and organisms containing at least one nucleic acid sequence or an expression cassette. The invention further relates to unsaturated fatty acids and triglycerides having an increased content of unsaturated fatty acids and use thereof.

32 Claims, No Drawings
DELTA 6 DESATURASES FROM PRIMULACEAE, EXPRESSING PLANTS AND PUFA-CONTAINING OILS

RELATED APPLICATIONS

This application is a divisional application of U.S. application Ser. No. 10/504,424 filed Aug. 13, 2004, which is a national stage application (under 35 U.S.C. §371) of PCT/EP2003/01161 filed Feb. 6, 2003, which claims benefit of United Kingdom application 0204676.1 filed Feb. 27, 2002. The entire content of each above-mentioned application is hereby incorporated by reference in its entirety.

SUBMISSION OF SEQUENCE LISTING

The Sequence Listing associated with this application is filed in electronic format via EFS-Web and hereby incorporated by reference into the specification in its entirety. The name of the text file containing the Sequence Listing is Sequence_List_12810_00051.txt. The size of the text file is 23 KB, and the text file was created on May 5, 2009.

FIELD OF THE INVENTION

The present invention relates to an improved method for the specific production of unsaturated α-3 fatty acids and a method for the production of triglycerides having an increased content of unsaturated fatty acids, in particular α-3 fatty acids having more than three double bonds. The invention relates to the production of a transgenic organism, preferably a transgenic plant or a transgenic microorganism, having an increased content of fatty acids, oils or lipids having Δ6 double bonds due to the expression of a Δ6-desaturase from Primulaceae.

The invention additionally relates to expression cassettes containing a nucleic acid sequence, a vector and organisms containing at least one nucleic acid sequence or an expression cassette. The invention further relates to unsaturated fatty acids and triglycerides having an increased content of unsaturated fatty acids and use thereof.

BACKGROUND OF THE INVENTION

Fatty acids and triglycerides have numerous applications in the food industry, animal nutrition, cosmetics and in the drug sector. Depending on whether they are free saturated or unsaturated fatty acids or are triglycerides having an increased content of saturated or unsaturated fatty acids, they are suitable for the most varied applications. Thus, for example, polyunsaturated fatty acids are added to infant formula to increase its nutritional value. The various fatty acids and triglycerides are mainly obtained from microorganisms such as Mortierella or from oil-producing plants such as soybean, oilseed rape, sunflower and others, and generally occur in the form of triacylglycerides. However, they may also be obtained from animals, e.g. fish. The free fatty acids are advantageously produced by saponification.

Depending on application purpose oils containing saturated or unsaturated fatty acids are preferred, thus in human nutrition for example, lipids containing unsaturated fatty acids, especially polyunsaturated fatty acids, are preferred since they have a positive effect on the level of cholesterol in the blood and hence on the possibility of heart disease. They are employed in various dietary foods or medicinal drugs.


To date, however, the various desaturases have been only inadequately characterized biochemically since the enzymes in the form of membrane-bound proteins are isolable and characterizable only with very great difficulty (McKeon et al., Methods in Enzymol., 71, 1981: 12141-12147, Wang et al., Plant Physiol. Biochem., 26, 1988: 777-792). Generally, membrane-bound desaturases are characterized by introduction into a suitable organism which is then investigated for enzyme activity by means of analysis of starting materials and products. Δ6-Desaturases are described in WO 93/06712, U.S. Pat. No. 5,614,393, U.S. Pat. No. 5,614,393, WO 96/21022, WO 96/21157 and WO 99/27111 and their application to production in transgenic organisms is also described, e.g. in WO 9846753, WO 9846754 and WO 9846757. At the same time the expression of various desaturases, as in WO 9564616 or WO 9846775, and the formation of polyunsaturated fatty acids is also described and claimed.

With regard to the effectiveness of the expression of desaturases and their effect on the formation of polyunsaturated fatty acids it may be noted that through expression of a single desaturase as described to date only low contents of Δ6 unsaturated fatty acids/lipids, such as by way of example gamma-linolenic acid and steardonic acid, have been achieved. Furthermore, a mixture of α-3 and α-6 fatty acids was usually obtained since all Δ6-desaturases described so far converted, for example, linoleic acid (α-6 fatty acid) as well as α-linolenic acid (α-3 fatty acid).

Accordingly, there is still a great demand for new and more suitable genes which encode enzymes which participate in the biosynthesis of unsaturated fatty acids and make it possible to produce certain fatty acids specifically on an industrial scale without unwanted byproducts forming.

In the selection of genes for biosynthesis two characteristics above all are particularly important. On the one hand, there is an ever a need for improved processes for obtaining the highest possible contents of polyunsaturated fatty acids. On the other hand, the enzymes employed should be highly specific to a certain substrate since as far as possible unwanted byproducts must not be produced which might have negative or so far undiscovered physiological effects in humans or animals due to food/feed intake.

SUMMARY OF THE INVENTION

Accordingly, it is an object of the present invention to introduce further genes of desaturase enzymes for the synthesis of polyunsaturated fatty acids into the seeds of an oil seed and in doing so to prevent the production of unwanted byproducts. We have found that this object is achieved by the isolated nucleic acid sequences according to the invention which encode polypeptides having Δ6-desaturase activity, wherein the Δ6-desaturases encoded by the nucleic acid sequences specifically convert α-3 fatty acids. This object was achieved in particular by cloning the isolated nucleic acid sequences according to the invention, wherein the nucleic acid sequences encode a polypeptide having Δ6-desaturase activity.
Allele variants include in particular functional variants obtainable by deletion, insertion or substitution of nucleotides in the sequences depicted in SEQ ID NO: 1 or SEQ ID NO: 3, the enzymatic activity of the derived synthesized proteins being retained.

Starting from the DNA sequence described in SEQ ID NO: 1 and SEQ ID NO: 3 or parts of said sequences such DNA sequences can be isolated using, for example, normal hybridization methods or the PCR technique from other eukaryotes such as those identified above for example. These DNA sequences hybridize under standard conditions with the said sequences. For hybridization use is advantageously made of short oligonucleotides of the conserved regions, for example, which can be determined by comparisons with other desaturase genes in the manner known to those skilled in the art. The histidine box sequences are advantageously employed. However, longer fragments of the nucleic acids according to the invention or the complete sequences may also be used for hybridization. Depending on the nucleic acid employed: oligonucleotide, longer fragment or complete sequence, or depending on which type of nucleic acid, DNA or RNA, is used for hybridization these standard conditions vary. Thus, for example, the melting temperatures of DNA:DNA hybrids are approximately 10\(^\circ\) C. lower than those of DNA:RNA hybrids of the same length.

By standard conditions is meant, for example, depending on the nucleic acid in question temperatures between 42\(^\circ\) C. and 58\(^\circ\) C. in an aqueous buffer solution having a concentration of between 0.1 and 5\(\times\)SSC (1\(\times\)SSC=0.15 M NaCl, 15 mM sodium citrate, pH 7.2) or additionally in the presence of 50\% formamide, such as by way of example 42\(^\circ\) C. in 5\(\times\)SSC, 50\% formamide. Hybridization conditions for DNA:DNA hybrids are advantageously 0.1\(\times\)SSC and temperatures between approximately 20\(^\circ\) C. and 45\(^\circ\) C. preferably between approximately 30\(^\circ\) C. and 45\(^\circ\) C. For DNA:RNA hybrids the hybridization conditions are advantageously 0.1\(\times\) SSC and temperatures between approximately 30\(^\circ\) C. and 55\(^\circ\) C. preferably between approximately 45\(^\circ\) C. and 55\(^\circ\) C. These specified temperatures for hybridization are melting temperature values calculated by way of example for a nucleic acid having a length of approximately 100 nucleotides and a G+C content of 50\% in the absence of formamide. The experimental conditions for DNA hybridization are described in relevant genetics textbooks such as by way of example Sambrook et al., “Molecular Cloning”, Cold Spring Harbor Laboratory, 1989, and may be calculated by formulae known to those skilled in the art, for example as a function of the length of the nucleic acids, the nature of the hybrids or the G+C content. Those skilled in the art may draw on the following textbooks for further information on hybridization: Ausubel et al. (eds), 1985, Current Protocols in Molecular Biology, John Wiley & Sons. New York, Hames and Higgins (eds), 1985, Nucleic Acids Hybridization: A Practical Approach, IRL Press at Oxford University Press, Oxford; Brown (ed), 1991, Essential Molecular Biology: A Practical Approach, IRL Press at Oxford University Press, Oxford.

Furthermore, by derivatives is meant homologues of the sequences SEQ ID NO: 1 and NO: 3, for example eukaryotic homologues, truncated sequences, single-stranded DNA of the encoding and noncoding DNA sequence or RNA of the encoding and noncoding DNA sequence.

In addition, by homologues of the sequences SEQ ID NO: 1 and SEQ ID NO: 3 is meant derivatives such as by way of example promoter variants. These variants may be modified by one or more nucleotide exchanges, by insertion(s) and/or deletion(s) without, however, adversely affecting the functionality or efficiency of the promoters. Furthermore, the
promoters can have their efficiency increased by altering their sequence or be completely replaced by more effective promoters even of foreign organisms.

By derivatives is also advantageously meant variants whose nucleotide sequence has been altered in the region from -1 to -2000 ahead of the start codon in such a way that the gene expression and/or the protein expression is modified, preferably increased. Furthermore, by derivatives is also meant variants which have been modified at the 3’ end.

By derivatives is also meant the antisense DNAs which may be employed for inhibiting protein biosynthesis of the proteins according to the invention. These antisense DNAs are numbered among the nonfunctional derivatives according to the invention such as derivatives which exhibit no enzymatic activity. Other methods known to those skilled in the art for the production of nonfunctional derivatives are what is known as cosuppression, the use of ribozymes and introns and the RNAi method. Ribozymes are catalytic RNA molecules having ribonuclease activity which can chop single-stranded nucleic acids, such as mRNA, with which they are complementary. In this way, using these ribozymes (Hauselhoff and Gerlach, Nature, 334, 1988: 585-591) mRNA transcripts can be catalytically cleaved and, thus, the translation of this mRNA is suppressed. Ribozymes of this type can be specially tailored to their purpose (U.S. Pat. No. 4,987,071; U.S. Pat. No. 5,116,742 and Bartel et al., Science 261, 1993: 1413-1418). By this means, with the aid of the antisense DNA, fatty acids, lipids or oils having an increased content of saturated fatty acids can be produced.

The nucleic acid sequence according to the invention which encodes a Δ6-desaturase may be produced by synthesis or obtained naturally or contain a mixture of synthetic and natural DNA components as well as consist of various heterologous Δ6-desaturase gene segments from different organisms. In general, synthetic nucleotide sequences are produced with codons which are preferred by the corresponding host organisms, plants for example. This usually results in optimum expression of the heterologous gene. These codons preferred by plants may be determined from codons having the highest protein frequency which are expressed in most of the plant species of interest. An example concerning Corynebacterium glutamicum is provided in Wada et al. (1992) Nucleic Acids Res. 20:2111-2118. Such experiments can be carried out using standard methods and are known to the person skilled in the art.

Functionally equivalent sequences which encode the Δ6-desaturase gene are those derivatives of the sequence according to the invention which despite differing nucleotide sequence still possess the desired functions, that is to say the enzymatic activity and specific selectivity of the proteins. Thus, functional equivalents include naturally occurring variants of the sequences described herein as well as artificial ones, e.g. artificial nucleotide sequences adapted to the codon use of a plant which have been obtained by chemical synthesis.

In addition, artificial DNA sequences are suitable, provided, as described above, they mediate the desired property, for example an increase in the content of Δ6 double bonds in fatty acids, oils or lipids in organisms such as in a plant by overexpression of the Δ6-desaturase gene in crop plants. Such artificial DNA sequences can exhibit Δ6-desaturase activity, for example by back-translation of proteins constructed by means of molecular modeling, or be determined by in vitro selection. Possible techniques for in vitro evolution of DNA to modify or improve the DNA sequences are described in PATTEN, P. A. et al., Current Opinion in Biotechnology 8, 724-735 (1997) or in MOORE, J. C. et al., Journal of Molecular Biology 272, 336-347 (1997). Particularly suitable are encoding DNA sequences which are obtained by back-translation of a polypeptide sequence in accordance with the codon use specific to the host plant. Those skilled in the art familiar with the methods of plant genetics can easily determine the specific codon use by computer analyses of other known genes of the plant to be transformed.

Other suitable equivalent nucleic acid sequences which may be mentioned are sequences that encode fusion proteins, a component of the fusion protein being a Δ6-desaturase polypeptide or a functionally equivalent part thereof. The second part of the fusion protein can be, for example, another polypeptide having enzymatic activity or an antigenic polypeptide sequence by means of which it is possible to demonstrate Δ6-desaturase expression (e.g. myc tag or his tag). Preferably, however, this is a regulatory protein sequence, such as by way of example a signal sequence for the endoplasmic reticulum (ER) which directs the Δ6-desaturase protein to the desired point of action, or regulatory sequences which influence the expression of the nucleic acid sequence according to the invention, such as promoters or terminators.

Advantageously, the Δ6-desaturase genes in the method according to the invention may be combined with other genes for fatty acid biosynthesis. Examples of such genes are the acetyl transferases, other desaturases or elongases such as Δ4-, Δ5-, Δ6-, or Δ8-desaturases or ω-3-and ω-6-elongases such as Δ12 for (C16 fatty acids), Δ15 for (C18 fatty acids) or Δ19 (C20, fatty acids) or such as Δ5- or Δ6-elongases. For in vivo and especially in vitro synthesis combination with e.g. NADH cytochrome B5 reductases which can take up or release reduction equivalents is advantageous.

By the amino acid sequences according to the invention is meant proteins which contain an amino acid sequence depicted in the sequences SEQ ID NO: 2 and SEQ ID NO: 4 or a sequence obtainable therefrom by substitution, inversion, insertion or deletion of one or more amino acid groups, the enzymatic activities of the proteins depicted in SEQ ID NO: 2 and NO: 4 being retained or not substantially reduced, that is they still possess the same enzymatic activity. By “not substantially reduced” or “the same enzymatic activity” is meant all enzymes which still exhibit at least 10%, preferably 20%, particularly preferably 30%, of the enzymatic activity of the initial enzyme obtained from the wild form of the said Prunuscereae organism. In doing this, for example, certain amino acids may be replaced by others having similar physicochemical properties (space filling, basicity, hydrophilicity, etc.). For example, arginine residues are exchanged for lysine residues, valine residues for isoleucine residues or aspartic acid residues for glutamic acid residues. However, one or more amino acids may also be swapped in sequence, added or removed, or a plurality of these measures may be combined with one another.

By derivatives is also meant functional equivalents which in particular also contain natural or artificial mutations of an originally isolated sequence encoding Δ6-desaturase which continue to exhibit the desired function, that is the enzymatic activity and substrate selectivity thereof is not substantially reduced. Mutations comprise substitutions, additions, deletions, exchanges or insertions of one or more nucleotide residues. Thus, for example, the present invention also encompasses those nucleotide sequences which are obtained by modification of the Δ6-desaturase nucleotide sequence. The aim of such a modification may be, e.g., to further bound the encoding sequence contained therein or also, e.g. to insert further restriction enzyme interfaces.
7 Functional equivalents also include those variants whose function by comparison with the initial gene or gene fragment is weakened (not substantially reduced) or reinforced (enzymatic activity higher than the activity of the initial enzyme, that is activity is higher than 100%, preferably higher than 110%, particularly preferably higher than 130%).

At the same time, the nucleic acid sequence may, for example, advantageously be a DNA or cDNA sequence. Suitable encoding sequences for insertion into an expression cassette according to the invention include by way of example those which encode a Δ9-desaturase with the sequences described above and lend the host the ability to overproduce fatty acids, oils or lipids having double bonds in the Δ9 position, it being advantageous when at the same time ω-3 fatty acids having at least four double bonds are produced. These sequences may be of homologous or heterologous origin.

By the expression cassette (= nucleic acid construct or fragment of gene construct) according to the invention is meant the sequences specified in SEQ ID NO: 1 and SEQ ID NO: 3 which result from the genetic code and/or functional or non-functional derivatives thereof which are functionally linked with one or more regulation signals advantageously to increase the gene expression and which control the expression of the encoding sequence in the host cell. These regulatory sequences should allow the selective expression of the genes and the protein expression. Depending on the host organism this may mean, for example, that the gene is expressed and/or overexpressed only after induction or that it is expressed and/or overexpressed immediately. Examples of these regulatory sequences are sequences to which inducers or repressors bind and in this way regulate the expression of the nucleic acid. In addition to these new regulation sequences or instead of these sequences the natural regulation of these sequences ahead of the actual structural genes may still be present and optionally have been genetically modified so that natural regulation was switched off and the expression of the genes increased. However, the gene construct can also be built up more simply, that is no additional regulation signals have been inserted ahead of the nucleic acid sequence or derivatives thereof and the natural promoter with its regulation has not been removed. Instead of this the natural regulation sequence was mutated in such a way that no further regulation ensues and/or the gene expression is heightened. These modified promoters in the form of part sequences (= promoter containing parts of the nucleic acid sequences according to the invention) can also be brought on their own ahead of the natural gene to increase the activity. In addition, the gene construct may advantageously also contain one or more so-called enhancer sequences functionally linked to the promoter which allow enhanced expression of the nucleic acid sequence. At the 3′ end of the DNA sequences additional advantageous sequences may also be inserted, such as further regulatory elements or terminators. The Δ9-desaturase gene may be present in one or more copies in the expression cassette (= gene construct).

As described above, the regulatory sequences or factors can preferably positively influence and so increase the gene expression of the introduced genes. Thus, reinforcement of the regulatory elements advantageously on the transcription level may be effected by using powerful transcription signals such as promoters and/or enhancers. However, in addition reinforcement of translation is also possible, for example by improving the stability of the mRNA.

Suitable promoters in the expression cassette are in principle all promoters which can control the expression of foreign genes in organisms such as microorganisms like protoplasts such as citrates, algae such as green, brown, red or blue algae, bacteria such as gram-positive or gram-negative bacteria, yeasts such as Saccharomyces, Pichia or Schizosaccharomyces or fungi such as Mortierella, Trametes or Schizosacharomyces, advantageously in plants or fungi. Use is preferably made in particular of plant promoters or promoters derived from a plant virus. Advantageous regulation sequences for the method according to the invention are found for example in promoters such as cos, tac, trp, tet, trp-tet, lpp, lac, lpp-lac, lacP-, lpp-lac, lacP-, lpp-lac, lacP-, T7, T5, T3, gal, trc, ara, SP6, λ-P(−1) or in λ-P2 promoters which are employed advantageously in gram-negative bacteria. Other advantageous regulation sequences are found, for example, in the gram-positive promoters amy and spo2, in the yeast or fungal promoters AD1C, M feast, ACP, CQYC1, GADPH1, TEF1, rps28, ADH1 or in the plant promoters CaMV 35S [Franck et al., Cell 21 (1980) 285-294], SU, OCS, lib4, STLS1, B33, nos (= Nopal Synthase Promoter) or in the ubiquitin promoter. The expression cassette may also contain a chemically inducible promoter by means of which the expression of the exogenous Δ9-desaturase gene in the organisms can be controlled advantageously in the plants at a particular time. Advantageous plant promoters of this type are by way of example the PRP1 promoter [Ward et al., Plant Mol. Biol. 22 (1993), 361-366], a promoter inducible by benzene sulfoximide (EP 388186), a promoter inducible by tetracycline (Gat et al., EP 1992), a promoter inducible by salicylic acid (WO 95/19443), a promoter inducible by ascorbic acid (EP 335528) and a promoter inducible by vitamin C (WO/93/21334). Other examples of plant promoters which can advantageously be used are the promoter of cystosolic FBPase from potato, the STLS1 promoter from potato (Stockhaus et al., EMBO J. 8 (1989) 2445-2450), the promoter of phosphoribosyl pyrophosphate amidotransferase from Glycine max (see also gene bank accession number U87999) or a nodule-specific promoter as described in EP 249676. Particularly advantageous are those plant promoters which ensure expression in tissues or plant parts/organisms in which fatty acid biosynthesis or the precursor stages thereof occurs, as in endosperm or in the developing embryo for example. Particularly noteworthy are advantageously promoters which ensure seed-specific expression such as by way of example the USP promoter or derivatives thereof, the LE4 promoter, the phaseolin promoter or the napin thereof. The particularly advantageous USP promoter cited according to the invention or its derivatives mediate very early gene expression in seed development (Baeumlein et al., Mol Gen Genet. 191, 225 (3): 459-67). Other advantageous seed-specific promoters which may be used for monocotyledonous or dicotyledonous plants are the promoters suitable for dicotyledons such as napin gene promoters, likewise cited by way of example, from oilseed rape (U.S. Pat. No. 5,608,152), the osbox promoter from Arabidopsis (WO 98/45461), the phaseolin promoter from Phaseolus vulgaris (U.S. Pat. No. 5,504,200), the Bcs4 promoter from Brassica (WO 91/13980) or the leguminous B4 promoter (Left4, Baumelein et al., Plant J., 2, 2, 1992: 233-239) or promoters suitable for monocotyledons such as the promoters of the ltp2 or ltp1 gene in barley (WO 95/15389 and WO 95/23230) or the promoters of the barley hordeine gene, the rice glutelin gene, the rice oryzin gene, the rice prolamin gene, the wheat gliadin gene, the white glutenin gene, the corn zein gene, the oats glutenin gene, the sorghum kasiin gene or the rye secalin gene which are described in WO98/16890.

Furthermore, particularly preferred are those promoters which ensure the expression in tissues or plant parts in which, for example, the biosynthesis of fatty acids, oils and lipids or
the precursor stages thereof takes place. Particularly noteworthy are promotors which ensure a seed-specific expression. Noteworthy are the promotors of the napin gene from oilseed rape (U.S. Pat. No. 5,608,152), the USP promotors from *Vicia faba* (USP-unknown seed protein, Baumelein et al., Mol Gen Genet, 1991, 225 (3): 459-67), the promotors of the oleosin gene from *Arabidopsis* (WO98/45461), the phaseolin promotors (U.S. Pat. No. 5,504,200) or the promotors of the legumin B4 gene (LeB4; Baumelein et al., 1992, Plant Journal, 2 (2): 233-9). Other promotors to be mentioned are those of the lpt2 or ltp1 gene from barley (WO95/15389 and WO95/23250) which mediate seed-specific expression in monocotyledonous plants.

As described above, the expression construct (=gene construct, nucleic acid construct) may contain yet other genes which are to be introduced into the organisms. These genes can be subject to separate regulation or be subject to the same regulation region as the Δ6-desaturase gene. These genes are by way of example other biosynthesis genes, advantageous for fatty acid biosynthesis, which allow increased synthesis. Examples which may be mentioned are the genes for Δ15, Δ12-, Δ9-, Δ6-, Δ5-, Δ4-desaturase, β-ketoacyl reductases, β-ketoacyl synthases, elongases or the various hydroxylases and acyl-ACP thioesterases. The desaturase genes are advantageously used in the nucleic acid constructs.

In principle all natural promotors with their regulation sequences can be used like those named above for the expression cassette according to the invention and the method according to the invention. Over and above this, synthetic promotors may also advantageously be used.

In the preparation of an expression cassette various DNA fragments can be manipulated in order to obtain a nucleotide sequence which usefully reads in the correct direction and is equipped with a correct reading raster. To connect the DNA fragments (=nucleic acids according to the invention) to one another adaptors or linkers may be attached to the fragments. The promoter and the terminator regions can usefully be provided in the transcription direction with a linker or polyn linker containing one or more restriction points for the insertion of this sequence. Generally, the linker has 1 to 10, mostly 1 to 8, preferably 2 to 6, restriction points. In general the size of the linker inside the regulatory region is less than 100 bp, frequently less than 60 bp, but at least 5 bp. The promoter may be both native or homologous as well as foreign or heterologous to the host organism, for example to the host plant. In the 5'-3’ transcription direction the expression cassette contains the promotor, a DNA sequence which encodes a Δ6-desaturase gene and a region for transcription termination. Different termination regions can be exchanged for one another in any desired fashion.

Furthermore, manipulations which provide suitable restriction interfaces or which remove excess DNA or restriction interfaces can be employed. Where insertions, deletions or substitutions, such as transitions and transversions, come into consideration, in vitro mutagenesis, primer repair, restriction or ligation may be used. In suitable manipulations such as restriction, chewing back or filling of overhangs for blunt ends complementary ends of the fragments can be provided for the ligation.

For an advantageous high expression the attachment of the specific ER retention signal SEKDEL inter alia can be of importance (Schouten, A. et al., Plant Mol. Biol. 30 (1996), 781-792). In this way the average expression level is tripled or even quadrupled. Other retention signals which occur naturally in plant and animal proteins located in the ER may also be employed for the construction of the cassette.

Preferred polyadenylation signals are plant polyadenylation signals, preferably those which substantially correspond to T-DNA polyadenylation signals from *Agrobacterium tumefaciens*, in particular gene 3 of the T-DNA (octopin thylase) of the Ti plasmid pTiACH5 (Gieden et al., EMBO J. 3 (1984), 835 et seq.) or corresponding functional equivalents.


In the preparation of an expression cassette various DNA fragments can be manipulated to produce a nucleotide sequence which usefully reads in the correct direction and is equipped with a correct reading raster. Adaptors or linkers can be attached to the fragments for joining the DNA fragments.

The promotors and the terminator regions can usefully be provided in the transcription direction with a linker or polyn linker containing one or more restriction points for the insertion of this sequence. Generally, the linker has 1 to 10, mostly 1 to 8, preferably 2 to 6, restriction points. In general the size of the linker inside the regulatory region is less than 100 bp, frequently less than 60 bp, but at least 5 bp. The promotors may be both native or homologous as well as foreign or heterologous to the host organism, for example to the host plant. In the 5’-3’ transcription direction the expression cassette contains the promotors, a DNA sequence which encodes a Δ6-desaturase gene and a region for transcription termination. Different termination regions can be exchanged for one another in any desired fashion.

In the preparation of an expression cassette various DNA fragments can be manipulated to produce a nucleotide sequence which usefully reads in the correct direction and is equipped with a correct reading raster. Adaptors or linkers can be attached to the fragments for joining the DNA fragments.

The DNA sequences encoding two Δ6-desaturases from *Muscarioldes vialis* and *Aleuritia farinosa* contain all the sequence characteristics needed to achieve correct localization of the site of fatty acid, lipid or oil biosynthesis. Accordingly, no further targeting sequences are needed per se. However, such a localization may be desirable and advantageous and hence artificially modified or reinforced so that such fusion constructs are also a preferred advantageous embodiment of the invention.

Particularly preferred are sequences which ensure targeting in plastids. Under certain circumstances targeting into other compartments (reported in: Kermode, C. R. Rev. Plant Sci. 15, 4 (1996), 285-243) may also be desirable, e.g. into vacuoles, the mitochondrion, the endoplasmic reticulum (ER), peroxisomes, lipid structures or due to lack of corresponding operative sequences retention in the compartment of origin, the cytosol.

Advantageously, the nucleic acid sequences according to the invention or the gene construct together with at least one reporter gene are cloned into an expression cassette which is introduced into the organism via a vector or directly into the genome. This reporter gene should allow easy detection via a growth, fluorescence, chemical, bioluminescence or resistance assay or via a photometric measurement. Examples of reporter genes which may be mentioned are antibiotic-
herbicide-resistance genes, hydrolase genes, fluorescence protein genes, bioluminescence genes, sugar or nucleotide metabolic genes or biosynthesis genes such as the Ura3 gene, the llv2 gene, the luciferase gene, the β-galactosidase gene, the gfp gene, the 2-deoxyglucose-6-phosphate phosphatase gene, the β-glucoronidase gene, β-lactamase gene, the neomycin phosphotransferase gene, the hygromycin phosphotransferase gene or the BASTA (γ-glutamylase-resistance) gene. These genes permit easy measurement and quantification of the transcription activity and hence of the expression of the genes. In this way genome positions may be identified which exhibit differing productivity.

In a preferred embodiment an expression cassette comprises upstream, i.e. at the 5′ end of the encoding sequence, a promoter and downstream, i.e. at the 3′ end, a polyadenylation signal and optionally other regulatory elements which are operably linked to the intervening encoding sequence for Δ6-desaturase and/or Δ6-desaturase DNA sequence. By an operable linkage is meant the sequential arrangement of promoter, encoding sequence, terminator and optionally other regulatory elements in such a way that each of the regulatory elements can fulfill its function in the expression of the encoding sequence in due sequence. The sequences preferred for operable linkage are targeting sequences for ensuring subcellular localization in plastids. However, targeting sequences for ensuring subcellular localization in the mitochondrion, in the endoplasmic reticulum (ER), in the nucleus, in oil corpules or other compartments may also be employed as well as translation promoters such as the 5′ lead sequence in tobacco mosaic virus (Galli et al., Nucl. Acids Res. 15 (1978), 8693-8711).

An expression cassette may, for example, contain a constitutive promoter or a tissue-specific promoter (preferably the USF or napin promoter) the gene to be expressed and the ER retention signal. For the ER retention signal the KDEL amino acid sequence (lysine, aspartic acid, glutamic acid, leucine) or the KXX amino acid sequence (lysine-lysine-X-stop, wherein X means every other known amino acid) is preferably employed.

For expression in a prokaryotic or eukaryotic host organism, for example a microorganism such as a fungus or a plant, the expression cassette is advantageously inserted into a vector such as by way of example a plasmid, a phage or other DNA which allows optimum expression of the genes in the host organism. Examples of suitable plasmids are: in E. coli plLG335, pACYC184, pBR series such as pBR322, pUC series such as pUC18 or pUC19, M13mp series, PKK30, Rep4, pHS1, pHS2, pIL2, p236, pMBI 24, plG200, plIR209, plIN 113-131, λgt11 or plBcl1, in Streptomyces plJ101, plJ364, plJ702 or plJ361, in Bacillus pUB110, pC194 or pBD214; in Corynebacterium pSA77 or pA667; in fungi plAS1, plIL2 or pBB116; other advantageous fungal vectors are described by Romanos, M. A. et al., (1992) “Foreign gene expression in yeasts: a review”, Yeast 8: 423-488) and by van den Hondel, C. A. M. J. J. et al. (1991) “Heterologous gene expression in filamentous fungi” as well as in More Gene Manipulations in Fungi J. W. Bennet & L. L. Lasure, eds., pp. 396-428: Academic Press: San Diego) and in “Gene transfer systems and vector development for filamentous fungi” (van den Hondel, C. A. M. J. J. & Pont, P. J. (1991) in: Applied Molecular Genetics of Fungi, Pobert, J. F. et al., eds., pp. 1-28, Cambridge University Press: Cambridge). Examples of advantageous yeast promoters are 2xM, pAG-1, YEp6, YEp13 or pEMBLYc23. Examples of algal or plant promoters are plGV3, pGHH, pB109, pAK2004, pVK10 or pDH51 (see Schmidt, R. and Willmitzer, L., 1988). The vectors identified above or derivatives of the vectors identified above are a small selection of the possible plasmids. Further plasmids are well known to those skilled in the art and may be found, for example, in the book Cloning Vectors (Eds. Poulwe P. H., et al. Elsevier, Amsterdam-New York-Oxford, 1985, ISBN 0 444 904018). Suitable plant vectors are described inter alia in "Methods in Plant Molecular Biology and Biotechnology" (CRC Press), Ch. 6/7, pp. 71-119. Advantageous vectors are known as shuttle vectors or binary vectors which replicate in E. coli and Agrobacterium. By vectors is meant with the exception of plasmids all other vectors known to those skilled in the art such as by way of example plages, viruses such as SV40, CMV, baculovirus, adenovirus, transposons, IS elements, plasmids, phageoids, cosmids, linear or circular DNA. Those vectors can be replicated autonomously in the host organism or be chromosomally replicated, chromosomal replication being preferred.

In a further embodiment of the vector the expression cassette according to the invention may also advantageously be introduced into the organisms in the form of a linear DNA and be integrated into the genome of the host organism by way of heterologous or homologous recombination. This linear DNA may be composed of a linearized plasmid or only of the expression cassette as vector or the nucleic acid sequences according to the invention.

In a further advantageous embodiment the nucleic acid sequence according to the invention can also be introduced into an organism on its own.

If in addition to the nucleic acid sequence according to the invention further genes are to be introduced into the organism, all together with a reporter gene in a single vector or each single gene with a reporter gene in a vector in each case can be introduced into the organism, whereby the different vectors can be introduced simultaneously or successively.

The vector advantageous contains at least one copy of the nucleic acid sequences according to the invention and/or the expression cassette (=gene construct) according to the invention.

By way of example the plant expression cassette can be installed in the pK1 transformation vector (a) Toepfer et al., 1993, Methods Enzymol., 217: 66-78; (b) Toepfer et al., 1987, Nucl. Acids. Res. 15: 5800 ff.).

Alternatively, a recombinant vector (=expression vector) can also be transcribed and translated in vitro, e.g. by using the T7 promoter and the T7 RNA polymerase.

Vectors expressing employed in prokaryotes frequently make use of inducible systems with and without fusion proteins or fusion oligopeptides, wherein these fusions can ensure in both N-terminal and C-terminal manner or in other useful domains of a protein. Such fusion vectors usually have the following purposes: i) to increase the RNA expression rate; ii) to increase the achievable protein synthesis rate; iii) to increase the solubility of the protein; iv) or to simplify purification by means of a binding sequence usable for affinity chromatography. Proteolytic cleavage points are also frequently introduced via fusion proteins which allows cleavage of a portion of the fusion protein and purification. Such recognition sequences for proteases are recognized, e.g. factor Xa, thrombin and enterokinase.


Other examples of E. coli expression vectors are pTrc [Aman et al., (1988) Gene 69:301-315] and pET vectors [Studier et al., Gene Expression Technology: Methods in

Alternatively, insect cell expression vectors can also be advantageously utilized, e.g. for expression in Sf9 cells. These are e.g. the vectors of the pAc series (Smith et al. (1983) Mol. Cell. Biol. 3:215-2165) and the pVL series (Lucklow and Summers (1989) Virology 170:31-39).


Furthermore, the nucleic acid sequences according to the invention may be expressed in mammalian cells, advantageously in nonhuman mammalian cells. Examples of corresponding expression vectors are pCDM8 and pMT2PC referred to in: Seed, B. (1987) Nature 329:840 or Kaufman et al. (1987) EMBO J. 6: 187-195. At the same time promoters preferred for use are of viral origin, such as by way of example promoters of polyoma, adenovirus 2, cytomegalovirus or simian virus 40. Other prokaryotic and eukaryotic expression systems are referred to in chapters 16 and 17 of Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

The introduction of the nucleic acids according to the invention, the expression cassette or the vector into organisms, plants for example, can in principle be done by all of the methods known to those skilled in the art. The introduction of the nucleic acid sequences gives rise to recombinant or transgenic organisms.


The transfer of foreign genes into the genome of a plant is called transformation. In doing this the methods described for the transformation and regeneration of plants from plant tissues or plant cells are utilized for transient or stable transformation. Suitable methods are protoplast transformation by polyethylene glycol-induced DNA uptake, the “biologic” method using the gene cannon—referred to as the particle bombardment method, electroporation, the incubation of dry embryos in DNA solution, microinjection and gene transfer mediated by Agrobacterium. Said methods are described by way of example in B. Jenes et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. I, Engineering and Utilization, eds. S. D. Kung and R. Wu, Academic Press (1993) 128-143 and in Potterkus Annu. Rev. Plant Physiol. Plant Molec. Biol. 42 (1991) 205-225. The construct to be expressed is preferably cloned into a vector which is suitable for transforming Agrobacterium tumefaciens, for example pBIN19 (Bevan et al., Nucl. Acids Res. 12 (1984) 8711). Agrobacteria transformed by such a vector may then be used in known manner for the transformation of plants, in particular of crop plants such as by way of example tobacco plants, for example by bathing bruised leaves or chopped leaves in an agrobacterial solution and then culturing them in suitable media. The transformation of plants by means of Agrobacterium tumefaciens is described, for example, by Höggen and Willmitzer in Nucl. Acid Res. (1988) 16, 9877 or is known inter alia from F. W. White, Vectors for Gene Transfer in Higher Plants; in Transgenic Plants, Vol. I, Engineering and Utilization, eds. S. D. Kung and R. Wu, Academic Press, 1993, pp. 15-38.

Agrobacteria transformed by an expression vector according to the invention may likewise be used in known manner for the transformation of plants such as test plants like Arabidopsis or crop plants such as cereal crops, corn, oats, rye, barley, wheat, soybean, rice, cotton, sugar beet, canola, sunflower, flax, hemp, potatoes, tobacco, tomatoes, carrots, paprika, oilseed rape, tapioca, cassava, arrowroot, targets, alfalfa, lettuce and the various tree, nut and vine species, in particular of oil-containing crop plants such as soybean, peanut, castor oil plant, sunflower, corn, cotton, flax, oilseed rape, coconut, oil palm, safflower (Carthamus Tinctorius) or cacao bean. e.g. by bathing bruised leaves or chopped leaves in an agrobacterial solution and then culturing them in suitable media. For the production of LAPAs, for example stearidonic acid, eicosapentaenoic acid and docosahexaenoic acid, borage or Primulaceae are advantageously suitable.

The genetically modified plant cells may be regenerated by all of the methods known to those skilled in the art. Appropriate methods can be found in the publications referred to above by S. D. Kung and R. Wu, Potterkus or Höggen and Willmitzer.

Accordingly, a further aspect of the invention relates to transgenic organisms transformed by at least one nucleic acid sequence, expression cassette or vector according to the invention as well as cells, cell cultures, tissue, parts—such as, for example, leaves, roots, etc. in the case of plant organism— or reproductive material derived from such organisms. The terms “host organism”, “host cell”, “recombinant (host) organism” and “transgenic (host) cell” are used here interchangeably. Of course these terms relate not only to the particular host organism or the particular target cell but also to the descendants or potential descendents of these organisms or cells. Since, due to mutation or environmental effects certain modifications may arise in successive generations, these descendents need not necessarily be identical with the parental cell but nevertheless are still encompassed by the term as used here.

For the purposes of the invention “transgenic” or “recombinant” means with regard for example to a nucleic acid sequence, an expression cassette (“gene construct”) or a vector containing the nucleic acid sequence according to the invention or an organism transformed by the nucleic acid sequences, expression cassette or vector according to the invention all those constructions produced by genetic engineering methods in which either:

(a) the nucleic acid sequence according to the invention or
(b) a genetic control sequence functionally linked to the nucleic acid sequence according to the invention, for example a promoter, or

c) (a) and (b) are not found in their natural, genetic environment or have been modified by genetic engineering methods, wherein the
modification may by way of example be a substitution, addition, deletion, inversion or insertion of one or more nucleotide residues. Natural genetic environment means the natural genomic or chromosomal locus in the organism of origin or presence in a genomic library. In the case of a genomic library the natural genetic environment of the nucleic acid sequence is preferably retained at least in part. The environment borders the nucleic acid sequence at least on one side and has a sequence length of at least 50 bp, preferably at least 500 bp, particularly preferably at least 1,000 bp, most particularly preferably at least 5,000 bp. A naturally occurring expression cassette—for example the naturally occurring combination of the natural promoter of the nucleic acid sequence according to the invention with the corresponding PSE gene—turns into a transgenic expression cassette when the latter is modified by unnatural, synthetic (“artificial”) methods such as by way of example a mutagenation. Appropriate methods are described by way of example in U.S. Pat. No. 5,565,350 or WO 00/15815.

Suitable organisms or host organisms for the nucleic acid, expression cassette or vector according to the invention are advantageously in principle all organisms which are able to synthesize fatty acids, especially unsaturated fatty acids or are suitable for the expression of recombinant genes. Examples which may be mentioned are plants such as Arabidopsis, Asteraceae such as Cardunula or crop plants such as soybean, peanut, castor oil plant, sunflower, corn, cotton, flax, oilseed rape, coconut, oil palm, sunflower (Carbamus tinctorius) or cocoa bean, microorganisms such as fungi, for example the genus Mortierella, Saprolegia or Pyramid, bacteria such as the genus Escherichia, yeasts such as the genus Saccharomyces, cyanobacteria, ciliates, algae or protozoa such as dinoflagellates like Cryptophycocium. Preference is given to organisms which can naturally synthesize oils in relatively large quantities such as fungi like Mortierella alpina, Pyramid insidiosum or plants such as soybean, oilseed rape, coconut, oil palm, sunflower, flax, castor oil plant, Cardunula, peanut, cocoa bean or sunflower, or yeasts such as Saccharomyces cerevisiae and particular preference is given to soybean, flax, oilseed rape, sunflower, Cardunula, Mortierella or Saccharomyces cerevisiae. In principle, apart from the transgenic organisms identified above, transgenic animals, advantageously nonhuman animals, are suitable, for example C. elegans.


A further object of the invention relates to the use of an expression cassette containing DNA sequences encoding a Δ6-desaturase gene or DNA sequences hybridizing therewith for the transformation of plant cells, tissues or parts of plants. The aim of use is to increase the content of fatty acids, oils or lipids having an increased content of double bonds in the Δ6 position.

In doing so, depending on the choice of promoter, the Δ6-desaturase gene can be expressed specifically in the leaves, in the seeds, in the nodes, in the root or other parts of the plant. Those transgenic plants overproducing fatty acids, oils or lipids having Δ6 double bonds, the reproductive material thereof, together with the plant cells, tissues or parts thereof are a further object of the present invention. A preferred object according to the invention comprises transgenic plants containing a functional or nonfunctional (antisense DNA or enzymatically inactive enzyme) nucleic acid sequence or a functional or nonfunctional expression cassette according to the invention.

The expression cassette or the nucleic acid sequences according to the invention containing a Δ6-desaturase gene sequence can, moreover, also be employed for the transformation of the organisms identified by way of example above such as bacteria, cyanobacteria, yeasts, filamentous fungi, ciliates and algae with the objective of increasing the content of fatty acids, oils or lipids possessing Δ6 double bonds.

Within the framework of the present invention, increasing the content of fatty acids, oils or lipids possessing Δ6 double bonds means, for example, the artificially acquired trait of increased biosynthetic performance due to functional overexpression of the Δ6-desaturase gene in the organisms according to the invention, advantageously in the transgenic plants according to the invention, by comparison with the nongenetically modified initial plants at least for the duration of at least one plant generation.

The preferred locus of biosynthesis, of fatty acids, oils or lipids for example, is generally the seed or cell layers of the seed so that a seed-specific expression of the Δ6-desaturase gene is appropriate. It is, however, obvious that the biosynthesis of fatty acids, oils or lipids not be limited to the seed tissue but can also occur in tissue-specific manner in all other parts of the plant—in epidemis cells or in the nodules for example.

A constitutive expression of the exogenous Δ6-desaturase gene is, moreover, advantageous. On the other hand, however, an inducible expression may also appear desirable.

The efficiency of the expression of the Δ6-desaturase gene can be determined, for example, in vitro by shoot meristem propagation. In addition, an expression of the Δ6-desaturase gene modified in nature and level and its effect on fatty acid, oil or lipid biosynthesis performance can be tested on test plants in greenhouse trials.

An additional object of the invention comprises transgenic organisms such as transgenic plants transformed by an expression cassette containing a Δ6-desaturase gene sequence according to the invention or DNA sequences hybridizing therewith, as well as transgenic cells, tissues, parts and reproduction material of such plants. Particular preference is given in this case to transgenic crop plants such as by way of example barley, wheat, rye, oats, corn, soybean, rice, cotton, sugar beet, oilseed rape and canola, sunflower, flax, hemp, thistle, potatoes, tobacco, tomatoes, oilseed rape, tapioca, cassava, arrowroot, alfalfa, lettuce and the various tree, nut and vine species.

For the purposes of the invention plants are mono- and dikotyledonous plants, mosses or algae.

A further refinement according to the invention are transgenic plants as described above which contain a functional or nonfunctional nucleic acid sequence according to the invention or a functional or nonfunctional expression cassette according to the invention. By nonfunctional is meant that an enzymatically active protein is no longer synthesized. Moreover, by nonfunctional nucleic acids or nucleic acid constructs is also means what is known as an antisense DNA which results in transgenic plants which show a reduction in enzymatic activity or no enzymatic activity. With the aid of the antisense technique, especially when the nucleic acid sequence is combined in the antisense DNA with other fatty acid synthesis genes, it is possible to synthesize triglycerides having an increased content of saturated fatty acids or saturated fatty acids. Furthermore, by means of what is known as coexpression or by means of the RNAi technique transgenic plants can be manipulated in such a way that no or reduced
enzymatic activity is produced in the plants. By transgenic
plants is meant single plant cells and cultures thereof on fixed
media or in liquid culture, parts of plants and entire plants.
Other objects of the invention are:

A method for the transformation of a plant comprising the
introduction of expression cassettes according to the
invention containing a Δ6-desaturase gene sequence
derived from Prunellaceae or DNA sequences hybridizing
therewith into a plant cell, into callus tissue, an entire
plant or protoplasts of plants.
A method for producing PUFA's, wherein the method com-
prises the growing of a transgenic organism comprising a
nucleic acid as claimed in claims 1 to 4, a gene con-
struct as claimed in claim 6 or a vector as claimed in
claim 7 encoding a Δ6-desaturase which specifically
desaturates ω-3 fatty acids, and wherein due to the ac-
tivity of the Δ6-desaturase PUFA's are formed in the or-
ganism which exhibit an increased content of ω-3 fatty
acids. In this method ω-3 fatty acids such as stearidonic
acid, eicosapentaenoic acid or docosahexaenoic acid are
advantageously produced.
Use of a Δ6-desaturase DNA gene sequence or DNA
sequences hybridizing therewith for the production of plants
having an increased content of fatty acids, oils or lipids hav-
ing Δ6 double bonds due to the expression of said Δ6-desatu-
rase DNA sequence in plants.
Use of a Δ6-desaturase DNA gene sequence DNA
sequences hybridizing therewith for the production of plants
having an increased content of fatty acids, oils or lipids hav-
ing Δ6 double bonds, particularly of ω-3 fatty acids, due to
the expression of said Δ6-desaturase DNA sequence in plants.
Proteins containing the amino acid sequences depicted in
SEQ ID NO: 2 or NO: 4.
Use of said proteins having the sequences SEQ ID NO: 2 or
NO: 4 for producing unsaturated fatty acids.
A further object according to the invention is a method for
producing unsaturated fatty acids comprising: introducing
at least one said nucleic acid sequence according to the inven-
tion or at least one nucleic acid construct according to the
invention into a preferably oil-producing plant; growing said
organism; isolating oil contained in said organism; and liber-
ating the fatty acids present in said oil. These unsaturated fatty
acids advantageously contain Δ6 double bonds. The fatty
acids may be liberated from the oils or lipids, for example by
basic hydrolysis, e.g. using NaOH or KOH.
A method for producing triglycerides having an increased
content of unsaturated fatty acids comprising: introducing at
least one said nucleic acid sequence according to the inven-
tion or at least one expression cassette according to the inven-
tion into an oil-producing organism; growing said organism;
and isolating oil contained in said organism; is also numbered
among the objects of the invention.
A further object according to the invention is a method for
producing triglycerides having an increased content of unsat-
urated fatty acids by incubating triglycerides containing satu-
rated or unsaturated or saturated and unsaturated fatty acids
with at least one of the proteins encoded by the sequences
SEQ ID NO: 2 or NO: 4. The method is advantageously
carried out in the presence of compounds which can take up or
release reduction equivalents. The fatty acids can then be
liberated from the triglycerides.
A further object according to the invention is a method for
producing triglycerides having an increased content of satu-
rated or unsaturated fatty acids or saturated and unsatur-
ated fatty acids advantageously having an increased content
of unsaturated fatty acids is a method wherein the fatty acids
are liberated from the triglycerides with the aid of basic
hydrolysis known to those skilled in the art or by means of an
enzyme such as a lipase.

The methods specified above advantageously allow the
synthesis of fatty acids or triglycerides having an increased
content of fatty acids containing Δ6 double bonds.

The methods identified above advantageously allow the
synthesis of fatty acids or triglycerides having an increased
content of fatty acids containing Δ6 double bonds, wherein
the substrate used for the reaction of the Δ6-desaturase is
preferably α-linolenic acid. In this way the method identified
above advantageously allows in particular the synthesis of
fatty acids derived from stearidonic acid (C_{18:3ω6,9,12}) such
as by way of example eicosapentaenoic acid and docosa-
hexaenoic acid.

Using what is known as antisense technology, in one
method fatty acids or triglycerides having an increased con-
tent of saturated fatty acids can also be produced.
Examples of organisms for the said methods which may be
mentioned are plants such as Arabidopsis, Prunellaceae, boro-
gage, barley, wheat, rape, oats, corn, soybean, rice, cotton, sugar
beet, oilseed rape and canola, sunflower, flax, hemp, potatoes,
tobacco, tomatoes, rape, tapioca, cassava, arrowroot, alfalfa,
peanut, castor oil plant, coconut, oil palm, safflower (Cartha-
nus tinctorius) or cocoa bean, microorganisms such as the
fungi Mortierella, Saprolegnia or Pythium, bacteria such as the
genus Escherichia, cyanobacteria, yeasts such as the
genus Saccharomyces, algae or protozoa such as dinoflagel-
lates like Cryptocodinium. Preference is given to organisms
which can naturally synthesize oils in relatively large quan-
tities such as fungi like Mortierella alpina, Pythium insidio-
sum or plants such as soybean, oilseed rape, coconut, oil
palm, safflower, castor oil plant, Calendula, peanut, cocoa
bean or sunflower, or yeasts such as Saccharomyces cerevi-
siae and particular preference is given to soybean, oilseed
rape, sunflower, flax, Prunellaceae, borage, Carthamus or
Saccharomyces cerevisiae.

Depending on the host organism, the organisms used in the
methods are grown or cultured in the manner known to those
skilled in the art. Microorganisms are usually grown in a
liquid medium containing a carbon source, usually in the
form of sugars, a nitrogen source, usually in the form of
organic nitrogen sources such as yeast extract or salts such as
ammonium sulfate, trace elements such as iron, manganese or
magnesium salts and optionally vitamins at temperatures of
between 10°C and 60°C with exposure to gaseous oxygen. In
doing so the pH of the nutrient liquid may be kept at a fixed
value, that is during growth it is or is not regulated. Growth
can ensue in batch mode, semibatch mode or continuously.

Nutrients can be provided at the start of fermentation or be fed
in semicontinuously or continuously.

After transformation plants are first of all regenerated as
described above and then cultured or cultivated as normal.

After growth the lipids are isolated from the organisms in
the usual way. For this purpose, after harvesting the organ-
isms may first of all be digested or used directly. The lipids are
advantageously extracted using suitable solvents such as apol-
lar solvents like hexane or ethanol, isopropanol or mixtures
such as hexane/isopropanol, phenol/chloroform/isooamyl
alcohol at temperatures of between 0°C and 30°C, prefer-
ably between 20°C and 50°C. The biomass is usually
extracted with an excess of solvent, for example an excess of
solvent to biomass of 1:4. The solvent is then removed, for
example by distillation. Extraction can also be done using
supercritical CO₂. After extraction the remaining biomass
may be removed, for example by filtration.
The crude oil isolated in this way can then be further purified, for example by removing cloudiness by treatment with polar solvents such as acetone or chloroform and then filtration or centrifugation. Further purification through columns is also possible.

In order to obtain the free acids from the triglycerides the latter are saponified in the usual way.

A further object of the invention comprises fatty acids and triglycerides having an increased content of unsaturated fatty acids produced by the methods identified above and use thereof for producing foods, animal feeds, cosmetics or pharmaceutically. For this purpose the latter are added in customary quantities to the foods, the animal feed, the cosmetics or pharmaceutically.

Said unsaturated fatty acids according to the invention as well as triglycerides having an increased content of unsaturated fatty acids produced by the methods identified above are the result of the expression of the nucleic acids according to the invention in the various host organisms. This results overall in a modification of the composition of the compounds in the host cell containing unsaturated fatty acids by comparison with the original starting host cells which do not contain the nucleic acids. These modifications are more marked in host organisms, for example plant cells, which naturally do not contain the proteins or enzymes encoded by the nucleic acids than in host organisms which naturally do contain the proteins or enzymes encoded by the nucleic acids. This gives rise to host organisms containing oils, lipids, phospholipids, sphingolipids, glycolipids, triacylglycerols and/or free fatty acids having a higher content of PUFA. For the purposes of the invention, by an increased content is meant that the host organisms contain at least 5%, advantageously at least 10%, preferably at least 20%, particularly preferably at least 30%, most particularly preferably at least 40% more polyunsaturated fatty acids by comparison with the initial organism which does not contain the nucleic acids according to the invention. This is particularly the case for plants which do not naturally contain longer-chain polyunsaturated C20 or C22 fatty acids such as DHA, EPA or ARA. Due to the expression of the nucleic acids novel lipid compositions are produced by said means these being a further aspect of the invention.

The invention is explained in more detail by the following examples.

EXAMPLES

General Cloning Methods

The cloning methods, such as by way of example restriction cleavages, agarose gel electrophoresis, purification of DNA fragments, transfer of nucleic acids to nitrocellulose and nylon membranes, linkage of DNA fragments, transformation of Escherichia coli cells, culture of bacteria and sequence analysis of recombinant DNA were carried out as described in Sambrook et al. (1989) (Cold Spring Harbor Laboratory Press: ISBN 0-87969-309-6).

Example 2

Sequence Analysis of Recombinant DNA

Sequencing of recombinant DNA molecules was done using a laser fluorescence DNA sequencer from the ABI company by the method of Sanger (Sanger et al. (1977) Proc. Natl. Acad. Sci. USA 74, 5463-5467). Fragments resulting from a polymerase chain reaction were sequenced and checked to prevent polymerase errors in the constructs to be expressed.

Example 3

Cloning of the Δ6-Desaturase from Muscariodides vialii (SEQ ID NO: 3)

Total RNA from young Muscariodides vialii leaves was isolated with the aid of the RNAeasy kit from the Qiagen company (Valencia, Calif., USA). With the aid of oligo-dT-cellulose poly-A+ RNA (mRNA) was isolated from the total RNA (Sambrook et al., 1989). Using the Reverse Transcription System kit from Promega the RNA was reverse transcribed and the synthesized cDNA was used for PCR amplification of the Δ6-desaturases. Degenerate primers were used for the amplification of the Δ6-desaturase. The nucleotide sequence was derived from the first and the third histidine box motif of borage Δ6-desaturase (Syanova et al., 1997, WO9621022).

Primer 1: GGTGGTCHGCGAAYAYYKSCCA (SEQ ID NO: 5)

Primer 2: GGAIAARYGOTTCYYCATTU (SEQ ID NO: 6)

In the primers identified here and in the primer sequences set out below the symbols or letters in accordance with Wobble IUPAC-IUB have the following meaning:

R=A/G; Y=C/T; M=A/C; K=G/T; S=G/C; W=A/T; H=A/C/T; B=G/T/C; V=G/C/A; D=G/T/A and N=G/A/T/C.

PCR Protocol

Addition temperature: 1 min at 45°C.

Denaturation temperature: 1 min at 94°C.

Elongation temperature: 2 min at 72°C.

Number of cycles: 35

The PCR mixture was separated on an agarose gel and a 660 bp fragment was isolated. The PCR fragment was cloned in the pGEM-T easy vector (Promega) and the insert was then sequenced.

The missing 5’ and 3’ region of the isolated gene fragment from Muscariodides vialii was isolated with the aid of the Smart RACE cDNA kit (Clontech) and then sequenced. Starting from 3’ and 5’ sequence primers were derived in order to isolate the complete clone. For this purpose primers were derived from the DNA regions around the start methionine and the stop codon. The PCR yielded a single band of the expected size. The cDNA was again cloned in the pGEM T easy vector and the now complete gene was sequenced.

Example 4

Cloning of the Δ6-Desaturase from Aleurita farinosa (SEQ ID NO: 1)

Total RNA from young Aleurita farinosa leaves was isolated with the aid of the RNAeasy kit from the Qiagen company (Valencia, Calif., USA). With the aid of oligo-dT-cellulose poly-A+ RNA (mRNA) was isolated from the total RNA (Sambrook et al., 1989). Using the Reverse Transcription System kit from Promega the RNA was reverse transcribed and the synthesized cDNA was used for PCR amplification of the Δ6-desaturases. Degenerate primers were used for the amplification of the Δ6-desaturase. The nucleotide sequence
was derived from the first and the third histidine box motif of borage Δ6-desaturase (Syanova et al., 1997, WO9621022).

Primer 1:
GTTTGTGTTGCGTAGGKYKSSCA (SEQ ID NO: 5)

Primer 2:
GRTAALAGRCTGYTTTCAATTTG (SEQ ID NO: 6)

PCR Protocol
Addition temperature: 1 min at 45°C.
Denaturing temperature: 1 min at 94°C.
Elongation temperature: 2 min at 72°C.
Number of cycles: 35

The PCR mixture was separated on an agarose gel and a 660-bp fragment was isolated. The PCR fragment was cloned in the pGEM-T easy vector (Promega) and the insert was then sequenced.

The missing 5′ and 3′ region of the isolated gene fragment from *Aleurita furinosa* was isolated with the aid of the Smart RACE cDNA kit (Clonetech) and then sequenced. Starting from 3′ and 5′ sequence primers were derived in order to isolate the complete clone. For this purpose primers were derived from the DNA regions around the start methionine and the stop codon. The PCR yielded a single band of the expected size. The cDNA was again cloned in the pGEM T easy vector and the now complete gene was sequenced.

Example 5
Cloning of Expression Plasmids for Constitutive Expression in Plants

By means of appropriate primers at the 5′ and 3′ end of both the new desaturases a CLA1 and a XbaI site was introduced. Primer design for the Δ6-desaturase from *M. vialii*:

atcgasttgctacaaacttctcccccc (ClaI) (SEQ ID NO: 7)
tctagattcgctgtgcttgagccct (XbaI) (SEQ ID NO: 8)

Primer design for the Δ6-desaturase from *A. furinosa*:

atcgasttgctacaaacttctcccccc (ClaI) (SEQ ID NO: 7)
tctagattcgctgtgcttgagccct (XbaI) (SEQ ID NO: 9)

The PCR products were separated in agarose gel, digested with ClaI/XbaI and ligated into the appropriately cut vector pSLJ4K1. The result plasmids contain 35S promoter (cauliflower mosaic virus; Franck et al. (1980) Cell 21, 285), the Δ6-desaturase from *Muscariodides vialii* or *Aleurita furinosa* and the 35S terminator in the vector pSLJ4K1. Apart from said promoters or terminators all constitutive promoters or all plant virus promoters such as advantageously the nos promoter (Wilkinson et al., Journal of Experimental Botany, 48, 1997: 307 et seq.) or the ubiquitin promotors may be used. The promoters and terminators identified in the description may also advantageously be used in principle for expression.

The constructs were used for the transformation of *Arabidopsis thaliana*, oilseed rape, tobacco and linsed.

Example 6
Production of Transgenic Plants

a) Production of transgenic plants (modified in accordance with Moloney et al., 1992, Plant Cell Reports, 8:238-242)

To produce transgenic oilseed rape plants binary vectors in *Agrobacterium tumefaciens* C58C1-pGV2260 or *Escherichia coli* were used (Deblaere et al, 1984, Nucl. Acids. Res. 13, 4777-4788). For transforming oilseed rape plants (var. Dukkar, NPZ Nordeutsche Pflanzenzucht, Holhenleith, Germany) a 1:50 dilution of an overnight culture of a positively transformed *agrobacteria* colony in Murashige-Skoog medium (Murashige and Skoog 1962 Physiol. Plant. 15, 473) containing 3% of succharose (3MS medium) was used. Petioles or hypocotyledons of freshly germinated sterile rape plants (approx. 1 cm each) were incubated in a Petri dish with a 1:50 *agrobacteria* dilution for 5-10 minutes. This was followed by 3-day co-culture in darkness at 25°C on MS medium containing 0.8% of Bacto–Agar. After three days, culturing was continued with 16 hours of light/8 hours of darkness and in a weekly cycle on MS medium containing 500 mg/l of Cloran (sodium cefotaxime), 50 mg/l of kanamycin, 20 microg of benzylaminopurine (BAP) and 1.6 g/l of glucose. Growing shoots were transferred onto MS medium containing 2% of succharose, 250 mg/l of Cloran
and 0.8% of Bacto-Agar. If after three weeks no roots had formed 2-indolybutyric acid was added to the medium as a growth hormone for rooting purposes.

Regenerated shoots were obtained on 2MS medium using kanamycin and Claron, transferred into soil after rooting and after culturing grown for two weeks in a climate-controlled chamber, brought to blossom and after harvesting of ripe seed investigated for Δ6-desaturase expression by means of lipid analyses. Lines having increased contents of double bonds at the Δ6 position were identified. In the stably transform transgenic lines functionally expressing the transgene it was found that there is an increased content of double bonds at the Δ6 position by comparison with untransformed control plants.

b) Transgenic flax plants may be produced, for example by the by the method Bell et al., 1999, In Vitro Cell. Dev. Biol. Plant. 35(6):456-465, by means of particle bombardment. Agrobacterium-mediated transformations can be produced, for example, as described by Mlynarova et al. (1994), Plant Cell Report 13: 282-285.

Example 7

Lipid Extraction from Seed

Plant material was first of all mechanically homogenized by means of triturators in order to render it more amenable to extraction.

It was then heated to 100° C. for 10 min and after cooling on ice sedimented again. The cell sediment was hydrolyzed with 1 M methanolic sulfuric acid and 2% dimethoxypropane for 1 h at 90° C. and the lipids were transmethyalted. The resultant fatty acid methyl esters (FAMEs) were finally extracted into petroleum ether. The extracted FAMEs were analyzed by gas-liquid chromatography using a capillary column (Chrompack, WCOT fused silica. CP wax 52 CB. 25 m. 0.32 mm) and a temperature gradient of from 170° C. to 240° C. in 20 min and 5 min at 240° C. The identity of the fatty acid methyl esters was confirmed by comparison with corresponding FAME standards (Sigma). The identity and the position of the double bond was further analyzed by means of GC-MS by suitable chemical derivatization of the FAME mixtures, e.g. to form 4,4-dimethoxyxazoline derivatives (Christie, 1998). The GC analyses of the fatty acid methyl esters obtained from the transgenic rape seeds exhibiting seed-specific expression of the Δ6-desaturase are presented in Table 1. The transgenic rape seeds contained up to 5% γ-linolenic acid in the seed.

Table 1

<table>
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<tr>
<th>Fatty Acid</th>
<th>yYES2</th>
<th>Borage</th>
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<th>M. vialli</th>
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Example 8

Expression of Δ6-Desaturases from Primulaeae in Yeast (Saccharomyces cerevisiae)

The open reading rasters of the Δ6-desaturases obtained from Mascarioides viallii and Aleurita farinosa were each cloned behind the galactose-inducible GAL1 promoter of the yeast expression vector pYES2 (Invitrogen). The open reading rasters were amplified by means of PCR. The interfaces used for cloning were KpnI and EcoRI.

Primer Design for M. vialli: (SEQ ID NO: 14)

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Primer Design for A. farinosa: (SEQ ID NO: 16)

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The vectors produced were used for expression in yeast. The substrate specificities were determined by feeding the transformed yeast strains with α-linoleic acid and linoleic acid. The methodology used is described, for example, in Nipper and Michaelson, 2001, Lipids. 36(8):761-766; Sayanova et al., 2001, Journal of Experimental Botany. 52(360): 1581-1585; Sperling et al., 2001, Arch. Biochem. Biophys. 389(2):293-298 and Michaelson et al., 1998, FEBS Letters. 459(3):215-218.

In order to compare the specificities the Δ6-desaturase from borago (Borago officinalis) was likewise expressed in yeast (Sayanova et al., 1999, Plant Physiol. 121(2):641-646).

Table 2

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LA = linoleic acid (C18:2 n-6) Δ6-desaturation produces C18:4 n-3
ALA = α-linolenic acid (C18:3 n-3) Δ6-desaturation produces C20:5 n-3
nd = not determined

It may be gathered from the tables that the nucleic acid sequences according to the invention encode Δ6-desaturases which are specific for α-3 fatty acids.
SEQUENCE LISTING

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20  25  30
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35  40  45
His Gly Gin Val Tyr Aep Val Ser Ser Trp Ala Ala Leu His Pro Gly

GCG act gcc cct ctc atg gcc ctt gcc caa cac gac tgt acc gat gct
50  55  60
Gly Thr Ala Pro Leu Met Ala Leu Ala Gly His Aep Val Thr Aep Ala

TTC ctc ggc tac cct ccc cct tcc act gcc cgt ctc ctt cct ccc
65  70  75  80
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115  120  125
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420 425 430

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Phe Leu Ala Tyr His Pro Pro Ser Thr Ala Arg Leu Leu Pro Pro Leu
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Arg Lys His Thr Ala Tyr Ala Thr Phe Val Ile Met Ile Val Met
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Trp Ile Gly His Asp Ser Gly His Tyr Arg Ile Met Ser Asp Arg Lys
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FEATURE:
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We claim:

1. An isolated nucleic acid that encodes a polypeptide having 46-desaturase activity, wherein the polypeptide exhibits higher 446-desaturase activity for ω-3 fatty acids as compared to ω-6 fatty acids, wherein said nucleic acid comprises a nucleotide sequence selected from the group consisting of:
   a) the nucleotide sequence as set forth in SEQ ID NO: 3;
   b) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence as set forth in SEQ ID NO: 4;
   c) a nucleotide sequence having at least 75% homology to the nucleic acid sequence as set forth in SEQ ID NO: 3; and
   d) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least 75% homology to the amino acid sequence as set forth in SEQ ID NO: 4.

2. The isolated nucleic acid of claim 1, wherein the nucleic acid is derived from a plant.

3. The isolated nucleic acid of claim 1, wherein the nucleic acid is derived from the genera <i>Mucor</i> or <i>Acremonium</i>.

4. The isolated nucleic acid of claim 1, wherein the nucleic acid comprises a nucleotide sequence selected from the group consisting of:
   a) a nucleotide sequence having at least 95% homology to the nucleic acid sequence as set forth in SEQ ID NO: 3; and
b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least 95% homology to the amino acid sequence as set forth in SEQ ID NO: 4.

5. An amino acid sequence which is encoded by the isolated nucleic acid of claim 1.

6. A gene construct containing the isolated nucleic acid of claim 1, wherein said nucleic acid is functionally linked to one or more regulation signals.

7. A vector containing the isolated nucleic acid of claim 1.

8. A transgenic nonhuman organism containing the isolated nucleic acid of claim 1, wherein the organism is a microorganism, yeast, or plant.

9. The transgenic nonhuman organism of claim 8, wherein the organism is a plant.

10. A method for producing polynsaturated fatty acids, wherein the method comprises growing a transgenic organism which comprises the isolated nucleic acid of claim 1, wherein, due to the activity of said Δ-6 desaturase, polynsaturated fatty acids are formed in said organism which exhibits an increased content of ω-3 fatty acids compared to a non-transformed organism.

11. The method of claim 10, wherein in the eicosapentaenoic acid, eicosapentaenoic acid, or docosahexaenoic acid is produced.

12. The method of claim 10, further comprising isolating polynsaturated fatty acid molecules from said organism in the form of an oil, lipid, or a free fatty acid.

13. The method of claim 10, wherein said organism is a microorganism, a yeast, or a plant.

14. The method of claim 10, wherein said organism is a transgenic plant.

15. The method of claim 12, wherein said polynsaturated fatty acid molecules comprise a C18 fatty acid having at least three double bonds.

16. The isolated nucleic acid of claim 1, wherein the Δ6-desaturase activity toward ω-3 fatty acids as compared to ω-6 fatty acids is higher by a factor of at least 1.5.

17. The isolated nucleic acid of claim 16, wherein the factor is at least 5.

18. The isolated nucleic acid of claim 16, wherein the factor is at least 5.

19. A vector containing the gene construct of claim 6.

20. A transgenic nonhuman organism containing the gene construct of claim 6, wherein the organism is a microorganism, yeast, or plant.

21. A gene construct of claim 6, wherein the one or more regulation signals comprise one or more promoter, terminator, or polyadenylation site.

22. The method of claim 10, which produces triglycerides having an increased content of saturated or unsaturated fatty acids as compared to an untransformed organism.

23. The method of claim 10, wherein said organism has an increased content of polynsaturated fatty acids as compared to an untransformed organism without said nucleic acid.

24. The method of claim 23, wherein said increased content of polynsaturated fatty acids is at least 10% increased as compared to an untransformed organism without said nucleic acid.

25. The method of claim 23, wherein said increased content of polynsaturated fatty acids is at least 20% increased as compared to an untransformed organism without said nucleic acid.

26. The method of claim 23, wherein said increased content of polynsaturated fatty acids is at least 40% increased as compared to an untransformed organism without said nucleic acid.

27. The method of claim 12, wherein said polynsaturated fatty acid molecules comprise fatty acids having an increased content of Δ-6 double bonds as compared to an untransformed organism.

28. The method of claim 12, wherein the oil, lipid, or fatty acid is further formulated as an animal feed, a foodstuff, a cosmetic, or a pharmaceutical.

29. An amino acid sequence which is encoded by an isolated nucleic acid that encodes a polypeptide having Δ-6-desaturase activity, wherein the polypeptide exhibits higher Δ-6-desaturase activity for ω-3 fatty acids as compared to ω-6 fatty acids, wherein said nucleic acid comprises a nucleotide sequence selected from the group consisting of:
   a) the nucleotide sequence as set forth in SEQ ID NO: 1;
   b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO: 2; and
   c) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least 75% sequence identity to the amino acid sequence as set forth in SEQ ID NO: 2, wherein the polypeptide has Δ-6-desaturase activity, and the polypeptide exhibits higher Δ-6-desaturase activity for ω-3 fatty acids as compared to ω-6 fatty acids.

30. The amino acid sequence of claim 29, wherein the nucleotide sequence is selected from the group consisting of:
   a) a nucleotide sequence having at least 85% sequence identity to the nucleic acid sequence of SEQ ID NO: 1; and
   b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least 85% sequence identity to the amino acid sequence of SEQ ID NO: 2.

31. The amino acid sequence of claim 29, wherein the nucleotide sequence is selected from the group consisting of:
   a) a nucleotide sequence having at least 95% sequence identity to the nucleic acid sequence of SEQ ID NO: 1; and
   b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 2.

32. The isolated nucleic acid of claim 1, wherein the nucleic acid comprises a nucleotide sequence selected from the group consisting of:
   a) a nucleotide sequence having at least 85% sequence identity to the nucleic acid sequence as set forth in SEQ ID NO: 3; and
   b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least 85% homology to the amino acid sequence as set forth in SEQ ID NO: 4.