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*Botryoccocus Braunii* Triterpene Synthase Proteins and Nucleic Acid Molecules, and Methods for Their Use

Joe Chappell  
*University of Kentucky*, chappell@uky.edu

Shigeru Okada

Tom Niehaus  
*University of Kentucky*, tomniehaus@uky.edu

Tim Devarenne

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**United States Patent**

Chappell et al.

**Field of Classification Search**

None

See application file for complete search history.

**References Cited**

**OTHER PUBLICATIONS**

Jarstfer CD (1990) Biosynthesis of Non-Head-to-Tail Terpenes—Formation of 1'-1 and 1'-3 Linkages. Accounts of Chemical Research 23: 70-77.

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Primary Examiner — Hope Robinson

Attorney, Agent, or Firm — Crowell & Moring LLP

**ABSTRACT**

This application relates to the functional identification and characterization of a nucleic acid molecule encoding a triterpene synthase, in particular botryococcene synthase. Also described are host cells comprising the nucleic acid molecules of this invention, proteins encoded by the nucleic acid molecules and methods for using the nucleic acid molecules, transformed hosts and encoded proteins to produce high levels of triterpene hydrocarbons.

6 Claims, 11 Drawing Sheets
FIG. 1
Hydrocracking of a typical, C₃₄ Botryococcene

\[
\text{Hydrocracking} \quad \downarrow \quad \text{1) hydrogenation} \quad \text{C=O} + \text{H}_2 \rightarrow \text{H} - \text{C} - \text{C} - \quad (~30 \text{ kcal})
\]

\[
\downarrow \quad \text{2) cracking} \quad \text{C} - \text{C} - \rightarrow \text{C} \cdot \cdot \cdot \text{C} 
\]

\[
\begin{align*}
\text{(% v/v)} & \quad \text{68.5} \quad \text{30.0} \quad \text{<0.2} \quad \text{1.4} \\
\text{Paraffins} & \quad \text{Naphthenes} \quad \text{Olefins} & \text{Aromatics} \\
\end{align*}
\]

\[
\begin{align*}
\text{(% v/v)} & \quad \text{67} \quad \text{15} \quad \text{15} \quad \text{3} \\
\text{Gasoline} & \quad \text{Kerosene} \quad \text{Diesel} \quad \text{Residuals} \\
\text{C5-C12, 40-} & \quad \text{C10-C18,} \quad +\text{C12, 250-} \quad +\text{C70, >600°C} \quad \text{205°C} \\
\text{205°C} & \quad 175-325°C \quad 350°C & \text{Hillen et al., 1982} \\
\end{align*}
\]
FIG. 3
FIG. 4

FIG. 5
FIG. 6
SDS-PAGE showing purification of H6-BBS expressed in E.coli

FIG. 7
Enzyme Assays for squalenesynthase and botryococcenesynthase

Algal or bacterial cell extracts

$1^{-3}H$-FPP

NADPH
Mg$^{2+}$

TLC: SiO$_2$, n-hexane

C$_{36}$botryococcene

squalene

FIG. 8
FIG. 9
FIG. 10
FIG. 12

Squalene accumulation (mg/l) vs. Time (days)
The current disclosure describes the functional identification and characterization of the gene coding for a triterpene synthase in particular a botryococcene synthase, BBS, enzyme. The identification of the botryococcene synthase gene now provides an alternative means of generating important raw materials for the reliable and cost-effective production of an energy-rich, renewable, and sustainable biofuel source (FIG. 3). For example, the co-expression of the botryococcene synthase gene in combination with a suitable FPP synthase and triterpene methyltransferase genes in transgenic terrestrial or aquatic plants could yield a production platform for the methylated triterpenes. These compounds could be derived from the metabolic diversion of CO₂ fixed in the process of photosynthesis flowing directly into triterpene biosynthesis and accumulation. The feasibility of this engineering strategy for the production of large amounts of high-valued sesquiterpenes, terpenes consisting of 15 carbons rather than the 30 carbons found in triterpenes, was recently demonstrated. (Wu et al., (2006) Nature Biotechnology 141,1147).

The botryococcene synthase of this invention is a triterpene synthase enzyme catalyzing the reductive condensation of 2 farnesyl diphosphate (FPP) substrate molecules yielding botryococcene, a 30-carbon, branched-chain hydrocarbon.

More specifically, disclosed herein is the DNA and protein sequence of, and the functional characterization for, the race B botryococcene synthase gene which, when expressed in a heterologous host such as bacteria, yeast or plants yields a protein that, when mixed with a lystate and reducing equivalents in the form of NADPH, provides an enzyme activity that catalyzes a unique chemical condensation of 2 FPP molecules, creating a branched, triterpene hydrocarbon known as botryococcene. A schematic diagram of the reaction catalyzed by the botryococcene synthase enzyme is shown in FIG. 1. Like squalene synthase (Blugg et al., (2002) J. Am. Chem. Soc. 88:46-8853), botryococcene synthase is predicted to catalyze a 2 step reaction. The first step condenses the 2 FPP substrate molecules into a pre-squalene diphosphate intermediate (PSPP). When NADPH is provided, squalene synthase reduces the PSPP to a linkage of carbons 1 and 1' of the respective FPP molecules. In contrast, when botryococcene synthase is provided NADPH, the PSPP undergoes a different reducing rearrangement to botryococcene with a linkage of carbon 3 of one FPP starter molecule to carbon 1' of the second FPP starter molecule.

FIG. 1 depicts the biosynthetic pathways for botryococcene and squalene. Both triterpenes are derived from an initial condensation of 2 FPP molecules to form presqualene diphosphate (PSPP), which is subsequently cleaved and reduced to form either botryococcene or squalene.

FIG. 2 depicts an overview of the hydrocracking process of a typical, C₃₄ botryococcene to yield fuel suitable for combustion engines. Briefly, botryococenes are treated with high pressure H₂ at high temperatures with a Pd catalyst to give a variety of organic molecules, which can be further distilled into various classes of fuel.

FIG. 3 depicts a strategy for engineering an alternative biofuels production platform into terrestrial or aquatic plants. Genes coding for the biochemical steps for synthesis of botryococenes would be introduced into plants such that the respective catalytic steps (FPP synthase, triterpene synthase and triterpene methyltransferase activities) would be targeted to the chloroplast compartment. The introduced enzyme activities would hence divert photosynthetically fixed CO₂ directly into methylated triterpene biosynthesis.
FIG. 4 presents the DNA sequence for the botryococcene synthase cDNA, SEQ ID NO: 1. The start and stop codons are shown in bold.

FIG. 5 presents the amino acid sequence for the botryococcene synthase protein, SEQ ID NO: 2, predicted from the corresponding cDNA sequence shown in FIG. 4.

FIG. 6 depicts an alignment comparison of selection regions/domains of various squalene synthases from Botryococcus(BBS), tobacco (N. tabacum), Arabidopsis (A. thaliana), corn (Z. mays), rape (R. ruttus) and yeast (S. cerevisiae) to that for the botryococcene synthase (BBS). Domains I-VI were identified as highly conserved amongst diverse squalene synthases, and domains III-V were previously correlated with the particular steps in catalysis as noted. Sequences displayed across the 5 domains are: BBS, SEQ ID NO: 3, 4, 5, 6, and 7; BSS, SEQ ID NO: 8, 9, 10, 11, and 12; N. tabacum SEQ ID NO: 13, 14, 15, 16, and 17; A. thaliana, SEQ ID NO: 18, 19, 20, 21, and 22; Z. mays, SEQ ID NO: 23, 24, 25, 26 and 27; R. ruttus, SEQ ID NO: 28, 29, 30, 31 and 32; and S. cerevisiae SEQ ID NO: 33, 34, 35, 36 and 37.

FIG. 7 depicts the purification of hexa-histidine tagged (SEQ ID NO: 44) BBS enzyme. E. coli cells over-expressing the botryococcene synthase gene harboring an amino terminal hexa-histidine purification tag (SEQ ID NO: 44) were used to prepare an initial cell lysate (crude lysate), which was then subjected to nickel affinity chromatography. The crude lysate was applied to the affinity column, followed by washing with buffer containing increasing concentrations of imidazole (flow buffer without imidazole, to buffer containing 150 mM imidazole) and the respective column fractions collected for SDS-PAGE analysis. Aliquots of each fraction were resolved by SDS-PAGE and the gel stained with Coomassie Blue, a general protein stain. Molecular weight standards are noted as marker and the expected size for the his-tagged BBS protein is noted by the arrow.

FIG. 8 illustrates the botryococcene synthase enzyme assay.

FIG. 9 depicts the enzyme activity of purified BBS protein, activity associated with a B. braunii lysate (boty lys), and BBS combined with lysate (BBS+boty lys) with or without NADPH. BBS containing an N-terminal hexa-histidine tag (SEQ ID NO: 44) was expressed in E. coli and purified from bacterial lysate by nickel affinity chromatography according to the manufacturer (Novagen) (see FIG. 7).

FIG. 10 depicts GC chromatograms of hexane extracts prepared from TN7 yeast (a) and TN7 yeast expressing BBS (b). The mass spectrum for the unique peak found in the TN7-BBS culture with a retention time of 16.20 is shown in panel c. The mass spectrum matches that of presqualene alcohol (PSOH) as described by Edmond et al. (1971) J. Biol. Chem. 6254-6251.

FIG. 11 depicts GC chromatograms of hexane extracts prepared from TN7 yeast (a) and TN7 yeast expressing a full length B. braunii squalene synthase gene (b). Identification of the novel compound accumulating in TN7 yeast expressing the squalene synthase gene (corresponding to the peak with a retention time of approximately 14) was based on mass spectral comparisons (not shown) and identical chromatographic behavior of an authentic squalene (25 ng) standard (c).

FIG. 12 depicts the accumulation of squalene in TN7 yeast over-expressing a Botryococcus braunii squalene synthase gene.

DETAILED DESCRIPTION OF THE INVENTION

The current disclosure describes the functional identification and characterization of the gene coding for a botryococcene synthase, BBS, enzyme, nucleic acid molecules e.g. SEQ ID NO: 1, encoding a botryococcene synthase, BBS, polypeptide of this invention, e.g., SEQ ID NO: 2 and methods for their use.

The polypeptides of this invention include for example polypeptides comprising the amino acid sequence set forth in SEQ ID NO:2 and fragments thereof. Preferably the polypeptide fragments have triterpene synthase activity. The polypeptides of this invention may comprise one or more peptide domains I, II, III, IV, V and VI, wherein domain I comprises LPQLQDPICFLPYL (SEQ ID NO: 3), domain II comprises LRLTDITIVDDMN LKSETK (SEQ ID NO: 4), domain III comprises YCHYVAGSGGLAV TKVIV (SEQ ID NO: 5), domain IV comprises GLLLQKANITID YNED (SEQ ID NO 6), and domain V comprises ALALLVTAGFHL S (SEQ ID NO: 7).

The polypeptides of this invention may also contain one or more modified amino acids. The presence of modified amino acids may be advantageous in, for example, increasing triterpene synthase catalytic activity or increasing polypeptide stability. Amino acid(s) are modified, for example, by post-translationally or post-translationally during recombinant production (e.g., N-linked glycosylation at N-X-S/T motifs during expression in mammalian cells) or modified by synthetic means. Accordingly, a “mutant”, “variant” or “modified” protein, enzyme, polynucleotide, gene, or cell, means a protein, enzyme, polynucleotide, gene, or cell, that has been altered or derived, or is in some way different or changed, from a parent protein, enzyme, polynucleotide, gene, or cell. A mutant or modified protein or enzyme is usually, although not necessarily, expressed from a mutant polynucleotide or gene.

A “parent” protein, enzyme, polynucleotide, gene, or cell, is any protein, enzyme, polynucleotide, gene, or cell, from which any other protein, enzyme, polynucleotide, gene, or cell, is derived or made, using any methods, tools or techniques, and whether or not the parent is itself native or mutant.

A parent polynucleotide or gene encodes for a parent protein or enzyme.

A “mutation” means any process or mechanism resulting in a mutant protein, enzyme, polynucleotide, gene, or cell. This includes any mutation in which a protein, enzyme, polynucleotide, or gene sequence is altered, and any detectable change in a cell arising from such a mutation. Typically, a mutation occurs in a polynucleotide or gene sequence, by point mutations, deletions, or insertions of single or multiple nucleotide residues. A mutation includes polynucleotide alterations arising within a protein-encoding region of a gene as well as alterations in regions outside of a protein-encoding sequence, such as, but not limited to, regulatory or promoter sequences. A mutation in a gene can be “silent”, i.e., not reflected in an amino acid alteration upon expression, leading to a “sequence-conservative” variant of the gene. This generally arises because of degeneracy of the genetic code wherein more than one codon codes for the same amino acid.

Non-limiting examples of a modified amino acid include a glycosylated amino acid, a sulfated amino acid, a prenylated (e.g., farnesylated, geranylgeranylated) amino acid, an acetylated amino acid, an acetylated amino acid, a prenylated amino acid, a biotinylated amino acid, a carboxyamidated amino acid, a phosphorylated amino acid, and the like. References adequate to guide one of skill in the modification of amino acids are replete throughout the literature. Example protocols are found in Walker (1998) Protein Protocols on CD-ROM (Humana Press, Towata, N.J.).

Recombinant methods for producing and isolating the triterpene synthase polypeptides and modified triterpene synthase polypeptides of the invention are described herein. In
addition to recombinant production, the polypeptides may be produced by direct peptide synthesis using solid-phase tech-
niques (e.g., Stewart et al. (1969) Solid-Phase Peptide Synthesis (WH Freeman Co, San Francisco); and Merrifield
(1963). J. Am. Chem. Soc. 85: 2140-2154; each of which is
incorporated by reference). Peptide synthesis may be per-
fomed using manual techniques or by automation. Auto-
nated synthesis may be achieved, for example, using Applied
Biosystems 431 A Peptide Synthesizer (Perkin Elmer, Foster
City, Calif.) in accordance with the instructions provided by
the manufacturer.

A “protein” or “polypeptide”, which terms are used inter-
changeably herein, comprises one or more chains of chemical
building blocks called amino acids that are linked together by
chemical bonds called peptide bonds. An “enzyme” means
any substance, composed wholly or largely of protein, that
catalyzes or promotes, more or less specifically, one or more
chemical or biochemical reactions. A “native” or “wild-type”
protein, enzyme, polynucleotide, gene, or cell, means a pro-
tein, enzyme, polynucleotide, gene, or cell that occurs in
nature (whose form predominates in natural populations).

Accordingly, in various embodiments, isolated or recom-
binant polypeptides comprising the amino acid sequence set
forth in SEQ ID NO:2 are provided. The polypeptides include
up to 35, 25, 10, 5, 4, 3, 2 or 1 conservative amino acid
substitutions.

“Conservative amino acid substitutions” or, simply, “con-
servative variations” of a particular sequence refers to the
replacement of one amino acid, or series of amino acids, with
essentially identical amino acid or series of amino acids. One
of skill will recognize that individual substitutions, deletions
or additions which alter, add or delete a single amino acid or
a percentage of amino acids in an encoded sequence result in
“conservative variations” where the alterations result in the
deletion of an amino acid, addition of an amino acid, or
substitution of an amino acid with a functionally similar
amino acid.

Conservative substitution tables providing functionally
similar amino acids are well known in the art. For example,
one conservative substitution group includes Alanine (A),
Serine (S), and Threonine (T). Another conservative substitu-
tion group includes Aspartic acid (D) and Glutamic acid
(E). Another conservative substitution group includes Aspar-
agine (N) and Glutamine (Q). Yet another conservative sub-
stitution group includes Arginine (R) and Lysine (K). Another
conservative substitution group includes Isoleucine, (I) Leu-
cine (L), Methionine (M), and Valine (V). Another conserva-
tive substitution group includes Phenylalanine (F), Tyrosine
(Y), and Tryptophan (W).

Thus, “conservative amino acid substitutions” of a listed
polypeptide sequence (e.g., SEQ ID NO:2) include substitu-
tions of a percentage, typically less than 10%, of the amino
acids of the polypeptide sequence, with an amino acid of the
same conservative substitution group. Accordingly, a conserva-
tively substituted variation of a polypeptide of the invention
can contain, for example, substitutions of 35, 25, 10, 5, 4, 3,
2 or 1 amino acid with an amino acid of the same conservative
substitution group.

It is understood that the addition of sequences that do not
alter the encoded activity of a nucleic acid molecule, such as
the addition of a non-functional or non-coding sequence, is a
conservative variation of the basic nucleic acid molecule. The
“activity” of an enzyme is a measure of its ability to catalyze
a reaction, i.e., to “function”, and may be expressed as the rate
at which the product of the reaction is produced. For example,
enzyme activity can be represented as the amount of product
produced per unit of time or per unit of enzyme (e.g., con-
centration or weight), or in terms of affinity or dissociation
constants. As used interchangeably herein a “triterpene syn-
thesis activity”, “biological activity of triterpene synthase” or
“functional activity of triterpene synthase” refers to an activ-
ity exerted by a triterpene synthase protein, polypeptide or
nucleic acid molecule on a triterpene synthase polypeptide
substrate, as determined in vivo, or in vitro, according to
standard techniques.

One of skill in the art will appreciate that many conserva-
tive substitutions of the nucleic acid constructs which are
disclosed herein yield a functionally identical construct. For
example, owing to the degeneracy of the genetic code, “silent
substitutions” (i.e., substitutions in a nucleic acid sequence
which do not result in an alteration in an encoded polypep-
tide) are an implied feature of every nucleic acid sequence
which encodes an amino acid.

Similarly, “conservative amino acid substitutions,” in
which one or a few amino acids in an amino acid sequence are
substituted with different amino acids with highly similar
properties, are also readily identified as being highly similar
to a disclosed construct. Families of amino acid residues
having similar side chains have been defined in the art. These
families include amino acids with basic side chains (e.g.,
lysine, arginine, histidine), acidic side chains (e.g., aspartic
acid, glutamic acid), uncharged polar side chains (e.g.,
glycine, asparagine, glutamine, serine, threonine, tyrosine, cys-
teine), nonpolar side chains (e.g., alanine, valine, leucine,
isoctane, proline, phenylalanine, methionine, tryptophan),
beta-branched side chains (e.g., threonine, valine, isoleucine)
and aromatic side chains (e.g., tyrosine, phenylalanine, tryp-
tophan, histidine). Such conservative variations of each disclo-
 sed sequence are a feature of the polypeptides provided
herein.

It will be appreciated by those skilled in the art that due to
the degeneracy of the genetic code, a multitude of nucleotide
sequences encoding modified triterpene synthase polypep-
tides of the invention may be produced, some of which bear
substantial identity to the nucleic acid sequences explicitly
disclosed herein. For instance, codons AGA, AGG, CGA,
CGC, CGG, and CGU all encode the amino acid arginine.
Thus, at every position in the nucleic acid molecules of the
invention where an arginine is specified by a codon, the codon
can be altered to any of the corresponding codons described
above without altering the encoded polypeptide. It is under-
stood that U in an RNA sequence corresponds to T in a DNA
sequence.

“Conservative variants” are proteins or enzymes in which a
given amino acid residue has been changed without altering
overall conformation and function of the protein or enzyme,
including, but not limited to, replacement of an amino acid
with one having similar properties, including polar or non-
polar character, size, shape and charge. Amino acids other
than those indicated as conserved may differ in a protein or
enzyme so that the percent protein or amino acid sequence
similarity between any two proteins of similar function may
vary and can be, for example, at least 30%, at least 50%, at
least 70%, at least 80%, at least 90%, at least 95%, at least
98% or at least 99%, as determined according to an alignment
scheme. As referred to herein, “sequence similarity” means
the extent to which nucleotide or protein sequences are
related. The extent of similarity between two sequences can
be based on percent sequence identity and/or conservation.
“Sequence identity” herein means the extent to which two
nucleotide or amino acid sequences are invariant. “Sequence
alignment” means the process of lining up two or more
sequences to achieve maximal levels of identity (and, in the
case of amino acid sequences, conservation) for the purpose
of assessing the degree of similarity. Numerous methods for aligning sequences and assessing similarity/identity are known in the art such as, for example, the Cluster Method, wherein similarity is based on the MEGALIGN algorithm, as well as BLASTN, BLASTP, and FASTA (Lipman and Pearson, 1985 Science 227:1435-41; Pearson and Lipman, 1988 Proc Natl Acad Sci USA 85(8):2444-8). When using all of these programs, the preferred settings are those that result in the highest sequence similarity.

Non-conservative modifications of a particular polypeptide are those which substitute any amino acid not characterized as a conservative substitution. For example, any substitution which crosses the bounds of the six groups set forth above. These include substitutions of basic or acidic amino acids for neutral amino acids, (e.g., Asp, Glu, Asn, or Gln for Val, Ile, Leu or Met), aromatic amino acid for basic or acidic amino acids (e.g., Phe, Tyr or Trp for Asp, Asn, Glu or Gln) or any other substitution not replacing an amino acid with a like amino acid. Basic amino acids include lysine (K), arginine (R), histidine (H); acidic amino acids include aspartic acid (D), glutamic acid (E); uncharged polar amino acids include glycine (G), asparagine (N), glutamine (Q), serine (S), threonine (T), tyrosine (Y), cysteine (C); nonpolar amino acids include alanine (A), valine (V), leucine (L), isoleucine (I), proline (P), phenylalanine (F), methionine (M), tryptophan (W); beta-branched amino acids include threonine (T), valine (V), isoleucine (I); aromatic amino acids include tyrosine (Y), phenylalanine (F), tryptophan (W), histidine (H).

A polynucleotide, polypeptide, or other component is “isolated” when it is partially or completely separated from components with which it is normally associated (other proteins, nucleic acid molecules, cells, synthetic reagents, etc.). A nucleic acid molecule or polypeptide is “recombinant” when it is artificial or engineered, or derived from an artificial or engineered protein or nucleic acid molecule. For example, a polynucleotide that is inserted into a vector or any other heterologous location, e.g., in a genome of a recombinant organism, such that it is not associated with nucleotide sequences that normally flank the polynucleotide as it is found in nature is a recombinant polynucleotide. A protein expressed in vitro or in vivo from a recombinant polynucleotide is an example of a recombinant polypeptide. Likewise, a polynucleotide sequence that does not appear in nature, for example a variant of a naturally occurring gene, is recombinant. For example, an “isolated” nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid molecule. For example, with regards to genomic DNA, the term “isolated” includes nucleic acid molecules which are separated from the chromosome with which the genomic DNA is naturally associated. Typically, an “isolated” nucleic acid molecule is free of sequences which normally flank the nucleic acid molecule (i.e., sequences located at the 5′ and 3′ ends of the nucleic acid molecule) in the genomic DNA of the organism from which the nucleic acid molecule is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which normally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid molecule is derived. Moreover, an “isolated” nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

In some embodiments, a polypeptide provided herein includes amino acid residue substitutions that correspond to positions in a particular sequence at least 80%, 85%, 90%, 95%, 98% or 99% of the time. In other words, the invention encompasses polypeptides that contain the recited amino acid substitutions at 80%, 85%, 90%, 95%, 98% or 99% of the recited positions in a given sequence. The skilled artisan will recognize that not every substitution from a group of substitutions is necessary to obtain a modified polypeptide that is active on a triterpene substrate.

“Sequence identity” herein means the extent to which two nucleotide or amino acid sequences are invariant. “Sequence alignment” means the process of lining up two or more sequences to achieve maximal levels of identity (and, in the case of amino acid sequences, conservation) for the purpose of assessing the degree of similarity. Numerous methods for aligning sequences and assessing similarity/identity are known in the art such as, for example, the Cluster Method, wherein similarity is based on the MEGALIGN algorithm, as well as BLASTN, BLASTP, and FASTA (Lipman and Pearson, 1985 Science 227:1435-41; Pearson and Lipman, 1988 Proc Natl Acad Sci USA 85(8):2444-8). When using all of these programs, the preferred settings are those that result in the highest sequence similarity. For example, the “identity” or “percent identity” with respect to a particular pair of aligned amino acid sequences can refer to the percent amino acid sequence identity that is obtained by ClustalW analysis (version W 1.8 available from European Bioinformatics Institute, Cambridge, UK), counting the number of identical matches in the alignment and dividing such number of identical matches by the greater of (i) the length of the aligned sequences, and (ii) 96, and using the following default ClustalW parameters to achieve slow/accurate pairwise alignments—Gap Open Penalty: 10; Gap Extension Penalty: 0.10; Protein weight matrix: Gonnet series; DNA weight matrix: IUB; Toggle Slow/Fast pairwise alignments—SLOW or FULL Alignment.

Two sequences are “optimally aligned” when they are aligned for similarity scoring using a defined amino acid substitution matrix (e.g., BLOSUM62), gap existence penalty and gap extension penalty so as to arrive at the highest score possible for that pair of sequences. Amino acid substitution matrices and their use in quantifying the similarity between two sequences are well-known in the art and described, e.g., in Dayhoff et al. (1978) “A model of evolutionary change in proteins” in “Atlas of Protein Sequence and Structure,” Vol. 5, Suppl. 3 (ed. M. O. Dayhoff), pp. 345-352, Natl. Biomed. Res. Found., Washington, D.C. and Henikoff et al. (1992) Proc Natl Acad Sci USA 89: 10915-10919 (each of which is incorporated by reference). The BLOSUM62 matrix is often used as a default scoring substitution matrix in sequence alignment protocols such as Gapped BLAST 2.0. The gap existence penalty is imposed for the introduction of a single amino acid gap in one of the aligned sequences, and the gap extension penalty is imposed for each additional empty amino acid position inserted into an already opened gap. The alignment is defined by the amino acids positions of each sequence at which the alignment begins and ends, and optionally by the insertion of a gap or multiple gaps in one or both sequences so as to arrive at the highest possible score. While optimal alignment and scoring can be accomplished manually, the process is facilitated by the use of a computer-implemented alignment algorithm, e.g., gapped BLAST 2.0, described in Altschul et al. (1997) Nucl. Acids Res. 25: 3389-3402 (incorporated by reference herein), and made available to the public at the National Center for Biotechnology Information (NCBI) Website (www.ncbi.nlm.nih.gov). Optimal alignments, including multiple alignments, can be prepared using, e.g., PSI-BLAST, available through the NCBI website.

With respect to an amino acid sequence that is optimally aligned with a reference sequence, an amino acid residue “corresponds to” the position in the reference sequence with which the residue is paired in the alignment. The “position” is denoted by a number that sequentially identifies each amino acid in the reference sequence based on its position relative to the N-terminus. For example, in SEQ ID NO: 2, position 1 is M, position 2 is T, position 3 is M, etc. When a test sequence is optimally aligned with SEQ ID NO: 2, a residue in the test sequence that aligns with the M at position 3 is said to “correspond to position 3” of SEQ ID NO: 2. Owing to deletions, insertions, truncations, fusions, etc., that must be taken into account when determining an optimal alignment, in general the amino acid residue number in a test sequence as determined by simply counting from the N-terminal will not necessarily be the same as the number of its corresponding position in the reference sequence. For example, in a case where there is a deletion in an aligned test sequence, there will be no amino acid that corresponds to a position in the reference sequence at the site of deletion. Where there is an insertion in an aligned reference sequence, that insertion will not correspond to any amino acid position in the reference sequence. In the case of truncations or fusions there can be stretches of amino acids in either the reference or aligned sequence that do not correspond to any amino acid in the corresponding sequence.

Also contemplated are fragments of the full length triterpene synthase polypeptides and polynucleotides, e.g., fragments of polypeptides comprising the amino acid sequence set forth in SEQ ID NO: 2 and fragments of nucleic acid molecules comprising the sequence set forth in SEQ ID NO: 1. A “fragment” is a unique portion of a triterpene synthase polypeptide or the polynucleotide encoding triterpene synthase which is identical in sequence to, but shorter in length than, the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues of a given nucleic acid molecule or polypeptide. A fragment used as a probe, primer, antigen, catalytic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing tables, and figures, may be encompassed by the present embodiments.

Also contemplated in this invention are isolated polypeptides that are triterpene synthases, that comprise 5 peptide domains I, II, III, IV, and V of the triterpene synthase of this invention may comprise respectively, e.g., SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, and SEQ ID NO: 7 (See FIG. 6, the 5 domains of B. braunii (BBS)). In an embodiment of the invention, domain I comprises an amino acid sequence that is at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 95% identical to the full-length of SEQ ID NO: 3, domain II comprises an amino acid sequence that is at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 95% identical to the full-length of SEQ ID NO: 4, domain III may comprise an amino acid sequence that is at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 95% identical to the full-length of SEQ ID NO: 5, domain IV comprises an amino acid sequence that is at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 95% identical to the full-length of SEQ ID NO: 6 and domain V comprises an amino acid sequence that is at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 95% identical to the full-length of SEQ ID NO: 7. In other embodiments, isolated nucleic acid molecules are provided. Described herein are nucleic acid molecules that encode a polypeptide having triterpene synthase activity, in particular a Botryococcus braunii triterpene synthase. The nucleic acid molecules of this invention include e.g., nucleic acid molecules that encode the amino acid sequence set forth in SEQ ID NO: 2, nucleic acid molecules that encode fragments of SEQ ID NO: 2, nucleic acid molecules that comprise SEQ ID NO: 1, and nucleic acid molecules that encode fragments of SEQ ID NO: 1. In one aspect, the invention provides a novel family of isolated or recombinant polynucleotides referred to herein as “triterpene synthase polynucleotides” or “triterpene synthase nucleic acid molecules.” Triterpene synthase polynucleotide sequences are characterized by the ability to encode a triterpene synthase polypeptide. In general, the invention includes any nucleotide sequence that encodes the polypeptide described herein. The terms “polynucleotide,” “nucleotide sequence,” and “nucleic acid molecule” are used to refer to a polymer of nucleotides (A, C, T, U, G, etc. or naturally occurring or artificial nucleotide analogues), e.g., DNA or RNA, or a representation thereof, e.g., a character string, etc., depending on the relevant context. A given polynucleotide or complementary polynucleotide can be determined from any specified nucleotide sequence.

In an aspect, the triterpene synthase polynucleotides comprise recombinant or isolated forms of naturally occurring nucleic acid molecules isolated from an organism, e.g., an algae strain. Exemplary triterpene synthase polynucleotides include those that encode the polypeptide set forth in SEQ ID NO: 2. In another aspect of the invention, triterpene synthase polynucleotides are produced by diversifying, e.g., mutating, a naturally occurring, isolated, or recombinant triterpene synthase polynucleotide, e.g., the nucleic acid sequence set forth in SEQ ID NO: 1. It is possible to generate diversified triterpene synthase polynucleotides encoding triterpene synthase polypeptides with superior functional attributes, e.g., increased catalytic function, increased stability, or higher expression level, than a triterpene synthase encoded by the polynucleotide used as a substrate or parent in the diversification process.

The polynucleotides of the invention have a variety of uses in, for example recombinant production (i.e., expression) of the triterpene synthase polypeptides of the invention and as substrates for further diversity generation, e.g., recombination reactions or mutation reactions to produce new and/or improved triterpene synthase homologues, and the like. It is important to note that certain specific, substantial and credible utilities of triterpene synthase polynucleotides do not require that the polynucleotide encode a polypeptide with substantial triterpene synthase activity or even variant triterpene synthase activity. For example, triterpene synthase polynucleotides that do not encode active enzymes can be valuable sources of parental polynucleotides for use in diversification procedures to arrive at triterpene synthase
polynucleotide variants, or non-triterpene synthase poly-
ucleotides, with desirable functional properties (e.g., high k_{on}, or k_{on}/K_{on}, low K_{on}, high stability towards heat or other
environmental factors, high transcription or translation rates,
resistance to proteolytic cleavage, etc.).
Triterpene synthase polynucleotides, including nucleotide
sequences that encode triterpene synthase polypeptides
and variants thereof, fragments of triterpene synthase polypep-
tides, related fusion proteins, or functional equivalents
thereof, are used in recombinant DNA molecules that direct
the expression of the triterpene synthase polypeptides in
appropriate host cells, such as plant cells. Due to the inherent
degeneracy of the genetic code, other nucleic acid sequences
which encode substantially the same or a functionally equiva-
 lent amino acid sequence can also be used to clone and
direct the triterpene synthase polynucleotides. The term
“host cell”, as used herein, includes any cell type which is
susceptible to transformation with a nucleic acid construct.
The term “transformation” means the introduction of a
foreign (i.e., extrinsic or extracellular) gene, DNA or RNA
sequence to a host cell, so that the host cell will express
the introduced gene or sequence to produce a desired substance,
typically a protein or enzyme coded by the introduced gene or
sequence. The introduced gene or sequence may include
regulatory or control sequences, such as start, stop, promoter,
signal, secretion, or other sequences used by the genetic
machinery of the host. A host cell that receives and expresses
introduced DNA or RNA has been “transformed” and is a
“transformant” or a “clone.” The DNA or RNA introduced to
a host cell can come from any source, including cells of the
same genus or species as the host cell, or cells of a different
genus or species.
As will be understood by those of skill in the art, it can be
advantageous to modify a coding sequence to enhance its
expression in a particular host. The genetic code is redundant
with 64 possible codons, but most organisms preferentially
use a subset of these codons. The codons that are utilized most
often in a species are called optimal codons, and those not
utilized very often are classified as rare or low-usage codons
(see, e.g., Zhang et al. (1991) Gene 105:61-72; incorporated
by reference herein). Codons can be substituted to reflect the
preferred codon usage of the host, a process sometimes called
codon optimization” or “controlling for species codon bias.”

Optimized coding sequences containing codons preferred
by a particular prokaryotic or eukaryotic host (see also, Mur-
ray et al. (1989) Nucleic Acids Res. 17:477-508; incorporated
by reference herein) can be prepared, for example, to increase
the rate of translation or to produce recombinant RNA trans-
scripts having desirable properties, such as a longer half-life,
as compared with transcripts produced from a non-optimized
sequence. Translation stop codons can also be modified to
reflect host preference. For example, preferred stop codons
for S. cerevisiae and mammals are UAA and UGA,
respectively. The preferred stop codon for monocotyledonous
plants is UGA, whereas insects and E. coli prefer to use UAA as
the stop codon (Dolphin et al. (1996) Nucleic Acids Res. 24: 216-
218; incorporated by reference herein). Methodology for
optimizing a nucleotide sequence for expression in a plant
is provided, for example, in U.S. Pat. No. 6,015,891, and
the references cited therein (incorporated herein by reference).

“Silent variations” are one species of “conservative substitu-
tions.” One of skill will recognize that each codon in a
nucleic acid sequence (except AUG, which is ordinarily the
only codon for methionine) can be modified by standard
techniques to encode a functionally identical polypeptide.
Accordingly, each silent variation of a nucleic acid sequence
that encodes a polypeptide is implicit in any described
sequence. The invention provides each and every possible
variation of nucleic acid sequence encoding a polypeptide of
the invention that could be made by selecting combinations
based on possible codon choices. These combinations are
made in accordance with the standard triplet genetic code as
applied to the nucleic acid sequence encoding a triterpene
synthase homologue polypeptide of the invention. All such
variations of every nucleic acid sequence herein are specifi-
cally provided and described by consideration of the
sequence in combination with the genetic code. Any variant
can be produced as noted herein.

In general, the invention includes any polypeptide encoded
by a modified triterpene synthase polynucleotide derived by
mutation, recursive sequence recombination, and/or diversi-
fication of the polynucleotide sequences described herein.
In some aspects of the invention, a triterpene synthase polypep-
tide is modified by single or multiple amino acid substitu-
tions, a deletion, an insertion, or a combination of one or more
of these types of modifications. Substitutions can be conser-
vatve or non-conservative, can alter function or not, and can
add new function. Insertions and deletions can be substantial,
such as the case of a truncation of a substantial fragment of
the sequence, or in the fusion of additional sequence, either
internally or at N or C terminal.

An aspect of the invention pertains to isolated nucleic acid
molecules that encode modified triterpene synthase polypep-
tides or biologically active portions thereof. As used herein,
the term “nucleic acid molecule” is intended to include DNA
molecules (e.g., cDNA or genomic DNA) and RNA mole-
cules (e.g., mRNA) and analogs of the DNA or RNA gener-
ated using nucleotide analogs. The nucleic acid molecule
can be single-stranded or double-stranded, but preferably is
double-stranded DNA.

A nucleic acid molecule of the present invention, e.g., a
nucleic acid molecule that encodes a polypeptide set forth in
SEQ ID NO:1, or having the nucleotide sequence of set forth
in SEQ ID NO:1, or a portion thereof, can be isolated using
standard molecular biology techniques and the sequence
information provided herein.

A nucleic acid molecule of the invention can be amplified
using cDNA, mRNA or alternatively, genomic DNA, as a
template and appropriate oligonucleotide primers according
to standard PCR amplification techniques. The nucleic acid
molecule so amplified can be cloned into an appropriate vec-
tor and characterized by DNA sequence analysis. Further-
more, oligonucleotides corresponding to nucleotide
sequences can be prepared by standard synthetic techniques,
e.g., using an automated DNA synthesizer. In some embed-
ments, an isolated nucleic acid molecule of the invention
comprises a nucleic acid molecule which is a complement of
a nucleotide sequence encoding a polypeptide set forth in
SEQ ID NO:2, or complement of the nucleotide sequence set
forth in SEQ ID NO:1. In still another embodiment, an
isolated nucleic acid molecule of the invention comprises a
nucleotide sequence which is at least about 50%, 52%, 55%,
60%, 62%, 65%, 70%, 75%, 78%, 80%, 85%, 88%, 90%,
95%, 97%, 98% or more identical to the nucleotide sequence
encoding a polypeptide set forth in SEQ ID NO:2, or the
nucleotide sequence set forth in SEQ ID NO:1, or a portion
of any of these nucleotide sequences.

In addition to the nucleotide sequences encoding a
polypeptide set forth in SEQ ID NO:2, or the nucleotide
sequence set forth in SEQ ID NO:1, it will be appreciated by
those skilled in the art that DNA sequence polymorphisms
that lead to changes in the amino acid sequences of the pro-
teins may exist within a population. Such genetic polymor-
phisms may exist among individuals within a population due
to natural allelic variation. Such natural allelic variations include both functional and non-functional proteins and can typically result in 1-5% variance in the nucleotide sequence of a gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in genes are the result of natural allelic variation and that do not alter the functional activity of a protein are intended to be within the scope of the invention.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention hybridizes under stringent conditions to a nucleic acid molecule comprising the nucleotide sequence encoding a polypeptide set forth in SEQ ID NO:2, or the nucleotide sequence set forth in SEQ ID NO:1. In other embodiments, the nucleic acid molecule is at least 30, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, or 600 nucleotides in length. Nucleic acid molecules are “hybridized” to each other when at least one strand of one nucleic acid molecule can anneal to another nucleic acid molecule under defined stringency conditions. Stringency of hybridization is determined, e.g., by (a) the temperature at which hybridization and/or washing is performed, and (b) the ionic strength and polarity (e.g., formamide) of the hybridization and washing solutions, as well as other parameters. Hybridization requires that the two nucleic acid molecules contain substantially complementary sequences; depending on the stringency of hybridization, however, mismatches may be tolerated. Typically, hybridization of two sequences at high stringency (such as, for example, an aqueous solution of 0.5xSSC at 65°C) requires that the sequences exhibit some degree of complementarity over their entire sequence. Conditions of intermediate stringency (such as, for example, an aqueous solution of 2xSSC at 65°C) and low stringency (such as, for example, an aqueous solution of 2xSSC at 55°C), require correspondingly less overall complementarity between the hybridizing sequences (1xSSC is 0.15 M NaCl, 0.015 M Na citrate).

Nucleic acid molecules that hybridize include those which anneal under suitable stringency conditions and which encode polypeptides or enzymes having the same function, such as the ability to catalyze the reductive condensation of 2 farnesyl diphasphate (FPP) substrate molecules yielding botryococcene, a 30-carbon branched-chain hydrocarbon, of the invention. Further, the term “hybridizes under stringent conditions” is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 30%, 40%, 50%, or 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 70%, more preferably at least about 80%, even more preferably at least about 85% or 90% homologous to each other typically remain hybridized to each other. In some cases, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleic acid sequence encoding a polypeptide set forth in any of SEQ ID NO:2, or the nucleotide sequence set forth in SEQ ID NO:1, corresponds to a naturally-occurring nucleic acid molecule. As used herein, a “naturally-occurring” nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein). Preferably the nucleic acid molecule that hybridizes to at least 30%, 40%, 50%, 60%, 70%, 80%, 85% or 90% of the length of a nucleic acid molecule consisting of SEQ ID NO:1 under stringent conditions. More preferably the nucleic acid molecule that hybridizes to at least about 80%, even more preferably at least about 85% or 90% of the length of a nucleic acid molecule consisting of SEQ ID NO:1. Preferably the nucleic acid molecule that hybridizes encodes a polypeptide having triterpene synthase activity.

The skilled artisan will appreciate that changes can be introduced by mutation into the nucleotide sequences of any nucleic acid sequence encoding a polypeptide set forth in SEQ ID NO:2, or having the nucleotide sequence set forth in SEQ ID NO:1, thereby leading to changes in the amino acid sequence of the encoded proteins. In some cases the alteration will lead to altered function of the polypeptide. In other cases the change will not alter the functional ability of the encoded polypeptide. In general, substitutions that do not alter the function of a polypeptide include nucleotide substitutions leading to amino acid substitutions at “non-essential” amino acid residues. Generally these substitutions can be made in, for example, the sequence encoding a polypeptide set forth in SEQ ID NO:2, or having the nucleotide sequence set forth in SEQ ID NO:1, without altering the ability of the enzyme to catalyze the reductive condensation of FPP substrate. A “non-essential” amino acid residue is a residue that can be altered from the parent sequence without altering the biological activity of the resulting polypeptide, e.g., catalyzing the reductive condensation of 2 FPP to yield botryococcene.

Also contemplated are those situations where it is desirable to alter the activity of a parent polypeptide such that the polypeptide has new or increased activity on a particular substrate. It is understood that these amino acid substitutions will generally not constitute “conservative” substitutions. Instead, these substitutions constitute non-conservative substitutions introduced in to a sequence in order to obtain a new or improved activity.

It is also understood that an isolated nucleic acid molecule encoding a polypeptide homologous to the polypeptide of SEQ ID NO:2 can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence encoding the particular polypeptide, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into the nucleic acid sequence by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. In contrast to those positions where it may be desirable to make a non-conservative amino acid substitutions (see above), in some positions it is preferable to make conservative amino acid substitutions.


Additional details regarding various diversity generating methods can be found in the following U.S. patents, PCT publications, and EPO publications: U.S. Pat. No. 5,605,793 to Stemmer (Feb. 25, 1997); U.S. Pat. No. 5,811,238 to Stemmer et al. (Sep. 22, 1998); U.S. Pat. No. 5,830,721 to Stemmer et al. (Nov. 3, 1998); U.S. Pat. No. 5,834,252 to Stemmer et al. (Nov. 10, 1998); U.S. Pat. No. 5,837,485 to Minshull et al. (Nov. 17, 1998); WO 95/22625, Stemmer and Crameri; WO 96/33207 by Stemmer and Lipschat; WO 97/20078 by Stemmer and Crameri; WO 97/35966 by Minshull and Stemmer; WO 99/41402 by Pumonen et al.; WO 99/41383 by Pumonen et al.; WO 99/41368 by Pumonen et al.; EP 752008 by Stemmer and Crameri; EP 99/52670 by Stemmer; WO 99/23107 by Stemmer et al.; WO 99/21979 by Apt et al.; WO 98/31837 by del Cardayre et al.; WO 98/27230 by Patten and Stemmer; WO 98/26549 by Stemmer; WO 98/42832 by Arnold et al.; WO 99/29902 by Arnold et al.; WO 98/41653 by Vind; WO 98/41622 by Borchert et al.; WO 98/42727 by Patti and Zarling; WO 00/590 by Patten et al.; WO 00/49190 by del Cardayre et al.; WO 00/42561 by Crameri et al.; WO 00/42559 by Selifonov and Stemmer; WO 00/42560 by Selifonov et al.; WO 00/23401 by Welch et al.; and WO 01/64864 by Affholter (each of which is incorporated by reference). The QUICKCHANGE™ protocol marketed by Stratagene of San Diego, Calif. is one specific method known to those skilled in the art for introducing site-directed mutations. This method relies on the use of oligo or DNA primer pairs, harboring specific DNA sequence changes to be introduced, annealed to the target DNA or gene to be modified. Copies of modified DNA/gene are amplified by standard PCR methodology. Confirmation of alteration of the target DNA sequence is verifiable by automated DNA sequencing.

Also provided are recombinant constructs comprising one or more of the nucleic acid sequences as broadly described above. The constructs comprise a vector, such as, a plasmid, a cosmid, a phage, a virus, a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences including, for example, a promoter operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

Accordingly, in other embodiments, vectors that include a nucleic acid molecule of the invention are provided. In other embodiments, host cells transfected with a nucleic acid molecule of the invention, or a vector that includes a nucleic acid molecule of the invention, are provided. Host cells include eucaryotic cells such as yeast cells, e.g., yeast cells having a ERG1 knockout, e.g., the yeast strain T7 described in co-pending application Ser. No. 12/489,938 incorporated herein in its entirety, insect cells, animal cells, or plant cells (e.g., algae cells or terrestrial plant cells). Host cells also include prokaryotic cells such as bacterial cells.

The terms “vector,” “vector construct” and “expression vector” mean the vehicle by which a DNA or RNA sequence (e.g. a foreign gene) can be introduced into a host cell, so as to transform the host and promote expression (e.g. transcription and translation) of the introduced sequence. Vectors typically comprise the DNA of a transmissible agent, into which foreign DNA encoding a protein is inserted by restriction enzyme technology. A common type of vector is a “plasmid,” which generally is a self-contained molecule of double-stranded DNA that can readily accept additional (foreign) DNA and which can readily introduced into a suitable host cell. A large number of vectors, including plasmid and viral vectors, have been described for replication and/or expression in a variety of eukaryotic and prokaryotic hosts. Non-limiting examples include pKK plasmids (Clonetech), pUC plasmids, pET plasmids (Novagen, Inc., Madison, Wis.), PRSET or pREP plasmids (Invitrogen, San Diego, Calif.), pMAL plasmids (New England Biolabs, Beverly, Mass.), and Ti plasmid vectors, and many appropriate host cells, using methods disclosed or cited herein or otherwise known to those skilled in the relevant art. Vectors can also be selected such that expression of the introduced sequence is targeted to a chloroplast in a plant cell. Recombinant cloning vectors will often include one or more replication systems for cloning or expression, one or more markers for selection in the host, e.g., antibiotic resistance, and one or more expression cassettes.

The terms “express” and “expression” mean allowing or causing the information in a gene or DNA sequence to become manifest, for example producing a protein by activating the cellular functions involved in transcription and translation of a corresponding gene or DNA sequence. A DNA sequence is expressed in or by a cell to form an “expression product” such as a protein. The expression product itself, e.g. the resulting protein, may also be said to be “expressed” by the cell. A polynucleotide or polypeptide is expressed recombinantly, for example, when it is expressed or produced in a foreign host cell under the control of a foreign or native promoter, or in a native host cell under the control of a foreign promoter.

Polynucleotides provided herein can be incorporated into any one of a variety of expression vectors suitable for expressing a polypeptide. Suitable vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, pseudorabies, adenovirus, adeno-associated viruses, retroviruses; Ti plasmids for the incorporation and expression of DNA in plant cells, and many others. Any vector that transduces genetic material into a cell, and if replication is desired, which is replicable and viable in the relevant host can be used.
Vectors can be employed to transform an appropriate host  

permitted the host to express an inventive protein or polypeptide. Examples of appropriate expression hosts include: bacterial cells, such as E. coli, B. subtilis, Streptomyces, and Salmonella typhimurium; fungal cells, such as Saccharomyces cerevisiae, Pichia pastoris, and Neurospora crassa; insect cells such as Drosophila and Spodoptera frugiperda; mammalian cells such as CHO, COS, BHK, HEK 293 br Bowes melanoma; plant cells e.g., Nicotiana tabacum, a dicot plant species, or corn, a monocot plant species; algal cells e.g., Chlamydomonas reinhardtii; or explants of any plant tissues, e.g., leaf, stem or root segments, etc.

In bacterial systems, a number of expression vectors may be selected depending upon the use intended for the triterpene synthase polypeptide. For example, when large quantities of triterpene synthase polypeptide or fragments thereof are needed, expression vectors for induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified can be desirable. Such vectors include, but are not limited to, multifunctional E. coli cloning and expression vectors such as BLUESCRIPT™ (Stratagene), in which the triterpene synthase polypeptide coding sequence may be ligated into the vector in-frame with sequences for the amino-terminal Met and the subsequent 7 residues of 6-galactosidase so that a hybrid protein is produced; pIN vectors (Van Hecke & Schuster [1989] J. Biol. Chem. 264: 5503-5509); pET vectors (Novagen, Madison Wis.); and the like.

Similarly, in the yeast Saccharomyces cerevisiae a number of vectors containing constitutive or inducible promoters isolated from, e.g., an alpha factor, an alcohol dehydrogenase or a PGK gene may be used for production of the triterpene synthase polypeptides of the invention. For reviews, see Ausubel (supra) and Grant et al. (1987) Methods in Enzymology 153:516-544 (incorporated herein by reference).


Also provided are engineered host cells that are transduced (transformed or transfected) with a vector provided herein (e.g., a cloning vector or an expression vector), as well as the production of polypeptides of the invention by recombinant techniques. The vector may be, for example, a plasmid, a viral particle, a pluge, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the triterpene synthase gene. Culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, e.g., Sambrook, Ausubel and Berger, as well as e.g., Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique, 3rd ed. (Wiley-Liss, New York) and the references cited therein.

In other embodiments, methods for producing a cell that catalyzes a unique chemical condensation of 2 FPP molecules creating a branched, triterpene hydrocarbon, botryococcene, are provided. Such methods generally include: (a) transforming a host cell with an isolated nucleic acid molecule encoding a triterpene synthase polypeptide, e.g., a nucleic acid molecule encoding a polypeptide comprising SEQ ID NO: 2, 5 a variant, preferably a conservative variant, of SEQ ID NO: 2, or a fragment of SEQ ID NO: 2 having triterpene synthase activity and (b) culturing the transformed cell to produce the botryococcene. For example a transformed yeast cell of this invention may be cultured by large scale fermentation, providing the added advantage of producing large amounts of triterpenes, particularly botryococcene.

In other embodiments, methods for selecting a cell that converts 2 FPP to botryococcene are provided. The methods generally include: (a) providing a host cell containing a nucleic acid construct that includes a nucleotide sequence that encodes a triterpene synthase polypeptide. The methods further include (b) culturing the cell in the presence of a suitable 2 FPP and under conditions where the triterpene synthase is expressed at an effective level; and (c) detecting the production of botryococcene.

In other embodiments, methods for producing botryococcene are provided. In one aspect, the methods for producing a botryococcene comprise culturing a host cell transfected with a nucleic acid molecule that encodes a triterpene synthase, preferably a triterpene synthase of this invention under conditions sufficient for production of a botryococcene. Optionally, the botryococcene produced by the host cells are isolated. The host cell may be, for example, a cell in culture, e.g., the yeast strain TN7 transfected with a vector of this invention, or it may be a cell which is part of an organism such as a transfected cell in a terrestrial plant. In addition to transfection with triterpene synthase-encoding nucleic acid molecule, such plant cells may also be cotransfected with nucleic acid molecules encoding for one or more other enzymes in the triterpene synthesis pathway, such as the genes for farnesyl diphosphate synthase or a triterpene synthase such as squelene synthase or triterpene methyltransferase. Plant cells for transfection include, for example algal cells such as Botryococcus spp. cells (e.g., Botryococcus braunii), Chlamydomonas spp. cells or terrestrial plant cells, such as a tobacco plant cell. Transfection of plant cells with exogenous genes may be directed to the cytosolic compartment, the chloroplast or both. In other embodiments, cells other than plant cells may be transformed with triterpene synthase-encoding nucleic acid molecules, and optionally with nucleic acid molecules encoding one or more other enzymes involved in triterpene synthesis. These cells include, for example, prokaryotic cells such as bacteria and eukaryotic cells, such as fungi or animal cells. In particular the cells may be a natural or recombinant yeast cells, e.g., yeast cells that accumulate FPP but do not metabolize squalene, e.g., yeast cells with a mutant or deleted or disrupted EGR1 gene such that it produces reduced or no squalene epoxidase, e.g., a yeast strain such as TN7. In any of the aforementioned embodiments, the cells may also be genetically altered to enhance the production of farnesyl diphosphate and thereby provide a larger precursor pool for triterpene synthesis, such as through gene knockout, so as to eliminate or reduce diversion of farnesyl diphosphate for use in synthesis of metabolites other than triterpenes, such as sesquiterpenes, sterols, or polyphenols, or to eliminate or reduce the action of phosphatase(s) on farnesyl diphosphate.
The production of triterpenes may also be enhanced by diverting other metabolic intermediates such as, e.g., isopentenyl diphosphate or dimethylallyl diphosphate (DMAPP) to the production of FPP, thereby providing enhanced carbon flux to a key intermediate for the biosynthesis of triterpenes.

Also an aspect of this invention is a method for producing triterpenes comprising transfecting a yeast strain having high intracellular concentrations of FPP and reduced levels of squalene epoxidase with a nucleic acid molecule encoding a triterpene synthase and culturing the transfected cells under conditions suitable for the production of triterpenes. The triterpene synthase may be, e.g., a botryococcene synthase or a squalene synthase. The botryococcene synthase may be, e.g., a botryococcene synthase of this invention, e.g., a botryococcene synthase comprising the amino acid sequence of SEQ ID NO:2 or a conservative variant thereof, or a fragment thereof having botryococcene synthase activity. The high intracellular concentrations of FPP may be, e.g., at least 10 mg/L, at least 20 mg/L, at least 30 mg/L, at least 40 mg/L, at least 50 mg/L, at least 60 mg/L, at least 70 mg/L, or at least 80 mg/L.

The reduced squalene epoxidase may be, e.g., less than the levels of squalene epoxidase found in the yeast strain CALI-7 (Ikkahashi et al., 2007) “Metabolic Engineering of Sesquiterpene Metabolism in Yeast” Biotech. Bioeng. 170-181). The reduced squalene epoxidase levels may also be undetectable levels, such as the levels in the yeast strain TN7.

In another aspect, cells transfected with a nucleic acid molecule encoding a triterpene synthase are cultured under conditions suitable for the expression of the triterpene synthase polypeptide and an extract rich in triterpene synthase is then prepared. This extract may be, for example, a cell paste or tissue homogenate, or it may be, for example, a purified or partially purified preparation of triterpene synthase. FPP, e.g., radiolabelled FPP, plus or minus reducing equivalents (NADPH) and algal lysates is then exposed to the extract rich in triterpene synthase under conditions which allow for propagation of botryococcene. The recombinant condensation may be via a batch process or a continuous process. Optionally the botryococcene may then be isolated.


These and other embodiments of the present invention will readily occur to those of ordinary skill in the art in view of the disclosure herein, and are specifically contemplated.

The invention is further understood by reference to the examples set forth herein, which are intended to be purely exemplary of the invention. The present invention is not limited in scope by the exemplified embodiments, which are intended as illustrations of single aspects of the invention only. Any methods that are functionally equivalent are within the scope of the invention. Various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description. Such modifications fall within the scope of the appended claims.

EXAMPLES

Example 1

Isolation of the Botryococcus braunii Botryococcene Synthase Gene

A cDNA library was constructed from mRNA isolated from cells in rapid growth phase, corresponding to 9 days after subculturing, converted to double stranded cDNAs, and the cDNAs inserted into the lambda ZAP™ vector (Stratagene, La Jolla, Calif.) as previously described by Okada et al. (2000) “Molecular characterization of squalene synthase from the green microalga Botryococcus braunii, race B”. Archives Of Biochemistry and Biophysics 307-317. Plaque lifts of the cDNA library were prepared and hybridized with an 32PdCTP-radiolabeled full-length squalene synthase cDNA probe (referred to as SS1386 because it is 1386 bp long) using the Prime-It™ kit (Stratagene) at 30°C. In hybridization buffer consisting of 5x SSPE, 2x Denhardt’s solution, 0.2% SDS, 100 g/ml salmon sperm DNA and 40% formamide, also according to Okada et al. (2000). The plaque lifts were then washed three times at room temperature for 5 min with 2xSSC, 0.1% SDS and hybridization detected by autoradiography. After 2 rounds of plaque purification, isolated plaques were converted to their plasmid forms following the procedures recommended by the manufacturer (Stratagene), and restriction digests of the isolated plasmids compared. Those plasmids exhibiting restriction patterns similar to that for the squalene synthase were discarded and only those showing distinctive differences examined further by automated DNA sequencing (ABI 310 genetic analyzer, PE applied Biosystems, Foster City, Calif.).

DNA sequence of the entire botryococcene synthase (BBS) cDNA clone (FIG. 4) yielded a putative full-length cDNA clone coding for a 402 amino acid protein having a predicted molecular size of 45,692 daltons as shown in FIG.
5. Alignment of the predicted amino acid sequence from the BBS cDNA to other well described squalene synthase proteins from plants, animals and microbes demonstrated that there were several highly conserved domains shared between the predicted BBS protein and the various squalene synthases, but also there were several regions highly conserved amongst the various squalene synthases not found in the BBS protein (Fig. 6). Several of the domains conserved between BBS and the squalene synthases have been associated with early steps in the squalene synthase enzymatic reactions (domains I-IV), while domain V, associated with the conversion of PSPP to squalene, and a membrane-spanning domain (domain VI) are not conserved in the BBS protein.

Example 2

Functional Characterization of the Botryococcene Synthase Enzyme

The entire open reading frame, ORF, region of the BBS cDNA was amplified using standard RT-PCR conditions with a forward primer (5’ CCGGCTACTGCAAGAGGCCACCACG 3’ SEQ ID NO: 38), a reverse primer (5’ CCTCGATGACATGACCCGCTGC 3’ SEQ ID NO: 39) (designed according to the DNA sequence obtained from the initial BBS cDNA isolated from the cDNA library) and first strand cDNA as template. First strand cDNA was prepared from RNA isolated from rapidly growing cells via the Triazol method according to the manufacturer’s instructions (Invitrogen, Carlsbad, Calif.), and converted to single-strand DNA using oligo-dT primer and reverse transcriptase (Okada et al. 2000). The PCR amplification product was subsequently cloned in the pGEM-T Easy vector (Promega, Madison, Wis.) and the resulting recombinant plasmid subjected to automated DNA sequencing. The BBS cDNA was then PCR amplified from the pGEM vector using various primer combinations for the insertion of the BBS cDNA into bacterial expression vectors and into yeast expression vectors. To create bacterial expression vectors, a forward-primer (5’ TTGCGCCTATGACTGCAAGAGGCCACCACG 3’ SEQ ID NO: 40) harboring an Ascl restriction site reverse-(in bold) and primer (5’ GGCGCGCCGCCTAGCTTGGTGGGCTGCGCGC 3’ SEQ ID NO: 41) containing an XhoI restriction site (in bold) to PCR amplify the intact BBS cDNA from the pGEM vector and the amplified DNA ligated into the Ascl and XhoI sites of a modified pET28b vector (Novagen, Madison Wis.) This vector was modified to contain an Ascl restriction site 3’ to the transcriptional elements within the vector. In order to generate a BBS protein with a hexa-histidine (SEQ ID NO: 44) amino-terminal extension, the full-length BBS cDNA was released from the pET28b vector by digestion with BamHII and XhoI, and the isolated fragment ligated into the corresponding sites of the pET28a vector. The pET28a expression vector is designed to include a DNA sequence coding for a hexa-histidine (SEQ ID NO: 44) amino acid extension fused in-frame with the amino terminus of the BBS cDNA, creating a fusion protein that facilitates nickel affinity purification of the bacterial expressed BBS protein. The recombinant pET28a vector was transformed into E. coli strain BL21 (DE3) according to the manufacturer’s recommendations (Novagen) and the engineered bacteria were selected for growth in the presence of a suitable antibiotic selection marker.

E. coli harboring the recombinant plasmid were grown in liquid LB broth at 37°C with vigorous shaking until the cultures reached an optical density of ~0.8 (OD nm), then expression of the BBS cDNA was induced by addition of 0.1 mM isopropylthio-B-D-galactoside (IPTG) and the cultures allowed to incubate for an additional 5 to 20 hours with shaking at room temperature. One hundred ml of the culture were subsequently collected by centrifugation at 4,000 g for 10 min, resuspended in 10 ml of lysis buffer (50 mM Tris-HCl, 2 mM MgCl2, 5 mM β-mercaptoethanol, 1 mM EDTA, 5% (v/v) glycerol, pH 7.5), then sonicated 5 times for 20 seconds with a microprobe sonicator at 60% maximum power. The samples were cooled on ice for 2 min between sonication treatments. The sonicate was centrifuged at 16,000 g for 15 min at 4°C and used either for purification of the hexa-histidine tagged (SEQ ID NO: 44) BBS enzyme or 5-20 µl of the supernatant (corresponding to 10-100 µg of total soluble protein) used for the botryococcene synthase enzyme assays as described by Okada et al., (2004)Arch. Biochem. Biophys. 110-118.

Purification of the bacterial expressed BBS enzyme was afforded by the amino-terminal hexa-histidine tag (SEQ ID NO: 44) using standard nickel affinity chromatography. In brief, aliquots of the bacterial lysate were applied to activated nickel columns according the manufacturer’s recommendations (Novagen) and non-associating proteins eluted from the column using wash buffer. Selective elution of the hexa-histidine (SEQ ID NO: 44) BBS enzyme was observed at increasing concentrations of the counter ion, imidazole, with maximum recovery of protein at 250 mM imidazole and recovery of protein with the expected molecular size of 49,000 daltons (Fig. 7). Lysate prepared from bacteria over-expressing the BBS cDNA was prepared, applied to a nickel affinity column, and then proteins eluted with increasing concentrations of imidazole. Aliquots of the eluted fractions were examined by SDS-PAGE and stained with Coomassie Blue. Bradford dye analysis indicated that the protein content in the 250mM imidazole fraction was 0.2 mg/ml.

Typical BBS enzyme assays were initiated by mixing aliquots of 5 µl of E. coli lysate or purified BBS enzyme with 50 mM Tris, pH 7.0, 10 mM MgCl2 5 mM-mercaptoethanol4 M [3H]-FPP (1,800, dpm/pmol), plus as indicated 2 mM NADPH and 5 µl of lysate prepared from cells according to Okada et al. (2004) in 50 l total volume. Reactions were incubated at 37°C for 1 h, then extracted with 100 µl hexane. Forty µl of the hexane extract was then spotted onto silica TLC plates with authentic standards of botryococcene and squalene, developed with hexane, and the standards visualized with iodine vapors. The TLC zones corresponding to squalene and botryococcene were scrapped and analyzed by scintillation spectrometry (see assay illustration, Fig. 8). After incubating lysates or purified BBS enzyme prepared from E. coli over-expressing the BBS cDNA with radiolabeled FPP, plus and minus reducing equivalents (NADPH) and algal lysates, the reaction products were separated by TLC prior to determining the amount of radioactivity incorporated in squalene (control) and botryococcene.

Botryococcus lystate was prepared as described by Okada et al., (2004) and enzyme assays were performed with the components indicated in Fig. 9, then incubated at 37°C for 1 h, and reaction products were then extracted with hexane. Aliquots of the hexane extracts were separated by silica TLC and the radioactivity migrating to zones corresponding to authentic standards of botryococcene and squalene determined by scintillation spectrometry. As shown in Fig. 9, incubation of the purified BBS enzyme with FPP, plus or minus the inclusion of NADPH, resulted in little, if any, botryococcene being formed. Similar low levels of background activity were observed in control incubations without any BBS enzyme being added. Botryococcene biosynthesis was evident at a very low level in incubations of the lysate, as
was reported by Okada et al. (2004) earlier, but was dependent upon the addition of NADPH to the reaction mixture. However, a 5 to 10 fold stimulation of botryococcene biosynthesis was observed when the purified BBS enzyme was incubated with the lysate (Fig. 9). This botryococcene synthase activity was dependent upon the addition of NADPH, was equally supported by the addition of NADH, was time dependent with maximal activity observed after 1 hr incubation, and suggested that the BBS required an accessory or complementary factor found in the algal lysate for full enzyme activity.

Additional experiments demonstrated that the BBS enzyme was essential to the formation of botryococcene in these assays. Incubation of the purified BBS enzyme at 95°C for 5 min prior to the enzyme assays eliminated all apparent botryococcene biosynthesis. Prior treatment of the lysate with proteinase K, likewise abolished the botryococcene biosynthetic activity.

Altogether, the experimental data suggest that the BBS enzyme was not sufficient for botryococcene biosynthesis by itself and that an additional partner factor, perhaps an accessory protein (as suggested by the proteinase K sensitivity) as provided by the algal lysate, was necessary to observe the full complement of enzyme activity. Additional evidence for this suggestion was provided by over-expression of the BBS gene in yeast.

Example 3

Over Expression of the BBS Enzyme in Yeast

A yeast line, CAL1-7, generates high intracellular concentrations of FPP (Takahashi et al., 2007) “Biotech. Bioeng. 170-181). One further modification was introduced into this yeast line i.e., an insertional mutation in the ERG1 gene. The ERG1 gene of yeast encodes for the enzyme squalene epoxidase (Androsit et al., 1991) Gene 155-60), which converts squalene to an epoxide form. The insertional mutation of this gene was created by introducing the TRP1 gene flanked by DNA sequences of the 5' and 3' region of the ERG1 gene into the CAL1-7 cells and subsequent selection for tryptophan auxotrophic growth according to the method of Wang et al. (2004) Methods 199-205. This modified yeast line is capable of accumulating high levels of FPP (Song, 2003) Anal. Biochem. 180-185), but not metabolizing squalene was denoted as TN7.

The BBS gene was then inserted into a standard yeast expression vector pYEP352 harboring an ADH1 promoter (Takahashi et al., 2007). This was accomplished by PCR amplification of the BBS gene with oligo nucleotide primers (5'-CGGGAATTCACAAATGACTATGCACCAAGA CCACGAG SEQ ID No. 42, EcoR1 restriction site in bold, 5'-CCCAAGCTTTATACGAGGTCGCCGCGCGC SEQ ID No. 43, HindIII restriction site in bold) that introduced unique restriction enzyme sites at the 5' and 3' ends of the amplification product, digestion of the PCR amplification product with EcoR1 and HindIII restriction enzymes, followed by ligation of the isolated BBS DNA fragment into the pYEP352 vector digested with corresponding enzymes. The recombinant yeast expression vector was designated as pYEP-BBS and was introduced into the TN7 yeast line via lithium acetate transformation (Takahashi et al., 2007), followed by selection for uracil auxotrophic growth. A yeast line confirmed to possess the pYEP-BBS expression vector was identified by colony PCR and designated as TN7-BBS.

Individual colonies of TN7 and TN7-BBS were subsequently grown in 25 ml of YPDE media for 8 days at room temperature before analyzing the cultures for production of novel triterpene components (Fig. 10). In brief, 1 ml aliquots of the culture were combined with 1 ml of acetone, vigorously mixed, and incubated at room temperature for 3 min. One ml of hexane was added and mixed vigorously for 60 seconds. The mixture was then centrifuged briefly at 100 g to separate the phases, and the organic phase removed and concentrated to dryness under a nitrogen stream. The dried extract was resuspended in 50 μl of hexane and a 1 μl aliquot injected into a Thermo-Finnigan GC-MS. Compounds were separated on a Restek Rtx-5 (30 m by 0.25 μm) column with an initial temperature of 200°C for 1 min, followed by an increase to 280°C at 4°C/min, then to 320°C with a 20°C/min ramp and a final 5 min hold at 320°C. Mass spectra were recorded in a DSO quadrupole with the ionization set at 70 eV.

Comparison of the compounds accumulating specifically in the TN7-BBS lines and not in the TN7 lines identified pre-squalene alcohol, the dephosphorylated product of PSPP, as the only unique compound correlated with expression of the BBS gene (Fig. 10). This is consistent with the observation that additional factors provided by the lysate are necessary for the BBS enzyme to convert FPP to PSPP and then onto the final product of botryococcene.

Example 4

Accumulation of Squalene in TN7 Yeast

Over-Expressing a B. Braunnii Squalene Synthase Gene

A yeast TN7 harboring the expression vector YEpD60 containing a squalene synthase gene was produced by transfecting TN7 with DNA sequence encoding the B. braunnii squalene synthase gene as described by Okada et al. (2002). Recombinant yeast, verified by colony PCR for the plasmid, were grown in defined media and aliquots of the cell culture collected at the indicated times. For squalene determination, equal volumes of acetone were added to the cell culture samples, vortexed, incubated 15 min, then exacted with 2 volumes of hexane. The collected hexane was passed over a silica column and flow-through analyzed by GC as described above. The accumulation of squalene in TN7 yeast is shown in FIGS. 11 and 12.

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US 7,985,568 B2

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Val Lys

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<222> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
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<210> SEQ ID NO 43
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<210> SEQ ID NO 44
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<222> OTHER INFORMATION: Description of Artificial Sequence: Synthetic 6xHis tag
<400> SEQUENCE: 44
His His His His His His

We claim:

1. An isolated polypeptide having triterpene synthase activity wherein the polypeptide comprises peptide domains I, II, III, IV, and V; and
   wherein:
   - domain I comprises the amino acid sequence of SEQ ID NO: 3;
   - domain II comprises the amino acid sequence of SEQ ID NO: 4;
   - domain III comprises the amino acid sequence of SEQ ID NO: 5;
   - domain IV comprises the amino acid sequence of SEQ ID NO: 6; and
   - domain V comprises the amino acid sequence of SEQ ID NO: 7.

2. The isolated polypeptide of claim 1, wherein:
   - (a) domain I is at least 95% identical to the amino acid sequence of SEQ ID NO: 3;
   - (b) domain II is at least 95% identical to the amino acid sequence of SEQ ID NO: 4;
   - (c) domain III is at least 95% identical to the amino acid sequence of SEQ ID NO: 5;
   - (d) domain IV is at least 95% identical to the amino acid sequence of SEQ ID NO: 6; and
   - (e) domain V is at least 95% identical to the amino acid sequence of SEQ ID NO: 7.

3. The isolated polypeptide of claim 1, which is a Botryococcus braunii triterpene synthase.

4. The isolated polypeptide of claim 1, which comprises the amino acid sequence of SEQ ID NO: 2.

5. The isolated polypeptide of claim 1, which comprises at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 2.

6. An isolated polypeptide that comprises the amino acid sequence of SEQ ID NO: 2, wherein said polypeptide has triterpene synthase activity.

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