US 20220204984A1

(19) United States

(12) Patent Application Publication (10) Pub. No.: US 2022/0204984 A1

Shanklin et al. (43) Pub. Date: Jun. 30, 2022

(54) METHODS AND COMPOSITIONS FOR MODIFYING PHENOTYPES OF PLANTS EXPRESSING FATTY ACID TRANSGENES AND REDUCED EXPRESSION OF BADC GENES

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(21) Appl. No.: **17/534,993**

(22) Filed: **Nov. 24, 2021**

Related U.S. Application Data

(60) Provisional application No. 63/131,755, filed on Dec. 29, 2020, provisional application No. 63/118,209, filed on Nov. 25, 2020.

Publication Classification

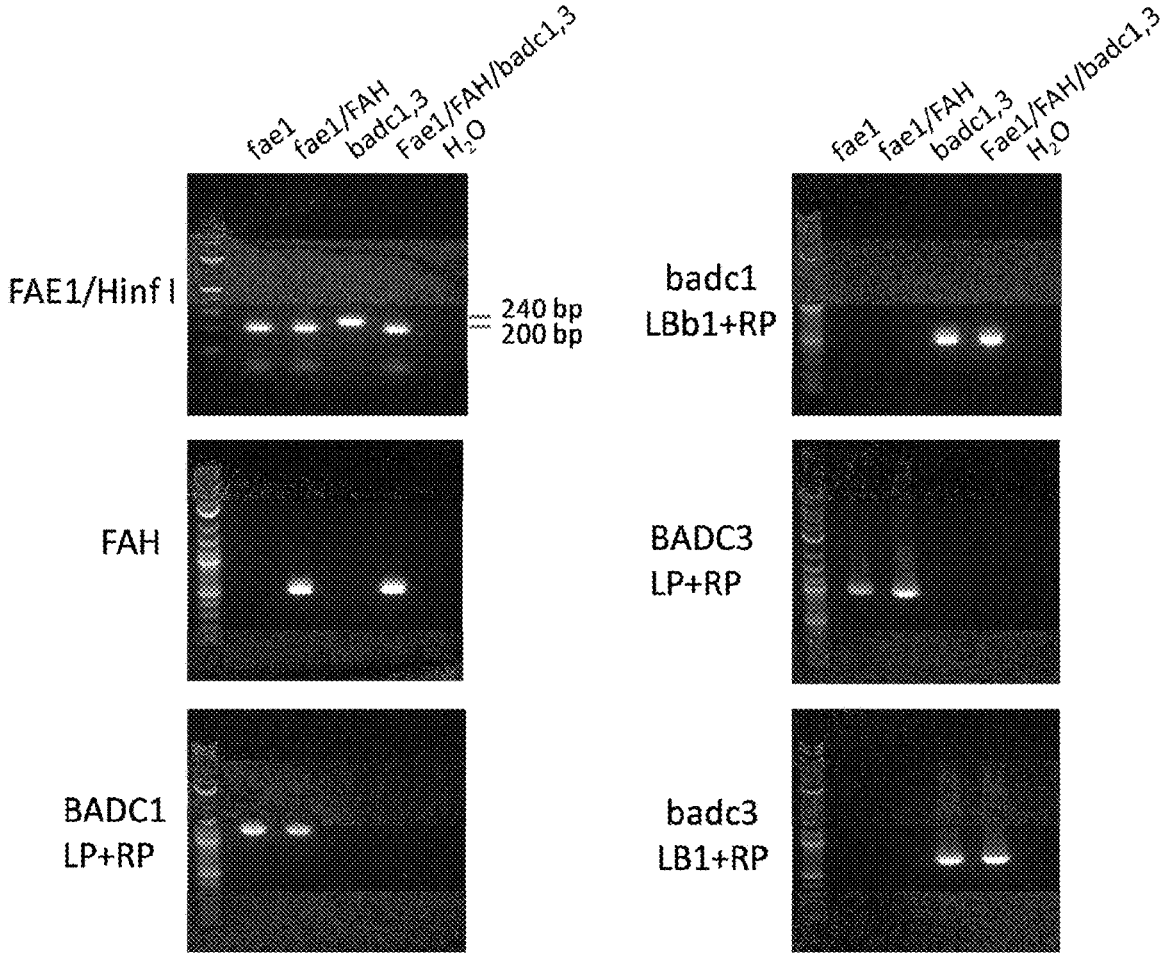
(51) **Int. Cl.**
C12N 15/82 (2006.01)

(52) **U.S. Cl.**
CPC *C12N 15/8247* (2013.01)

(57) **ABSTRACT**

Compositions that are plants, seeds or crops that have a combination of defective BADC genes and genes for making hydroxy fatty acids produced normal levels of oil containing specialty fatty acids, and exhibited an increases in total oil accumulation, increase in absolute hydroxy (specialized) fatty acid accumulation per seed and/or per plant and/or per unit land area. Defective BADC genes and genes for synthesizing hydroxy fatty acids are combined to produce specialized fatty acids without substantially slowing production of endogenous fatty acids. Methods are also described for increasing production of unusual fatty acids and increasing total fatty acid levels in plants by a mechanism involving combining defective BADC genes and genes for making hydroxy fatty acids to produce steady or increased levels of oil containing the increased specialty products as described herein.

Specification includes a Sequence Listing.



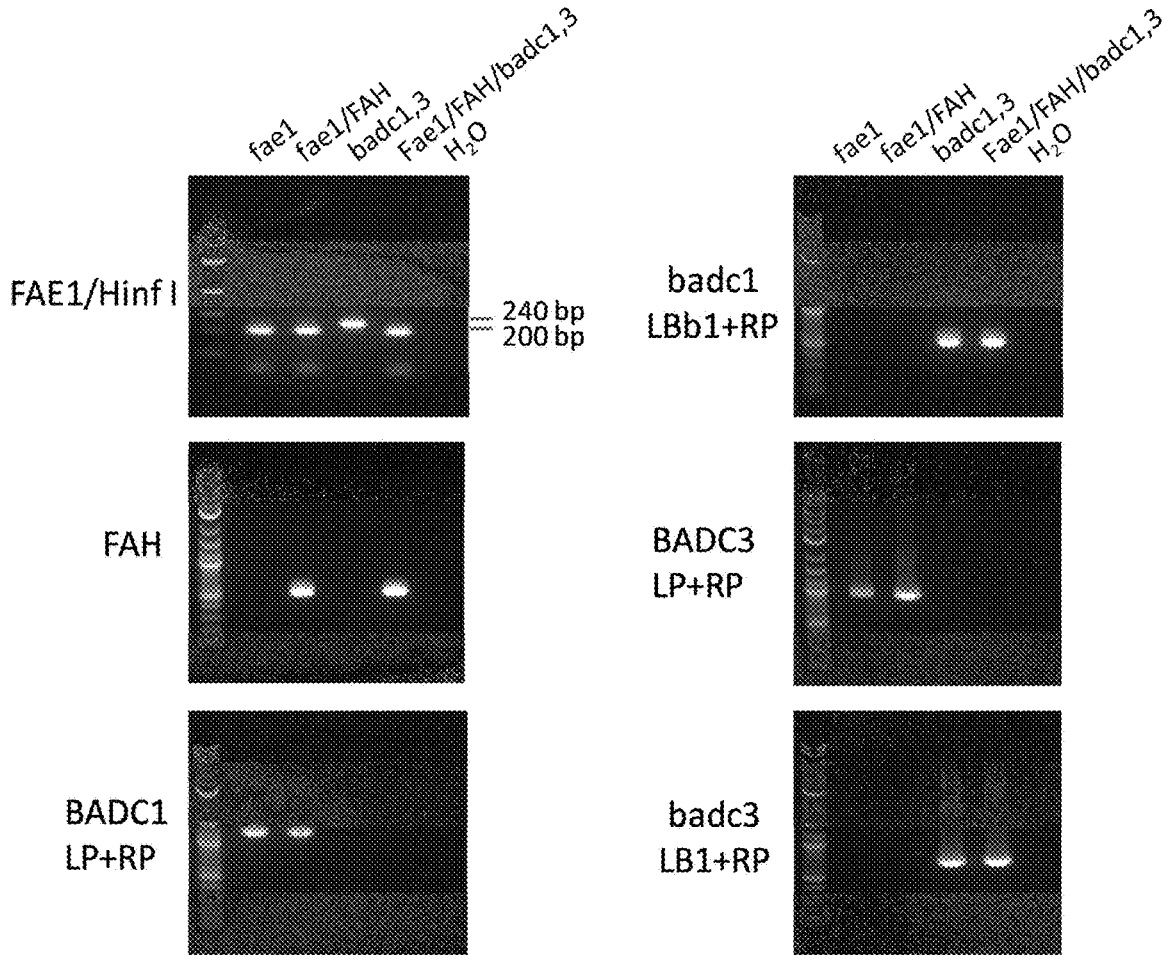

fae1
fae1/FAH
badc1,3
Fae1/FAH/badc1,3
H2O
FAE1/Hinf I
240 bp
200 bp
FAH
BADC1
LP+RP
badc1
LBb1+RP
BADC3
LP+RP
badc3
LB1+RP

Figure 1.

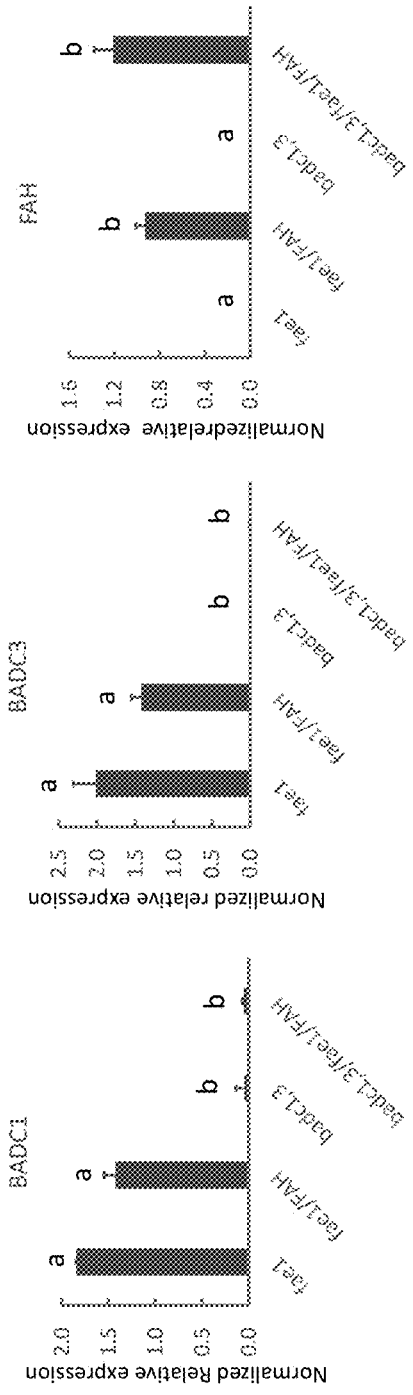
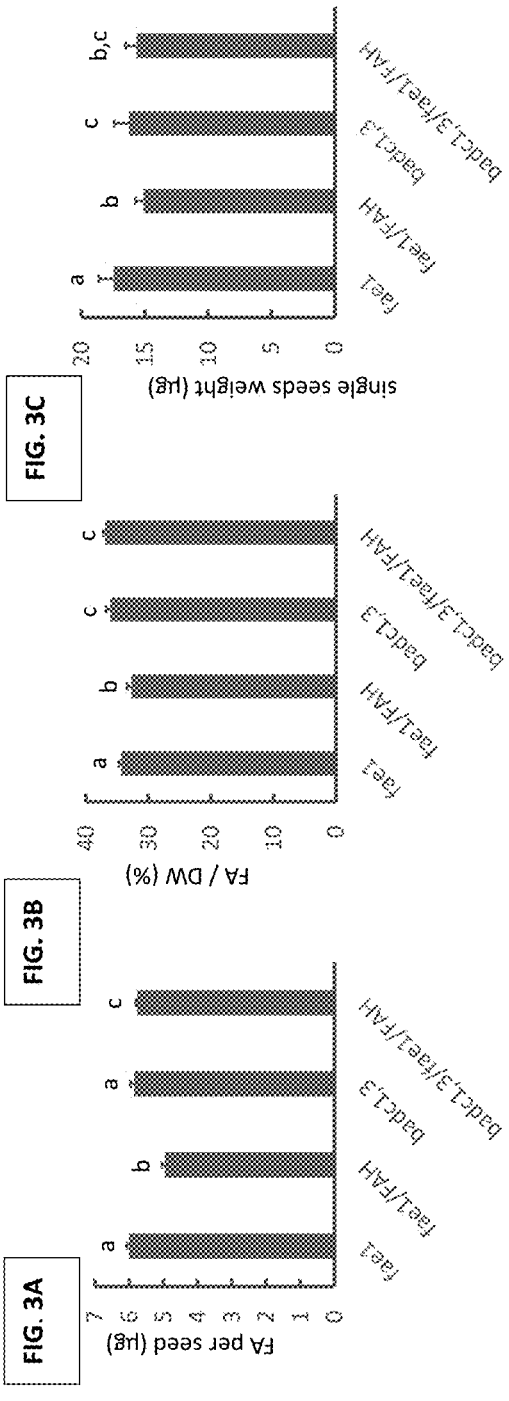

Normalized Relative expression
2.0
1.5
1.0
0.5
0.0
BADC1
a
a
b
b
faeI
faeI/FAH
badc1,3
badc1,3/faeI/FAH
Normalized relative expression
2.5
2.0
1.5
1.0
0.5
0.0
BADC3
a
a
b
b
faeI
faeI/FAH
badc1,3
badc1,3/faeI/FAH
Normalizedrelative expression
1.6
1.2
0.8
0.4
0.0
FAH
a
b
a
b
faeI
faeI/FAH
badc1,3
badc1,3/faeI/FAH

Figure 2.



Figures 3.A-3.C

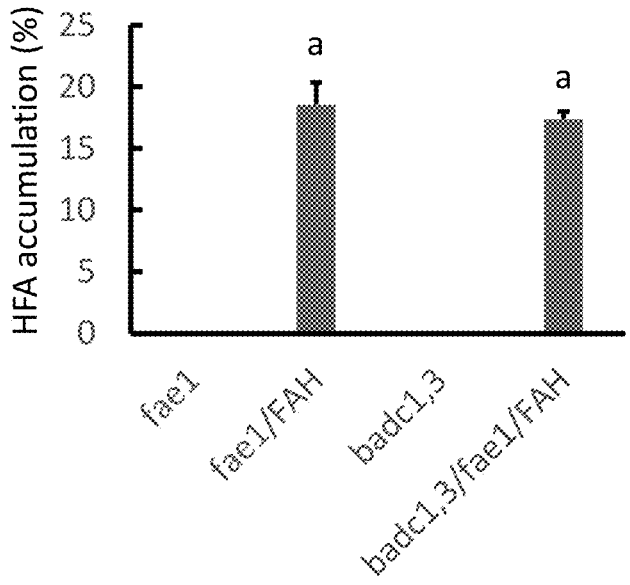

HFA accumulation (%)
25
20
15
10
5
0
a
a
fae1
fae1/FAH
badc1,3
badc1,3/fae1/FAH

Figure 4

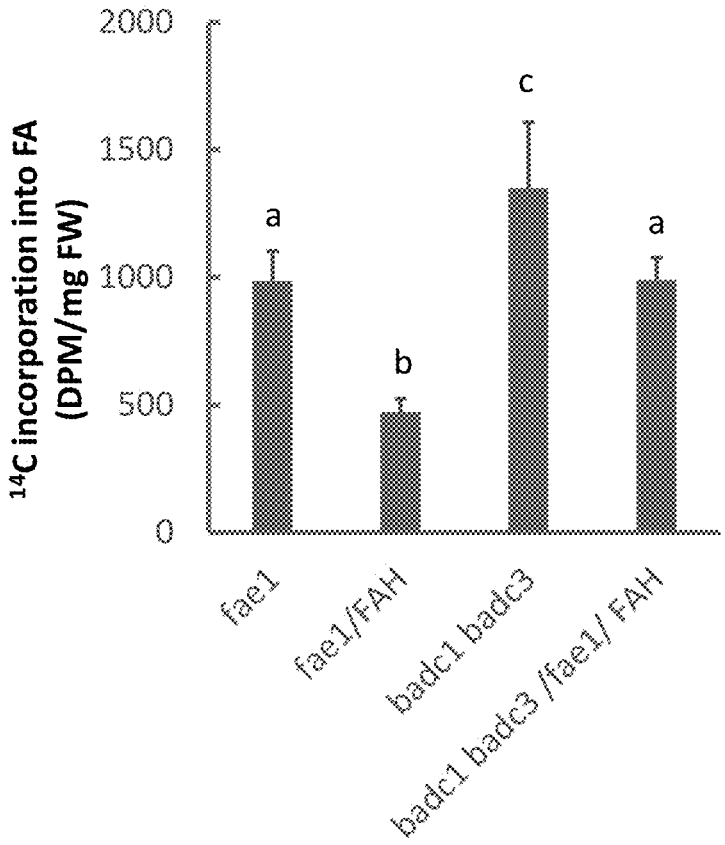
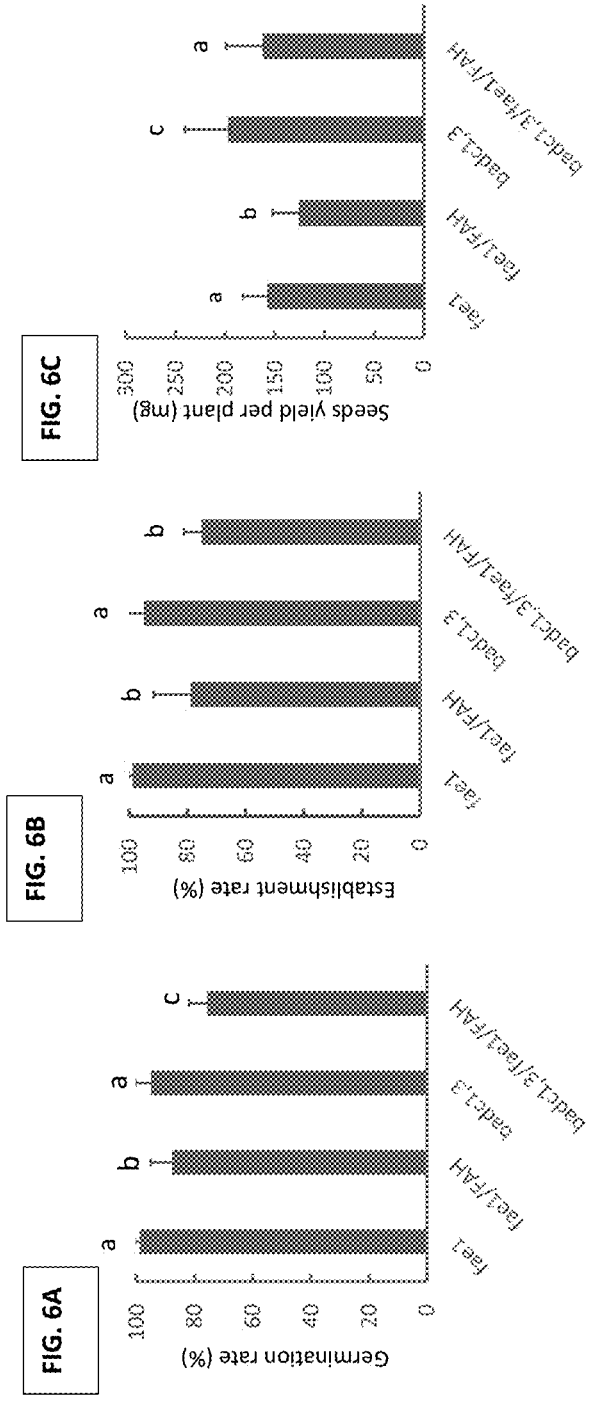

2000
1500
1000
500
0
^{14}C incorporation into FA (DPM/mg FW)
a
b
c
a
fae1
fae1/FAH
badc1 badc3
badc1 badc3 /fae1/ FAH

Figure 5



Figures 6.A-6.C

Figure 7. EMS mutation caused truncation of FAE1 in *fae1* mutant. FAE1 gene was amplified from fae1 mutant and its sequence showed a mutated codon (TGG1395TGA, highlighted in green). **SEQ ID NO: 3.**

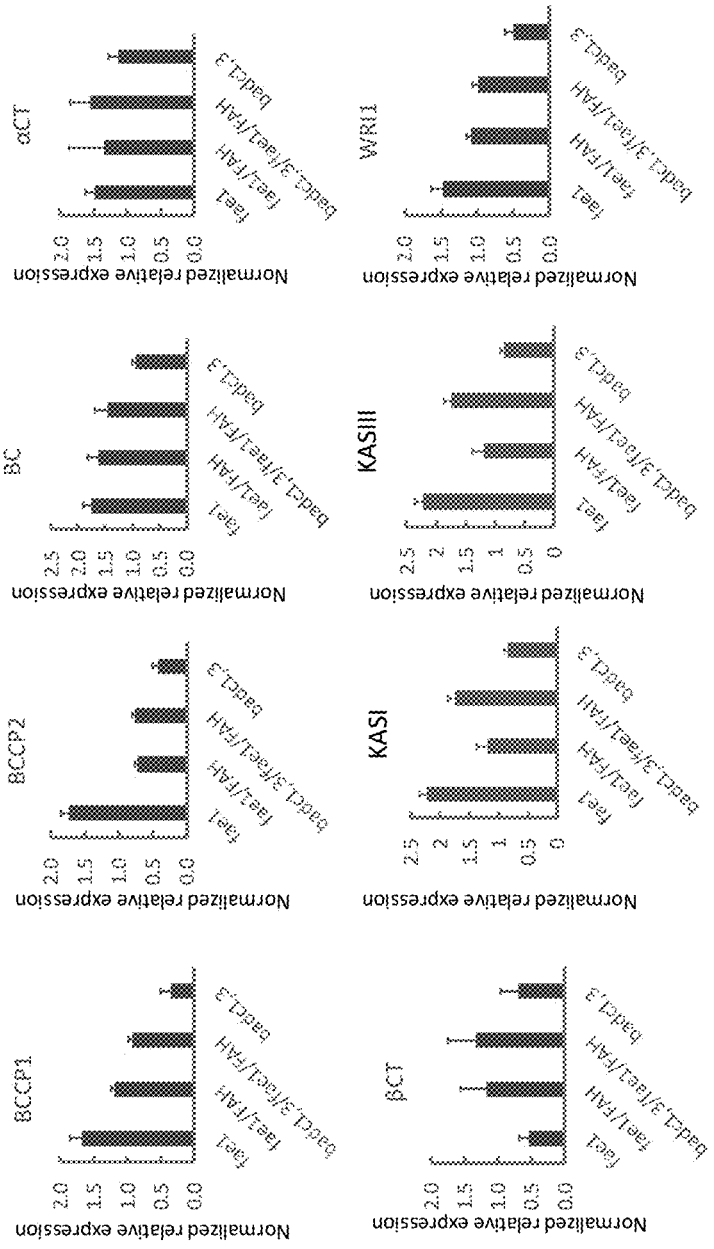

αCT
WRI1
BC
KASIII
BCCP2
KASI
BCCP1
βCT
Normalized relative expression
faeI
faeI/FAH
badc1,3/faeI/FAH
badc1,3

Figure 8

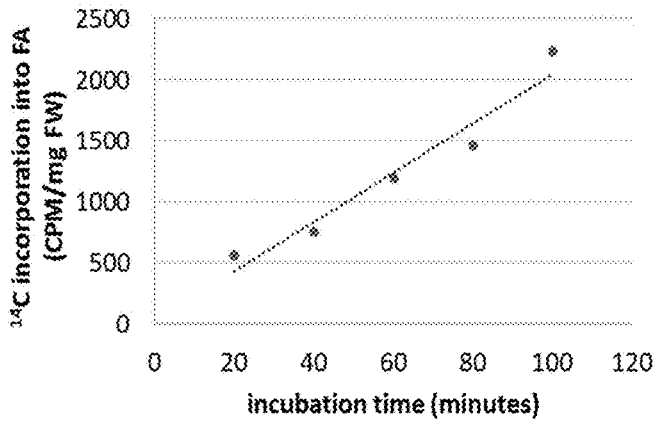


Figure 9

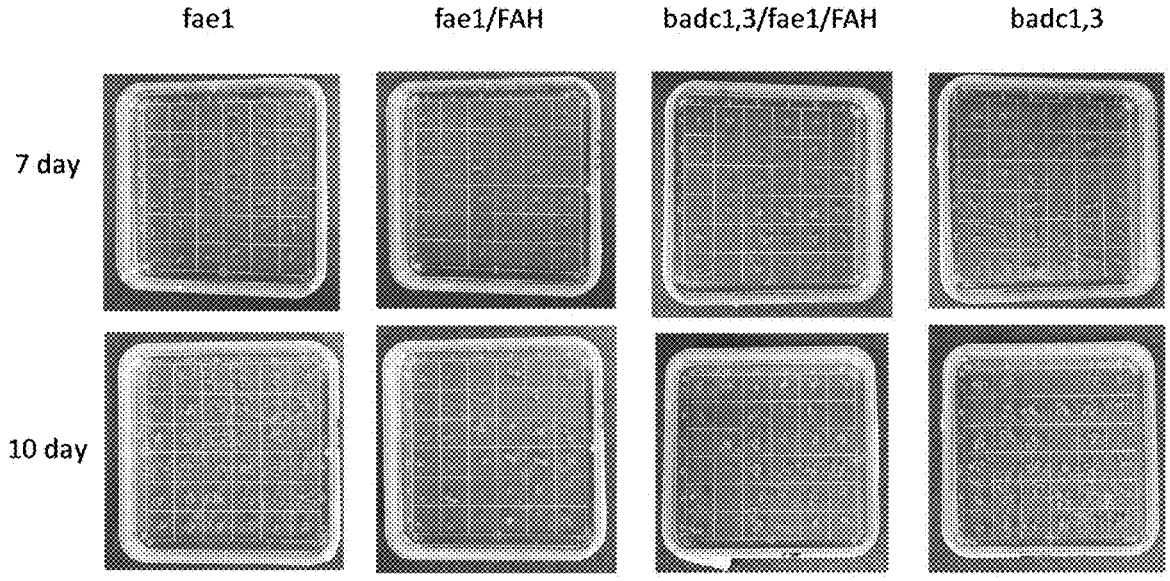


Figure 10

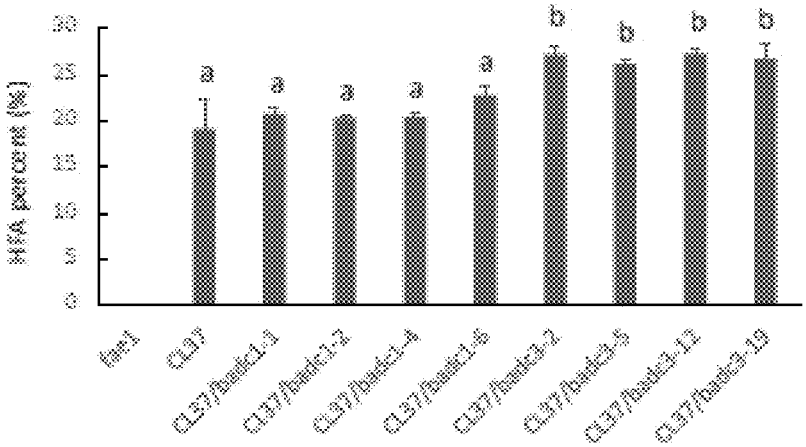


FIG. 11

FIG. 12A

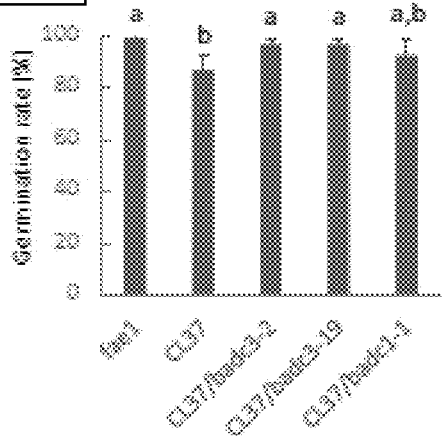


FIG. 12B

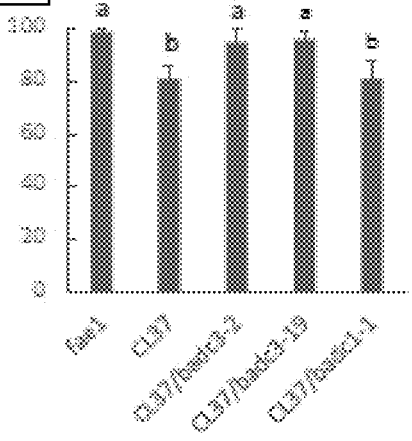


FIG. 12A - B

FIG. 13A

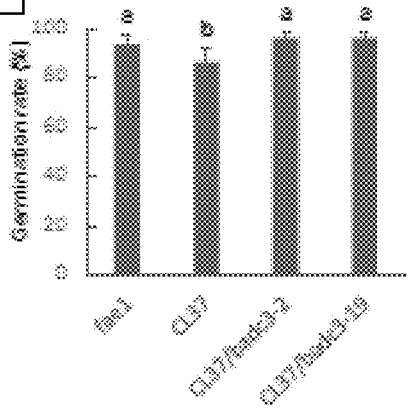


FIG. 13B

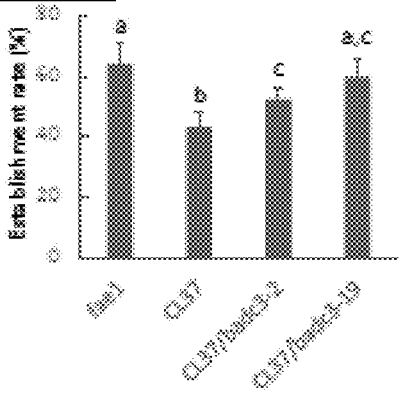


FIG. 13A - B

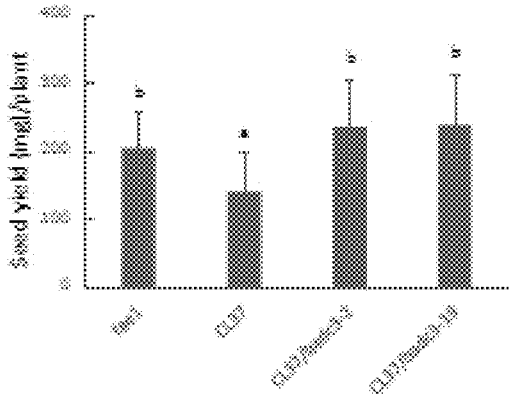


FIG. 14

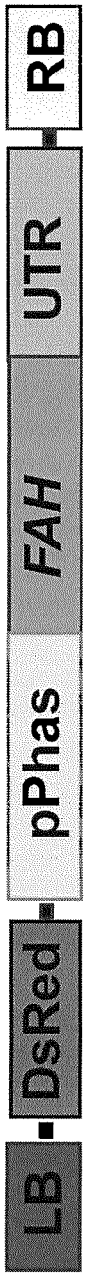


FIG. 15

FIG. 16 A: FAH exemplified by RcFAH nucleotide sequence: Gene ID # 8267837
>NM_001323721.1 FAH mRNA SEQ ID NO: 4

ATGGGAGGTGGTGGTCGCATGTCCACTGTCATAACCAGCAACAACAGTGAGAAGAAAGGAGGAAGCAGCC
ACCTTAAGCGAGCGCCGCACACGAAGCCTCCTTTCACACTTGGTGACCTCAAGAGAGCCATCCCACCCCA
TTGCTCTGAACGCTCTTTTGTGCGCTCATTCTCCTATGTTGCCTATGATGTCTGCTTAAGTTTTCTTTTC
TACTCGATCGCCACCAACTTCTTCCCTTACATCTCTTCTCCGCTCTCGTATGTCGCTTGGCTGGTTTACT
GGCTCTTCCAAGGCTGCATTCTCACTGGTCTTTGGGGTCATCGGCCATGAATGTGGCCATCATGCTTTTAG
TGAGTATCAGCTGGCTGATGACATTGTTGGCCTAATTGTCCATTCTGCACTTCTGGTTCCATATTTTTCA
TGGAAATATAGCCATCGCCGCCACCATTCTAACATAGGATCTCTCGAGCGAGACGAAGTGTTCGTCCCGA
AATCAAAGTCGAAAATTTCATGGTATTCTAAGTACTTAAACAACCCGCCAGGTCGAGTTTTGACACTTGC
TGCCACGCTCCTCCTTGGCTGGCCTTTATACTTAGCTTTCAATGTCTCTGGTAGACCTTACGATCGCTTT
GCTTGCCATTATGATCCCTATGGCCCAATATTTTCCGAAAGAGAAAGGCTTCAGATTTACATTGCTGACC
TCGGAATCTTTGCCACAACGTTTGCGCTTTATCAGGCTACAATGGCAAAAGGGTTGGCTTGGGTAATGCG
TATCTATGGGGTGCCATTGCTTATTGTTAACTGTTTCCTTGTTATGATCACATACTTGCAGCACACTCAC
CCAGCTATTCCACGCTATGGCTCATCGGAATGGGATTGGCTCCGGGGAGCAATGGTGACTGTCGATAGAG
ATTATGGGGTGTTGAATAAAGTATTCCATAACATTGCAGACACTCAGGTAGCTCATCATCTCTTTGCTAC
AGTGCCACATTACCATGCAATGGAGGCCACTAAAGCAATCAAGCCTATAATGGGTGAATATTACCGGTAT
GATGGTACCCCATTTTACAAGGCATTGTGGAGGGAGGCAAAGGAGTGCTTGTTCGTCGAGCCAGATGAAG
GAGCTCCTACACAAGGCGTTTTCTGGTACCGGAACAAGTATTAA
NCBI Reference Sequence: NP_001310650.1

FIG. 16 B: FAH amino acid sequence: NP_001310650.1 oleate hydroxylase FAH12 [Ricinus communis] SEQ ID NO: 7

MGGGGRMETVTSNNSEKKGGSSHLKRAPHTKPPFTLGDLKRAIPPHCFERSFVRSFSYVAYDVCLSFLF
YSLATMFPVISSPLSYVAWLVYWLFQGCILTGLWVIGHECGHHAFSEYQLADDIVGLIVHSALLVPYFS
WKYSHRRHHSNIGSLERDEVFVPKSKSKISWYSKYLNNPPGRVLTLAATLLLGWPLYLAFNVSGRPYDRF
ACHYDPYGPIFSERERLQIYIADLGIFATTFALYQATMAKGLAWVMRIYGVPLLIVNCFLVMITYLQHTH
PAIPRYGSSEWDWLRGAMVTVDRDYGVLNKVFHNIADTQVAHHLFATVPHYHAMEATKAIKPILGEYYRY
DGTPFYKALWREAKECLFVEPDEGAPTQGVFWYRNKY

FIG. 16 C: Camelina BADC1 SEQ ID NO: 8
First isoform nucleotide sequence: >Csa04g042500.1

ATGGCGTCTTCTGCAGCTCTCGGATCTCTTCATCAGACTTTAGGGTCACAGAGTGAGCTT
CATTTGCTTTCTGGAAACTGGTCTGCCTCTGGTACTTCTTGCGTTCCACGGTGGAGATTA
TCCAACAGGAGTAGCAATTACACGCTTGTGTTACGTGCAAAGGCCTCTAAAACTTCGACA
ACAACCAAAAGCGATGATTCATCTGATGCGACTGTGTCAAACGGGAAGAAATCTGTTCGA
CGGACAACCTTCCCGAAAGAAGTGGAGGCACTGGTTCACGAGATGTGTGATGAGACTGAG
GTTGCTGTCCTGAAACTTAAGGTTGGAGATTTCGAGATGAACCTAAAACGGAAGATTGGA
GCGGCCACAAACCCCATTCCTGTGGAGGATATATCTCCAACCGTAGCACCTCCGATTCCT
TCTGAGCCCATGGATAAATCTGTTTCTTCTGCTCCCAGCCCATCTAAAGCAAAACCGTCT
GAAAAAGTATCTCCATTTATGAATACATCATATGGGAAACCAGCGAAGTTGGTAGCTTTG
GAGGCATCTGGATCAAACAATTATGTTCTAGTCAAATCTCCCTCAGTTGGCGAGTTTCAC

AGAAGCAGAACTGTAAAAGGAAAGAAACTATCTCCTAGCTGCAAAGAGGGTGATGAAATA

AAGGAAGGCCAAGTTATTGGATACTTACATCAGTTGGGAACAGAACTTCCAGTGACGTCG

GATGTAGCTGGGGAAGTCCTCAAGCTTCTTTCAGATGACGGAGACTCCGTAGGTTATGGT

GATCCTCTGGTTGCGGTCTTGCCATCGTTCCACGATATCAACATCCAGTGA

FIG. 16 D: Camelina BADC1 SEQ ID NO: 9
First isoform amino acid sequence >Csa04g042500.1

MASSAALGSLHQTLGSQSELHLLSGNWSASGTSCVPRWRLSNRSSNYTLV

LRAKASKTSTTTKSDDSSDATVSNGKKSVRRTTPPKEVEALVHEMCDETE

VAVLRLKVGDFEMNLKRKIGAATNPIPVEDISPTVAPPPSEPMDKSVSS

APSPSKAKPSEKVSPPMNTSYGKPAELVALEASGSNNYVLVKSPSVGEPH

RSRTVEGKKLSPSCKEGDEIKEGQVIGYLHQLGTELPVTSDVAGEVLKLL

SDDGDSVGYGDPLVAVLPSPHDINQ

FIG. 16 E: Camelina BADC1 SEQ ID NO: 10
Second isoform nucleotide sequence >Csa06g030800.1

ATGGCGTCTTCTGCAGCTCTCGGATCTCTTCATCAGACTTTAGGGTCACAGAGTGAGCTT

CACTTGCTTTCTGGAAATTGGTCTGCTTCTGGTACTTCTTGTGTACCACGGTGGAGATTA

TCCAACAGGAGCAGCAATTACACGCTTGTGTTACGTGCAAAGGCCTCTAAAACTTCGACA

ACAACCAAAAGCGATGATTCATCTGATGCGACTGTGTCAAACGGGAAGAAATCTGTTCGA

CGGACAACTTTCCCGAAAGAAGTGGAGGCACTGGTTCACGAGATGTGTGATGAGACTGAG

GTTGCTGTCCTGAAACTTAAGGCAAGTTACTCTGGCGTTGGAGATTTCGAGATGAACCTA

AAACGGAAGATTGAAGCGGCCACAAACCCCATTCCTGTGGAGGATATATCTCCAACCGTA

GCACCTCCGATTCCTTCTGAGCCCATGAATCAATCGGTTTCCTCTATTCCTAGCCCATCT

AAAGCAAAACCTTCTGAAAAAGTATCTCCATTTATAAATACATCATATGGGAAACCAGCA

AAGTTGGCAGCTTTGGAGGCATCTGGATCAAATAATTATGTTCTAGTCAAATCTCCCTCA

GTTGGCGAGTTTCACAGAAGCAGAACTGTAAAAGGAAAGAAACTATCTCCTAGCTGCAAA

GAGGGTGATGAAATAAAGGAAGGGCAAGTTATTGGATACTTACATCAGTTGGGAACAGAA

CTTCCAGTGACGTCGGATGTAGCTGGGGAAGTCCTCAAGCTTCTTTCAGATGACGGAGAC

TCCGTAGGTTATGGTGATCCTCTGGTTGCGGTCTTGCCATCGTTCCACGATATCAACATC

CAGTGA

FIG. 16 F: Camelina BADC1 SEQ ID NO: 11
Second isoform amino acid sequence >Csa06g030800.1

MASSAALGSLHQTLGSQSELHLLSGNWSASGTSCVPRWRLSNRSSNYTLV

LRAKASKTSTTTKSDDSSDATVSNGKKSVRRTTPPKEVEALVHEMCDETE

FIG. 16A - V

VAVLKLKASYSGVGDFEMNLKRKIEAATNPIPVEDISPTVAPPIPSEPMQN

QSVSSIPSPSKAKPSEKVSPFINTSVGKPAKLAALEASGSNNYVLVKSPS

VGEFHRSRTVKGKKLSPSCKEGDEIKEGQVIGYLHQLGTELPVTSDVAGE

VLKLLSDDGDSVGYGDPLVAVLPSFHDINIQ

FIG. 16 G: Camelina BADC1 SEQ ID NO: 12
Third isoform nucleotide sequence >Csa09g068300.1

ATGGCGTCTTCTGCAGCTCTCGGATCTCTTCATCATCCGATCTTTTTGTGGCAATTGGTT

GTTGTGGTGACTGAATTAGAGACTTTAGGGTCACAGAGTGAGCTTCACTTGCTTTCTGGA

AATTGGTCTGCTTCTGGTACTTCTTGTGTACCACGGTGGAGATTATCCAACAGGAGCAGC

AATTACACGCTTGTGTTACGTGCAAAGGCCTCTAAAACTTCGACAACAACCAAAAGCGAT

GATTCATCTGATGCAACTGTGTCAAACGGGAAGAAATCTGTTCGAAGGACAACTTTCCCC

AAAGAAGTGGAGACACTGGTTCACGAGATGTGTGATGAGACTGAGGTTGCTGTCCTGAAA

CTCAAGGCAAGATACTCTGGCGTTGGAGATTTCGAGATGAACCTAAAACGGAAGATTGGA

GCTACCACAAACCCCATTCCTGTGGAGGATATATCTCCAACCGTAGCACCTCCAATTCCT

TCTGAGCCCATGAATCAATCGGTTTCCTCTGCTCCCAGCCCATCTACAGCAAAACCGTCT

GAAAAAGTATCTCCATTTATGAATACATCATATGGGAAACCAGCAAAGTTGGCAGCTTTG

GAGGCATCTGGATCAAACAATTATGTTCTAGTCAAATCTCCCTCAGTTGGCGAGTTTCAC

AGAAGCAGAACTGTAAAAGGAAAGAAACTATCTCCTAGCTGCAAAGAGGGTGATGAAATA

AAGGAAGGCCAAGTGATTGGATACTTACATCAGTTGGGAACAGAACTTCCAGTGACGTCG

GATGTAGCTGGGGAAGTCCTCAAGCTTCTTTCAGATGACGGAGACTCCATAGG

TTATGGTGATCCTCTGGTTG

CGGTCTTGCCATCGTTCCACGATATCAACATCCAGTGA

FIG. 16 H: Camelina BADC1 SEQ ID NO: 13
Third isoform amino acid sequence >Csa09g068300.1

MASSAALGSLHHPIFLWQLVVVVIELETLGSQSELHLLSGNWSASGTSCV

PEWRLSNRSSNYTLVLRAKASKTSTTTKSDDSSDATVSNGKKSVRRTTPT

KEVETLVHEMCDETEVAVLKLKARYSGVGDFEMNLKRKIGATTNPIPVED

ISPTVAPPIPSEPMNQSVSSAPSPSTAKPSEKVSPFMNTSVGKPAKLAAL

EASGSNNYVLVKSPSVGEFHRSRTVKGKKLSPSCKEGDEIKEGQVIGYLH

QLGTELPVTSDVAGEVLKLLSDDGDSIGYGDPLVAVLPSFHDINIQ

FIG. 16 I: Camelina BADC3 SEQ ID NO: 14

First isoform nucleotide sequence >Csa15g020290.1

ATGGCTTCCTGTAGCCTAGGAGTTCCTAAAATTAAAATCTCAGCAGTAGACCTTAGTAGA
GTAAGTTCTGGAAGCTTACTGATACCATTCAGCCAAAGATCATTGCTTGGACAAAGGCCG
GTGAAGTACTTGAGTCTCAGGACAACTTTTGGATCTGTGAAAGCTGTCCAAGTATCTACT
GTCCCAACCGCAGAAACATCAGCTACTATAGAAGTAGAAGATTCTGAAGAAACCAAGTCA
TCTCCATTGAACGCTCAGCTAGTTCCCAAGCCATCTGAGGTGGAAGCTCTTGTCACTGAA
ATATGCGATTCCTCATCAATTGCAGAGTTTGAATTGAAACTGGGGGGGTTTCCGCCTATAT
GTAGCAAGGGATCTAACTGACAAAAGTAGTCCGCAGCCTCATCCAGTTCCTGCTGTGGCT
GCTGCCAGTGAAACTACCAAGAGTCCTGATTCGAATGGATCAACTCCTTCTACTTCATTG
GCTATCACAAGACCAGCATCCTCAGCTGCTGATCACGCTTTGATGATTCTCCAATCTCCA
AAAGTAGGGTTCTTCAGGAGATCCAAAACTATAAAGGGTAAACGCATGCCTTCGTCATGT
AAAGAGAAAGACCAAGTGAAAGAAGGTCAAATTCTGTGCTACATTGAACAACTCGGTGGC
CAATTCCCAATAGAGTCTGATGTCAGCGGCGAGGTTGTCAAAATACTCCGAGAAGATGGA
GAGCCTGTAGGATACAATGATGCTCTCATCTCGATCCTTCCCTCTTTCCCTGGGATCAAG
AAGCTTCAGTAA

FIG. 16 J: Camelina BADC3 SEQ ID NO: 15

First isoform amino acid sequence >Csa15g020290.1

MASCSLGVPXIKISAVDLSRVSSGSLLPFSQRSLLGQRPVKVLSLRTTF
GEVKAVQVSTVPTARTSATIEVEDSEETKSSPLNAQLVPEPSEVEALVTE
KCDSSSIAEFELKLGGFRLYVARDLTDESSFQPHPVPAVAAASETTKSPD
SNGSTPSTSLAITRPASSAADHGLMILQSPKVGFFRRSKTIKGKRSMPSSC
KEKDQVKEGQILCYIRQLGGQFPIESDVSGEVVKILREDGEPVGYNDALI
SILPSFPGIKKLQ

FIG. 16 K: Camelina BADC3 SEQ ID NO: 16

Second isoform nucleotide sequence >Csa19g022480.1

ATGGCATCCTGTAGCCTAGGAGTTCCTAAAATTAAAATCTCAGCAGTAGACCTTAGTAGA
GTAAGTTCTGGAAGCTTACTGATACCATTCAGTCAAAGATCATTGCTTGGACAAAGGCCG
GTGAAGTACTTGAGTCTGAGGACAACTTTTGGATCTGTGAAAGCTGTACAAGTATCTACT
GTCCCAGCTGCAGAAACATCAGCTACTGTAGGAGTAGAAGATTCTGAAGAAACCAAGTCA

FIG. 16A - V

TCCCCATTGAACGCTCAGCTAGTTCCCAAGCGATCTGAGGTGGAAGCTCTTGTCACTGAA
ATATGCGACTCCTCATCAATTGCAGAGTTTGAACTGAAACTGGGGGGTTTCCGCCTATAT
GTAGCAAGGGATCTAGCTGACAAAAGTAGTCCGCAGCCTCATCCAATTCCTGCTGTGGCT
GCTGCAAGTGAAACTACCAAGAGTCCTGATTCGAATGGATCAACACCTTCTACTTCATTG
GCTATCACAAGACCAGCATCTTCAGCTGCTGATCAGGGTTTGATGATTCTCCAATCTCCA
AAAGTAGGGTTCTTTAGGAGATCCAAAACCATAAAGGGTAAACGCATGCCTTCGTCATGT
AAAGAGAAAGACCAAGTGAAAGAAGGTCAAATTCTGTGCTACATTGAACAACTCGGTGGC
CAATTCCCAATAGAGTCTGATGTCAGCGGTGAGGTTGTCAAAATACTCCGCGAAGATGGA
GAACCTGTAGGATACAATGATGCTCTCATCTCGATCCTTCCCTCTTTCCCTGGGATCAAG
AAGCTTCAGTAA

FIG. 16 L: Camelina BADC3 SEQ ID NO: 17

Second isoform amino acid sequence >Csa19g022480.1

MASCSLGVPKIKISAVDLSRVSSGSLLPFSQRSLLGQRFVKYLSLRTTP
GSVKAVQVSTVPAAETSATVGVEDSEETKSSPLNAQLVPKRSEVEALVTE
ICDGSSIAEPELKLGGFBLYVARDLADKSSPQPHPPAVAAASETTKSPD
SNGSTPSTSLAITPASSAADQGLMSLQSPKVGFFRRSKTIKGKRMPSSC
KEKDQVKEGQILCYEQLGGQFMESDVSGEVVKILREDGEPVGYNDALI
SILPSFPGIKKLQ

FIG. 16 M: Camelina BADC3 SEQ ID NO: 18

Third isoform nucleotide sequence >Csa01g018320.1

TGCTTCGCTGTACAAAGACCACTCTGGTTGTATCGAACAGAGCGAACCCAACCAACGACG
AGCGTTAACCTCAATTTGATCATCTCCACACTCGTCAAATCTTTGGTGTCCTCCTCCTCC
TCGTTCGTATCGTTATCGTATCAGCTCACAAATCTCATTCTCTTCCTTACATTCTTCTTC
TTCTGCTTCTCGAATCCTCCTTTGTCTCCCTCCATGGCTTCCTGTAGCCTAGGAGTTCCT
AAAATTAAAATCTCAGCAGTAGACCTTAGTAGAGTAAGTTCTGGAAGCTTGCTGGTACCA
TTCAGTCAAAGATCATTGCTTGGACAAAGGACGGTGAAGTACTTGAGTCTGAGGAAAACT
TTTGGATCTGTGAAAGCTGTACAACTATCTACTGTCCCAGCTGCAGAAACATCAGCTACT
GTAGGAGTAGAAGATTCTGAAGAAACCAAGTCATCTCCATTGAACGCTCAGCTAGTTCCC
AATCCATCTGAGGTGGAAGCTCTTGTCACTGAAATATGCGACTCCTCATCAATTGCAGAG
TTTGAACTGAAACTGGGGGGTTTCCGCCTATATGTAGCAAGGGATCTAGCTGACAAAAGT
AGTCCGCAGCCTCATCCAATTCCTGCTGTGGCTGCTGCAAGTGAAACTACCAAGAGTCCT

FIG. 16A - V

GATTCGAATGGATCAACACCTTCTACTTCATTGGCTATCACAAGACCAGCATCTTCAGCT

GCTGATCAGGGTTTGATGATTCTCCAATCTCCAAAAGTAGGGTTCTTTAGGAGATCCAAA

ACCATAAAGGGTAAACGCATGCCTTCGTCATGTAAAGAGAAAGACCAAGTGAAAGAAGGT

CAAATTCTGTGCTACATTGAACAACTCGGTGGCCAATTCCCAATAGAGTCTGATGTCAGC

GGCGAGGTTGTCAAAATACTCCGAGAAGATGGAGAGCCTGTAGGGTACAATGATGCTCTC

ATCTCGATCCTTCCCTCTTTCCCTGGGATCAAGAAGCTTCAGTAA

FIG. 16 N: Camelina BADC3 SEQ ID NO: 19

Third isoform amino acid sequence >Csa01g018320.1

MASCSLGVPKIKISAVDLSRVSSGSLLVPFSQRSLLGQRTVKVLSLRKTF

GSVKAVQLSTVPAARTSAIVGVEDSEETKSSPLNAQLVPNPSEVEALVTE

ICDSSSIAEFELKLGGFRLYVARDLADRSSPQPHPIAVAAASETTKSPD

SNGSTPSTSLAITRPAGSAADQQLMILQSPKVGFFRRSKTIKGKRMPSSC

KEKDQVKEGQILCYEQLGGQFPIESDVSGEVVKILREDGEPVGYNDALI

SILPSFPGIKELQ

FIG. 16 O: FAE1, AT4G34520, Coding sequence: SEQ ID NO: 20

ATGACGTCCGTTAACGTTAAGCTCCTTTACCGTTACGTCTTAACCAACTTTTTCAACCTCTGTTTGTTCCCGTTAACG
GCGTTCCTCGCCGGAAAAGCCTCTCGGCTTACCATAAACGATCTCCACAACTTCCTTTCCTATCTCCAACACAA
CCTTATAACAGTAACTTTACTCTTTGCTTTCACTGTTTTCGGTTTGGTTCTCTACATCGTAACCCGACCCAATCC
GGTTTATCTCGTTGACTACTCGTGTTACCTTCCACCACCGCATCTCAAAGTTAGTGTCTCTAAAGTCATGGATA
TTTTCTACCAAATAAGAAAAGCTGATACTTCTTCACGGAACGTGGCATGTGATGATCCGTCCTCGCTCGATTTC
CTGAGGAAGATTCAAGAGCGTTCAGGTCTAGGTGATGAGACGTACAGTCCTGAGGGACTCATTCACGTACCA
CCGCGGAAGACTTTTGCAGCGTCACGTGAAGAGACAGAGAAGGTTATCATCGGTGCGCTCGAAAATCTATTC
GAGAACACCAAAGTTAACCCTAGAGAGATTGGTATACTTGTGGTGAACTCAAGCATGTTTAATCCAACTCCTT
CGCTATCCGCTATGGTCGTTAATACTTTCAAGCTCCGAAGCAACATCAAAAGCTTTAATCTAGGAGGAATGGG
TTGTAGTGCTGGTGTTATTGCCATTGATTTGGCTAAAGACTTGTTGCATGTTCATAAAAACACTTATGCTCTTG
TGGTGAGCACTGAGAACATCACACAAGGCATTTATGCTGGAGAAAATAGATCAATGATGGTTAGCAATTGCTT
GTTTCGTGTTGGTGGGGCCGCGATTTTGCTCTCTAACAAGTCGGGAGACCGGAGACGGTCCAAGTACAAGCTA
GTTCACACGGTCCGAACGCATACTGGAGCTGATGACAAGTCTTTTCGATGTGTGCAACAAGAAGACGATGAG
AGCGGCAAAATCGGAGTTTGTCTGTCAAAGGACATAACCAATGTTGCGGGGACAACACTTACGAAAAATATA
GCAACATTGGGTCCGTTGATTCTTCCTTTAAGCGAAAAGTTCTTTTTTTCGCTACCTTCGTCGCCAAGAAACT
TCTAAAGGATAAAATCAAGCATTACTATGTTCCGGATTTCAAGCTTGCTGTTGACCATTTCTGTATTCATGCCG
GAGGCAGAGCCGTGATCGATGAGCTAGAGAAGAACTTAGGACTATCGCCGATCGATGTGGAGGCATCTAGAT
CAACGTTACATAGATTTGGGAATACTTCATCTAGCTCAATTTGGTATGAATTAGCATACATAGAGGCAAAGGG
AAGAATGAAGAAAGGGAATAAAGCTTGGCAGATTGCTTTAGGATCAGGGTTTAAGTGTAATAGTGCGGTTTG
GGTGGCTCTACGCAATGTCAAGGCATCGGCAAATAGTCCTTGGCAACATTGCATCGATAGATATCCGGTTAAA
ATTGATTCTGATTTGTCAAAGTCAAAGACTCATGTCCAAAACGGTCGGTCCTAA

FIG. 16 P: FAE1, AT4G34520, Protein Sequence SEQ ID NO: 21

MTSVNVKLLYRYVLTNFFNLCLPFLIAFLAGRAASRLTRDLHNPLSYLQHNLITVTLLFAFTVFGLVLYIVTRPNPVYLV
DYSCYLPPPHLKVSVSKVMDFYQRKADTSRNVACDDPSSLDFLRKIQERSGLGDETYSPEGLIHVPPRKTFAASR
EETEKVIFGALENLFENTKVNPREIGILVVNSSMFNPTPSLSAMVVNTFKLRSNIKSFNLGGMGCSAGVIAIDLAKDL

LHVHKNTYALVVSTENTTQGIYAGENRSMGVSNCLFRVGGAAILSNKSGDRRRSKVKLVHTVRTHTGADDKSFR
CVQQEDDESGKIGVCLSKDITNVAGTTLTKNIATLGPLILPLSEKFLFFATFVAKKLLKDKIKHYYVPDFKLAVDHF
CIHAGGRAVIDELEKNLGLSPIDVEASRSTLHRFGNTSSSSIWYELAYIEAKGRMKKGNRLAWQIALGSGFKCNSAV
WVALRNVKASANSPWQHCIDRYPVKIDSDLSRKSETHVQNGRS

FIG. 16 Q: Arabidopsis FAD2, AT3G12120.1, Coding sequence: SEQ ID NO: 22

ATGGGTGCAGGTGGAAGAATGCCGGTTCCTACTTCTTCCAAGAAATCGGAAACCGACACCACAAAGCGTGTGCCG
TGCGAGAAACCGCCTTTCTCGGTGGGAGATCTGAAGAAAGCAATCCCGCCGCATTGTTTCAAACGCTCAATCC
CTCGCTCTTTCTCCTACCTTATCAGTGACATCATTATAGCCTCATGCTTCTACTACGTCGCCACCAATTACTTCT
CTCTCCTCCCTCAGCCTCTCTCTTACTTGGCTTGGCCACTCTATTGGGCCTGTCAAGGCTGTGTCCTAACTGGTA
TCTGGGTCATAGCCCACGAATGCGGTCACCACGCATTCAGCGACTACCAATGGCTGGATGACACAGTTGGTCT
TATCTTCCATTCCTTCCTCCTCGTCCCTTACTTCTCCTGGAAGTATAGTCATCGCCGTCACCATTCCAACACTGG
ATCCCTCGAAAGAGATGAAGTATTTGTCCCAAAGCAGAAATCAGCAATCAAGTGGTACGGGAAATACCTCAA
CAACCCTCTTGGACGCATCATGATGTTAACCGTCCAGTTTGTCCTCGGGTGGCCCTTGTACTTAGCCTTTAACG
TCTCTGGCAGACCGTATGACGGGTTCGCTTGCCATTTCTTCCCCAACGCTCCCATCTACAATGACCGAGAACG
CCTCCAGATATACCTCTCTGATGCGGGTATTCTAGCCGTCTGTTTGGTCTTTACCGTTACGCTGCTGCACAAG
GGATGGCCTCGATGATCTGCCTCTACGGAGTACCGCTTCTGATAGTGAATGCGTTCCTCGTCTTGATCACTTAC
TTGCAGCACACTCATCCCTCGTTGCCTCACTACGATTCATCAGAGTGGGACTGGCTCAGGGGAGCTTTGGCTA
CCGTAGACAGAGACTACGGAATCTTGAACAAGGTGTTCCACAACATTACAGACACACACGTGGCTCATCACC
TGTTCTCGACAATGCCGCATTATAACGCAATGGAAGCTACAAAGGCGATAAAGCCAATTCTGGGAGACTATTA
CCAGTTCGATGGAACACCGTGGTATGTAGCGATGTATAGGGAGGCAAAGGAGTGTATCTATGTAGAACCGGA
CAGGGAAGGTGACAAGAAAGGTGTGTACTGGTACAACAATAAGTTATGA

FIG. 16 R: Arabidopsis FAD2, AT3G12120.1, Protein Sequence SEQ ID NO: 23

MGAGGRMVPTSKKSETDTTERVPCEKPPFSVGDLKKAIPPHCFKRSIPRSFSYLISDIIIASCFYYVATNYFSLLPQPLSY
LAWTLYWACQGCVLTGIWVLAHECGHHAFSDYQWLDDTVGLIFHSFLLVPYFSWKYSHRRHHSNTGSLERDEVF
VPKQKSAIKWYGKYLNNPLGRIMMLTVQFVLGWPLYLAFNVSGRPYDGFACHFFPNAPIYNDRERLQIYLSDAGIL
AVCFGLYRYAAAQGMASMICLYGVPLLIVNAFLVLITYLQHTHPSLPHYDSSEWDWLRGALATVDRDYGILNKVF
HNITDTHVAHHLFSTMPHYNAMEATKAIKPILGDYYQFDGTPWYVAMYREAKECIYVEPDRQGDKKGVYWYNN
KL

FIG. 16 S: Arabidopsis FAD3, AT2G29980.1, CDS SEQ ID NO: 24

ATGGTTGTTGCTATGGACCAACGCACCAATGTGAACGGAGATCCCGGCGCCGGAGACCGGAAGAAAGAAGAAAG
GTTTGATCCGAGTGCACAACCACCGTTCAAGATCGGAGATATAAGGGCGGCGATTCCTAAGCACTGTTGGGTT
AAGAGTCCTTTGAGATCAATGAGTTACGTCGTCAGAGACATTATCGCCGTCGCGGCTTTGGCCATCGCTGCCG
TGTATGTTGATAGCTGGTTCCTTTGGCCTCTTTATTGGGCCGCCCAAGGAACACTTTTCTGGGCCATCTTTGTTC
TCGGCCACGACTGTGGACATGGGAGTTTCTCAGACATTCCTCTACTGAATAGTGTGGTTGGTCACATTCTTCAT
TCTTTCATCCTCGTTCCTTACCATGGTTGGAGAATAAGCCACCGGACACACCACCAGAACCATGGCCATGTTG
AAAACGACGAGTCATGGGTTCCGTTACCAGAAAGGGTGTACAAGAAATTGCCCCACAGTACTCGGATGCTCA
GATACACTGTCCCTCTCCCCATGCTCGCATATCCTCTCTATTTGTGCTACAGAAGTCCTGGAAAAGAAGGATCA
CATTTTAACCCATACAGTAGTTTATTTGCTCCAAGCGAGAGAAAGCTTATTGCAACTTCAACTACTTGTTGGTC
CATAATGTTCGTCAGTCTTATCGCTCTATCTTTCGTCTTCGGTCCACTCGCGGTTCTTAAAGTCTACGGTGTACC
GTACATTATCTTTGTGATGTGGTTGGATGCTGTCACGTATTTGCATCATCATGGTCACGATGAGAAGTTGCCTT
GGTATAGAGGCAAGGAATGGAGTTATCTACGTGGAGGATTAACAACAATTGATAGAGATTACGGAATCTTTA
ACAACATTCATCACGACATTGGAACTCACGTGATCCATCATCTCTTCCCACAAATCCCTCACTATCACTTGGTC
GACGCCACGAAAGCAGCTAAACATGTGTTGGGAAGATACTACAGAGAACCAAAGACGTCAGGAGCAATACC
GATCCACTTGGTGGAGAGTTTGGTCGCAAGTATTAAGAAAGATCATTACGTCAGCGACACTGGTGATATTGTC
TTCTACGAGACAGATCCAGATCTCTACGTTTACGCTTCTGACAAATCTAAAATCAATTAA

FIG. 16 T: Arabidopsis FAD3, AT2G29980.1, Protein SEQ ID NO: 25

MVVAMDQRTNVNGDPGAGDRKKEERFDPSAQPPFKIGDIRAAIPKHCWVKSPLRSMSYVVRDIIAVAALAIAAVYVDS
WFLWPLYWAAQGTLFWAIFVLGHDCGHGSFSDIPLLNSVVGHILHSFILVPYHGWRISHRTHHQNHGHVENDESW
VPLPEKVYKKLPHSTRMLRYTVPLPMLAYPLYLCYRSPGKEGSHFNPYSSLFAPSERKLIATSTTCWSIMFVSLIALS
FVFGPLAVLKVYGVPYIIFVMWLDAVTYLHHHGHDEKLPWYRGKEWSYLRGGLTTIDRDVGIFNMHHEDIGTHVI
HHLFPQIPHYHLVDATKAAKHVLGRYYREPKTSGAIPIHLVESLVASIKKDHYVSDTGDIVFYETDPDLYVYASDKS
KIN

FIG. 16A - V

FIG. 16 U: mutant fatty acid elongation 1 (FAE1) DNA sequence (also see FIG.. 7) SEQ ID NO: 26

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ATGACGTCCGTTAACGTTAAGCTCCTTTACCGTTACGTCTTAACCAACTTTTTCAACCTC
    TGTTTGTTCCCGTTAACGGCGTTCCTCGCCGGAAAAGCCTCTCGGCTTACCATAAACGAT
    CTCCACAACTTCCTTTCCTATCTCCAACACAACCTTATAACAGTAACTTTACTCTTTGCT
    TTCACTGTTTTCGGTTTGGTTCTCTACATCGTAACCCGACCCAATCCGGTTTATCTCGTT
    GACTACTCGTGTTACCTTCCACCACCGCATCTCAAAGTTAGTGTCTCTAAAGTCATGGAT
    ATTTTCTACCAAATAAGAAAAGCTGATACTTCTTCACGGAACGTGGCATGTGATGATCCG
    TCCTCGCTCGATTTCCTGAGGAAGATTCAAGAGCGTTCAGGTCTAGGTGATGAGACGTAC
    AGTCCTGAGGGACTCATTCACGTACCACCGCGGAAGACTTTTGCAGCGTCACGTGAAGAG
    ACAGAGAAGGTTATCATCGGTGCGCTCGAAAATCTATTCGAGAACACCAAAGTTAACCCT
    AGAGAGATTGGTATACTTGTGGTGAACTCAAGCATGTTTAATCCAACTCCTTCGCTATCC
    GCTATGGTCGTTAATACTTTCAAGCTCCGAAGCAACATCAAAAGCTTTAATCTAGGAGGA
    ATGGGTTGTAGTGCTGGTGTTATTGCCATTGATTTGGCTAAAGACTTGTTGCATGTTCAT
    AAAAACACTTATGCTCTTGTGGTGAGCACTGAGAACATCACACAAGGCATTTATGCTGGA
    GAAAATAGATCAATGATGGTTAGCAATTGCTTGTTTCGTGTTGGTGGGGCCGCGATTTG
    CTCTCTAACAAGTCGGGAGACCGGAGACGGTCCAAGTACAAGCTAGTTCACACGGTCCGA
    ACGCATACTGGAGCTGATGACAAGTCTTTTCGATGTGTGCAACAAGAAGACGATGAGAGC
    GGCAAAATCGGAGTTTGTCTGTCAAAGGACATAACCAATGTTGCGGGGACAACACTTACG
    AAAAATATAGCAACATTGGGTCCGTTGATTCTTCCTTTAAGCGAAAAGTTTCTTTTTTTC
    GCTACCTTCGTCGCCAAGAAACTTCTAAAGGATAAAATCAAGCATTACTATGTTCCGGAT
    TTCAAGCTTGCTGTTGACCATTTCTGTATTCATGCCGGAGGCAGAGCCGTGATCGATGAG
    CTAGAGAAGAACTTAGGACTATCGCCGATCGATGTGGAGGCATCTAGATCAACGTTACAT
    AGATTTGGGAATACTTCATCTAGCTCAATTTGGTATGAATTAGCATACATAGAGGCAAAG
    GGAAGAATGAAGAAAGGGAATAAAGCTTGGCAGATTGCTTTAGGATCAGGGTTTAAGTGT
    AATAGTGCGGTTTGAGTGGCTCTACGCAATGTCAAGGCATCGGCAAATAGTCCTTGGCAA
    CATTGCATCGATAGATATCCGGTTAAAATTGATTCTGATTTGTCAAAGTCAAAGACTCAT
    GTCCAAAACGGTCGGTCCTAA
```

FIG. 16 V: mutant fatty acid elongation 1 (fae1) protein sequence (also see FIG.. 7) SEQ ID NO: 27

```
MTSVSVKLLYRIVLTNFPNLCLPPLTAFLAGKASRLTENDLHNFLSYLQHNLITVTLLPAFTVPGLVLYIVTRPKPVTLV
    DYSCVLPPHLEVSVSKVMDFVQRKADTSSRNVACDDPSSLDFLREIQERSGLGDETYSPEGLIHVPPRKTPAASR
    EETEKVIEQALENLFENTKVNPREIGLVVVNSSMFNPTPSLSAMVVNTFKLRSNIKSFNLGGMGCSAGVIAIDLAKDL
    LHVHKNTYALVVSTEMITQGIVAGENRSMMVSNCLFRVGGAAILLSNERSDERRSKYKLVHTVRTHTGADDKSFR
    CVQQEDDESGKIGVCLSKDIPVAGTTLTKNIATLGPLILPLSEKFLFFATFVARKLLKDKIKHYYVPDFKLAVDHF
    CIHAGGRAVIDELEKNLGLSPIDVEASRSTLHRFGNTSSSSIWYELAYIEAKGRMKRGNKAWQIALGSGFKCNSAV
```

FIG. 16A - V

FIG. 17 A: *E. coli* Cyclopropane fatty acid synthase (EcCPS1) DNA, NCBI Gene ID:944811; >NC_000913.3:1741413-1742561 SEQ ID NO: 28

ATGAGTTCATCGTGGTATAGAAGAAGTCAGTGTACCGGATGACAACTGGTACCGTATCGCCAACGAATTAC
TTAGCCGTGCCGGTATAGCCATTAACGGTTCTGCCCCGGCGGATATTCGTGTGAAAAACCCCGATTTTTT
TAAACGCGTTCTGCAAGAAGGCTCTTTGGGGTTAGGCGAAAGTTATATGGATGGCTGGTGGGAATGTGAC
CGACTGGATATGTTTTTTAGCAAAGTCTTACGCGCAGGTCTCGAGAACCAACTCCCCCATCATTTCAAAG
ACACGCTGCGTATTGCCGGCGCTCGTCTCTTCAATCTGCAGAGTAAAAAACGTGCCTGGATAGTCGGCAA
AGAGCATTACGATTTGGGTAATGACTTGTTCAGCCGCATGCTTGATCCCTTCATGCAATATTCCTGCGCT
TACTGGAAAGATGCCGATAATCTGGAATCTGCCCAGCAGGCGAAGCTCAAAATGATTTGTGAAAAATTGC
AGTTAAAACCAGGGATGCGCGTACTGGATATTGGCTGCGGCTGGGGCGGACTGGCACACTACATGGCATC
TAATTATGACGTAAGCGTGGTGGGCGTCACCATTTCTGCCGAACAGCAAAAAATGGCTCAGGAACGCTGT
GAAGGCCTGGATGTCACCATTTTGCTGCAAGATTATCGTGACCTGAACGACCAGTTTGATCGTATTGTTT
CTGTGGGGATGTTCGAGCACGTCGGACCGAAAAATTACGATACCTATTTTGCGGTGGTGGATCGTAATTT
GAAACCGGAAGGCATATTCCTGCTCCATACTATCGGTTCGAAAAAAACCGATCTGAATGTTGATCCCTGG
ATTAATAAATATATTTTTCCGAACGGTTGCCTGCCCTCTGTACGCCAGATTGCTCAGTCCAGCGAACCCC
ACTTTGTGATGGAAGACTGGCATAACTTCGGTGCTGATTACGATACTACGTTGATGGCGTGGTATGAACG
ATTCCTCGCCGCATGGCCAGAAATTGCGGATAACTATAGTGAACGCTTTAAACGAATGTTTACCTATTAT
CTGAATGCCTGTGCAGGTGCTTTCCGCGCCCGTGATATTCAGCTCTGGCAGGTCGTGTTCTCACGCGGTG
TTGAAAACGGCCTTCGAGTGGCTCGCTAA

FIG. 17 B: *E. coli* Cyclopropane fatty acid synthase (EcCPS1) protein, NP_416178.1 SEQ ID NO: 29

MSSSCIEEVSVPDDNWYRIANELLSRAGIAINGSAPADIRVKNPDFFKRVLQEGSLGLGESYMDGWWECD
RLDMFFSKVLRAGLENQLPHHFKDTLRIAGARLFNLQSEKRAWIVGKEHYDLGNDLFSRMLDPFMQYSCA
YWKDADNLESAQQAKLEMICEKLQLKPGMRVLDIGCGWGGLARYMASNYDVSVVGVTISAEQQKDMAQERC
EGLDVTILLQDYRDLNDQFDRIVSVGMFEHVGKKNYDTYFAVVDRMLKPEGIFLLHTIGSKKTDLNVDPW
INKYIFPNGCLPSVRQIAQSSEPHFVMEDWHNFGADYDTTLMAWYERFLAAWPELADNYSERFKRMFTYY
LNACAGAFRARDIQLWQVVFSRGVENGLPVAR

FIG. 17 C: Crepis palaestina delta 12 fatty acid epoxygenase GenBank#: Y16283.1;>Y16283.1:30-1154 Crepis palaestina mRNA for delta 12 fatty acid epoxygenase SEQ ID NO: 30

ATGGGTGCCGGCGGTCGTGGTCGGACATCGGAAAAATCGGTCATGGAACGTGTCTCAGTTGATCCAGTAA
CCTTCTCACTGAGTGAATTGAAGCAAGCAATCCCTCCCCATTGCTTCCAGAGATCTGTAATCCGCTCATC
TTACTATGTTGTTCAAGATCTCATTATTGCCTACATCTTCTACTTCCTTGCCAACACATATATCCCTACT
CTTCCTACTAGTCTAGCCTACTTAGCTTGGCCCGTTTACTGGTTCTGTCAAGCTAGCGTCCTCACTGGCT
TATGGATCCTCGGCCACGAATGTGGTCACCATGCCTTTAGCAACTACACATGGTTTGACGACACTGTGGG
CTTCATCCTCCACTCATTTCTCCTCACCCCGTATTTCTCTTGGAAATTCAGTCACCGGAATCACCATTCC
AACACAAGTTCGATTGATAACGATGAAGTTTACATTCCGAAAAGCAAGTCCAAACTCGCGCGTATCTATA
AACTTCTTAACAACCCACCTGGTCGGCTGTTGGTTTTGATTATCATGTTCACCCTAGGATTTCCTTTATA
CCTCTTGACAAATATTTCCGGCAAGAAATACGACAGGTTTGCCAACCACTTCGACCCCATGAGTCCAATT
TTCAAAGAACGTGAGCGGTTTCAGGTCTTCCTTTCGGATCTTGGTCTTCTTGCCGTGTTTTATGGAATTA
AAGTTGCTGTAGCAAATAAAGGAGCTGCTTGGGTAGCGTGCATGTATGGAGTTCCGGTATTAGGCGTATT
TACCTTTTTCGATGTGATCACCTTCTTGCACCACACCCATCAGTCGTCGCCTCATTATGATTCAACTGAA
TGGAACTGGATCAGAGGGGCCTTGTCAGCAATCGATAGGGACTTTGGATTCCTGAATAGTGTTTTCCATG
ATGTTACACACACTCATGTCATGCATCATTTGTTTTCATACATTCCACACTATCATGCAAAGGAGGCAAG
GGATGCAATCAAGCCAATCTTGGGCGACTTTTATATGATCGACAGGACTCCAATTTTAAAAGCAATGTGG
AGAGAGGGCAGGGAGTGCATGTACATCGAGCCTGATAGCAAGCTCAAAGGTGTTTATTGGTATCATAAAT
TGTGA

FIG. 17 D: >CAA76156.1 delta 12 fatty acid epoxygenase [Crepis palaestina] SEQ ID NO: 31

MGAGGRGRTSEKSVMERVSVDPVTFSLSELKQAIPPHCFQRSVIRSSYYVVQDLIIAVIFYFLANTYIPT
LPTSLAVLAWPVYWTCQASVLTGLWILGHECGHHAFSNYTWTDDTVGFILHSFLLTPYFSWKFSHRNHHS
NTGSIDNDEVYIPKSKSKLAPIYKLLNNPPGRLLVLIIMFTLGFPLYLLTNIGGKKYDRFANHFDPMSPI
FKERERFQVFLSDLGLLAVFYGIKVAVANKGAAWVACMYGVPVLGVFTFFDVTIFLHHTHQSSPHYDSTE
WNWIRGALSAIDRDFGFLNSVFHDVTHTHVMHHLFSVIPHYHAKEARDAIKPILGDFYMIDRTPILKAMW
REGRECMYIEPDSKLKGVYWYHKI

FIG. 17 E: Crepis alpina delta-12 fatty acid acetylenase GenBank#: DQ289485.1; SEQ ID NO: 32

>DQ289485.1 Crepis alpina delta-12 fatty acid acetylenase (vFAD2) gene, complete cds

AAGATGGGTGGCGGTGGCCGTGGTCGGACTTCGCAAAAACCCCTCATGGAACGTGTCTCAGTTGATCCAC
CCTTCACCGTGAGTGATCTCAAGCAAGCAATCCCTCCCCATTGCTTCAAGCGATCTGTAATCCGTTCCTC
TTACTACATAGTCCACGATGCTATTATCGCCTACATCTTCTACTTCCTTGCCGACAAATACATTCCGATT
CTCCCTGCCCCTCTAGCCTACCTCGCTTGGCCCCTTTACTGGTTCTGTCAAGCTAGCATCCTCACCGGCT
TATGGGTCATCGGTCACGAATGCGGTCACCATGCCTTCAGCGACTACCAGTGGGTTGACGACACTGTGGG
CTTCATCCTCCACTCGTTTCTCATGACCCCGTATTTCTCCTGGAAATACAGCCACCGGAACCACCATGCC
AACACAAATTCGCTTGACAACGATGAAGTTTACATCCCCAAAAGCAAGGCCAAAGTCGCGCTTTACTATA
AAGTTCTCAACCACCCACCTGGCCGACTGTTGATTATGTTCATCACCTTCACCCTAGGCTTCCCTCTATA
CCTCTTTACCAATATTTCCGGCAAGAAGTATGAAAGGTTTGCCAACCATTTCGACCCCATGAGTCCGATT
TTCAAAGAGCGTGAGCGGTTTCAGGTCTTGCTATCGGATCTTGGCCTTCTTGCTGTGCTTTACGGAGTTA
AACTTGCGGTAGCAGCGAAAGGCGCCGCTTGGGTGACGTGCATTTACGGAATTCCAGTTTTAGGCGTGTT
TATCTTTTTCGATATCATCACCTACTTGCACCACACCCATCTGTCGTTGCCTCATTATGATTCATCTGAA
TGGAACTGGCTCAGAGGGGCTTTGTCAACAATCGATAGGGACTTTGGGTTCCTGAATAGTGTGCTCCATG
ATGTTACACACACTCACGTTATGCATCATCTGTTTTCATACATTCCACACTATCATGCGAAGGAGGCAAG
GGATGCAATCAACACAGTCTTGGGCGACTTTTATAAGATCGATAGGACTCCAATTCTGAAAGCAATGTGG
AGAGAGGCCAAGGAATGCATCTTCATCGAGCCTGAAAAAGGTAGGGAGTCCAAGGGTGTATATTGGTACA
ATAAATTCTGA

FIG. 17 F: >ABC00769.1 delta-12 fatty acid acetylenase [Crepis alpina] SEQ ID NO: 33

MGGGGRGETSQKPLMERVSVDPPFTVSDLKQAIPPHCFERSVIRSSYYVVHDAIIAYIFYFLADKYIPL
PAPLAYLAWPLYWFCQASILTGLWVIGHECGHHAFSDYQWVDDTVGFILHSFLLVPYFSWKYSHRNHHAN
TNSLDNDEVYIPKSKAKVALYYKVLNHPPGRLLMFITFTLGFPLYLFTNISGRKYERFANHFDPMSPIF
KERERPQVLLSDLGLLAVLYGVKLAVAAKGAAWVTCIYGIPVLGVPIFFDHITYLHHTHLSLPHYDSSEW
NWLRGALSTIDRDFGFLNSVLHDVTHTHVNHHLFSYIPHYHAKEARDAINTVLGDFYKIDRTPILRAMWR
EAKECIFIEPEKGRESKGVYWYNKF

FIG. 17 G: Momordica Momordica charantia Conjugase (FadX) GenBank#: AF182521.1;

>AF182521.1 Momordica charantia delta-12 oleic acid desaturase-like protein (FadX) mRNA, complete cds SEQ ID NO: 34

AATAAATTAGCTTCTTTTTTTAAGTGAGTGAAGGGAGATCTGGAGGCAATGGGGGGGCAGAGGAGCTATTG
GAGTACTGAGGAACGGTGGCGGCCCAAAAAAGAAAATGGGGCCGGGGCAGGGGCTGGGGCCGGGGGAGCG
CATTACACATGCCAGGCCTCCCTTCAGCATCAGCCAGATCAAGAAGGCCATTCCCCCCCACTGCTTTCAG
CGATCCCTCCGCCGCTCTTTTTCCTACCTTCTTTCCGACATTGCCCTCGTCTCTGCCTTTTATTACGTTG
CCGACACCTACTTCCACCGCCTGCCCCACCCCCTACTCCACTACCTGGCCTGGCCCGTTTACTGGTTCTG
TCAGGGCGCCGTACTCACCGGCATGTGGGGCATCGCTCACGACTGCGGCCACCACGCCTTCAGCGACTAC
CAATTGGTAGACGACGTGGTTGGGTTCCTCATCCACTCTTTGGTTTTTGTCCCTTACTTCTCCTTCAAGA
TCAGCCACCGCCGCCACCACTCCAACACCTCATCCGTGGACCGGGACGAGGTGTTCGTCCCCAAGCCGAA
GGCCAAAATGCCCTGGTACTTCAAGTACTTGACAAACCCGCCCGCCAGGGTCTTCATTATTTTATCACG
CTCACTCTCGGGTGGCCAATGTACCTGACCTTCAACATCTCCGGCCGGTACTACGGCCGGTTCACCAGCC
ACTTCGACCCGAACAGCCCCATATTCAGCCCAAAGGAGCGCGTTCTCGTTCATATCTCCAACGCTGGGCT
TGTGGCGACCGGGTATTTGCTGTACAGGATCGCAATGGCGAAGGGGGTGGGGTGGTTGATCCGCTTGTAC
GGAGTGCCGCTGATCGTTTTAAACGCGTGCGTAGTTCTGATCACAGCGCTGCAGCACACCCACCCTTCGT
TCCCGTATTACGACTCGACGGAATGGGATTGGCTGAGAGGGAATCTGGTGACGGTGGACAGAGATTACGG
GCCTATAATGAATAGAGTGTTTCATCACATAACGGACACGCACGTGGTTCACCATTTGTTTCCTTCGATG
CCGCACTACAACGGGAAAGAGGCGACGGTTGCAGCAAAGCGAATACTGGGAGAGTACTACCAGTTTGATG
GGACCCCAATTTGGAAGGCGGCCTGGAGGGAATTCAGAGAGTGCGTTTATGTAGAGCCAGACGAAGACGA
TGGGGCCACTTCCGGCTCCAGTAGTAAGGGTGTTTTCTGGTACCACAACAAGCTCTGAATTCAATAATAT
CCTCTTTCACCTCTCTTTTTCATAAAAAAAAAAAAAAA

FIG. 17 H: >AAF05916.1 delta-12 oleic acid desaturase-like protein [Momordica charantia] SEQ ID NO: 35

MGGRGAIGVLRNGGGPKKKMGPGQGLGPGERITHARPPFSISQIKKAIPPHCFQRSLRRSFSYLLSDIAL
VSAFVYVADTYFHRLPHPLLHYLAWPVYWFCQGAVLTGMWGIAHDCGHHAFSDYQLVDDVVGFLIHSLVF
VPYFSFKISHRRHHSNTSSVDRDEVFVPKPKAKMPWYFKYLTNPPARVFTIFITLTLGWPMYLTPNISGR
YYGRFTSHFDPNSPIFSPKERVLVHISNAGLVATGYLLYRIAMAKGVGWLIRLYGVPLIVLNACVVLITA
LQHTHPSFPYYDSTEWDWLRGNLVTVDRDYGFIMNRVFHHITDTHVVHHLFPSMPHYNGKEATVAAKRIL
GEVYQFDGTPIWKAAWREFRECVYVEPDEDDGATSGSSSKGVFWYHNKL

FIG. 17A - H

METHODS AND COMPOSITIONS FOR MODIFYING PHENOTYPES OF PLANTS EXPRESSING FATTY ACID TRANSGENES AND REDUCED EXPRESSION OF BADC GENES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a Non-Provisional application which claims benefit of U.S. Patent Application Ser. No. 63/131,755, filed on Dec. 29, 2020, now expired, which is herein incorporated by reference in its entirety.

GOVERNMENT SUPPORT

[0002] This invention was made with Government support under contract numbers DE-SC0012704 and DE-SC0018420 awarded by the U.S. Department of Energy and IOS-13-39385 awarded by the National Science Foundation. The Government has certain rights in the invention.

SEQUENCE

[0003] A Sequence Listing has been submitted in an ASCII text file named "19963.txt" created on Mar. 23, 2022, consisting of 101,032 bytes, the entire content of which is herein incorporated by reference.

FIELD OF THE INVENTION

[0004] BADC (biotin attachment domain-containing) mutants specifically badc1, badc3 for beneficial effects on unusual fatty acid (also known as specialized fatty acid accumulation).

SUMMARY OF THE INVENTION

[0005] When enzymes that convert common fatty acids to unusual fatty acids (hydroxy, epoxy, conjugated or cyclopropane fatty acids) are expressed in plants like *Arabidopsis* or *Camelina*, the unusual fatty acid accumulates but the total yield of fatty acids decreases. Mutations in the badc1,badc3 genes i.e., negative regulators of acetyl CoA carboxylase (ACCase) may mitigate this effect and restore or maintain total fatty acid levels thereby facilitating the accumulation of unusual fatty acids.

[0006] The present discovery may be a way to reverse a roadblock in plants to specialty oil production thereby providing a pathway to grow crops that produce industrially important high-value fatty acids. Hundreds of naturally occurring specialty fatty acids (building blocks of oils) may have potential for use as raw materials for making for example, lubricants, plastics, or pharmaceuticals, if they can be produced at large scale by crop plants. Prior attempts to put genes for making these specialty building blocks into crops have resulted in the adverse effect, namely, transgenic seeds making the specialty fatty acids experienced a reduction in their oil accumulation.

[0007] The mechanism behind the oil-production slowdown is described herein. Model plants were crossbred and detailed biochemical-genetic analyses were conducted that demonstrate a strategy for reversing the roadblock and increasing production. This may provide potential for making at least one or more industrially important specialty fatty acid in plants, crops or seeds.

[0008] While the genes responsible for making specialty fatty acids were discovered several decades ago, this present mechanism may allow them to be put into compositions such as plants, crops or seeds to make renewable sources of desired fatty acids without slowing fatty acid and oil synthesis. The study focused on challenges associated with specialized fatty acid production in plants, and on deciphering the biochemical feedback loop that plants use to regulate ordinary or regular fatty acid (FA) and oil production. This study led to the discovery of a mechanism by which plants down-regulate oil synthesis when levels of a plant's ordinary or regular (endogenous) fatty acids (FAs) get too high. In other words, the system operates or functions like a thermostat. When endogenous FA (heat) gets above a certain set point, the system (furnace) turns off.

[0009] With plant oils, the machinery that controls production is an enzyme called ACCase (acetyl coA carboxylase). It has four parts, or subunits: biotin carboxylase (BC), biotin carboxyl carrier protein (BCCP), and two carboxyltransferases, α-carboxyltransferase and β-carboxyltransferase. As long as endogenous fatty acids are below a certain level, the four subunits act coordinately to convert acetyl-CoA to malonyl-CoA. But feeding plants additional endogenous fatty acids triggers a substitution in the machinery in which the BCCP subunit is gets replaced by biotin attachment domain-containing protein (BADC), a homolog of BADC that lacks a critical biotin attachment amino acid and is therefore inactive. ACCase in which BCCP has been replaced by BADC slows the production of malonyl-CoA and therefor the synthesis of fatty acids. In contrast, the shutdown mechanism triggered by the accumulation of specialty fatty acids (ones being produced by genes expressed in the plant) kicks in when even small amounts of the "foreign" fatty acids are present, and endogenous fatty acids aren't in excess. Because of this, they appeared to be two separate processes. But it was speculated whether the specialty fatty acids were triggering the same off switch triggered by high levels of ordinary fatty acids.

[0010] In a strain of *Arabidopsis* (a model plant) with two of its BADC genes deleted, the downregulation of ACCase is disabled and the plants make high levels of endogenous fatty acids. Further study looked at what would happen if the BADC genes were disabled in plants engineered to produce specialty fatty acids. A research strategy was designed to crossbreed the defective off-switch plants with an *Arabidopsis* strain engineered to produce hydroxy fatty acids-one of the specialty types scientists would like to produce for industrial applications. This latter strain could make the hydroxy fatty acids, but its rate of oil synthesis was only half that of normal (unmodified) plants and it accumulated significantly less oil in its seeds.

[0011] When crossing four separate genetic factors (two mutant BADC genes, a mutant in fatty acid elongase 1 (FAE1) and an overexpression of the *Ricinus communis* 12-hydroxylase gene (FAH), it takes several plant generations to produce and identify plants homozygous for the four desired genes (see FIGS. **16**A and **16**B FAH sequences; FIGS. **16**O and **16**P FAE1 sequences; FIGS. **16**U and **16**V mutant FAE1 sequences). Polymerase chain reaction (PCR) tests were run for analyses of greater many hundreds of plants to find those homozygous for all four alleles. Those plants were biochemically characterized, to compare their rates of ACCase activity with those of the two parental *Arabidopsis* lines used to make the new genetic combina-

tions. Plants that had the combination of defective BADC genes and genes required for making hydroxy fatty acids produced normal (unaltered) levels of oil containing the specialty products. Compared with plants that had normal (wild-type) BADC genes, the new plants exhibited increases in the total amount of fatty acid per seed, the total seed oil content per plant, and the seed yield per plant. The BADC-defective plants were unresponsive to the presence of hydroxy fatty acids and the usual response of turning off the ACCase was gone. The results prove that BADC is the mechanism for reducing ACCase activity in both scenarios—the accumulation of excess endogenous fatty acids and the presence of hydroxy fatty acid.

[0012] The BADC mechanism may be specific to the accumulation of hydroxy fatty acids, or may be common to other 'foreign' fatty acids that also reduce ACCase activity. BADC may be a general mechanism, and mutations that reduce their activity may allow for the accumulation of additional specialty fatty acids in oil-rich seeds of crop plants with minimal reduction of oil yield. This fundamental mechanistic understanding of biochemical regulation may be useful towards a viable, sustainable bioeconomy. This approach may also be used to make valuable renewable industrial starting materials at low cost in plants from carbon dioxide and sunlight, rather than relying on petrochemicals.

[0013] Thus, in one embodiment, the invention provides a composition comprising one or more mutated BADC genes for accumulating unusual fatty acids and maintaining or increasing total fatty acid levels, oil content in the composition as described herein.

[0014] The invention also provides a composition produced by any one or more of the methods of the invention, wherein the composition is a seed, plant or crop.

[0015] The invention also provides a plant composition comprising a combination of defective BADC genes and genes for synthesizing hydroxy fatty acids for producing specialized fatty acids without slowing production of endogenous fatty acids as described herein.

[0016] The invention also provides a method of increasing production of unusual fatty acids and increasing total fatty acid levels in plants, crops or seeds by a mechanism involving combining defective BADC genes and genes for making hydroxy fatty acids to produce steady or increased levels of oil containing the specialty products as described herein.

[0017] In one embodiment, the invention provides a method of modifying a plant or part thereof, comprising producing a transgenic plant or part thereof that comprises a transgenic plant cell, said transgenic plant cell comprising a) reduced (e.g., lacks) expression of one or both of endogenous BADC1 and BADC3 genes, and b) expression of one or more transgenes that alters metabolism of a target fatty acid. In one embodiment, said transgenic plant exhibits one or more phenotypes of a) an increased amount of total seed fatty acid per plant, b) improved establishment of one or both of roots and plant aerial parts, and c) rescued or increased seed yield per plant. In one embodiment, said transgenic plant produces seeds, said seeds exhibiting one or more of rescued or increased seed germination rate, rescued or increased amount of total seed fatty acid per seed, rescued or increased amount of said target fatty acid per seed, and rescued or increased proportion of said target fatty acid relative to said total seed fatty acid per seed. In one embodiment, said transgenic plant cell comprises wild type BADC1 gene and reduced (or lacks) expression of said endogenous BADC3 gene. In one embodiment, said transgenic plant cell comprises wild type BADC1 gene and lacks expression of said endogenous BADC3 gene. In one embodiment, said producing comprises deleting at least a portion of said wild type BADC3 gene. In one embodiment, said deleting comprises using clusters of regularly interspaced short palindromic repeats (CRISPR) gene editing. In one embodiment, said transgenic plant cell lacks an alteration in one or both the enzyme activity and protein expression level of wild type acetyl CoA carboxylase (ACCase). In one embodiment, said target fatty acid comprises a foreign fatty acid that is not naturally produced in a wild type of said cell. In one embodiment, said target fatty acid comprises one or more of hydroxyl fatty acids, medium-chain fatty acids, very-long-chain fatty acids (VLCFAs), monounsaturated fatty acids (MUFAs), γ-linolenic acid, stearidonic acids, α-eleostearic acid, conjugated fatty acids, expoxy fatty acids, cyclic fatty acids and acetylenic fatty acids. In one embodiment, said target fatty acid comprises a hydroxyl fatty acid exemplified by ricinoleic acid. In one embodiment, said plant cell is selected from a *Camelina sativa* plant cell, a *Brassica napus* plant cell and *Glycine max* plant cell. In one embodiment, said transgenic plant cell comprises a genomic mutation such as fad2, fad3 and fae1 or any combination thereof. In one embodiment, said genomic mutation is selected from fad2/fae1 and fad3/fae1. In one embodiment, said transgenic plant cell is a cell from *Arabidopsis thaliana* and comprises genomic mutation fad2/fae1. In one embodiment, said transgenic plant cell is a cell from a plant selected from *Camelina sativa, Brassica napus* and *Glycine max*, and comprises a genomic mutation fad3/fae1. In one embodiment, said transgenic plant cell is a cell from a plant selected from *Camelina sativa, Brassica napus* and *Glycine max*, and comprises a genomic mutation fad3/fae1, wherein said transgene that alters metabolism of said target fatty acid encodes one or more of acetylanase, conjugase and epoxygenase. In one embodiment, said transgene that alters metabolism of said target fatty acid comprises a transgene encoding fatty acid hydroxylase exemplified by *Ricinus* fatty acid hydroxylase (RcFAH) mutant fatty acid elongation 1 (FAE1) (see exemplary FIGS. **16**A and **16**B FAH sequences; FIGS. **16**O and **16**P FAE1 sequences; FIGS. **16**U and **16**V mutant FAE1 sequences), *E. coli* Cyclopropane fatty acid synthase (see exemplary FIGS. **17** A and **17** B), epoxygenase exemplified by *Crepis palaestina* delta 12 fatty acid epoxygenase (see exemplary FIGS. **17** C and **17** D), acetylenase exemplified by *Crepis alpina* delta-12 fatty acid acetylenase (see exemplary FIGS. **17** E and **17** F), conjugase exemplified by *Momordica charantia* Conjugase (FadX) (see exemplary FIG. **17** G). In one embodiment, said transgene comprises a transgene encoding *Ricinus* fatty acid hydroxylase (FAH). In one embodiment, said transgene comprises a transgene encoding *E. coli* cyclopropane fatty acid synthase. In one embodiment, said one or more transgene that alters metabolism of said target fatty acid is under control of a seed-specific promoter. In one embodiment, said transgenic plant or part thereof that comprises reduced (or lacks) expression of one or both of said endogenous BADC1 and BADC3 genes contains a mutation in said one or both of said endogenous BADC1 and BADC3 genes. In one embodiment, said transgenic plant or part thereof is homozygous for said mutation in said one or both of said endogenous BADC1 and BADC3 genes. In one embodiment, said transgenic plant or part thereof is homozygous

null for said one or both of said endogenous BADC1 and BADC3 genes. In one embodiment, said transgenic plant or part thereof is homozygous for said one or more transgene that alters metabolism of said target fatty acid. In one embodiment, said transgenic plant or part thereof is heterozygous for said mutation in said one or both of said endogenous BADC1 and BADC3 genes. In one embodiment, said transgenic plant or part thereof is heterozygous for said one or more transgene that alters metabolism of said target fatty acid. In one embodiment, said transgenic plant cell or part thereof is stably transformed with said transgene that alters metabolism of said target fatty acid. In one embodiment, said producing comprises transforming a plant cell with one or more recombinant nucleotide sequences that partially or totally silence of one or both of said endogenous BADC1 and BADC3 genes. In one embodiment, said producing comprises transforming said plant cell with one or more recombinant nucleotide sequences that alter metabolism of said target fatty acid. In one embodiment, said producing comprises transforming said plant cell with one or more recombinant nucleotide sequences that partially or totally silence of one or both of said endogenous BADC1 and BADC3 genes. In one embodiment, said producing comprises transforming said plant cell with one or more recombinant nucleotide sequences that (a) partially or totally silence of one or both of said endogenous BADC1 and BADC3 genes, and (b) alter metabolism of said target fatty acid. In one embodiment, said producing comprises crossing a first transgenic plant comprising said reduced or lacking expression of one or both of said endogenous BADC1 and BADC3 genes to a second transgenic plant comprising said one or more transgene that alters metabolism of said target fatty acid.

[0018] In one embodiment, the present invention provides a method of modifying a plant or part thereof, comprising producing a transgenic plant or part thereof that comprises a transgenic plant cell, said transgenic plant cell comprising a) reduced expression of one or both of endogenous BADC1 and BADC3 genes, and b) expression of one or more transgenes that alters metabolism of a target fatty acid. In one embodiment, said transgenic plant exhibits one or more phenotypes of a) increased amount of total seed fatty acid per plant, b) improved establishment of one or both of roots and plant aerial parts, and c) rescued or increased seed yield per plant. In one embodiment, said transgenic plant produces seeds, said seeds exhibiting one or more of rescued or increased seed germination rate, rescued or increased amount of total seed fatty acid per seed, rescued or increased amount of said target fatty acid per seed, and rescued or increased proportion of said target fatty acid relative to said total seed fatty acid per seed. In one embodiment, said transgenic plant cell comprises wild type BADC1 gene and reduced expression of said endogenous BADC3 gene. In one embodiment, said transgenic plant cell comprises wild type BADC1 gene and lacks expression of said endogenous BADC3 gene. In one embodiment, said producing comprises deleting at least a portion of said wild type BADC3 gene. In one embodiment, said deleting comprises using clusters of regularly interspaced short palindromic repeats (CRISPR) gene editing. In one embodiment, said transgenic plant cell lacks an alteration in one or both the enzyme activity and protein expression level of wild type acetyl CoA carboxylase (ACCase). In one embodiment, said target fatty acid comprises a foreign fatty acid that is not naturally produced in a wild type of said cell. In one embodiment, said target fatty acid comprises one or more of hydroxyl fatty acids, medium-chain fatty acids, very-long-chain fatty acids (VLCFAs), monounsaturated fatty acids (MUFAs), 7-linolenic acid, stearidonic acids, α-eleostearic acid, conjugated fatty acids, expoxy fatty acids, cyclic fatty acids and acetylenic fatty acids. In one embodiment, said target fatty acid comprises a hydroxyl fatty acid. In one embodiment, said hydroxyl fatty acid comprises ricinoleic acid. In one embodiment, said plant cell is selected from a *Camelina sativa* plant cell, a *Brassica napus* plant cell and *Glycine max* plant cell. In one embodiment, said transgenic plant cell comprises a genomic mutation such as fad2, fad3 and fae1 or any combination thereof. In one embodiment, said genomic mutation is selected from fad2/fae1 and fad3/fae1. In one embodiment, said transgenic plant cell is a cell from *Arabidopsis thaliana* and comprises genomic mutation fad2/fae1. In one embodiment, said transgenic plant cell is a cell from a plant selected from *Camelina sativa, Brassica napus* and *Glycine max*, and comprises a genomic mutation fad3/fae1. In one embodiment, said transgenic plant cell is a cell from a plant selected from *Camelina sativa, Brassica napus* and *Glycine max*, and comprises a genomic mutation fad3/fae1, wherein said transgene that alters metabolism of said target fatty acid encodes one or more of acetylanase, conjugase and epoxygenase. In one embodiment, said transgene that alters metabolism of said target fatty acid comprises a transgene encoding *Ricinus* fatty acid hydroxylase (FAH), mutant fatty acid elongation 1 (FAE1), *E. coli* Cyclopropane fatty acid synthase, *Crepis palaestina* delta 12 fatty acid epoxygenase, *Crepis alpina* delta-12 fatty acid acetylenase, *Momordica charantia* Conjugase (FadX), RcFAH, cyclopropane fatty acid synthase. In one embodiment, said transgene comprises a transgene encoding *Ricinus* fatty acid hydroxylase (FAH). In one embodiment, said transgene comprises a transgene encoding *E. coli* cyclopropane fatty acid synthase. In one embodiment, said one or more transgene that alters metabolism of said target fatty acid is under control of a seed-specific promoter. In one embodiment, said transgenic plant or part thereof that comprises reduced expression of one or both of said endogenous BADC1 and BADC3 genes contains a mutation in said one or both of said endogenous BADC1 and BADC3 genes. In one embodiment, said transgenic plant or part thereof is homozygous for said mutation in said one or both of said endogenous BADC1 and BADC3 genes. In one embodiment, said transgenic plant or part thereof is homozygous null for said one or both of said endogenous BADC1 and BADC3 genes. In one embodiment, said transgenic plant or part thereof is homozygous for said one or more transgene that alters metabolism of said target fatty acid. In one embodiment, said transgenic plant or part thereof is heterozygous for said mutation in said one or both of said endogenous BADC1 and BADC3 genes. In one embodiment, said transgenic plant or part thereof is heterozygous for said one or more transgene that alters metabolism of said target fatty acid. In one embodiment, said transgenic plant cell or part thereof is stably transformed with said transgene that alters metabolism of said target fatty acid. In one embodiment, said producing comprises transforming a plant cell with one or more recombinant nucleotide sequences that partially or totally silence of one or both of said endogenous BADC1 and BADC3 genes. In one embodiment, said producing comprises transforming said plant cell with one or more

recombinant nucleotide sequences that alter metabolism of said target fatty acid. In one embodiment, said producing comprises transforming said plant cell with one or more recombinant nucleotide sequences that partially or totally silence of one or both of said endogenous BADC1 and BADC3 genes. In one embodiment, said producing comprises transforming said plant cell with one or more recombinant nucleotide sequences that (a) partially or totally silence of one or both of said endogenous BADC1 and BADC3 genes, and (b) alter metabolism of said target fatty acid. In one embodiment, said producing comprises crossing a first transgenic plant comprising said reduced expression of one or both of said endogenous BADC1 and BADC3 genes to a second transgenic plant comprising said one or more transgene that alters metabolism of said target fatty acid.

[0019] The invention also provides a transgenic plant or part thereof that comprises a transgenic plant cell that comprises a) reduced or lacks expression of one or both of said endogenous BADC1 and BADC3 genes, and b) one or more transgene that alters metabolism of said target fatty acid. In one embodiment, the transgenic plant exhibits one or more phenotype of a) increased amount of total seed fatty acid per plant, b) improved establishment of one or both of roots and plant aerial parts, and c) rescued or increased seed yield per plant. In one embodiment, the transgenic plant produces seeds, said seeds exhibiting one or more of rescued or increased seed germination rate, rescued or increased amount of total seed fatty acid per seed, rescued or increased amount of said target fatty acid per seed, and rescued or increased proportion of said target fatty acid relative to said total seed fatty acid per seed. In one embodiment, the transgenic plant or part thereof is produced by any one or more of the invention's methods.

[0020] In one embodiment, the present invention provides a transgenic plant or part thereof that comprises a transgenic plant cell, wherein said plant cell comprises a) reduced or lacks expression of one or both of said endogenous BADC1 and BADC3 genes, and b) one or more transgene that alters metabolism of a target fatty acid. In one embodiment, said transgenic plant exhibits one or more phenotype of a) increased amount of total seed fatty acid per plant, b) improved establishment of one or both of roots and plant aerial parts, and c) rescued or increased seed yield per plant. In one embodiment, said transgenic plant produces seeds, said seeds exhibiting one or more of rescued or increased seed germination rate, rescued or increased amount of total seed fatty acid per seed, rescued or increased amount of said target fatty acid per seed, and rescued or increased proportion of said target fatty acid relative to said total seed fatty acid per seed.

[0021] In one embodiment, the present invention provides a transgenic plant or part thereof that comprises a transgenic plant cell, wherein said plant cell comprises a) reduced or lack of expression of one or both of said endogenous BADC1 and BADC3 genes, and b) one or more transgene that alters metabolism of a target fatty acid.

[0022] In one embodiment, the present invention provides a transgenic plant or part thereof that comprises: a) a genomic mutation selected from the group consisting of a mutation of fad2, fad3, and fae1, or any combination of such mutations, b) the reduced expression of one or both endogenous BADC1 and BADC3 genes, and c) one or more transgenes that alter metabolism of a target fatty acid. In one embodiment, the present invention provides a transgenic plant or part thereof that comprises: a) genomic mutation of fad2, fad3, fae1 or any combination thereof, b) reduced expression of one or both endogenous BADC1 and BADC3 genes, and c) one or more transgenes that alter metabolism of a target fatty acid. In one embodiment, said transgenic plant part comprises wild type BADC1 gene and reduced expression of said endogenous BADC3 gene. In one embodiment, said transgenic plant part comprises reduced expression of said endogenous BADC1 gene and BADC3 gene. In one embodiment, said plant is *Camelina sativa, Brassica napus* or *Glycine max*. In one embodiment, said genomic mutation is fad2/fae1 or fad3/fae1. In one embodiment, said one or more transgenes encode *Ricinus* fatty acid hydroxylase (FAH), *E. coli* cyclopropane fatty acid synthase, *Crepis palaestina* delta 12 fatty acid epoxygenase, *Crepis alpina* delta-12 fatty acid acetylenase, or *Momordica charantia* Conjugase (FadX). In one embodiment, said one or more transgenes are under control of a seed-specific promoter. In one embodiment, said target fatty acid comprises one or more of hydroxyl fatty acids, medium-chain fatty acids, very-long-chain fatty acids (VLCFAs), monounsaturated fatty acids (MUFAs), gamma-linolenic acid, stearidonic acids, alpha-eleostearic acid, conjugated fatty acids, epoxy fatty acids, cyclic fatty acids and acetylenic fatty acids. In one embodiment, said transgenic plant part is from *Camelina sativa, Brassica napus* or *Glycine max*, said genomic mutation is fad3/fae1, and said transgene encodes acetylanase, conjugase, epoxygenase or any combinations thereof. In one embodiment, said transgenic plant part is from *Camelina sativa, Brassica napus* or *Glycine max*, said genomic mutation is fad2/fae1, and said transgene encodes *Ricinus* fatty acid hydroxylase. In one embodiment, said transgenic plant part is from *Camelina sativa, Brassica napus* or *Glycine max*, said genomic mutation is fae1, and said transgene encodes *Ricinus* fatty acid hydroxylase. In one embodiment, said reduced expression comprises complete silencing. In one embodiment, said reduced expression comprises complete silencing. In one embodiment, said reduced expression comprises complete silencing.

[0023] The invention further provides a progeny plant of the any of the transgenic plants of the invention.

[0024] In one embodiment, the present invention provides a method of modifying a plant or part thereof, comprising producing a transgenic plant or part thereof that comprises a transgenic plant cell, said transgenic plant cell comprising a) reduced expression of one or both of endogenous BADC1 and BADC3 genes, and b) expression of one or more transgenes that alters metabolism of a target fatty acid.

[0025] In one embodiment, the present invention provides a progeny plant of a transgenic plant or part thereof that comprises a transgenic plant cell, wherein said plant cell comprises a) reduced or lacks expression of one or both of said endogenous BADC1 and BADC3 genes, and b) one or more transgene that alters metabolism of said target fatty acid.

[0026] In one embodiment, the present invention provides a progeny plant of a transgenic plant or part thereof that comprises: a) genomic mutation of fad2, fad3, fae1 or any combination thereof, b) reduced expression of one or both endogenous BADC1 and BADC3 genes, and c) one or more transgenes that alter metabolism of a target fatty acid.

[0027] The invention additionally provides a transgenic seed produced by any one or more of the methods the

invention, wherein said transgenic seed comprises a transgenic plant cell having a) reduced or lacking expression of one or both of said endogenous BADC1 and BADC3 genes, and b) one or more transgene that alters metabolism of said target fatty acid. In one embodiment, said seed exhibits one or more of a) rescued or increased amount of total seed fatty acid per seed, b) rescued or increased amount of said target fatty acid per seed, and c) rescued or increased proportion of said target fatty acid relative to said total seed fatty acid per seed.

[0028] In one embodiment, the present invention provides a method of modifying a plant or part thereof for providing a transgenic seed, comprising producing a transgenic plant or part thereof that comprises a transgenic plant cell, said transgenic plant cell comprising a) reduced expression of one or both of endogenous BADC1 and BADC3 genes, and b) expression of one or more transgenes that alters metabolism of a target fatty acid. In one embodiment, said transgenic seed comprises a transgenic plant cell having a) reduced expression of one or both of said endogenous BADC1 and BADC3 genes, and b) one or more transgene that alters metabolism of said target fatty acid. In one embodiment, said seed exhibits one or more of a) a rescued or increased amount of total seed fatty acid per seed, b) rescued or increased amount of said target fatty acid per seed, and c) rescued or increased proportion of said target fatty acid relative to said total seed fatty acid per seed.

[0029] In one embodiment, the present invention provides a transgenic seed that produces a transgenic plant or part thereof that comprises: a) genomic mutation of fad2, fad3, fae1 or any combination thereof, b) reduced expression of one or both endogenous BADC1 and BADC3 genes, and c) one or more transgenes that alter metabolism of a target fatty acid.

[0030] The invention further provides a transgenic seed that produces the plant or part thereof of any one or more of the invention's methods, wherein said transgenic seed A) comprises a transgenic plant cell having a) reduced or lacking expression of one or both of said endogenous BADC1 and BADC3 genes, and b) one or more transgene that alters metabolism of said target fatty acid, and B) exhibits one or more phenotype of producing a plant with a) increased amount of total seed fatty acid per plant, b) improved establishment of one or both of roots and plant aerial parts, c) rescued or increased seed yield per plant, d) rescued or increased seed germination rate, e) rescued or increased amount of total seed fatty acid per seed, f) rescued or increased amount of said target fatty acid per seed, g) rescued or increased seed yield per plant, and h) rescued or increased proportion of said target fatty acid relative to said total seed fatty acid per seed.

[0031] In one embodiment, the present invention provides a transgenic seed that produces a transgenic plant or part thereof that comprises a transgenic plant cell, said transgenic plant cell comprising a) reduced expression of one or both of endogenous BADC1 and BADC3 genes, and b) expression of one or more transgenes that alters metabolism of a target fatty acid, wherein said transgenic seed A) comprises a transgenic plant cell having i) reduced expression of one or both of said endogenous BADC1 and BADC3 genes, and ii) one or more transgene that alters metabolism of said target fatty acid, and B) exhibits one or more phenotype of producing a plant with i) increased amount of total seed fatty acid per plant, ii) improved establishment of one or both of roots and plant aerial parts, iii) rescued or increased seed yield per plant, iv) rescued or increased seed germination rate, v) rescued or increased amount of total seed fatty acid per seed, vi) rescued or increased amount of said target fatty acid per seed, vii) rescued or increased seed yield per plant, and viii) rescued or increased proportion of said target fatty acid relative to said total seed fatty acid per seed.

[0032] The invention also provides a tissue culture of regenerable cells of any one or more of the transgenic plant or part thereof of the invention.

[0033] In one embodiment, the present invention provides a tissue culture of regenerable cells of a transgenic plant or part thereof that comprises a transgenic plant cell, wherein said transgenic plant cell comprises a) reduced or lacks expression of one or both of said endogenous BADC1 and BADC3 genes, and b) one or more transgene that alters metabolism of said target fatty acid, wherein said transgenic plant or plant part exhibits one or more phenotype of a) increased amount of total seed fatty acid per plant, b) improved establishment of one or both of roots and plant aerial parts, and c) rescued or increased seed yield per plant.

[0034] In one embodiment, the present invention provides a method of producing a target fatty acid using a transgenic plant or part thereof that comprises: a) genomic mutation of fad2, fad3, fae1 or any combination thereof, b) reduced expression of one or both endogenous BADC1 and BADC3 genes, and c) one or more transgenes that alter metabolism of said target fatty acid.

BRIEF DESCRIPTION OF THE DRAWINGS

[0035] The file of this patent contains at least one drawing executed in color. Copies of this patent with color drawings will be provided by the Patent and Trademark Office upon request and payment of the necessary fee.

[0036] FIG. **1** Genotyping of badc1,3/fae1/FAH. Individual plants were genotyped to be fae1 homozygous via HinfI digested PCR fragment of FAE1 gene fragment; badc1 or badc3 homozygous were verified using PCR with the indicated gene-specific primer pairs and combinations with T-DNA-specific primer LBb1.

[0037] FIG. **2**A-C Analysis of FIG. **2**A BADC1, FIG. **2**B BADC3 and FIG. **2**C FAH gene expression in developing seeds. Transcript levels of BADC1, 3 were analyzed by qRT-PCR in 11- to 13-DAF developing seeds of fae1, fae1/FAH, badc1,3/fae1/FAH and badc1,3, n=3 biological replicates, and error bars represent SE. The relative expression levels are reported relative to the expression of the UBQ10 (At4g05320) transcript. Columns with different letters are significantly different ($P<0.05$) computed by the relative expression (REST) software algorithm using three biological replicates (Pfaffl et al., 2002).

[0038] FIG. **3**A-**3**C Seed weight and FA content in seeds. (FIG. **3**A) FA per seed. FA was determined by 5 pooled sets of 100 seeds each. (FIG. **3**B) Oil content in seeds as a proportion of dry seed weight. Seed oil content, represented by total acyl lipids, was quantified by GC of fatty acid methyl esters. (FIG. **3**C) Mean weight of transgenic seeds determined by five pooled sets of 100 seeds each. Error bars represent SE. Columns with different letters are significantly different using the Student's t test ($P<0.05$) and five biological replicates.

[0039] FIG. **4** Hydroxy FA content in seeds. HFA is expressed as a weight percentage of the total seed FA. Values represent the mean±standard deviation (n=3 pooled sets of

100 seeds). Student t test analysis found no significant difference between fae1/FAH and badc1,3/fae1/FAH (P<0.05).

[0040] FIG. **5** ACCase activity in developing seeds. [^{14}C] Acetate incorporation into total lipids showed ACCase activity in 11- to 13-DAF developing seeds of fae1, fae1/FAH/badc1,3 and badc1,3. Specified different letters indicate significant differences (P<0.05) as determined by Student's t test using three biological replicates. Values are presented as means±SD of three biological replicates.

[0041] FIG. **6**A-**6**C Seed germination and establishment. A total of 180 seeds in five equal replicates from each line were plated in ½ MS media containing 1% sucrose for 14 d. Germination is scored as seeds that produced a radicle, and seedlings that produced roots and green cotyledons were counted as being able to establish. The germination rates (FIG. **6**A) and establishment rates (FIG. **6**B) are calculated as to the percentage of total seeds plated. Values are presented as means±SD of five biological replicates. FIG. **6**C Seed yield per plant. n=10, and error bars represent ±SE. Columns with different letters are significantly different (P<0.05) of the five replicates.

[0042] FIG. **7** EMS mutation caused truncation of FAE1 in fae1 mutant. FAE1 gene was amplified from fae1 mutant an its sequence showed a mutated codon (TGG1395TGA, highlighted in green).

[0043] FIG. **8** Analysis of fatty acid synthesis related gene expression in developing seeds. Transcript levels of genes were analyzed by qRT-PCR in 11- to 13-DAF developing seeds of fae1, fae1/FAH, badc1,3/fae1/FAH and badc1,3, n=3 biological replicates, and error bars represent SD. RT-qPCR values are presented as percentages of internal control normalized as described in "Materials and Methods." No values were found to differ significantly (P<0.05) using three biological replicates computed by the relative expression (REST) software algorithm (Pfaffl et al., 2002).

[0044] FIG. **9** [^{14}C]acetate incorporation assay in developing seeds of badc1,3. Developing seeds 11-13 days after flowering were collected from badc1,3 seeds and their fatty acid synthesis rates were determined by measuring the rate of [^{14}C]acetate incorporation into FAs by total lipid extraction and scintillation counting. Incorporation of [^{14}C]acetate between 20 and 100 minutes at a 20 minutes interval.

[0045] FIG. **10** Seed germination and establishment. Seeds from fae1, fae1/FAH, badc1,3/fae1/FAH and badc1,3 were germinated on ½ MS medium with 1% sugar plate and 7 and 10 day old plants were photographed.

[0046] FIG. **11** Hydroxy FA content in seeds. HFA is expressed as a weight percentage of the total seed FA. Values represent the mean±standard deviation (n=5 pooled sets of 100 seeds representing 5 biological replicates). Student t test analysis found no significant difference between CL37 and CL37/badc1 lines, but significant difference between CL37 and 4 CL37/badc3 lines (P<0.05).

[0047] FIG. **12**A-**12**B Seed germination and establishment on media supplemented with sucrose. A total of 180 seeds in five replicates from each line were plated in ½ MS media supplemented with 1% sucrose. Germination is scored as seeds that produced a radicle, and seedlings that produced roots and green cotyledons were scored as establishment. The germination rates (FIG. **12**A) and establishment rates (FIG. **12**B) are calculated as to the percentage of total seeds plated. Values are presented as means±SD of five biological replicates. Genotypes with different letters are significantly different (P<0.05).

[0048] FIG. **13**A-B Seed germination and establishment on media without sucrose. A total of 180 seeds in five replicates from each line were plated in ½ MS media. Germination is scored as seeds that produced a radicle, and seedlings that produced roots and green cotyledons were scored as being able to establish. The germination rates (FIG. **13**A) and establishment rates (FIG. **13**B) are calculated as to the percentage of total seeds plated. Values are presented as means±SD of five biological replicates. Genotypes with different letters are significantly different (P<0.05) of the five replicates.

[0049] FIG. **14** Seed production per plant. Plants of fae1, CL37, and CL37/badc3 lines 2 and 19 were grown side by side, and seeds were collected at maturity. Seed yields per plant were weighed. n=18, and error bars represent ±SE. Columns with different letters are significantly different (P<0.05).

[0050] FIG. **15** Vector diagram of FAH plant expression vector. RcFAH gene is placed under the control of seed-specific phaseolin promoter.

[0051] FIG. **16**A: FAH (also referred to as RcFAH) nucleotide sequence: Gene ID #8267537, >NM_001323721.1 FAH mRNA.

[0052] FIG. **16**B: FAH amino acid sequence: NP_001310650.1 oleate hydroxylase FAH12 [*Ricinus communis*].

[0053] FIG. **16**C: *Camelina* BADC1, First isoform nucleotide sequence: >Csa04g042500.1.

[0054] FIG. **16**D: *Camelina* BADC1, First isoform amino acid sequence >Csa04g042500.1.

[0055] FIG. **16**E: *Camelina* BADC1, Second isoform nucleotide sequence >Csa06g030800.1.

[0056] FIG. **16**F: *Camelina* BADC1, Second isoform amino acid sequence >Csa06g030800.1.

[0057] FIG. **16**G: *Camelina* BADC1, Third isoform nucleotide sequence >Csa09g068300.1.

[0058] FIG. **16**H: *Camelina* BADC1, Third isoform amino acid sequence >Csa09g068300.1.

[0059] FIG. **16**I: *Camelina* BADC3, First isoform nucleotide sequence >Csa15g020290.1.

[0060] FIG. **16**J: *Camelina* BADC3, First isoform amino acid sequence >Csa15g020290.1.

[0061] FIG. **16**K: *Camelina* BADC3, Second isoform nucleotide sequence >Csa19g022480.1.

[0062] FIG. **16**L: *Camelina* BADC3, Second isoform amino acid sequence >Csa19g022480.1.

[0063] FIG. **16**M: *Camelina* BADC3, Third isoform nucleotide sequence >Csa01g018320.1.

[0064] FIG. **16**N: *Camelina* BADC3, Third isoform amino acid sequence >Csa01g018320.1.

[0065] FIG. **16**O: FAE1, AT4G34520, Coding sequence.

[0066] FIG. **16**P: FAE1, AT4G34520, Protein Sequence.

[0067] FIG. **16**Q: *Arabidopsis* FAD2, AT3G12120.1, Coding sequence.

[0068] FIG. **16**R: *Arabidopsis* FAD2, AT3G12120.1, Protein Sequence.

[0069] FIG. **16**S: *Arabidopsis* FAD3, AT2G29980.1, CDS.

[0070] FIG. **16**T: *Arabidopsis* FAD3, AT2G29980.1, Protein.

[0071] FIG. **16**U: mutant fatty acid elongation 1 (FAE1) DNA sequence (also see FIG. **7**).

[0072] FIG. **16**V: mutant fatty acid elongation 1 (fae1) protein sequence (also see FIG. **7**).

[0073] FIG. **17**A: *E. coli* Cyclopropane fatty acid synthase (EcCPS1) DNA, NCBI Gene ID: 944811; >NC_000913.3: 1741413-1742561.

[0074] FIG. **17**B: *E. coli* Cyclopropane fatty acid synthase (EcCPS1) protein, NP_416178.1.

[0075] FIG. **17**C: *Crepis palaestina* delta 12 fatty acid epoxygenase GenBank #: Y16283.1; >Y16283.1:30-1154 *Crepis palaestina* mRNA for delta 12 fatty acid epoxygenase.

[0076] FIG. **17**D: >CAA76156.1 delta 12 fatty acid epoxygenase [*Crepis palaestina*].

[0077] FIG. **17**E: *Crepis alpina* delta-12 fatty acid acetylenase GenBank #: DQ289485.1; >DQ289485.1 *Crepis alpina* delta-12 fatty acid acetylenase (vFAD2) gene, complete cds

[0078] FIG. **17**F: ABC00769.1 delta-12 fatty acid acetylenase [*Crepis alpina*].

[0079] FIG. **17**G: *Momordica charantia* Conjugase (FadX) GenBank #: AF182521.1; >AF182521.1 *Momordica charantia* delta-12 oleic acid desaturase-like protein (FadX) mRNA, complete cds.

[0080] FIG. **17**H: >AAF05916.1 delta-12 oleic acid desaturase-like protein [*Momordica charantia*].

DEFINITIONS

[0081] "Wild-type" and "normal" are interchangeably used when in reference to any molecule or its level (e.g., amino acid sequence, and nucleic acid sequence, etc.) and/or phenomenon or its level (e.g., expression of a gene, transcription of a DNA sequence, translation of an mRNA molecule to an amino acid sequence) and/or phenotype or its level (e.g., seed yield per plant, amount of total seed fatty acid per seed, amount of a target fatty acid per seed, seed yield per plant, seed germination rate, proportion of a target fatty acid relative to total seed fatty acid per seed, amount of total seed fatty acid per plant, establishment of roots, establishment of plant aerial parts) to mean that the molecule or its level and/or phenomenon or its level and/or phenotype or its level is the same as found in nature without alteration by the hand of man (such as by chemical and/or molecular biological techniques, etc.).

[0082] "Expression" refers to the transcription and stable accumulation of sense or anti-sense RNA derived from a nucleic acid. "Expression" may also refer to translation of mRNA into a polypeptide or protein. As used herein, the term "antisense RNA" refers to an RNA transcript that is complementary to all or a part of a mRNA that is normally produced in a cell. The complementarity of an antisense RNA may be with any part of the specific gene transcript, i.e., at the 5' non-coding sequence, 3' non-translated sequence, introns, or the coding sequence. As used herein, the term "RNA transcript" refers to the product resulting from RNA polymerase-catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complimentary copy of the DNA sequence, it is referred to as the primary transcript or it may be an RNA sequence derived from post-transcriptional processing of the primary transcript and is referred to as the mature RNA.

[0083] "Reducing gene expression" and grammatical equivalents refers to a reduction in one or both of DNA transcription into mRNA, and mRNA translation into a protein molecule. In one embodiment, reducing gene transcription refers to the absence (or observable decrease) in the level of protein and/or mRNA product from the target gene. Specificity refers to the ability to inhibit the target gene without manifest effects on other genes of the cell and without any effects on any gene within the cell that is producing the dsRNA molecule. The inhibition of gene expression of a target gene as described herein may result in novel phenotypic traits in the plant. Reduced gene expression may be achieved by completely silencing or down-regulating expression of a gene and/or partial or incomplete silencing or down-regulation of a gene and/or introducing a mutation into the gene. Post-transcriptional gene suppression by anti-sense or sense-oriented RNA to regulate gene expression in plant cells is known in the art, as is the use of dsRNA to suppress genes in plants. Post-transcriptional gene suppression in plants may employ both sense-oriented and anti-sense-oriented, transcribed RNA that is stabilized, e.g., as a hairpin or stem-and-loop structure. In one embodiment, BADC genes are partially or totally silenced by expression of an RNAi cassette as described in WO 2017/039834 and WO 2018/009626.

[0084] "Mutation" for reducing gene expression includes deletion, insertion and/or substitution of one or more nucleotides of the gene or of sequences regulating expression of the gene. In one embodiment, said mutation comprises deleting at least a portion of the coding region, deleting the entire gene, deleting at least a portion of sequences that regulates transcription of the gene, introducing an insertion and/or a frameshift mutation, etc. so that at least one mutated allele contains a deletion of the translation start site, transcription start codon, at least a portion of the promoter region, at least a portion of the coding region, or any combination thereof. In one embodiment, said deleted sequences may be replaced with polynucleotides that are exogenous to the deleted gene sequences and that are flanked by sequences that are complementary to polynucleotide regions of the endogenous gene that flank the deleted gene sequences. In a further embodiment, at least one mutated allele is generated by site specific recombination, frame shift mutation, homologous recombination, CRISPR gene editing, or any combination thereof, in a cell such as an embryonic stem cell or germ cell.

[0085] "Genome editing" refers to the process of modifying (by insertion and/or deletion and/or substitution) of the nucleotide sequence of a genome sequence (e.g., coding sequence, non-coding sequence, tandem repeats, transposable elements, retrotransposons, long terminal repeats (LTRs), Non-long terminal repeats (Non-LTRs), etc.), preferably in a pre-determined targeted manner. In some embodiments, genome editing methods are exemplified by the CRISPR-endonuclease system, which produces a site-specific modification of a target DNA as described in Doudna et al., U.S. Pat. No. 10,000,772 (incorporated by reference). "CRISPR" ("clusters of regularly interspaced short palindromic repeats") gene editing is exemplified in Examples 9 and 10, and is used to knockout plant genes in melon (Hooghvorst et al. (2019) Scientific Reports 9:17077) and *Brassica napus* FAD2 (Okuzaki et al. (2018) Plant Physiology and Biochemistry, Volume 131, October 2018, Pages 63-69).

[0086] "Transformation" is a process of introducing a DNA sequence or construct (e.g., a vector or expression cassette) into a cell or protoplast in which that exogenous DNA is incorporated into a chromosome or is capable of autonomous replication.

[0087] "Stable transformation" of a cell with a transgene means that the transgene is integrated within the cell's genome. Methods for genetic transformation of plants (including use of regulatory elements, terminators, marker genes) and for production and characterization of stably transformed plants are known in the art (WO 2018/009626).

[0088] "Transgenic" and "genetically engineered" cell refer to a cell whose genome has been manipulated by any molecular biological technique, including, for example, the introduction of a transgene, homologous recombination, knockin of a gene, knockout of a gene, and/or CRISPR gene editing.

[0089] The term "transgene" refers to any nucleic acid sequence that is introduced into the cell by experimental manipulations. A transgene may be an "endogenous" DNA sequence or a "heterologous DNA sequence."

[0090] "Endogenous" molecule (such as nucleotide sequence, amino acid sequence, fatty acid) is a molecule natively found in nature in a host cell or a cell of the same species. In one embodiment, an endogenous sequence may be overexpressed or expressed at a higher level compared to wildtype and still be considered endogenous.

[0091] "Heterologous" and "foreign" molecule (such as nucleotide sequence, amino acid sequence, fatty acid) is a molecule that is not endogenous. In one embodiment, a heterologous sequence contains some modification (e.g., mutation, the presence of a selectable marker gene, etc.) relative to the naturally-occurring sequence. In this respect, the heterologous sequence may be native to the host genome, but be rearranged with respect to other genetic sequences within the host sequence. For example, a regulatory sequence may be heterologous in that it is linked to a different coding sequence relative to the native regulatory sequence. In addition, a particular sequence can be "heterologous" with respect to a cell or organism into which it is introduced (for example, a sequence that does not naturally occur in that particular cell or organism).

[0092] "BADC1" gene refers to accession AT3G56130 and/or orthologs thereof. In one embodiment, BADC1 gene is exemplified by one or more of the three isoform sequences in FIGS. **16**C, **16**E and **16**G, including nucleotide sequences that comprise from about 34%, 40%, 50%, 60%, 62%, 70%, 80%, 85%, 90%, 95% to about 100% sequence identity to sequences in FIGS. **16**C, **16**E and **16**G, or a complement thereof. In another embodiment, BADC1 gene encodes a polypeptide comprising from about 34%, 40%, 50%, 60%, 62%, 70%, 80%, 85%, 90%, 95% to about 100% sequence identity to any one of the three isoform polypeptide sequences in FIGS. **16**D, **16**F and **16**H. In one embodiment, BADC1 gene is exemplified by sequences described in WO 2018/009626, including nucleotide sequences that comprise from about 34%, 40%, 50%, 60%, 62%, 70%, 80%, 85%, 90%, 95% to about 100% sequence identity to WO 2018/009626's nucleotide sequence SEQ ID NO: 2, or a complement thereof. In another embodiment, BADC1 gene encodes a polypeptide comprising from about 34%, 40%, 50%, 60%, 62%, 70%, 80%, 85%, 90%, 95% to about 100% sequence identity to WO 2018/009626's polypeptide sequence SEQ ID NO: 1.

[0093] "BADC3" gene refers to accession AT3G15690 and/or orthologs thereof. In one embodiment, BADC3 gene is exemplified by one or more of the three isoform sequences in FIGS. **16**I, **16**K and **16**M, including nucleotide sequences that comprise from about 34%, 40%, 50%, 60%, 62%, 70%, 80%, 85%, 90%, 95% to about 100% sequence identity to sequences in FIGS. **16**I, **16**K and **16**M, or a complement thereof. In another embodiment, BADC3 gene encodes a polypeptide comprising from about 34%, 40%, 50%, 60%, 62%, 70%, 80%, 85%, 90%, 95% to about 100% sequence identity to any one of the three isoform polypeptide sequences in FIGS. **16**J, **16**L and **16**N. In one embodiment, BADC3 gene is exemplified by sequences described in WO 2018/009626, including nucleotide sequences that comprise from about 34%, 40%, 50%, 60%, 62%, 70%, 80%, 85%, 90%, 95% to about 100% sequence identity to WO 2018/009626's nucleotide sequence SEQ ID NO: 6, or a complement thereof. In another embodiment, BADC1 gene encodes a polypeptide comprising from about 34%, 40%, 50%, 60%, 62%, 70%, 80%, 85%, 90%, 95% to about 100% sequence identity to WO 2018/009626's polypeptide sequence SEQ ID NO: 5.

[0094] "Ortholog" genes refers to genes that are related by vertical descent from a common ancestor and encode proteins with the same function in different species. In one embodiment, ortholog nucleotide sequences comprise from about 34%, 40%, 50%, 60%, 62%, 70%, 80%, 85%, 90%, 95% to about 100% sequence identity. In another embodiment, ortholog polypeptide sequences comprise from about 34%, 40%, 50%, 60%, 62%, 70%, 80%, 85%, 90%, 95% to about 100% sequence identity. By contrast, "paralogs" are homologous genes that have evolved by duplication and code for protein with similar, but not identical functions. Exemplary orthologs of BADC1 gene and BADC3 gene, and proteins encoded by these genes, are described in WO 2018/009626, and the following Table 1 with respect to *Camelina sativa, Glycine max* and *Brassica napus*.

TABLE 1

BADC orthologs

A. thaliana gene	TAIR ID	sub-genome/ block[1]	Ensembl Plants gene ID	species
BADC1	AT3G56130	LF	Csa04g042500	*Camelina sativa*
BADC1	AT3G56130	MF1	Csa06g030800	*Camelina sativa*
BADC1	AT3G56130	MF2	Csa09g068300	*Camelina sativa*
BADC1	AT3G56130	A LF	GSBRNA2T00037117001	*Brassica napus*
BADC1	AT3G56130	C LF	GSBRN A2T00155998001	*Brassica napus*
BADC1	AT3G56130	n/a	GLYMA_11G35740	*Glycine max*
BADC1	AT3G56130	n/a	GLYMA_18G02670	*Glycine max*
BADC2	AT1G52670	LF	Csa17g092720	*Camelina sativa*
BADC2	AT1G52670	MF1	Csa14g061920	*Camelina sativa*
BADC2	AT1G52670	MF2	Csa03g059640	*Camelina sativa*

TABLE 1-continued

BADC orthologs				
A. thaliana gene	TAIR ID	sub-genome/ block[1]	Ensembl Plants gene ID	species
BADC3	AT3G15690	LF	Csa15g020290	*Camelina sativa*
BADC3	AT3G15690	MF1	Csa19g022480	*Camelina sativa*
BADC3	AT3G15690	MF2	Csa01g018320	*Camelina sativa*
BADC3	AT3G15690	A MF1	GSBRNA2T00010009001	*Brassica napus*
BADC3	AT3G15690	A LF	GSBRNA2T00104942001	*Brassica napus*
BADC3	AT3G15690	C MF1	GSBRNA2T00018165001	*Brassica napus*
BADC3	AT3G15690	C LF	GSBRNA2T00044654001	*Brassica napus*
BADC2/3[2]	AT1G52670/ AT3G15690	n/a	GLYMA_13G44040	*Glycine max*
BADC2/3	AT1G52670/ AT3G15690	n/a	GLYMA_15G01300	*Glycine max*

[0095] In Table 1, sub-genome information is only given for Brassicaceae species. BADC2 and BADC3 are thought to be derived through a gene duplication event at the base of the Brassicaceae. Therefore, GLYMA13G44040 and GLYMA15G01300 are homologs to an ancient precursor of BADC2 and BADC3.

[0096] "Seed-specific" promoter refers to a promoter that preferentially controls expression of an operably linked transgenes in seed products. Seed specific promoters are exemplified by the seed-specific phaseolin promoter, Napin promoter, β-conglycinin promoter, pea legumin legA promoter, and foxtail millet pF128 promoter.

[0097] "Fatty acid" refers to a carboxylic acid consisting of a hydrocarbon chain and a terminal carboxyl group, especially any of those occurring as esters in fats and oils. Fatty acid includes "unusual fatty acid," "special fatty acid" and "specialty fatty acid," which interchangeably refer to any fatty acid that is naturally found in a plant or plant part (such as seed) at less than 2 mole percent. Unusual fatty acids in seed oils from different species have identified more than 200 naturally occurring fatty acids of which 18 representatives are listed in the following Table 2 (David Hildebrand, "Production of Unusual Fatty Acids in Plants—AOCS Lipid Library" 2018):

[0098] In one embodiment, the fatty acid comprises one or more of hydroxyl fatty acids, medium-chain fatty acids, very-long-chain fatty acids (VLCFAs), monounsaturated fatty acids (MUFAs), γ-linolenic acid, stearidonic acids, α-eleostearic acid, conjugated fatty acids, epoxy fatty acids, cyclic fatty acids and acetylenic fatty acids, medium-chain fatty acids such as lauric acid and derivatives; very-long-chain fatty acids (VLCFAs) such as erucic acid; monounsaturated fatty acids (MUFAs) such as palmitoleic acid (also referred to as cis-9-hexadecenoic acid (16:1Δ9)), oleic acid (18:1Δ9) and petroselinic acid (18:1Δ6); γ-Linolenic acid (Δ6,9,12-18:3); stearidonic acids such as octadecatetraenoic acid (Δ6,9,12,15-18:4); conjugated fatty acids such as α-Eleostearic acid (9-cis,11-trans,13-trans-octadecatrienoic acid), calendic acid (trans-8,trans-10,cis-12-octadecatrienoic acid), punicic acid (cis-9,trans-11,cis-13-octadecatrienoic acid, parinaric acid (cis-9,trans-11,trans-13,cis-15-octadecatetraenoic acid), licanic acid (4-oxo-cis-9,trans-11, trans-13-octadecatrienoic acid), and catalpic acid (trans-9, trans-11,cis-13-octadecatrienoic acid); epoxy fatty acids, such as vemolic (cis-12,13-epoxyoctadeca-cis-9-enoic) and coronaric (cis-9,10-epoxyoctadeca-cis-12-enoic) acids, acetylenic fatty acids, 9,10-epoxystearic acid, alchornoic acid (14,15-epoxycis-11-eicosenoic acid), and 15-epoxy-

TABLE 2

Common name	Chemical name	High accumulator	% UFA
alchornoic	14-epoxy,cis-11-eicosenoic	*Alchornea cordifolia*	50
axillarenic	11,13-dihydroxy-tetracos-trans-9-enoic	*Baliospermum axillare*	3
calendic	trans-8,trans-10,cis-12-octadecatrienoic	*Calendula officinalis*	63
catalpic	trans-9,trans-11,cis-13-octadecatrienoic	*Catalpa bignonioides*	
dimorphecolic	9-hydroxy-trans,10-trans-12-octadecadienoic	*Dimorphotheca pluvialis*	60
coronaric	9-epoxy,cis-12-octadecenoic	*Chrysanthemum coronarium*	
crepenynic	octadec-cis-9-en-12-ynoic	*Crepis alpina*	74
eleostearic	cis-9,trans-11,trans-13-octadecatrienoic	*Aleurites fordii*	80
epoxystearic	9-epoxy-octadecanoic	*Tragopogon porrifolius*	3
isanolic	8-hydroxy-octadec-17-en-9,11-diynoic	*Ongokea gore*	
isoricinoleic	9-hydroxy-12-cis-octadecenoic	*Wrightia coccinea*	76
licanic	4-oxo-cis-9,trans-11,trans-13-octadecatrienoic	*Licania rigida*	78
lesquerolic	14-hydroxy-cis-11-eicosenoic	*Lesquerella fendleri*	55
parinaric	cis-9,trans-11,trans-13,cis-15-octadecatetraenoic	*Parinarium laurunum*	54
punicic	cis-9,trans-11,cis-13-octadecatrienoic	*Punicia granatum*	86
phloionolic	9,10,18-trihydroxy octadecanoic	*Chamaepeuce afra*	9
ricinoleic	12-hydroxy-9-cis-octadecenoic	*Ricinus communis*	88
vernolic	12-epoxy,cis-9-octadecenoic	*Vernonia galamensis*	80

cis-9,cis-12-octadecadienoic acid; and acetylenic fatty acids such as crepenynic acid (octadec-9-en-12-ynoic acid) (David Hildebrand, "Production of Unusual Fatty Acids in Plants—AOCS Lipid Library" 2018). Examples of hydroxyl fatty acids include ricinoleic acid (A-12-hydroxy-9-cis-octadecanoic acid or 12-d-hydroxy-octadeca-cis-9-enoic acid) and densipoleic acid (9Z,12R,15Z)-12-hydroxyoctadeca-9,15-dienoate.

[0099] "Rescued" means that if a first plant exhibits a first phenotype that is altered (increased or decreased) by a first mutation to a first nucleotide or polypeptide sequence, then a second mutation to the same or different nucleotide or polypeptide sequence is said to "rescue" the first phenotype if a second plant that has both the first and second nucleotide or polypeptide mutations exhibits substantially the same phenotype as the first plant, and the phenotype is said to be "rescued" by the second mutation. For example, if a wild type plant exhibits a first level of seed germination that is decreased by overexpression of FAH gene, then a mutation to genomic BADC3 gene is said to rescue the seed germination phenotype if a second plant that has both the FAH gene and mutant genomic BADC3 gene exhibits substantially the same level of seed germination as the wild type plant, and the seed germination phenotype is said to be "rescued" by the BADC3 gene mutation.

[0100] "Seed yield" means the number of seeds and/or weight of seeds.

[0101] "Germination" refers to the process whereby the seed coat splits and root and cotyledons start to poke out of the seed, after a dry seed is exposed to desired germination conditions such as water, light, soil, etc.

[0102] "Establishment" refers to the process whereby roots and aerial parts of a plant start to grow as a seedling starts to develop after a dry seed is exposed to desired germination conditions such as water, light, soil, etc. "Improved establishment" of roots or aerial parts of the plant refers to an increase in one or more of the length, girth and branching or roots and/or aerial parts of the plant.

[0103] "Plant" refers to a living thing that grows in the earth and has a stem, leaves, and roots, exemplified by organisms that contain orthologs to the *Arabidopsis thaliana* BADC genes, such as *Amborella trichopoda, Arabidopsis lyrata, Arabidopsis alpine, Arachis hypogaea, Auxenochlorella protothecoides, Brassica napus, Brassica rapa, Camelina sativa, Capsella rubella, Cathamus tinctorius, Chlamydomonas reinhardtii, Chlorella variabilis, Cicer arietinum, Citrus clementina, Citrus sinensis, Coccomyxa subellipsoideas* C-169, *Coffea canephora, Cucumis melo, Cucumis sativus, Elaeis guineensis, Erythranthe guttata, Eucalyptus grandis, Eutrema salsugineum, Fragaria vesca, Genlisea aurea, Glycine max, Helianthus annuus, Helicosporidium* ATCC 50920, *Jatropha curcas, Lotus japonicas, Medicago truncatula, Marus notabilis, Musa acuminate, Nelumbo nuciera, Nicotiana sylvestris, Nicotiana tomentosiformis, Phaseolus vulgaris, Pheonix dactylifera, Physcomitrella patens, Picea sitchensis, Polytomella parva, Populus trichocarpa, Prunus mume, Prunes persica, Pyrus* x *bretschneideri, Ricinus communis, Selaginella moellendorffli, Sesamum indicum, Solanum lycopersicum, Solanum tuberosum, Theobroma cacao, Thlaspi arvense, Vitis viniera*, or *Volvox carteri.*

[0104] A cell or organism is "homozygous" for a particular gene when identical alleles of the gene are present on all the homologous chromosomes. Thus, a diploid cell is homozygous for a particular gene when the cell contains two identical alleles of the gene. A cell or organism is "homozygous null" (also referred to as "nullizygous" and "nullizygote") for a particular gene when it contains only mutant alleles for the same gene, and all the mutant alleles are complete loss-of-function (i.e., "null") alleles. Thus, a diploid cell is homozygous null for a particular gene when the cell contains two null alleles of the gene. Null mutant BADC (i.e., BADC1 and/or BADC3) plants may be generated by crossing a male transgenic plant and a female transgenic plant each bearing one artificially mutated BADC allele in its germ cells.

[0105] A cell or organism is "heterozygous" for a particular gene when different alleles of the gene are present on the homologous chromosomes. Thus, a diploid cell is heterozygous for a particular gene when the cell contains two different alleles (e.g., one wild-type allele and one mutant allele) of the gene.

[0106] "Breeding" and "crossing" and "crossbreeding" interchangeably refers to the process of selectively propagating plants with desirable characteristics using closely or distantly related individuals to produce new plant varieties or lines with desirable properties. In one embodiment, crossing a plant line having one or more transgenes and/or genomic modifications relative to a starting plant line means the techniques that result in the one or more transgenes and/or genomic modifications of the invention being introduced into a plant line by crossing a plant of a starting line with a plant of a donor plant line that comprises one or more transgenes and/or genomic modifications of the invention. Methods for breeding (such as to produce plants that are homozygous for a transgene) are disclosed herein and known in the art (WO 2018/009626).

[0107] Plant "part" refers to a plant cell and/or tissue and/or organ, exemplified by seed, leaf, pollen, ovule, fruit, rootstock, flower and scion. In one embodiment, the plant tissue comprises tissue obtained directly or indirectly (e.g., by tissue culture of regenerable cells) from the plant. In a further embodiment, the plant part comprises a seed that produces, and/or is produced by, a plant produced by the presently disclosed methods.

[0108] "Regenerable" plant cells include protoplasts and embryogenic cells. Illustrative methods for tissue culture for the regeneration of cereals from protoplasts have been described (Toriyama et al., 1986; Yamada et al., 1986; Abdullah et al., 1986; Omirulleh et al., 1993 and U.S. Pat. No. 5,508,184; each specifically incorporated herein by reference in its entirety).

[0109] "Progeny" denotes the offspring of any generation of a parent plant prepared in accordance with the instant invention. In one embodiment, the progeny exhibits one or more phenotypes of the parent plant, and comprises one or more of the transgenes and one or more of the genomic modifications of the parent plant.

[0110] The terms "reduce," "inhibit," "diminish," "suppress," "decrease," and grammatical equivalents (including "lower," "smaller," etc.) when in reference to the level of any molecule (e.g., amino acid sequence, and nucleic acid sequence, etc.) and/or phenomenon (e.g., level of expression of a gene, level of transcription of a DNA sequence, level of translation of an mRNA molecule to an amino acid sequence) and/or phenotype (e.g., seed yield per plant, amount of total seed fatty acid per seed, amount of a target fatty acid per seed, seed yield per plant, seed germination

rate, proportion of a target fatty acid relative to total seed fatty acid per seed, amount of total seed fatty acid per plant, establishment of roots, establishment of plant aerial parts) in a first composition (e.g., first plant cell) relative to a second composition (e.g., second plant cell), mean that the quantity of molecule and/or phenomenon and/or phenotype in the first composition is lower than in the second composition by any amount that is statistically significant using any art-accepted statistical method of analysis. In one embodiment, the quantity of molecule and/or phenomenon and/or phenotype in the first composition is at least 10% lower than, at least 25% lower than, at least 50% lower than, at least 75% lower than, at least 90% lower and/or 100% lower than the quantity of the same molecule and/or phenomenon and/or phenotype in the second composition. In one embodiment, the first composition lacks (i.e., contains 0% of) the molecule and/or phenomenon and/or phenotype.

[0111] The terms "increase," "elevate," "raise," and grammatical equivalents (including "higher," "greater," etc.) when in reference to the level of any molecule (e.g., amino acid sequence, and nucleic acid sequence, etc.) and/or phenomenon (e.g., level of expression of a gene, level of transcription of a DNA sequence, level of translation of an mRNA molecule to an amino acid sequence) and/or phenotype (e.g., seed yield per plant, amount of total seed fatty acid per seed, amount of a target fatty acid per seed, seed yield per plant, seed germination rate, proportion of a target fatty acid relative to total seed fatty acid per seed, amount of total seed fatty acid per plant, establishment of roots, establishment of plant aerial parts) in a first composition (e.g., first plant cell) relative to a second composition (e.g., second plant cell), mean that the quantity of molecule and/or phenomenon and/or phenotype in the first composition is higher than in the second composition by any amount that is statistically significant using any art-accepted statistical method of analysis. This includes, without limitation, a quantity of molecule and/or phenomenon and/or phenotype in the first composition that is at least 10% greater than, at least 15% greater than, at least 20% greater than, at least 25% greater than, at least 30% greater than, at least 35% greater than, at least 40% greater than, at least 45% greater than, at least 50% greater than, at least 55% greater than, at least 60% greater than, at least 65% greater than, at least 70% greater than, at least 75% greater than, at least 80% greater than, at least 85% greater than, at least 90% greater than, and/or at least 95% greater than the quantity of the same molecule and/or phenomenon and/or phenotype in the second composition.

[0112] The terms "alter" and "modify" when in reference to the level of any molecule (e.g., amino acid sequence, and nucleic acid sequence, etc.) and/or phenomenon (e.g., level of expression of a gene, level of transcription of a DNA sequence, level of translation of an mRNA molecule to an amino acid sequence) and/or phenotype (e.g., seed yield per plant, amount of total seed fatty acid per seed, amount of a target fatty acid per seed, seed yield per plant, seed germination rate, proportion of a target fatty acid relative to total seed fatty acid per seed, amount of total seed fatty acid per plant, establishment of roots, establishment of plant aerial parts) in a first composition (e.g., first plant cell) relative to a second composition (e.g., second plant cell), mean that the quantity of molecule and/or phenomenon and/or phenotype in the first composition refer to an increase and/or decrease in the level of molecule and/or phenomenon and/or phenotype.

DESCRIPTION OF THE INVENTION

[0113] Hundreds of naturally occurring specialized fatty acids (FA) may have potential as chemical feedstocks if they can be produced at large scale by crop plants. However, transgenic expression of their biosynthetic genes has generally been accompanied by undesirable reductions in oil yield. For example, expression of *Ricinus* fatty acid hydroxylase (FAH) in the *Arabidopsis* fatty acid elongation mutant fae1 resulted in a 50% reduction of FA synthesis rate that was attributed to inhibition of acetyl Co-A carboxylase (ACCase) by an undefined mechanism. The hypothesis that the ricinoleic acid-dependent decrease in ACCase activity is mediated by biotin attachment domain-containing (BADC) proteins was tested.

[0114] BADCs are inactive homologs of biotin carboxy carrier protein that lack a biotin cofactor and can inhibit ACCase. *Arabidopsis* contains three BADC genes. To reduce expression levels of BADC1 and BADC3 in fae1/FAH, homozygous badc1,3/fae1/FAH was created. The rate of FA synthesis in badc1, 3/fae1/FAH seeds doubled relative to fae1/FAH, restoring it to fae1 levels, increasing both native FA and HFA accumulation. Total FA per seed, seed oil content and seed yield per plant all increased in badc1,3/fae1/FAH, to 5.8 μg, 37% and 162 mg, respectively, relative to 4.9 μg, 33% and 126 mg, respectively, for fae1/FAH. Transcript levels of fatty acid synthesis-related genes including ACCase subunits did not significantly differ between badc1,3/fae1/FAH and fae1/FAH. These results demonstrate that BADC1 and BADC3 mediate ricinoleic acid-dependent inhibition of FA synthesis. It is proposed that BADC-mediated FAS (fatty acid synthesis) inhibition may be a general mechanism that limits FA accumulation in specialized FA-accumulating seeds.

[0115] A longstanding crop improvement goal has been to exploit knowledge of specialized fatty acid synthesis from plants and microbes by reconstructing their synthetic pathways in crop production plants (Napier, 2007). If successful, this would allow the production of chiral fatty acid feedstocks in an inexpensive and scalable manner. However, a barrier to progress in this area was the discovery that upon the accumulation of specialized fatty acids seed oil yields are significantly decreased (Cahoon et al., 2007; Haslam et al., 2013; Vanhercke et al., 2013; Bates et al., 2014). An example of this comes from attempts to increase the accumulation of hydroxy fatty acid (HFA) in seed oils, of which much of the work has been performed in the model system *Arabidopsis* (Lu et al., 2006).

[0116] HFAs contain one or more hydroxy group(s) on a fatty acid backbone, which confer beneficial properties such as higher viscosity and chemical reactivity. The hydroxyl group of HFAs make them useful chemical feedstocks for the production of a wide range of industrial products including but not limited to: resins, waxes, nylons, plastics, lubricants, cosmetics, and additives for coatings and paints (Kim et al., 2000). Moreover, HFAs could be used as intermediates in the production of biodegradable plastics, cyclic lactones and pharmaceuticals (Wang et al., 2012). Industrial use of HFAs are available from natural sources such as castor beans which may limit their availability. Isolation of the oleate hydroxylase FAH from castor bean

over two decades ago raised the possibility of ricinoleic acid production in high-yielding oilcrops (van de Loo et al., 1995). However, in contrast to castor beans that accumulate approximately 90% of its FA as ricinoleic acid, transgenic *Arabidopsis* fatty acid elongation1 (fae1) mutant expressing the FAH i.e., fae1/FAH, (a line designated CL37) accumulated only 17% HFA in its total seed oil (Lu et al., 2006). The seeds of fae1/FAH also displayed many physiological deficits including reduced oil content and seed weight, low seed yield per plant compared with its parental fae1 line, and seed germination was also delayed (Adhikari et al., 2016).

[0117] Investigation of the reduced oil content of fae1/FAH revealed its FA synthesis rate was reduced compared to the parental fae1 line (Bates et al., 2014). While the molecular basis for this reduction in FA synthesis has not been reported, several attempts at overcoming it have proved at least partially successful. For example, overexpressing a master transcriptional regulator of fatty acid synthesis WRINKLED1 (Adhikari et al., 2016) or a lipid droplet associated factor SEIPIN1 to increase lipid droplet size (Lunn et al., 2018). Development defects of HFA-accumulating seeds are partially mitigated upon the expression of several castor acyltransferases (Lunn et al., 2018). Stacking the expression of several castor acyltransferases, including GPAT9, LPAT2, and PDAT1A along with the castor hydroxylase fae1/FAH seeds produced abundant tri-HFA TAG, restored seed oil content and partially restored seedling establishment (Lunn et al., 2019). The expression of phosphatidylcholine:diacylglycerol cholinephosphotransferase (PDCT), encoded by the REDUCED OLEATE DESATURATION1 (ROD1) gene (Lu et al., 2009) which channels about 40% of the flux of polyunsaturated fatty from PC into DAG for TAG synthesis was found to potentiate efficient accumulation of HFA in *Arabidopsis* (Hu et al., 2012).

[0118] In dicotyledonous plants, heteromeric acetyl-CoA carboxylase (ACCase) catalyzes the first committed step of de novo fatty acid biosynthesis. This enzyme complex consists of four catalytic subunits: biotin carboxylase (BC), carboxyltransferase (CT)-α, CT-β, and biotin carboxyl carrier protein (BCCP) (Salie et al., 2016). The two BCCP isoforms (BCCP1 and BCCP2) of *Arabidopsis* ACCase can interact with Biotin/lipoyl attachment domain containing (BADC) proteins (Feria Bourrellier et al., 2010). BADCs are BCCP homologs that contain a biotin attachment motif, but critically lack a biotinylation site. BADC proteins can act as negative regulators of ACCase due to their lack of the biotin adduct required for carboxylation (Salie et al., 2016) and a role for them in ACCase assembly was recently proposed. These proteins have been reported to significantly inhibit ACCase activity in both *E. coli* and *Arabidopsis* (Salie et al., 2016), and it was recently proposed that they can sense pH changes (Ye et al., 2020). An additional role for BADCs in ACCase assembly has also been proposed (Shivaiah et al., 2020).

[0119] Three BADC genes have been identified in *Arabidopsis*, single badc1, badc2, badc3 *Arabidopsis* knock-out mutants do not exhibit significant changes in oil content relative to wild type plants (Keereetaweep et al., 2018), while the badc1badc3 (badc1,3) double mutant showed increased fatty acid synthesis rate and a remarkable 25% increase in seed oil content (Keereetaweep et al., 2018).

[0120] In this context, badc1,3/fae1/FAH homozygous plant were generated by crossing badc1,3 double mutant with CL37, an *Arabidopsis* fae1 line expressing FAH (Lu et al., 2006). Downregulation of BADC1 and BADC3 in fae1/FAH doubled the rate of FA synthesis in developing seeds, restoring it to fae1 levels, and increased both native FA and HFA accumulation.

DISCUSSION OF EXEMPLARY EMBODIMENTS

[0121] It was previously reported that the accumulation of HFA in *Arabidopsis* seeds resulted in feedback inhibition of FA synthesis (Bates et al., 2014), with ACCase activity reduced by approximately 50% relative to the parental fae1 line. ACCase is often considered a rate limiting enzyme for FA synthesis and is therefore under tight genetic and biochemical regulation by a variety of mechanisms (Salie et al., 2016; Ye et al., 2020). In this study, we investigated the effects of null mutations in two negative regulatory subunits of ACCase i.e., badc1 and badc3 in FAH-expressing *Arabidopsis* seeds with respect to FA synthesis, common FA and HFA accumulation. The data demonstrates that eliminating BADC1 and BADC3 alleviates the HFA-dependent feedback inhibition of ACCase that results in a doubling FAS rate in badc1,3/fae1/FAH seeds restoring them to that of the parental fae1 line. Seed FA content of badc1,3/fae1/FAH was also restored to that of the parental fae1 line. That no significant increases were observed for transcripts corresponding to key FA synthesis-related genes in badc1,3/fae1/FAH is consistent with the increases being attributed to relief of BADC1 and BADC3-dependent inhibition of ACCase. Thus, data presented here employing badc1,3 null mutants demonstrates both the mechanism of HFA-dependent inhibition of ACCase and an approach to largely mitigating its effects by reducing or eliminating BADC isoforms 1 and 3. That the increased seed oil content in badc1,3/fae1/FAH didn't fully rescue seed weight relative to the parental fae1 line is consistent with previous reports in which the badc1,3 double mutant exhibited a small decrease in seed weight compare to that of wild type seeds, that likely resulted from a buildup of non-esterified FA under conditions in which their supply exceeds cellular demand. Support for this view comes from studies showing excess FAs can be associated with negative cellular consequences, including reductions in axillary bud growth in tobacco (Tso, 1964), microalgal growth (Bosma et al., 2008), cell elongation in *Arabidopsis* (Li et al., 2011) and cell death in *Arabidopsis* (Fan et al., 2013; Yang et al., 2015).

[0122] The work presented here is an extension of previous studies that focused on understanding mechanisms underlying lipid homeostasis under conditions in which FA supply exceeds that of cellular demand. Using a *Brassica napus* suspension cell culture we fed FA in the form of Tween esters and monitored reductions in the rate of FAS. Exposure of oleoyl-Tween for up to 2 days resulted in oleoyl-ACP-dependent reversible inhibition of ACCase (Andre et al., 2012); whereas prolonged exposure resulted in irreversible BADC-dependent inhibition (Keereetaweep et al., 2018). That BADC-dependent inhibition of ACCase activity can be elicited by chronic exposure to excesses oleate, a common naturally occurring monounsaturated FA, and ricinoleic acid, a non-native fatty acid, is intriguing. Evidence is accumulating that BADCs are conditional inhibitors of ACCase activity, i.e., that upon the accumulation of excess FA, biotin-lacking, and therefore inactive BADC subunits, replace active BCCP subunits in the

BC/BCCP ACCase subcomplex (Salie et al., 2016) (Keereetaweep et al., 2018)(Liu et al., 2019). Based on in vitro studies in which a one-unit pH change caused small changes in the dissociation constants of BADCs and BCCP for BC, it has been proposed that this might contribute to in vivo changes in the inhibition of ACCase related to light- and dark-dependent pH changes (Ye et al., 2020). However, in vivo evidence to support this hypothesis is lacking, and the experiments were conducted under non-physiological conditions. Thus, whether excess FA causes BCCP to dissociate from BC, allowing BADC to join the complex, or whether excess FA drives BADCs into the complex displacing BCCP subunits is an open question that requires additional investigation to resolve.

[0123] Due to the desirability of creating an HFA-accumulating variant of a high-yielding crop, work to date has mostly focused on increasing the accumulation of HFA without deleterious effects on seed oil content. Previous studies have shown that negative HFA-dependent deficits including decreased seed oil and seed weight could be mitigated by the overexpression of several common fatty acid accumulation factors. For example, overexpression of OLEOSIN1, a lipid droplet protection protein involved in TAG biosynthesis with FAH was shown to enhance HFA accumulation (Lu et al., 2006). Likewise, overexpression of SEIPIN, a lipid droplet development factor that was previously reported to increase total seed oil (Cai et al., 2015), when expressed in HFA-accumulating seed, increased both total oil and HFA content by more than 60%, likely by increasing LD size and creating a larger sink for TAG-accumulation (Lunn et al., 2018). Seed-specific expression of the WRINKLED1 transcription factor in fae1/FAH restored FA content (Adhikari et al., 2016). Other efforts have focused on the use of factors isolated from species that naturally accumulate modified fatty acid (mFA), in which FA-metabolizing enzymes have evolved preference for mFA. These studies were initially focused on enhancing the transfer of mFA from PC into TAG (Burgal et al., 2008; Kim et al., 2011; van Erp et al., 2011; Hu et al., 2012; Li et al., 2012). In another interesting example, the 18C ricinoleic acid is elongated to the corresponding 20 C lesquerolic acid by a specialized *Physaria* elongase (Snapp et al., 2014). That lesquerolic acid alleviates feedback inhibition of FAS likely reflects decreased discrimination against lesquerolic relative to ricinoleic in its transfer from PC to TAG. Co-expression of multiple mFA-preferring enzymes, e.g., three castor acyltransferases: GPAT9, LPAT2, and PDAT1A in fae1/FAH seeds resulted in the production of abundant tri-HFA TAG and restored seed oil content relative to the parental fae1 line (Lunn et al., 2019).

[0124] The reduced levels of seed oil accumulation reported for HFA-accumulating seed is a general phenomenon common to other mFAs including epoxy (Li et al., 2012), conjugated (Cahoon et al., 2006) and cyclopropane (Yu et al., 2014) FA. The findings presented here demonstrating that knocking out BADC1 and BADC3 in FAH-producing *Arabidopsis* seeds restored the FA synthesis rate, total FA, seed yield may not be specific for HFA. Indeed, data herein suggests that reducing or eliminating BADC1 and BADC3 gene expression in other mFA-accumulating plants may have similar beneficial effects on mFA accumulation. Further, combining our BADC reduction strategy with the coexpression of other genes, or combinations of genes and/or factors described above will likely increase mFA accumulation to levels equivalent to, or exceeding those of, their natural hosts.

[0125] Germination rates typically decline with increasing accumulation levels of mFA (modified fatty acid) accumulation in non-native hosts, even in plants that accumulate normal levels of TAG such as described herein and in previous studies (Lunn et al., 2019). This suggests that mFA generally impair the mobilization of lipid reserves needed for energy production during the critical stages of germination (Lunn et al., 2019). Thus, cellular components that participate in the mobilization mFA-containing TAG, mFA transport and β-oxidation represent additional targets for characterization and expression in non-native hosts to improve cellular energy supplies needed for germination to create robust mFA crops of the future.

[0126] We tested the hypothesis that HFA-dependent reduction in FA synthesis can be mediated by BADCs by the introgression of badc1,3 into fae1/FAH. Consistent with the hypothesis, knocking out BADC1 and BADC3 expression increased FA synthesis rates in developing seeds by two-fold, restoring the FA synthesis rate to that of the parental fae1 line. This equally increased both normal FA and HFA accumulation in seeds. The total FA per seed and total oil content in seeds and seeds yield per plant all increased, to an average of 5.8 μg, 37% and 162 mg respectively, compared to 4.9 μg, 33% and 126 mg of fae1/FAH respectively. That fatty acid synthesis-related genes including ACCase subunits, FA condensing enzymes and transcription factors were not significantly increased upon knockout of BADC1 and BADC3, is consistent with the role of BADCs as inhibitors of FA synthesis. Knocking out BADC1 and BADC3 alleviated the inhibition of ACCase, providing a corresponding increase in the FA synthesis rate and steady or improvement in seedling establishment. Combining the deceased expression of BADCs described herein along with the expression of other demonstrated mFA accumulating factors will likely realize the goal of creating crops with industrially relevant levels of HFA-accumulation. This strategy will likely be generalizable to increasing accumulation of many other mFA in seed oils.

[0127] The badc1,3/fae1/FAH *Arabidopsis* showed better establishment than fae1/FAH although their establishment rates are similar. Roots of ten-day old plants were longer and better developed as were aerial parts of the plants. The seed yield per plant was also rescued.

[0128] Data herein shows (Example 10) that disruption of badc3 alone in CL37 (fae1/FAH) *Arabidopsis* increased HFA percentage. Surprisingly, although one expects this disruption to decrease FAS and seed weight and impair seed germination, nonetheless it was empirically determined that the seed weight and seed yield per plant were both increased significantly, and seed germination rate was restored to wild type levels. BADC3 are edited/silenced in specialized fatty acid (sFA) producing crops such as *Camelina*, soybean and *Brassica napus* in the same manner as disclosed herein regarding editing/silencing badc1,3. Disruption/silencing of BADC3 in specialized FA-producing crops should lead to increased sFA, crop yield and recovered seed germination.

EXPERIMENTAL

[0129] The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques

disclosed in the examples, which follow represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments, which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

Example 1

[0130] Materials and Methods

[0131] A. Plant Growth Conditions

[0132] *Arabidopsis* badc1,3 double mutant, CL37 (fae1/FAH) and fae1 mutant were used in this study. Seeds were surface sterilized with 70% (v/v) ethanol, followed by 20% (v/v) bleach with 0.01% (v/v) Triton X-100, and washed three to four times with sterile water. Seeds were stratified for 2 d at 4° C. in the dark and germinated on half-Murashige and Skoog (MS) medium supplemented with 1% (w/v) sucrose at 23° C. with a light/dark cycle of 18 h/6 h, photon flux density at 250 μmol m^{-2} s^{-1} plants were grown in walk-in growth chambers at 22° C. with 16 h photoperiod with photon flux density of 70 μmol m^{-2} s^{-1}.

[0133] B. Seed Germination and Establishment

[0134] Seeds of fae1, fae1/FAH, badc1,3/fae1/FAH and badc1,3 were sterilized with ethanol and bleach as described above. A total of 180 seeds in five replicates from each line were sown in plates with ½ MS media containing 1% sucrose under the conditions described above for 14 d. Germination is scored as seeds that produced a radicle, and seedlings that produced roots and green cotyledons were counted as being able to establish (Adhikari et al., 2016).

[0135] C. *Arabidopsis* Cross and Screening of Homozygous Plants

[0136] badc1,3/fae1!FAH were generated by crossing the CL37 (frteI!FAH) with badc1,3 double mutant. Homozygous lines were identified by genotyping using PCR coupled with HinfI digestion of PCR products and GC/MS analysis of FA of individual seeds. The genotyping primers used for BADC 1 and 3 are described previously (Keereetaweep et al., 2018). To genotyping fae1, fae1 gene was amplified from CL37 with primer (gFAE-F0: catgagtttgagtatacacatgtcta (SEQ ID NO: 36) and gF AE-R0: aaagaaatcatgtaaacctaaatagaaacgc (SEQ ID NO: 37) and purified for sequencing. According to the fae1 gene sequence information, primer fae-LP: gtgatcgatgagctagagaagaac (SEQ ID NO: 38) and fae-RP: caaggacta TTTGCCGATGCCTTGACATTGCGT AGAGCGAC (SEQ ID NO: 39) were designed to introduce a HinfI restriction site to the fae1 mutant. PCR fragment were restricted with HinfI and the fae1 mutant resulted in two fragments of 200 bp and 40 bp.

[0137] D. RNA Extraction and RT-qPCR

[0138] RNA from *Arabidopsis* seeds was extracted according to Wu et al (Wu et al., 2002). RNA quality and concentration were determined by Nanodrop spectroscopy. cDNA was prepared using SuperScript IV VILO Master Mix with ezDNase enzyme (Invitrogen) following manufacture's manual. So Advanced Universal SYBR Green Supermix (Bio-Rad) was used in the reaction mix. RT-qPCR was carried out on the CFX96 Real-time PCR Detection System (Bio-Rad). Gene-specific primers used in the analysis for BADC1 and BADC3 are the same as previously described (Keereetaweep et al., 2018).

[0139] FAH-qFI, AATATAGCCATCGCCGCCACCATT (SEQ ID NO: 40) and FAH-qRI: TGGCAAGCAAAGCGA TCGT AAGGT (SEQ ID NO: 41) were used for F AH. The primers used for reference gene UBQIO qF, ACCATCACTTTGGAGGTGGA (SEQ ID NO: 42) and UBQIO qR, GTCAATGGTGTCGGAGCTTT (SEQ ID NO: 43). Statistical analysis of RT-qPCR data was carried out with REST2009 (Pfaffl et al., 200

[0140] E. Fatty Acid Analyses

[0141] Fatty acid analyses were carried out as described (Broadwater et al., 2002). Lipids were extracted in methanol/chloroform/formic acid (20:10:1) from seeds and heptadecanoic acid (17:0) was added as an internal standard. Total seed lipids were converted into fatty acid methyl esters (FAMEs) in 5% H_2SO_4 in methanol at 90° C. for 60 minutes and extracted with hexane. FAMEs from single seeds were prepared by incubating the seed with 30 μL 0.2M trimethylsulfonium hydroxide in methanol (Butte et al., 1982). Lipid profiles and acyl group identification were analyzed on a Hewlett Packard 6890 gas chromatograph equipped with a 5973 mass selective detector and Agilent DB-FATWAX UI capillary column (30 m×0.25 μm×0.25 μm). The injector was held at 225° C. and the oven temperature was set at 170° C. for one minute and then increased to 250° C. at 10° C./min, finally hold at 250° C. for 7 minutes. The FA percentage values were presented as a mean of at least three biological replicates.

[0142] F. [^{14}C]Acetate Incorporation Assay

[0143] [1-^{14}C]Acetic acid, sodium salt, was purchased from PerkinElmer. Developing seeds at 11-13 days after flower were collected. Approximately 10 mg fresh developing seeds were labeled by incubating in 0.2 mCi of [^{14}C] acetate for 60 min at room temperature with constant shaking. Cells were subsequently rinsed three times with water. Total lipids were extracted with 500 μL of methanol: chloroform:formic acid (20:10:1, v/v). The organic phase was then extracted with 370 μL of 1 M KCl and 0.2 M H_3PO4 and suspended in 2 mL of Ultima Gold liquid scintillation cocktail (PerkinElmer). The incorporated radioactivity was measured in cpm with a scintillation counter (Packard BioScience).

Example 2

[0144] Generation of Badc1,3/Fae1/FAH Plants

[0145] To test the hypothesis that HFA-induced inhibition of fatty acid synthesis results from BADC-dependent inhibition of ACCase, we crossed the badc1,3 double mutant with CL37, a single-insertion homozygous FAH transgenic line in a homozygous mutant fatty acid elongase1 (fae1) background (Kunst L, 1992), the seeds of which are reported to contain 17% HFA (Lu et al., 2006). The level of 18:1, FAH's substrate, is only 13% of TFA in wild type Columbia, therefore fae1, which contains much higher levels (33%) of 18:1 in its seed oil was used. Seeds resulting from this cross were germinated and genetically screened to identify heterozygous badc1,3/fae1/FAH plants. F2 seeds from the heterozygous badc1,3/fae1/FAH plants were planted to screen for homozygous plants which were used for the following studies. The fae1 mutant (Kunst L, 1992), the badc1 and badc3 T-DNA insertion lines (Bohannon and Kleiman, 1978; Bolle et al., 2013) all in the *Arabidopsis thaliana* Columbia-0 background.

[0146] To screen for fae1 homozygous individuals, we first needed to determine the genetic lesion underlying the

fae1 mutant. To do this we amplified the fae1 open reading frame from CL37 and sequenced it. We identified a mutation encoding a premature termination at 1395 bp (TGG1393TGA) in the fae1 mutant allele (FIG. **7**). We next designed primers to introduce a HinfI restriction site to the PCR amplification of fae1 allele around the mutation site. Subsequent restriction digestion with HinfI of a 240 bp PCR fragment produced two fragments of 200 bp and 40 bp in the fae1 mutant, and only a single 240 bp fragment in the wide type. While the 40 bp fragment is weakly detectable on our gel system, the fae1 mutant displays the 200 bp fragment which can be distinguished from the wild type fragment which is characterized by the larger 240 bp band (FIG. **1**).

[0147] The genotypes of badc1 or badc3 were determined using gene specific primer pairs in combination with T-DNA specific primer. After screening more than 500 plants 5 badc1,3/fae1 homozygous plants carrying FAH gene were identified. GC/MS analysis of 20 individual seeds for HFA accumulation from each of the 5 badc1,3/fae1 homozygous lines was used to identify FAH expressing homozygotes lines characterized by the accumulation of HFA in all 20 seeds. Finally, we identified two badc1,3/fae1/FAH homozygous individuals.

Example 3

[0148] Knocking Out BADC1 and BADC3 Did not Change FAH Transcription

[0149] To assess whether badc1,3/fae1/FAH plants were null mutants for BADC1 (AT3G56130) and BADC3 (AT3G15690), we harvested developing seeds from siliques 11 to 13 day after flowering (DAF), and for comparison from fae1, fae1/FAH and badc1,3 seeds grown in parallel. Reverse transcription-quantitative PCR (RT-qPCR) of total RNA extracted from developing seeds confirmed that both BADC1 and BADC3 transcription were dramatically decreased in badc1,3/fae1/FAH and the badc1,3 double mutant (FIGS. **2**A and **2**B). To evaluate whether knocking out BADC1,3 affects FAH expression, we also quantified FAH transcription. As shown in FIG. **2**C, FAH transcription showed no significant change between badc1,3/fae1/FAH and fae1/FAH seeds, showing that knocking out BADC1 and BADC3 genes did not significantly affect FAH expression (FIG. **2**C).

Example 4

[0150] Disruption of BADC1 and BADC3 Did not Significantly Alter Transcript Levels of Other FA Synthesis Genes.

[0151] To investigate whether disrupting BADC1 and BADC3 expression affects the transcription of FA synthetic genes, the expression of several genes involved in the FA biosynthetic pathway were quantified by RT-qPCR. Using relative expression (REST)-specific analysis (Pfaffl et al., 2002) designed for comparing qPCR data, no significant changes in transcript abundance were observed for ACCase subunit-encoding genes including BCCP1 (AT5G16390), BCCP2 (AT5G15530), ACCASE BIOTIN CARBOXYLASE (BC, AT5G35360), α-CT (AT2G38040) and β-CT (ATCG00500) or 3-KETOACYL ACP SYNTHASE I (KASI; AT5G46290), and KASIII (AT1G62640) (Maeo et al., 2009; To et al., 2012), two key genes in FA synthesis (FIG. **8**). WRI1 was previously shown to regulate a number of FA synthesis genes (Maeo et al., 2009) and all three BADC genes (Liu et al., 2019). Analysis of WRI1 from the same materials showed no significant changes in WRI1 transcript levels (FIG. **8**). That the levels of transcripts corresponding to these genes were not significantly different from controls, suggests that the alleviation of inhibition of FA synthesis is not the result of increased transcription of other FA synthesis genes.

Example 5

[0152] Badc1,3/Fae1/FAH Plants Exhibited Increased FA Content and Seed Yield

[0153] FA content in seeds was quantified to determine if badc1,3 alleviated the feedback inhibition of FA synthesis in seeds with HFA production. fae1 seeds contain 6.00±0.07 μg of total FA, and overexpression of FAH in fae1 significantly reduced FA to 4.94±0.10 g per seed. After introduction of badc1,3, the FA content of the seeds significantly increase by 16.8% to 5.77±0.04 μg per seed (FIG. **3**A). Correspondingly, seeds of fae1 plants yielded 34.3±0.4% oil content, expression of FAH significantly decreased the oil content to 32.7±0.7% and the introduction of badc1,3 increased the oil content to 36.9±0.3% (FIG. **3**B). The lower oil content in fae1/FAH has been reported to reduce seed weight (Adhikari et al., 2016). Indeed, expression of FAH in fae1 seeds decreased average seed weight from 17.5±1.1 μg to 15.1±0.7 μg (FIG. **3**C), but introduction of badc1,3 did not significantly increase seed weight (15.6±1.0 μg per seed). The small significant differences in FA content and seed yield reported herein can be attributed to differences in BADC and FAE gene expression because that both of the T-DNA lines (Bolle et al., 2013) and the fae1 (Kunst L, 1992) line were created in the *Arabidopsis* Columbia-0 (*Arabidopsis* Genome, 2000) background.

Example 6

[0154] Both HFA and Unmodified FA Increased in Badc1,3/Fae1/FAH

[0155] The badc1,3 double mutant increased total FA in badc1,3/fae1/FAH seeds. To determine whether the increase of FA was specific for either unmodified FAs or HFAs, FAMEs from the respective seed backgrounds were analyzed. HFA in fae1/FAH and badc1,3/fae1/FAH were 18.6±1.8% and 17.4 f 0.6% of the total FAs respectively (FIG. **4**), showing that badc1,3 didn't significantly change the HFA percentage in mature seeds (student t test, $p>0.05$), rather, the increases are in both HFAs and native FAs.

Example 7

[0156] FA Synthesis Rate is Restored in Badc1,3/Fae1/FAH

[0157] It was previously reported that the production of HFA in fae1 seeds expressing FAH was associated with a reduced rate of de novo FA synthesis that resulted in the observed decrease in oil content compared with the fae1 parental line (Bates et al., 2014). The introduction of badc1,3 in the fae1/FAH line restored the FA content suggesting that it had alleviated the previously observed inhibition of FA synthesis reported in non-HFA producing lines (Salie et al., 2016; Keereetaweep et al., 2018). To test this hypothesis, mid-phase developing seeds 11-13 days after flowering were collected and their fatty acid synthesis rates were determined by measuring the rate of [^{14}C]acetate incorporation into FAs by total lipid extraction and scintillation counting. We first

validated the assay by showing linear incorporation of [^{14}C]acetate between 20 and 100 minutes using badc1,3 seeds (FIG. **9**) and chose a 60 minute incubations for subsequent experiments. As shown in FIG. **5**, compared to fae1, the badc1,3 double mutant showed a 36.8% increase in fatty acid synthesis rate, whereas expression of FAH in fae1 decreased fatty acid synthesis rate by 52.2% with respect to that of fae1. When FAH was expressed in badc1,3/fae1, the fatty acid synthesis rate was fully restored to that of parental fae1 seeds.

Example 8

[0158] Seed Germination and Development

[0159] Overexpression of FAH in fae1 has been reported to decrease seed germination (Adhikari et al., 2016; Lunn et al., 2018; Lunn et al., 2018). To test if the restored FA content in badc1,3 can mitigate the germination defects, seeds of badc1,3/fae1/FAH were tested for germination and seedling establishment relative to the fae1/FAH, badc1,3 parental lines and fae1. Emergence of the radicle was used as a germination marker, and the appearance of roots and green cotyledons was used as a marker for establishment. Germination of fae1/FAH lines was reduced to 88% compared with 99% for fae1 (FIG. **6**A). The germination rate of badc1,3/fae1/FAH was even lower than fae1/FAH at 76%. badc1,3 showed a germination rate of 95%, i.e., similar to that of fae1. The seedling establishment rates of fae1 and badc1,3 were the same as their germination rates (FIG. **6**B). 90% of geminated fae1/FAH seedlings continued to establishment, whereas 99% of germinated badc1,3/fae1/FAH seeds continued to establishment, resulting in similar establishment rates with respect to all seeds for these two genotypes. Comparison of seedling establishment rates at 7 and 10 days showed the combining badc1,3 with fae1/FAH had the effect of reducing germination while increasing seedling establishment (FIG. **10**). While the growth rate of badc1,3/fae1/FAH was higher than that of fae1/FAH, at maturity no visible differences were observed with respect to plant height and leaf size. However, fae1 plants produced 158 mg of seeds per plant, which decreased to 126 mg in fae1/FAH, while the introduction of badc1,3 in the fae1/FAH lines more than compensated, increasing seed yield per plant to 162 mg (FIG. **6**C). In summary, combining badc1,3 with fae1/FAH improved seedling establishment and restored seed yield.

Example 9

[0160] Increasing Specialty Oil in Exemplary *Camelina* Crop Plants.

[0161] We use a fad2/fae1 *Camelina* background generated through RNAi suppression of FAD2 and FAE1 that accumulates over 60% 18:1 FA in mature seed (Nguyen et al. (2013)) (see FIGS. **16**Q and **16**R *Arabidopsis* sequences). RcFAH gene is placed under the control of seed-specific phaseolin promoter (see vector diagram of FIG. **15**) and transformed into fad2/fae1 *Camelina*. Independently transformed lines are analyzed by gas chromatography-linked mass spectrometry (GC-MS) to determine their lipid composition. Homozygous lines with high HFA accumulation are chosen for disruption of BADC 1 and BADC3 gene expression with the use of CRISPR/Cas9 gene editing. *Camelina* is a hexaploid so the following target sites are identified to simultaneously disrupt all 3 isoforms of each gene: i.e, either CGGTGGAGATTATCCAACAG (SEQ ID NO: 44) or TTATGGTGATCCTCTGGTTG (SEQ ID NO: 45) are used as the target site for editing *Camelina* BADC1, including Csa04g042500.1, Csa06g030800.I and Csa09g068300.I; and AAAATTAAAATCTCAGCAGT (SEQ ID NO: 46) is the target site for editing *Camelina* BADC3 including Csa15g020290.1, Csa19g022480.1 and Csa01g018320.1. The transgenic seeds are screened in media supplemented with Hygromycin B and DNA is extracted and BADC 1 and BADC3 genes are amplified and sequenced to identify the CRISPR/cas9-induced lesion and verify the target gene disruption. The fatty acid synthesis rate in developing seed of fad2/fae1 !FAHIbadc1,3 is evaluated. Mature seeds are collected, seed size and seed weight are measured, and fatty acid methyl esters are prepared from the seeds for GC-MS analysis for FA composition and total FA quantification.

Example 10

[0162] Disruption of Specific BADC Gene(s) Increases Both Hydroxy Fatty Acid Accumulation and Seed Germination in Plants Expressing a Fatty Acid Hydroxylase FAH Enzyme

[0163] In order to test whether knock out either BADC or BADC3 effects hydroxy fatty acid (HFA) accumulation in plants, we used a CRISPR/cas9 strategy to disrupt single BADC genes in *Arabidopsis* Columbia-0 line CL37 comprising a mutation in fatty acid elongase 1 (fae1) and overexpressing the *Ricinus communis* fatty acid hydroxylase gene (FAH), that accumulates approximately 17% HFA in seeds. Target sites in the exon of BADC1 and 3 were chosen using online genome-wide prediction of plant CRISPR/Cas9 target sites, and target specificities were evaluated on the website of potential off-target finder. Finally, we constructed two vectors, one targeting the 2^{nd} and 5^{th} exons of BADC1, the other targeting the 2^{nd} and 4^{th} exons of BADC3 and transformed each into CL37. Transformed progenies were genotyped and sequence analysis confirmed editing of BADC1 or BADC3 had resulted four CL37 lines with truncated BADC1 (CL37/badc1) and 4 lines with truncated BADC3 (CL37/badc3).

[0164] A. CL37/Badc3 Plants Exhibited Increased HFA Content

[0165] FA composition in seeds was analyzed to determine if badc1 or badc3 influenced HFA accumulation. CL37 seeds contain 19.1% HFA, 4 CL37/badc1 lines showed similar percentage of HFA, implying disrupting BADC1 did not change HFA accumulation. Surprisingly, disruption of badc3 significantly increased the HFA percentage in all 4 CL37/badc3 lines by more than 30% with values ranging from 26.1 to 27.2% (FIG. **11**). Notably, the increased HFA percentage didn't further inhibit FA synthesis, CL37/badc3 retained similar ACCase activity as that of CL37.

[0166] B. CL37/Badc3 Rescued Seed Germination and Increased Seed Yield

[0167] Overexpression of FAH in fae1 is reported to decrease seed germination (Adhikari et al., 2016; Lunn et al., 2018; Lunn et al., 2018). To test if increased HFA in CL37/badc3 seeds would further impair seed germination, seeds of CL37/badc3 were tested for germination and seedling establishment relative to CL37 and fae1. Emergence of the radicle was used as a germination marker, and the appearance of roots and green cotyledons was used as a marker for establishment. On plates comprising ½ MS supplemented with sucrose plate, germination of CL37 lines

was 87% compared with 99% for fae1 (FIG. **12**A). Surprisingly, the germination rate of CL37/badc3 was much higher than CL37 at 97%. The seedling establishment rates of fae1 and CL37/badc3 were similar to their germination rates (FIG. **12**B), whereas establishment rates dropped to 81% in both CL37 and CL37/badc1. Consistently, seed germination and seedling establishment in % MS plate without sugar were also rescued in CL37/badc3 line (FIG. **13**A-B). While the growth rate of CL37/badc3 was similar as that of CL37, no visible differences were observed with respect to plant height and leaf size during plants growth and maturity. However, fae1 plants produced 205 mg of seeds per plant, which decreased to 141 mg in CL37, while disruption of badc3 in the CL37 lines increased seed yield per plant by 67%, to more than 235 mg, that is an increase of 15% relative to fae1 (FIG. **14**). In summary, disruption of badc3 in CL37 rescued seed germination and seedling establishment, and significantly increased seed yield.

REFERENCES

[0168] Adhikari N D, Bates P D, Browse J (2016) WRINKLED1 Rescues Feedback Inhibition of Fatty Acid Synthesis in Hydroxylase-Expressing Seeds. Plant Physiol 171: 179-191

[0169] Andre C, Haslam R P, Shanklin J (2012) Feedback regulation of plastidic acetyl-CoA carboxylase by 18:1-acyl carrier protein in *Brassica napus*. Proc Natl Acad Sci USA 109: 10107-10112

[0170] *Arabidopsis* Genome I (2000) Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. Nature 408: 796-815

[0171] Bates P D, Johnson S R, Cao X, Li J, Nam J W, Jaworski J G, Ohlrogge J B, Browse J (2014) Fatty acid synthesis is inhibited by inefficient utilization of unusual fatty acids for glycerolipid assembly. Proc Natl Acad Sci USA 111: 1204-1209

[0172] Bohannon M B, Kleiman R (1978) Cyclopropene Fatty-Acids of Selected Seed Oils from Bombacaceae, Malvaceae, and Sterculiaceae. Lipids 13: 270-273

[0173] Bolle C, Huep G, Kleinbolting N, Haberer G, Mayer K, Leister D, Weisshaar B (2013) GABI-DUPLO: a collection of double mutants to overcome genetic redundancy in *Arabidopsis thaliana*. Plant J 75: 157-171

[0174] Bosma R, Miazek K, Willemsen S M, Vermue M H, Wijffels R H (2008) Growth inhibition of *Monodus subterraneus* by free fatty acids. Biotechnol Bioeng 101: 1108-1114

[0175] Broadwater J A, Whittle E, Shanklin J (2002) Desaturation and hydroxylation. Residues 148 and 324 of *Arabidopsis* FAD2, in addition to substrate chain length, exert a major influence in partitioning of catalytic specificity. J Biol Chem 277: 15613-15620

[0176] Burgal J, Shockey J, Lu C, Dyer J, Larson T, Graham I, Browse J (2008) Metabolic engineering of hydroxy fatty acid production in plants: RcDGAT2 drives dramatic increases in ricinoleate levels in seed oil. Plant Biotechnol J 6: 819-831

[0177] Butte W, Eilers J, Hirsch K (1982) Trialkysulfonium-hydroxides and trialkylselonium-hydroxides for the pyrolytic alkylation of acidic compounds. Anal. Lett. 15: 841-850

[0178] Cahoon E B, Dietrich C R, Meyer K, Damude H G, Dyer J M, Kinney A J (2006) Conjugated fatty acids accumulate to high levels in phospholipids of metabolically engineered soybean and *Arabidopsis* seeds. Phytochemistry 67: 1166-1176

[0179] Cahoon E B, Shockey J M, Dietrich C R, Gidda S K, Mullen R T, Dyer J M (2007) Engineering oilseeds for sustainable production of industrial and nutritional feedstocks: solving bottlenecks in fatty acid flux. Current Opinion in Plant Biology 10: 236-244

[0180] Cai Y, Goodman J M, Pyc M, Mullen R T, Dyer J M, Chapman K D (2015) *Arabidopsis* SEIPIN Proteins Modulate Triacylglycerol Accumulation and Influence Lipid Droplet Proliferation. Plant Cell 27: 2616-2636

[0181] Fan J, Yan C, Xu C (2013) Phospholipid:diacylglycerol acyltransferase-mediated triacylglycerol biosynthesis is crucial for protection against fatty acid-induced cell death in growing tissues of *Arabidopsis*. Plant J 76: 930-942

[0182] Feria Bourrellier A B, Valot B, Guillot A, Ambard-Bretteville F, Vidal J, Hodges M (2010) Chloroplast acetyl-CoA carboxylase activity is 2-oxoglutarate-regulated by interaction of PII with the biotin carboxyl carrier subunit. Proc Natl Acad Sci USA 107: 502-507

[0183] Haslam R P, Ruiz-Lopez N, Eastmond P, Moloney M, Sayanova O, Napier J A (2013) The modification of plant oil composition via metabolic engineering-better nutrition by design. Plant Biotechnology Journal 11: 157-168

[0184] Hu Z H, Ren Z H, Lu C F (2012) The Phosphatidylcholine Diacylglycerol Cholinephosphotransferase Is Required for Efficient Hydroxy Fatty Acid Accumulation in Transgenic *Arabidopsis*. Plant Physiology 158: 1944-1954

[0185] Keereetaweep J, Liu H, Zhai Z, Shanklin J (2018) Biotin Attachment Domain-Containing Proteins Irreversibly Inhibit Acetyl CoA Carboxylase. Plant Physiol 177: 208-215

[0186] Kim H, Gardner H W, Hou C T (2000) Production of isomeric 9,10,13 (9,12,13)-trihydroxy-11E (10E)-octadecenoic acid from linoleic acid by *Pseudomonas aeruginosa* PR3. Journal of Industrial Microbiology & Biotechnology 25: 109-115

[0187] Kim H U, Lee K R, Go Y S, Jung J H, Suh M C, Kim J B (2011) Endoplasmic Reticulum-Located PDAT1-2 from Castor Bean Enhances Hydroxy Fatty Acid Accumulation in Transgenic Plants. Plant and Cell Physiology 52: 983-993

[0188] Kunst L T D, Underhill E W (1992) Fatty acid elongation in developing seeds of *Arabidopsis thaliana* Plant Physiol Biochem 30: 425-434

[0189] Li M, Bahn S C, Guo L, Musgrave W, Berg H, Welti R, Wang X (2011) Patatin-related phospholipase pPLAIIIbeta-induced changes in lipid metabolism alter cellulose content and cell elongation in *Arabidopsis*. Plant Cell 23: 1107-1123

[0190] Li R, Yu K, Wu Y, Tateno M, Hatanaka T, Hildebrand D F (2012) *Vernonia* DGATs can complement the disrupted oil and protein metabolism in epoxygenase-expressing soybean seeds. Metab Eng 14: 29-38

[0191] Liu H, Zhai Z, Kuczynski K, Keereetaweep J, Schwender J, Shanklin J (2019) WRINKLED1 Regulates BIOTIN ATTACHMENT DOMAIN-CONTAINING Proteins that Inhibit Fatty Acid Synthesis. Plant Physiol 181: 55-62

[0192] Lu C, Fulda M, Wallis J G, Browse J (2006) A high-throughput screen for genes from castor that boost hydroxy fatty acid accumulation in seed oils of transgenic *Arabidopsis*. Plant J 45: 847-856

[0193] Lu C F, Xin Z G, Ren Z H, Miquel M, Browse J (2009) An enzyme regulating triacylglycerol composition is encoded by the ROD1 gene of *Arabidopsis*. Proceedings of the National Academy of Sciences of the United States of America 106: 18837-18842

[0194] Lunn D, Smith G A, Wallis J G, Browse J (2018) Development Defects of Hydroxy-Fatty Acid-Accumulating Seeds Are Reduced by Castor Acyltransferases. Plant Physiol 177: 553-564

[0195] Lunn D, Wallis J G, Browse J (2018) Overexpression of Seipin1 Increases Oil in Hydroxy Fatty Acid-Accumulating Seeds. Plant Cell Physiol 59: 205-214

[0196] Lunn D, Wallis J G, Browse J (2019) Tri-Hydroxy-Triacylglycerol Is Efficiently Produced by Position-Specific Castor Acyltransferases. Plant Physiol 179: 1050-1063

[0197] Maeo K, Tokuda T, Ayame A, Mitsui N, Kawai T, Tsukagoshi H, Ishiguro S, Nakamura K (2009) An AP2-type transcription factor, WRINKLED1, of *Arabidopsis thaliana* binds to the AW-box sequence conserved among proximal upstream regions of genes involved in fatty acid synthesis. Plant J 60: 476-487

[0198] Napier J A (2007) The production of unusual fatty acids in transgenic plants. Annu Rev Plant Biol 58: 295-319

[0199] Nguyen et al. (2013) Plant Biotechnol J 11: 759-769)

[0200] Pfaffl M W, Horgan G W, Dempfle L (2002) Relative expression software tool (REST) for group-wise comparison and statistical analysis of relative expression results in real-time PCR. Nucleic Acids Res 30: e36

[0201] Salie M J, Zhang N, Lancikova V, Xu D, Thelen J J (2016) A Family of Negative Regulators Targets the Committed Step of de Novo Fatty Acid Biosynthesis. Plant Cell 28: 2312-2325

[0202] Shivaiah K K, Ding G, Upton B, Nikolau B J (2020) Non-Catalytic Subunits Facilitate Quaternary Organization of Plastidic Acetyl-CoA Carboxylase. Plant Physiology 182: 756-775

[0203] Snapp A R, Kang J, Qi X, Lu C (2014) A fatty acid condensing enzyme from *Physaria fendleri* increases hydroxy fatty acid accumulation in transgenic oilseeds of *Camelina sativa*. Planta 240: 599-610

[0204] To A, Joubes J, Barthole G, Lecureuil A, Scagnelli A, Jasinski S, Lepiniec L, Baud S (2012) WRINKLED transcription factors orchestrate tissue-specific regulation of fatty acid biosynthesis in *Arabidopsis*. Plant Cell 24: 5007-5023

[0205] Tso T C (1964) Plant-Growth Inhibition by Some Fatty Acids and Their Analogues. Nature 202: 511-512

[0206] van de Loo F J, Broun P, Turner S, Somerville C (1995) An oleate 12-hydroxylase from *Ricinus communis* L. is a fatty acyl desaturase homolog. Proc. Natl. Acad. Sci. USA 92: 6743-6747

[0207] van Erp H, Bates P D, Burgal J, Shockey J, Browse J (2011) Castor phospholipid:diacylglycerol acyltransferase facilitates efficient metabolism of hydroxy fatty acids in transgenic *Arabidopsis*. Plant Physiol 155: 683-693

[0208] Vanhercke T, Wood C C, Stymne S, Singh S P, Green A G (2013) Metabolic engineering of plant oils and waxes for use as industrial feedstocks. Plant Biotechnology Journal 11: 197-210

[0209] Wang X, Li L, Zheng Y, Zou H, Cao Y, Liu H, Liu W, Xian M (2012) Biosynthesis of long chain hydroxyfatty acids from glucose by engineered *Escherichia coli*. Bioresour Technol 114: 561-566

[0210] Wu Y R, Llewellyn D J, Dennis E S (2002) A quick and easy method for isolating good-quality RNA from cotton (*Gossypium hirsutum* L.) tissues. Plant Molecular Biology Reporter 20: 213-218

[0211] Yang Y, Munz J, Cass C, Zienkiewicz A, Kong Q, Ma W, Sanjaya, Sedbrook J, Benning C (2015) Ectopic Expression of WRINKLED1 Affects Fatty Acid Homeostasis in Brachypodium distachyon Vegetative Tissues. Plant Physiol 169: 1836-1847

[0212] Ye Y, Fulcher Y G, Sliman D J, 2nd, Day M T, Schroeder M J, Koppisetti R K, Bates P D, Thelen J J, Van Doren S R (2020) The BADC and BCCP subunits of chloroplast acetyl-CoA carboxylase sense the pH changes of the light-dark cycle. J Biol Chem

[0213] Yu X H, Prakash R R, Sweet M, Shanklin J (2014) Coexpressing *Escherichia coli* cyclopropane synthase with *Sterculia foetida* Lysophosphatidic acid acyltransferase enhances cyclopropane fatty acid accumulation. Plant Physiol 164: 455-465

[0214] Each and every publication and patent mentioned in the above specification is herein incorporated by reference in its entirety for all purposes. Various modifications and variations of the described methods and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific embodiments, the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in the art and in fields related thereto are intended to be within the scope of the following claims.

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tgtttgttcc cgttaacggc gttcctcgcc ggaaaagcct ctcggcttac cataaacgat 120

ctccacaact tcctttccta tctccaacac aaccttataa cagtaacttt actctttgct 180

ttcactgttt tcggtttggt tctctacatc gtaacccgac ccaatccggt ttatctcgtt 240

gactactcgt gttaccttcc accaccgcat ctcaaagtta gtgtctctaa agtcatggat 300

attttctacc aaataagaaa agctgatact tcttcacgga acgtggcatg tgatgatccg 360

tcctcgctcg atttcctgag gaagattcaa gagcgttcag gtctaggtga tgagacgtac 420

agtcctgagg gactcattca cgtaccaccg cggaagactt ttgcagcgtc acgtgaagag 480

acagagaagg ttatcatcgg tgcgctcgaa aatctattcg agaacaccaa agttaaccct 540

agagagattg gtatacttgt ggtgaactca agcatgttta atccaactcc ttcgctatcc 600

gctatggtcg ttaatacttt caagctccga agcaacatca aaagctttaa tctaggagga 660

atgggttgta gtgctggtgt tattgccatt gatttggcta aagacttgtt gcatgttcat 720

aaaaacactt atgctcttgt ggtgagcact gagaacatca cacaaggcat ttatgctgga 780

gaaaatagat caatgatggt tagcaattgc ttgtttcgtg ttggtggggc cgcgattttg 840

ctctctaaca agtcgggaga ccggagacgg tccaagtaca agctagttca cacggtccga 900

acgcatactg gagctgatga caagtctttt cgatgtgtgc aacaagaaga cgatgagagc 960

ggcaaaatcg gagtttgtct gtcaaaggac ataaccaatg ttgcggggac aacacttacg 1020

aaaaatatag caacattggg tccgttgatt cttcctttaa gcgaaaagtt tctttttttc 1080

gctaccttcg tcgccaagaa acttctaaag gataaaatca agcattacta tgttccggat 1140

ttcaagcttg ctgttgacca tttctgtatt catgccggag gcagagccgt gatcgatgag 1200

ctagagaaga acttaggact atcgccgatc gatgtggagg catctagatc aacgttacat 1260

agatttggga atacttcatc tagctcaatt tggtatgaat tagcatacat agaggcaaag 1320

ggaagaatga agaaagggaa taaagcttgg cagattgctt taggatcagg gtttaagtgt 1380

aatagtgcgg tttgggtggc tctacgcaat gtcaaggcat cggcaaatag tccttggcaa 1440

cattgcatcg atagatatcc ggttaaaatt gattctgatt tgtcaaagtc aaagactcat 1500

gtccaaaacg gtcggtccta a 1521

<210> SEQ ID NO 4
<211> LENGTH: 1164
<212> TYPE: DNA
<213> ORGANISM: Ricinus communis

<400> SEQUENCE: 4

atgggaggtg gtggtcgcat gtccactgtc ataaccagca acaacagtga gaagaaagga 60

ggaagcagcc accttaagcg agcgccgcac acgaagcctc ctttcacact tggtgacctc 120

aagagagcca tcccacccca ttgctctgaa cgctcttttg tgcgctcatt ctcctatgtt 180

gcctatgatg tctgcttaag ttttcttttc tactcgatcg ccaccaactt cttcccttac 240

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atctcttctc cgctctcgta tgtcgcttgg ctggtttact ggctcttcca aggctgcatt 300

ctcactggtc tttgggtcat cggccatgaa tgtggccatc atgcttttag tgagtatcag 360

ctggctgatg acattgttgg cctaattgtc cattctgcac ttctggttcc atatttttca 420

tggaaatata gccatcgccg ccaccattct aacataggat ctctcgagcg agacgaagtg 480

ttcgtcccga aatcaaagtc gaaaatttca tggtattcta agtacttaaa caacccgcca 540

ggtcgagttt tgacacttgc tgccacgctc ctccttggct ggcctttata cttagctttc 600

aatgtctctg gtagacctta cgatcgcttt gcttgccatt atgatcccta tggcccaata 660

ttttccgaaa gagaaaggct tcagatttac attgctgacc tcggaatctt tgccacaacg 720

tttgcgcttt atcaggctac aatggcaaaa gggttggctt gggtaatgcg tatctatggg 780

gtgccattgc ttattgttaa ctgtttcctt gttatgatca catacttgca gcacactcac 840

ccagctattc cacgctatgg ctcatcggaa tgggattggc tccggggagc aatggtgact 900

gtcgatagag attatggggt gttgaataaa gtattccata acattgcaga cactcaggta 960

gctcatcatc tctttgctac agtgccacat taccatgcaa tggaggccac taaagcaatc 1020

aagcctataa tgggtgaata ttaccggtat gatggtaccc cattttacaa ggcattgtgg 1080

agggaggcaa aggagtgctt gttcgtcgag ccagatgaag gagctcctac acaaggcgtt 1140

ttctggtacc ggaacaagta ttaa 1164

<210> SEQ ID NO 5
<211> LENGTH: 263
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 5

Met Ala Ser Cys Ser Leu Gly Val Pro Lys Ile Lys Ile Ser Ala Val
1 5 10 15

Asp Leu Ser Arg Val Arg Ser Gly Ser Leu Leu Ile Pro Tyr Asn Gln
20 25 30

Arg Ser Leu Leu Arg Gln Arg Pro Val Lys Tyr Leu Ser Leu Lys Thr
35 40 45

Thr Phe Gly Ser Val Lys Ala Val Gln Val Ser Thr Val Pro Thr Ala
50 55 60

Glu Thr Ser Ala Thr Ile Glu Val Lys Asp Ser Lys Glu Ile Lys Ser
65 70 75 80

Ser Arg Leu Asn Ala Gln Leu Val Pro Lys Pro Ser Glu Val Glu Ala
85 90 95

Leu Val Thr Glu Ile Cys Asp Ser Ser Ser Ile Ala Glu Phe Glu Leu
100 105 110

Lys Leu Gly Gly Phe Arg Leu Tyr Val Ala Arg Asn Ile Ala Asp Asn
115 120 125

Ser Ser Leu Gln Pro Pro Pro Thr Pro Ala Val Thr Ala Ser Asn Ala
130 135 140

Thr Thr Glu Ser Pro Glu Ser Asn Gly Ser Ala Ser Ser Thr Ser Leu
145 150 155 160

Ala Ile Ser Lys Pro Ala Ser Ser Ala Ala Asp Gln Gly Leu Met Ile
165 170 175

Leu Gln Ser Pro Lys Val Gly Phe Phe Arg Arg Ser Lys Thr Ile Lys
180 185 190

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Gly Lys Arg Leu Pro Ser Ser Cys Lys Glu Lys Asp Gln Val Lys Glu
        195                 200                 205

Gly Gln Ile Leu Cys Tyr Ile Glu Gln Leu Gly Gly Gln Phe Pro Ile
    210                 215                 220

Glu Ser Asp Val Thr Gly Glu Val Val Lys Ile Leu Arg Glu Asp Gly
225                 230                 235                 240

Glu Pro Val Gly Tyr Asn Asp Ala Leu Ile Ser Ile Leu Pro Ser Phe
                245                 250                 255

Pro Gly Ile Lys Lys Leu Gln
            260
```

<210> SEQ ID NO 6
<211> LENGTH: 2698
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 6

```
accactctgg ttgtatcgaa cgagcgaaac ccaaccaacg acgagcgttc acctcaaata     60

ttttgatttg atcaaatcat ctccacactc gccaaatcgt tgtgtcctcg ttcatatcgt    120

tatcgtatca gctcaaaaat ctcaatctct cttccttaca ttcttctgtt tctcgaatcc    180

ttgtctccct ccatggcttc ctgtaagttt ctctacctgt ctcttgttgt cttgcttgtt    240

ccagttttct tgggatcgta cactaaattg ggtttgtgtt tcctcattca aatttgaatg    300

ctttcgtagt tttctgctct catagaatca tattcatcga aaggttgtaa ctttggggat    360

tctgtttatt gagtgatagg aaaactcaga aagggactta actttgaaca attaggttga    420

ttttggtata aattagagat ctaaagttga agaatttgtc ttcagtatct gtttcaatgg    480

agatgagatt caagttactt catttgatat tgaattgcca agctaatcta attgatgagt    540

ttggcagtga taagttaatt tcataatttg tatctcttaa tatgaattac tcgacaacat    600

tacttaatct ttcactgttg agtatacgtg gagatcggtt aacgtgagtt tattctaaga    660

cattatattt tgaattactt aaaactttct ggagctatct tggattgagt gtataagatt    720

tgcttatgct caattttaaa aagtgaggga tcatattgaa gataagtgct tatttagtct    780

ttctttttga ctctgtcttg ttttggctga tttcccatat tgagaccttg gcgtatgacg    840

tatgttacag gtagcctagg agttcctaaa attaaaatct cggcagtaga ccttagtaga    900

gtaagatctg gaagcttact gataccatac aatcaaagat cattgcttcg acaaaggcca    960

gtgaagtact tgagtctgaa gacaacattt ggatctgtga aagctgtcca agtgtctact   1020

gtcccaactg cagaaacatc aggtacactt atctctatat gttttcttaa cttgaatatg   1080

ctcattttta ccgattttac tatcgatatg ttttgcacat cgagtgtgtt cacatgtggg   1140

ctgatgtgtt cctagaaagt ctcttttagt tttcctttaa tgctttctga tttattcttg   1200

ttatcaacag ctactataga agtaaaagat tctaaagaga tcaagtcatc tcgattaaac   1260

gctcagcttg ttcccaagcc ttctgaggtg ggttttgatt ttccatttaa tgttagaatg   1320

tcaatttaag aactctggtt cttctccctt attgtcaaat ggaagagaag aaatgtgttg   1380

tcttgaggat taagtggaga attcacttgt tgcctgcaca ataaaaccat ttgagtctgt   1440

ttttttaatt ggatgcattc aatatgattt ctttttcgat cttttaggtg gaagcccttg   1500

taactgaaat atgcgattct tcatcaattg cagagtttga actgaaagta aggctctact   1560

caattgaatt gttgtcatgt tattgctctt ttgcagagtc atctcagcta agtttttgaa   1620
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taggattctt atctaataat ttcggcctct ttcatttgca cattctaata gctgggggt 1680

ttccgactat atgtagcaag gaacatagct gacaatagta gtctacaacc tccgccaact 1740

cctgctgtga ctgcttcaaa tgcaactacc gagagtcctg agtcgaatgg atcagcttcc 1800

tctacttcac tggctatctc aaaaccagca tcgtcagccg ctgatcaggg tttgatgatt 1860

ctccaatctc caaaagtaag agaccacaca actcaaaggc aaaatgtcat atactctgtt 1920

ggaaaatgct atattttata gtttcaatca gaaagttgat cccaatctaa atggtgtgta 1980

atatgtgcag gtagggttct tcaggagatc caaaaccata aagggtaaac gcctgccttc 2040

gtcttgtaaa gaggtataac caatcttctt gaacagaaga gagtgtttga tttcatgggg 2100

gaaaccactg actaatctct tatttgctct tgtttaatct gacagaaaga ccaagtgaaa 2160

gaaggtcaaa ttctgtgcta cattgaacaa ctcggtggcc aatttccaat cgaggttaga 2220

taatattcca ttttaattcc tgatttagta attactatca cttgcttcaa ccaactcagt 2280

taaattgctt ctctgtttat cgatcaatct tctagtctga tgttaccggc gaggtagtca 2340

agatactccg agaagatgga ggcaagtctc tcgtcttctt taacctttct tcgtttttct 2400

taaaacctcg gtgtaatgat ttttcttatc gttttctcat tcggaacaga gcctgtagga 2460

tacaatgatg ctctcatctc catccttcca tccttccctg ggatcaagaa gcttcagtaa 2520

aaccaaattc gagctggttt tgagttatga cactgtgcct tgtgtatgct tttagataaa 2580

gaaacttcat tcatatttgt atttgtcttt tgcttgtatg aaagttcttc tttaagactc 2640

ttttattctg tatgcttttt cttatatata aaaacattat ggtatttttt tttaatcg 2698

<210> SEQ ID NO 7
<211> LENGTH: 387
<212> TYPE: PRT
<213> ORGANISM: Ricinus communis

<400> SEQUENCE: 7

Met Gly Gly Gly Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser
1 5 10 15

Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys
            20 25 30

Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys
        35 40 45

Ser Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
    50 55 60

Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
65 70 75 80

Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
                85 90 95

Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
            100 105 110

His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
        115 120 125

Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
    130 135 140

His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
145 150 155 160

Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu

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               165                 170                 175

Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
            180                 185                 190

Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
        195                 200                 205

Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
    210                 215                 220

Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
225                 230                 235                 240

Phe Ala Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
                245                 250                 255

Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
            260                 265                 270

Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
        275                 280                 285

Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
    290                 295                 300

Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr Gln Val
305                 310                 315                 320

Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
                325                 330                 335

Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
            340                 345                 350

Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
        355                 360                 365

Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
    370                 375                 380

Asn Lys Tyr
385
```

<210> SEQ ID NO 8
<211> LENGTH: 831
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 8

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atggcgtctt ctgcagctct cggatctctt catcagactt tagggtcaca gagtgagctt     60

catttgcttt ctggaaactg gtctgcctct ggtacttctt gcgttccacg gtggagatta    120

tccaacagga gtagcaatta cacgcttgtg ttacgtgcaa aggcctctaa aacttcgaca    180

acaaccaaaa gcgatgattc atctgatgcg actgtgtcaa acgggaagaa atctgttcga    240

cggacaacct tcccgaaaga agtggaggca ctggttcacg agatgtgtga tgagactgag    300

gttgctgtcc tgaaacttaa ggttggagat ttcgagatga acctaaaacg gaagattgga    360

gcggccacaa accccattcc tgtggaggat atatctccaa ccgtagcacc tccgattcct    420

tctgagccca tggataaatc tgtttcttct gctcccagcc catctaaagc aaaaccgtct    480

gaaaaagtat ctccatttat gaatacatca tatgggaaac cagcgaagtt ggtagctttg    540

gaggcatctg gatcaaacaa ttatgttcta gtcaaatctc cctcagttgg cgagtttcac    600

agaagcagaa ctgtaaaagg aaagaaacta tctcctagct gcaaagaggg tgatgaaata    660
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aaggaaggcc aagttattgg atacttacat cagttgggaa cagaacttcc agtgacgtcg 720

gatgtagctg gggaagtcct caagcttctt tcagatgacg gagactccgt aggttatggt 780

gatcctctgg ttgcggtctt gccatcgttc cacgatatca acatccagtg a 831

<210> SEQ ID NO 9
<211> LENGTH: 276
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 9

Met Ala Ser Ser Ala Ala Leu Gly Ser Leu His Gln Thr Leu Gly Ser
1 5 10 15

Gln Ser Glu Leu His Leu Leu Ser Gly Asn Trp Ser Ala Ser Gly Thr
20 25 30

Ser Cys Val Pro Arg Trp Arg Leu Ser Asn Arg Ser Ser Asn Tyr Thr
35 40 45

Leu Val Leu Arg Ala Lys Ala Ser Lys Thr Ser Thr Thr Thr Lys Ser
50 55 60

Asp Asp Ser Ser Asp Ala Thr Val Ser Asn Gly Lys Lys Ser Val Arg
65 70 75 80

Arg Thr Thr Phe Pro Lys Glu Val Glu Ala Leu Val His Glu Met Cys
85 90 95

Asp Glu Thr Glu Val Ala Val Leu Lys Leu Lys Val Gly Asp Phe Glu
100 105 110

Met Asn Leu Lys Arg Lys Ile Gly Ala Ala Thr Asn Pro Ile Pro Val
115 120 125

Glu Asp Ile Ser Pro Thr Val Ala Pro Pro Ile Pro Ser Glu Pro Met
130 135 140

Asp Lys Ser Val Ser Ser Ala Pro Ser Pro Ser Lys Ala Lys Pro Ser
145 150 155 160

Glu Lys Val Ser Pro Phe Met Asn Thr Ser Tyr Gly Lys Pro Ala Lys
165 170 175

Leu Val Ala Leu Glu Ala Ser Gly Ser Asn Asn Tyr Val Leu Val Lys
180 185 190

Ser Pro Ser Val Gly Glu Phe His Arg Ser Arg Thr Val Lys Gly Lys
195 200 205

Lys Leu Ser Pro Ser Cys Lys Glu Gly Asp Glu Ile Lys Glu Gly Gln
210 215 220

Val Ile Gly Tyr Leu His Gln Leu Gly Thr Glu Leu Pro Val Thr Ser
225 230 235 240

Asp Val Ala Gly Glu Val Leu Lys Leu Leu Ser Asp Asp Gly Asp Ser
245 250 255

Val Gly Tyr Gly Asp Pro Leu Val Ala Val Leu Pro Ser Phe His Asp
260 265 270

Ile Asn Ile Gln
275

<210> SEQ ID NO 10
<211> LENGTH: 846
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 10

atggcgtctt ctgcagctct cggatctctt catcagactt tagggtcaca gagtgagctt 60

cacttgcttt ctggaaattg gtctgcttct ggtacttctt gtgtaccacg gtggagatta 120

tccaacagga gcagcaatta cacgcttgtg ttacgtgcaa aggcctctaa aacttcgaca 180

acaaccaaaa gcgatgattc atctgatgcg actgtgtcaa acgggaagaa atctgttcga 240

cggacaactt tcccgaaaga agtggaggca ctggttcacg agatgtgtga tgagactgag 300

gttgctgtcc tgaaacttaa ggcaagttac tctggcgttg gagatttcga gatgaaccta 360

aaacggaaga ttgaagcggc cacaaacccc attcctgtgg aggatatatc tccaaccgta 420

gcacctccga ttccttctga gcccatgaat caatcggttt cctctattcc tagcccatct 480

aaagcaaaac cttctgaaaa agtatctcca tttataaata catcatatgg gaaaccagca 540

aagttggcag ctttggaggc atctggatca aataattatg ttctagtcaa atctccctca 600

gttggcgagt ttcacagaag cagaactgta aaaggaaaga aactatctcc tagctgcaaa 660

gagggtgatg aaataaagga agggcaagtt attggatact tacatcagtt gggaacagaa 720

cttccagtga cgtcggatgt agctggggaa gtcctcaagc ttctttcaga tgacggagac 780

tccgtaggtt atggtgatcc tctggttgcg gtcttgccat cgttccacga tatcaacatc 840

cagtga 846

<210> SEQ ID NO 11
<211> LENGTH: 281
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 11

Met Ala Ser Ser Ala Ala Leu Gly Ser Leu His Gln Thr Leu Gly Ser
1 5 10 15

Gln Ser Glu Leu His Leu Leu Ser Gly Asn Trp Ser Ala Ser Gly Thr
20 25 30

Ser Cys Val Pro Arg Trp Arg Leu Ser Asn Arg Ser Ser Asn Tyr Thr
35 40 45

Leu Val Leu Arg Ala Lys Ala Ser Lys Thr Ser Thr Thr Thr Lys Ser
50 55 60

Asp Asp Ser Ser Asp Ala Thr Val Ser Asn Gly Lys Lys Ser Val Arg
65 70 75 80

Arg Thr Thr Phe Pro Lys Glu Val Glu Ala Leu Val His Glu Met Cys
85 90 95

Asp Glu Thr Glu Val Ala Val Leu Lys Leu Lys Ala Ser Tyr Ser Gly
100 105 110

Val Gly Asp Phe Glu Met Asn Leu Lys Arg Lys Ile Glu Ala Ala Thr
115 120 125

Asn Pro Ile Pro Val Glu Asp Ile Ser Pro Thr Val Ala Pro Pro Ile
130 135 140

Pro Ser Glu Pro Met Asn Gln Ser Val Ser Ser Ile Pro Ser Pro Ser
145 150 155 160

Lys Ala Lys Pro Ser Glu Lys Val Ser Pro Phe Ile Asn Thr Ser Tyr
165 170 175

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Gly Lys Pro Ala Lys Leu Ala Ala Leu Glu Ala Ser Gly Ser Asn Asn
            180                 185                 190

Tyr Val Leu Val Lys Ser Pro Ser Val Gly Glu Phe His Arg Ser Arg
        195                 200                 205

Thr Val Lys Gly Lys Lys Leu Ser Pro Ser Cys Lys Glu Gly Asp Glu
    210                 215                 220

Ile Lys Glu Gly Gln Val Ile Gly Tyr Leu His Gln Leu Gly Thr Glu
225                 230                 235                 240

Leu Pro Val Thr Ser Asp Val Ala Gly Glu Val Leu Lys Leu Leu Ser
                245                 250                 255

Asp Asp Gly Asp Ser Val Gly Tyr Gly Asp Pro Leu Val Ala Val Leu
            260                 265                 270

Pro Ser Phe His Asp Ile Asn Ile Gln
        275                 280


<210> SEQ ID NO 12
<211> LENGTH: 891
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 12

Ala Thr Gly Gly Cys Gly Thr Cys Thr Thr Cys Thr Gly Cys Ala Gly
1               5                   10                  15

Cys Thr Cys Thr Cys Gly Gly Ala Thr Cys Thr Cys Thr Thr Cys Ala
            20                  25                  30

Thr Cys Ala Thr Cys Cys Gly Ala Thr Cys Thr Thr Thr Thr Thr Gly
        35                  40                  45

Thr Gly Gly Cys Ala Ala Thr Thr Gly Gly Thr Thr Gly Thr Thr Gly
    50                  55                  60

Thr Gly Gly Thr Gly Ala Cys Thr Gly Ala Ala Thr Thr Ala Gly Ala
65                  70                  75                  80

Gly Ala Cys Thr Thr Thr Ala Gly Gly Gly Thr Cys Ala Cys Ala Gly
                85                  90                  95

Ala Gly Thr Gly Ala Gly Cys Thr Thr Cys Ala Cys Thr Thr Gly Cys
            100                 105                 110

Thr Thr Thr Cys Thr Gly Gly Ala Ala Ala Thr Thr Gly Gly Thr Cys
        115                 120                 125

Thr Gly Cys Thr Thr Cys Thr Gly Gly Thr Ala Cys Thr Thr Cys Thr
    130                 135                 140

Thr Gly Thr Gly Thr Ala Cys Cys Ala Cys Gly Gly Thr Gly Gly Ala
145                 150                 155                 160

Gly Ala Thr Thr Ala Thr Cys Cys Ala Ala Cys Ala Gly Gly Ala Gly
                165                 170                 175

Cys Ala Gly Cys Ala Ala Thr Thr Ala Cys Ala Cys Gly Cys Thr Thr
            180                 185                 190

Gly Thr Gly Thr Thr Ala Cys Gly Thr Gly Cys Ala Ala Ala Gly Gly
        195                 200                 205

Cys Cys Thr Cys Thr Ala Ala Ala Ala Cys Thr Thr Cys Gly Ala Cys
    210                 215                 220

Ala Ala Cys Ala Ala Cys Cys Ala Ala Ala Ala Gly Cys Gly Ala Thr
225                 230                 235                 240
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Gly Ala Thr Thr Cys Ala Thr Cys Thr Gly Ala Thr Gly Cys Ala Ala
                245                 250                 255

Cys Thr Gly Thr Gly Thr Cys Ala Ala Ala Cys Gly Gly Gly Ala Ala
            260                 265                 270

Gly Ala Ala Ala Thr Cys Thr Gly Thr Thr Cys Gly Ala Ala Gly Gly
        275                 280                 285

Ala Cys Ala Ala Cys Thr Thr Thr Cys Cys Cys Gly Ala Ala Ala Gly
    290                 295                 300

Ala Ala Gly Thr Gly Gly Ala Gly Ala Cys Ala Cys Thr Gly Gly Thr
305                 310                 315                 320

Thr Cys Ala Cys Gly Ala Gly Ala Thr Gly Thr Gly Thr Gly Ala Thr
                325                 330                 335

Gly Ala Gly Ala Cys Thr Gly Ala Gly Gly Thr Thr Gly Cys Thr Gly
            340                 345                 350

Thr Cys Cys Thr Gly Ala Ala Ala Cys Thr Cys Ala Ala Gly Gly Cys
        355                 360                 365

Ala Ala Gly Ala Thr Ala Cys Thr Cys Thr Gly Gly Cys Gly Thr Thr
    370                 375                 380

Gly Gly Ala Gly Ala Thr Thr Thr Cys Gly Ala Gly Ala Thr Gly Ala
385                 390                 395                 400

Ala Cys Cys Thr Ala Ala Ala Ala Cys Gly Gly Ala Ala Gly Ala Thr
                405                 410                 415

Thr Gly Gly Ala Gly Cys Thr Ala Cys Cys Ala Cys Ala Ala Ala Cys
            420                 425                 430

Cys Cys Cys Ala Thr Thr Cys Cys Thr Gly Thr Gly Gly Ala Gly Gly
        435                 440                 445

Ala Thr Ala Thr Ala Thr Cys Thr Cys Cys Ala Ala Cys Cys Gly Thr
    450                 455                 460

Ala Gly Cys Ala Cys Cys Thr Cys Cys Ala Ala Thr Thr Cys Cys Thr
465                 470                 475                 480

Thr Cys Thr Gly Ala Gly Cys Cys Cys Ala Thr Gly Ala Ala Thr Cys
                485                 490                 495

Ala Ala Thr Cys Gly Gly Thr Thr Thr Cys Cys Thr Cys Thr Gly Cys
            500                 505                 510

Thr Cys Cys Cys Ala Gly Cys Cys Cys Ala Thr Cys Thr Ala Cys Ala
        515                 520                 525

Gly Cys Ala Ala Ala Ala Cys Cys Gly Thr Cys Thr Gly Ala Ala Ala
    530                 535                 540

Ala Ala Gly Thr Ala Thr Cys Thr Cys Cys Ala Thr Thr Thr Ala Thr
545                 550                 555                 560

Gly Ala Ala Thr Ala Cys Ala Thr Cys Ala Thr Ala Thr Gly Gly Gly
                565                 570                 575

Ala Ala Ala Cys Cys Ala Gly Cys Ala Ala Ala Gly Thr Thr Gly Gly
            580                 585                 590

Cys Ala Gly Cys Thr Thr Thr Gly Gly Ala Gly Gly Cys Ala Thr Cys
        595                 600                 605

Thr Gly Gly Ala Thr Cys Ala Ala Ala Cys Ala Ala Thr Thr Ala Thr
    610                 615                 620

Gly Thr Thr Cys Thr Ala Gly Thr Cys Ala Ala Ala Thr Cys Thr Cys
625                 630                 635                 640
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Cys Cys Thr Cys Ala Gly Thr Thr Gly Gly Cys Gly Ala Gly Thr Thr
                645                 650                 655

Thr Cys Ala Cys Ala Gly Ala Ala Gly Cys Ala Gly Ala Ala Cys Thr
            660                 665                 670

Gly Thr Ala Ala Ala Ala Gly Gly Ala Ala Ala Gly Ala Ala Ala Cys
        675                 680                 685

Thr Ala Thr Cys Thr Cys Cys Thr Ala Gly Cys Thr Gly Cys Ala Ala
    690                 695                 700

Ala Gly Ala Gly Gly Gly Thr Gly Ala Thr Gly Ala Ala Ala Thr Ala
705                 710                 715                 720

Ala Ala Gly Gly Ala Ala Gly Gly Cys Cys Ala Ala Gly Thr Gly Ala
                725                 730                 735

Thr Thr Gly Gly Ala Thr Ala Cys Thr Thr Ala Cys Ala Thr Cys Ala
            740                 745                 750

Gly Thr Thr Gly Gly Gly Ala Ala Cys Ala Gly Ala Ala Cys Thr Thr
        755                 760                 765

Cys Cys Ala Gly Thr Gly Ala Cys Gly Thr Cys Gly Gly Ala Thr Gly
    770                 775                 780

Thr Ala Gly Cys Thr Gly Gly Gly Gly Ala Ala Gly Thr Cys Cys Thr
785                 790                 795                 800

Cys Ala Ala Gly Cys Thr Thr Cys Thr Thr Thr Cys Ala Gly Ala Thr
                805                 810                 815

Gly Ala Cys Gly Gly Ala Gly Ala Cys Thr Cys Cys Ala Thr Ala Gly
            820                 825                 830

Gly Thr Thr Ala Thr Gly Gly Thr Gly Ala Thr Cys Cys Thr Cys Thr
        835                 840                 845

Gly Gly Thr Thr Gly Cys Gly Gly Thr Cys Thr Thr Gly Cys Cys Ala
    850                 855                 860

Thr Cys Gly Thr Thr Cys Cys Ala Cys Gly Ala Thr Ala Thr Cys Ala
865                 870                 875                 880

Ala Cys Ala Thr Cys Cys Ala Gly Thr Gly Ala
                885                 890


<210> SEQ ID NO 13
<211> LENGTH: 296
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 13

Met Ala Ser Ser Ala Ala Leu Gly Ser Leu His His Pro Ile Phe Leu
1               5                   10                  15

Trp Gln Leu Val Val Val Val Thr Glu Leu Glu Thr Leu Gly Ser Gln
            20                  25                  30

Ser Glu Leu His Leu Leu Ser Gly Asn Trp Ser Ala Ser Gly Thr Ser
        35                  40                  45

Cys Val Pro Arg Trp Arg Leu Ser Asn Arg Ser Ser Asn Tyr Thr Leu
    50                  55                  60

Val Leu Arg Ala Lys Ala Ser Lys Thr Ser Thr Thr Thr Lys Ser Asp
65                  70                  75                  80

Asp Ser Ser Asp Ala Thr Val Ser Asn Gly Lys Lys Ser Val Arg Arg
                85                  90                  95
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```
Thr Thr Phe Pro Lys Glu Val Glu Thr Leu Val His Glu Met Cys Asp
            100                 105                 110

Glu Thr Glu Val Ala Val Leu Lys Leu Lys Ala Arg Tyr Ser Gly Val
        115                 120                 125

Gly Asp Phe Glu Met Asn Leu Lys Arg Lys Ile Gly Ala Thr Thr Asn
    130                 135                 140

Pro Ile Pro Val Glu Asp Ile Ser Pro Thr Val Ala Pro Pro Ile Pro
145                 150                 155                 160

Ser Glu Pro Met Asn Gln Ser Val Ser Ser Ala Pro Ser Pro Ser Thr
                165                 170                 175

Ala Lys Pro Ser Glu Lys Val Ser Pro Phe Met Asn Thr Ser Tyr Gly
            180                 185                 190

Lys Pro Ala Lys Leu Ala Ala Leu Glu Ala Ser Gly Ser Asn Asn Tyr
        195                 200                 205

Val Leu Val Lys Ser Pro Ser Val Gly Glu Phe His Arg Ser Arg Thr
    210                 215                 220

Val Lys Gly Lys Lys Leu Ser Pro Ser Cys Lys Glu Gly Asp Glu Ile
225                 230                 235                 240

Lys Glu Gly Gln Val Ile Gly Tyr Leu His Gln Leu Gly Thr Glu Leu
                245                 250                 255

Pro Val Thr Ser Asp Val Ala Gly Glu Val Leu Lys Leu Leu Ser Asp
            260                 265                 270

Asp Gly Asp Ser Ile Gly Tyr Gly Asp Pro Leu Val Ala Val Leu Pro
        275                 280                 285

Ser Phe His Asp Ile Asn Ile Gln
    290                 295
```

<210> SEQ ID NO 14
<211> LENGTH: 792
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 14

```
atggcttcct gtagcctagg agttcctaaa attaaaatct cagcagtaga ccttagtaga     60

gtaagttctg gaagcttact gataccattc agccaaagat cattgcttgg acaaaggccg    120

gtgaagtact tgagtctcag gacaactttt ggatctgtga aagctgtcca agtatctact    180

gtcccaaccg cagaaacatc agctactata gaagtagaag attctgaaga aaccaagtca    240

tctccattga acgctcagct agttcccaag ccatctgagg tggaagctct tgtcactgaa    300

atatgcgatt cctcatcaat tgcagagttt gaattgaaac tgggggggttt ccgcctatat    360

gtagcaaggg atctaactga caaaagtagt ccgcagcctc atccagttcc tgctgtggct    420

gctgccagtg aaactaccaa gagtcctgat tcgaatggat caactccttc tacttcattg    480

gctatcacaa gaccagcatc ctcagctgct gatcacggtt tgatgattct ccaatctcca    540

aaagtagggt tcttcaggag atccaaaact ataaagggta aacgcatgcc ttcgtcatgt    600

aaagagaaag accaagtgaa agaaggtcaa attctgtgct acattgaaca actcggtggc    660

caattcccaa tagagtctga tgtcagcggc gaggttgtca aaatactccg agaagatgga    720

gagcctgtag gatacaatga tgctctcatc tcgatccttc cctctttccc tgggatcaag    780

aagcttcagt aa                                                        792
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<210> SEQ ID NO 15
<211> LENGTH: 263
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 15

Met Ala Ser Cys Ser Leu Gly Val Pro Lys Ile Lys Ile Ser Ala Val
1 5 10 15

Asp Leu Ser Arg Val Ser Ser Gly Ser Leu Leu Ile Pro Phe Ser Gln
20 25 30

Arg Ser Leu Leu Gly Gln Arg Pro Val Lys Tyr Leu Ser Leu Arg Thr
35 40 45

Thr Phe Gly Ser Val Lys Ala Val Gln Val Ser Thr Val Pro Thr Ala
50 55 60

Glu Thr Ser Ala Thr Ile Glu Val Glu Asp Ser Glu Glu Thr Lys Ser
65 70 75 80

Ser Pro Leu Asn Ala Gln Leu Val Pro Lys Pro Ser Glu Val Glu Ala
85 90 95

Leu Val Thr Glu Ile Cys Asp Ser Ser Ser Ile Ala Glu Phe Glu Leu
100 105 110

Lys Leu Gly Gly Phe Arg Leu Tyr Val Ala Arg Asp Leu Thr Asp Lys
115 120 125

Ser Ser Pro Gln Pro His Pro Val Pro Ala Val Ala Ala Ala Ser Glu
130 135 140

Thr Thr Lys Ser Pro Asp Ser Asn Gly Ser Thr Pro Ser Thr Ser Leu
145 150 155 160

Ala Ile Thr Arg Pro Ala Ser Ser Ala Ala Asp His Gly Leu Met Ile
165 170 175

Leu Gln Ser Pro Lys Val Gly Phe Phe Arg Arg Ser Lys Thr Ile Lys
180 185 190

Gly Lys Arg Met Pro Ser Ser Cys Lys Glu Lys Asp Gln Val Lys Glu
195 200 205

Gly Gln Ile Leu Cys Tyr Ile Glu Gln Leu Gly Gly Gln Phe Pro Ile
210 215 220

Glu Ser Asp Val Ser Gly Glu Val Val Lys Ile Leu Arg Glu Asp Gly
225 230 235 240

Glu Pro Val Gly Tyr Asn Asp Ala Leu Ile Ser Ile Leu Pro Ser Phe
245 250 255

Pro Gly Ile Lys Lys Leu Gln
260

<210> SEQ ID NO 16
<211> LENGTH: 792
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 16

atggcatcct gtagcctagg agttcctaaa attaaaatct cagcagtaga ccttagtaga 60

gtaagttctg gaagcttact gataccattc agtcaaagat cattgcttgg acaaaggccg 120

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gtgaagtact tgagtctgag gacaactttt ggatctgtga aagctgtaca agtatctact 180

gtcccagctg cagaaacatc agctactgta ggagtagaag attctgaaga aaccaagtca 240

tccccattga acgctcagct agttcccaag cgatctgagg tggaagctct tgtcactgaa 300

atatgcgact cctcatcaat tgcagagttt gaactgaaac tgggggttt ccgcctatat 360

gtagcaaggg atctagctga caaaagtagt ccgcagcctc atccaattcc tgctgtggct 420

gctgcaagtg aaactaccaa gagtcctgat tcgaatggat caacaccttc tacttcattg 480

gctatcacaa gaccagcatc ttcagctgct gatcagggtt tgatgattct ccaatctcca 540

aaagtagggt tctttaggag atccaaaacc ataaagggta aacgcatgcc ttcgtcatgt 600

aaagagaaag accaagtgaa agaaggtcaa attctgtgct acattgaaca actcggtggc 660

caattcccaa tagagtctga tgtcagcggt gaggttgtca aaatactccg cgaagatgga 720

gaacctgtag gatacaatga tgctctcatc tcgatccttc cctctttccc tgggatcaag 780

aagcttcagt aa 792

<210> SEQ ID NO 17
<211> LENGTH: 263
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 17

Met Ala Ser Cys Ser Leu Gly Val Pro Lys Ile Lys Ile Ser Ala Val
1 5 10 15

Asp Leu Ser Arg Val Ser Ser Gly Ser Leu Leu Ile Pro Phe Ser Gln
20 25 30

Arg Ser Leu Leu Gly Gln Arg Pro Val Lys Tyr Leu Ser Leu Arg Thr
35 40 45

Thr Phe Gly Ser Val Lys Ala Val Gln Val Ser Thr Val Pro Ala Ala
50 55 60

Glu Thr Ser Ala Thr Val Gly Val Glu Asp Ser Glu Glu Thr Lys Ser
65 70 75 80

Ser Pro Leu Asn Ala Gln Leu Val Pro Lys Arg Ser Glu Val Glu Ala
85 90 95

Leu Val Thr Glu Ile Cys Asp Ser Ser Ser Ile Ala Glu Phe Glu Leu
100 105 110

Lys Leu Gly Gly Phe Arg Leu Tyr Val Ala Arg Asp Leu Ala Asp Lys
115 120 125

Ser Ser Pro Gln Pro His Pro Ile Pro Ala Val Ala Ala Ala Ser Glu
130 135 140

Thr Thr Lys Ser Pro Asp Ser Asn Gly Ser Thr Pro Ser Thr Ser Leu
145 150 155 160

Ala Ile Thr Arg Pro Ala Ser Ser Ala Ala Asp Gln Gly Leu Met Ile
165 170 175

Leu Gln Ser Pro Lys Val Gly Phe Phe Arg Arg Ser Lys Thr Ile Lys
180 185 190

Gly Lys Arg Met Pro Ser Ser Cys Lys Glu Lys Asp Gln Val Lys Glu
195 200 205

Gly Gln Ile Leu Cys Tyr Ile Glu Gln Leu Gly Gly Gln Phe Pro Ile
210 215 220

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Glu Ser Asp Val Ser Gly Glu Val Val Lys Ile Leu Arg Glu Asp Gly
225 230 235 240

Glu Pro Val Gly Tyr Asn Asp Ala Leu Ile Ser Ile Leu Pro Ser Phe
245 250 255

Pro Gly Ile Lys Lys Leu Gln
260

<210> SEQ ID NO 18
<211> LENGTH: 1005
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 18

tgcttcgctg tacaaagacc actctggttg tatcgaacag agcgaaccca accaacgacg 60

agcgttaacc tcaatttgat catctccaca ctcgtcaaat ctttggtgtc ctcctcctcc 120

tcgttcgtat cgttatcgta tcagctcaca aatctcattc tcttccttac attcttcttc 180

ttctgcttct cgaatcctcc tttgtctccc tccatggctt cctgtagcct aggagttcct 240

aaaattaaaa tctcagcagt agaccttagt agagtaagtt ctggaagctt gctggtacca 300

ttcagtcaaa gatcattgct tggacaaagg acggtgaagt acttgagtct gaggaaaact 360

tttggatctg tgaaagctgt acaactatct actgtcccag ctgcagaaac atcagctact 420

gtaggagtag aagattctga agaaaccaag tcatctccat tgaacgctca gctagttccc 480

aatccatctg aggtggaagc tcttgtcact gaaatatgcg actcctcatc aattgcagag 540

tttgaactga aactgggggg tttccgccta tatgtagcaa gggatctagc tgacaaaagt 600

agtccgcagc ctcatccaat tcctgctgtg gctgctgcaa gtgaaactac caagagtcct 660

gattcgaatg gatcaacacc ttctacttca ttggctatca caagaccagc atcttcagct 720

gctgatcagg gtttgatgat tctccaatct ccaaaagtag ggttctttag gagatccaaa 780

accataaagg gtaaacgcat gccttcgtca tgtaaagaga aagaccaagt gaaagaaggt 840

caaattctgt gctacattga acaactcggt ggccaattcc caatagagtc tgatgtcagc 900

ggcgaggttg tcaaaatact ccgagaagat ggagagcctg tagggtacaa tgatgctctc 960

atctcgatcc ttccctcttt ccctgggatc aagaagcttc agtaa 1005

<210> SEQ ID NO 19
<211> LENGTH: 263
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 19

Met Ala Ser Cys Ser Leu Gly Val Pro Lys Ile Lys Ile Ser Ala Val
1 5 10 15

Asp Leu Ser Arg Val Ser Ser Gly Ser Leu Leu Val Pro Phe Ser Gln
20 25 30

Arg Ser Leu Leu Gly Gln Arg Thr Val Lys Tyr Leu Ser Leu Arg Lys
35 40 45

Thr Phe Gly Ser Val Lys Ala Val Gln Leu Ser Thr Val Pro Ala Ala
50 55 60

Glu Thr Ser Ala Thr Val Gly Val Glu Asp Ser Glu Glu Thr Lys Ser

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65                  70                  75                  80

Ser Pro Leu Asn Ala Gln Leu Val Pro Asn Pro Ser Glu Val Glu Ala
                85                  90                  95

Leu Val Thr Glu Ile Cys Asp Ser Ser Ser Ile Ala Glu Phe Glu Leu
            100                 105                 110

Lys Leu Gly Gly Phe Arg Leu Tyr Val Ala Arg Asp Leu Ala Asp Lys
        115                 120                 125

Ser Ser Pro Gln Pro His Pro Ile Pro Ala Val Ala Ala Ala Ser Glu
    130                 135                 140

Thr Thr Lys Ser Pro Asp Ser Asn Gly Ser Thr Pro Ser Thr Ser Leu
145                 150                 155                 160

Ala Ile Thr Arg Pro Ala Ser Ser Ala Ala Asp Gln Gly Leu Met Ile
                165                 170                 175

Leu Gln Ser Pro Lys Val Gly Phe Phe Arg Arg Ser Lys Thr Ile Lys
            180                 185                 190

Gly Lys Arg Met Pro Ser Ser Cys Lys Glu Lys Asp Gln Val Lys Glu
        195                 200                 205

Gly Gln Ile Leu Cys Tyr Ile Glu Gln Leu Gly Gly Gln Phe Pro Ile
    210                 215                 220

Glu Ser Asp Val Ser Gly Glu Val Val Lys Ile Leu Arg Glu Asp Gly
225                 230                 235                 240

Glu Pro Val Gly Tyr Asn Asp Ala Leu Ile Ser Ile Leu Pro Ser Phe
                245                 250                 255

Pro Gly Ile Lys Lys Leu Gln
            260


<210> SEQ ID NO 20
<211> LENGTH: 1521
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 20

atgacgtccg ttaacgttaa gctcctttac cgttacgtct taaccaactt tttcaacctc     60

tgtttgttcc cgttaacggc gttcctcgcc ggaaaagcct ctcggcttac cataaacgat    120

ctccacaact tcctttccta tctccaacac aaccttataa cagtaacttt actctttgct    180

ttcactgttt tcggtttggt tctctacatc gtaacccgac ccaatccggt ttatctcgtt    240

gactactcgt gttaccttcc accaccgcat ctcaaagtta gtgtctctaa agtcatggat    300

attttctacc aaataagaaa agctgatact tcttcacgga acgtggcatg tgatgatccg    360

tcctcgctcg atttcctgag gaagattcaa gagcgttcag gtctaggtga tgagacgtac    420

agtcctgagg gactcattca cgtaccaccg cggaagactt ttgcagcgtc acgtgaagag    480

acagagaagg ttatcatcgg tgcgctcgaa aatctattcg agaacaccaa agttaaccct    540

agagagattg gtatacttgt ggtgaactca agcatgttta atccaactcc ttcgctatcc    600

gctatggtcg ttaatacttt caagctccga agcaacatca aaagctttaa tctaggagga    660

atgggttgta gtgctggtgt tattgccatt gatttggcta aagacttgtt gcatgttcat    720

aaaaacactt atgctcttgt ggtgagcact gagaacatca cacaaggcat ttatgctgga    780

gaaaatagat caatgatggt tagcaattgc ttgtttcgtg ttggtggggc cgcgattttg    840
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ctctctaaca agtcgggaga ccggagacgg tccaagtaca agctagttca cacggtccga 900

acgcatactg gagctgatga caagtctttt cgatgtgtgc aacaagaaga cgatgagagc 960

ggcaaaatcg gagtttgtct gtcaaaggac ataaccaatg ttgcggggac aacacttacg 1020

aaaaatatag caacattggg tccgttgatt cttccttaa gcgaaaagtt tctttttttc 1080

gctaccttcg tcgccaagaa acttctaaag gataaaatca agcattacta tgttccggat 1140

ttcaagcttg ctgttgacca tttctgtatt catgccggag gcagagccgt gatcgatgag 1200

ctagagaaga acttaggact atcgccgatc gatgtggagg catctagatc aacgttacat 1260

agatttggga atacttcatc tagctcaatt tggtatgaat tagcatacat agaggcaaag 1320

ggaagaatga agaaagggaa taaagcttgg cagattgctt taggatcagg gtttaagtgt 1380

aatagtgcgg tttgggtggc tctacgcaat gtcaaggcat cggcaaatag tccttggcaa 1440

cattgcatcg atagatatcc ggttaaaatt gattctgatt tgtcaaagtc aaagactcat 1500

gtccaaaacg gtcggtccta a 1521

<210> SEQ ID NO 21
<211> LENGTH: 506
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 21

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
1 5 10 15

Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
20 25 30

Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
35 40 45

Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50 55 60

Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65 70 75 80

Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
85 90 95

Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
100 105 110

Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
115 120 125

Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
130 135 140

Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
145 150 155 160

Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
165 170 175

Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
180 185 190

Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
195 200 205

Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
210 215 220

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Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225                 230                 235                 240

Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
                245                 250                 255

Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
            260                 265                 270

Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
        275                 280                 285

Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
    290                 295                 300

Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
305                 310                 315                 320

Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
                325                 330                 335

Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
            340                 345                 350

Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
        355                 360                 365

Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
    370                 375                 380

Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
385                 390                 395                 400

Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
                405                 410                 415

Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
            420                 425                 430

Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
        435                 440                 445

Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
    450                 455                 460

Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
465                 470                 475                 480

His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
                485                 490                 495

Ser Lys Thr His Val Gln Asn Gly Arg Ser
            500                 505


<210> SEQ ID NO 22
<211> LENGTH: 1152
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 22

Ala Thr Gly Gly Gly Thr Gly Cys Ala Gly Gly Thr Gly Gly Ala Ala
1               5                   10                  15

Gly Ala Ala Thr Gly Cys Cys Gly Gly Thr Thr Cys Cys Thr Ala Cys
            20                  25                  30

Thr Thr Cys Thr Thr Cys Cys Ala Ala Gly Ala Ala Ala Thr Cys Gly
        35                  40                  45

Gly Ala Ala Ala Cys Cys Gly Ala Cys Ala Cys Cys Ala Cys Ala Ala
    50                  55                  60
```

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```
Ala Gly Cys Gly Thr Gly Thr Gly Cys Cys Gly Thr Gly Cys Gly Ala
65                  70                  75                  80

Gly Ala Ala Ala Cys Cys Gly Cys Cys Thr Thr Thr Cys Thr Cys Gly
                85                  90                  95

Gly Thr Gly Gly Gly Ala Gly Ala Thr Cys Thr Gly Ala Ala Gly Ala
            100                 105                 110

Ala Ala Gly Cys Ala Ala Thr Cys Cys Cys Gly Cys Cys Gly Cys Ala
        115                 120                 125

Thr Thr Gly Thr Thr Thr Cys Ala Ala Ala Cys Gly Cys Thr Cys Ala
    130                 135                 140

Ala Thr Cys Cys Cys Thr Cys Gly Cys Thr Cys Thr Thr Thr Cys Thr
145                 150                 155                 160

Cys Cys Thr Ala Cys Cys Thr Thr Ala Thr Cys Ala Gly Thr Gly Ala
                165                 170                 175

Cys Ala Thr Cys Ala Thr Thr Ala Thr Ala Gly Cys Cys Thr Cys Ala
            180                 185                 190

Thr Gly Cys Thr Thr Cys Thr Ala Cys Thr Ala Cys Gly Thr Cys Gly
        195                 200                 205

Cys Cys Ala Cys Cys Ala Ala Thr Thr Ala Cys Thr Thr Cys Thr Cys
    210                 215                 220

Thr Cys Thr Cys Cys Thr Cys Cys Cys Thr Cys Ala Gly Cys Cys Thr
225                 230                 235                 240

Cys Thr Cys Thr Cys Thr Thr Ala Cys Thr Thr Gly Gly Cys Thr Thr
                245                 250                 255

Gly Gly Cys Cys Ala Cys Thr Cys Thr Ala Thr Thr Gly Gly Gly Cys
            260                 265                 270

Cys Thr Gly Thr Cys Ala Ala Gly Gly Cys Thr Gly Thr Gly Thr Cys
        275                 280                 285

Cys Thr Ala Ala Cys Thr Gly Gly Thr Ala Thr Cys Thr Gly Gly Gly
    290                 295                 300

Thr Cys Ala Thr Ala Gly Cys Cys Cys Ala Cys Gly Ala Ala Thr Gly
305                 310                 315                 320

Cys Gly Gly Thr Cys Ala Cys Cys Ala Cys Gly Cys Ala Thr Thr Cys
                325                 330                 335

Ala Gly Cys Gly Ala Cys Thr Ala Cys Cys Ala Ala Thr Gly Gly Cys
            340                 345                 350

Thr Gly Gly Ala Thr Gly Ala Cys Ala Cys Ala Gly Thr Thr Gly Gly
        355                 360                 365

Thr Cys Thr Thr Ala Thr Cys Thr Thr Cys Cys Ala Thr Thr Cys Cys
    370                 375                 380

Thr Thr Cys Cys Thr Cys Cys Thr Cys Gly Thr Cys Cys Cys Thr Thr
385                 390                 395                 400

Ala Cys Thr Thr Cys Thr Cys Cys Thr Gly Gly Ala Ala Gly Thr Ala
                405                 410                 415

Thr Ala Gly Thr Cys Ala Thr Cys Gly Cys Cys Gly Thr Cys Ala Cys
            420                 425                 430

Cys Ala Thr Thr Cys Cys Ala Ala Cys Ala Cys Thr Gly Gly Ala Thr
        435                 440                 445

Cys Cys Cys Thr Cys Gly Ala Ala Ala Gly Ala Gly Ala Thr Gly Ala
    450                 455                 460

Ala Gly Thr Ala Thr Thr Thr Gly Thr Cys Cys Cys Ala Ala Ala Gly
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465                 470                 475                 480

Cys Ala Gly Ala Ala Ala Thr Cys Ala Gly Cys Ala Ala Thr Cys Ala
                485                 490                 495

Ala Gly Thr Gly Gly Thr Ala Cys Gly Gly Gly Ala Ala Ala Thr Ala
            500                 505                 510

Cys Cys Thr Cys Ala Ala Cys Ala Ala Cys Cys Cys Thr Cys Thr Thr
        515                 520                 525

Gly Gly Ala Cys Gly Cys Ala Thr Cys Ala Thr Gly Ala Thr Gly Thr
    530                 535                 540

Thr Ala Ala Cys Cys Gly Thr Cys Cys Ala Gly Thr Thr Thr Gly Thr
545                 550                 555                 560

Cys Cys Thr Cys Gly Gly Gly Thr Gly Gly Cys Cys Cys Thr Thr Gly
                565                 570                 575

Thr Ala Cys Thr Thr Ala Gly Cys Cys Thr Thr Thr Ala Ala Cys Gly
            580                 585                 590

Thr Cys Thr Cys Thr Gly Gly Cys Ala Gly Ala Cys Cys Gly Thr Ala
        595                 600                 605

Thr Gly Ala Cys Gly Gly Gly Thr Thr Cys Gly Cys Thr Thr Gly Cys
    610                 615                 620

Cys Ala Thr Thr Thr Cys Thr Thr Cys Cys Cys Cys Ala Ala Cys Gly
625                 630                 635                 640

Cys Thr Cys Cys Cys Ala Thr Cys Thr Ala Cys Ala Ala Thr Gly Ala
                645                 650                 655

Cys Cys Gly Ala Gly Ala Ala Cys Gly Cys Cys Thr Cys Cys Ala Gly
            660                 665                 670

Ala Thr Ala Thr Ala Cys Cys Thr Cys Thr Cys Thr Gly Ala Thr Gly
        675                 680                 685

Cys Gly Gly Gly Thr Ala Thr Thr Cys Thr Ala Gly Cys Cys Gly Thr
    690                 695                 700

Cys Thr Gly Thr Thr Thr Thr Gly Gly Thr Cys Thr Thr Thr Ala Cys
705                 710                 715                 720

Cys Gly Thr Thr Ala Cys Gly Cys Thr Gly Cys Thr Gly Cys Ala Cys
                725                 730                 735

Ala Ala Gly Gly Gly Ala Thr Gly Gly Cys Cys Thr Cys Gly Ala Thr
            740                 745                 750

Gly Ala Thr Cys Thr Gly Cys Cys Thr Cys Thr Ala Cys Gly Gly Ala
        755                 760                 765

Gly Thr Ala Cys Cys Gly Cys Thr Thr Cys Thr Gly Ala Thr Ala Gly
    770                 775                 780

Thr Gly Ala Ala Thr Gly Cys Gly Thr Thr Cys Cys Thr Cys Gly Thr
785                 790                 795                 800

Cys Thr Thr Gly Ala Thr Cys Ala Cys Thr Thr Ala Cys Thr Thr Gly
                805                 810                 815

Cys Ala Gly Cys Ala Cys Ala Cys Thr Cys Ala Thr Cys Cys Cys Thr
            820                 825                 830

Cys Gly Thr Thr Gly Cys Cys Thr Cys Ala Cys Thr Ala Cys Gly Ala
        835                 840                 845

Thr Thr Cys Ala Thr Cys Ala Gly Ala Gly Thr Gly Gly Gly Ala Cys
    850                 855                 860

Thr Gly Gly Cys Thr Cys Ala Gly Gly Gly Gly Ala Gly Cys Thr Thr
865                 870                 875                 880
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```
Thr Gly Gly Cys Thr Ala Cys Cys Gly Thr Ala Gly Ala Cys Ala Gly
                885                 890                 895

Ala Gly Ala Cys Thr Ala Cys Gly Gly Ala Ala Thr Cys Thr Thr Gly
            900                 905                 910

Ala Ala Cys Ala Ala Gly Gly Thr Gly Thr Thr Cys Cys Ala Cys Ala
        915                 920                 925

Ala Cys Ala Thr Thr Ala Cys Ala Gly Ala Cys Ala Cys Ala Cys Ala
    930                 935                 940

Cys Gly Thr Gly Gly Cys Thr Cys Ala Thr Cys Ala Cys Cys Thr Gly
945                 950                 955                 960

Thr Thr Cys Thr Cys Gly Ala Cys Ala Ala Thr Gly Cys Cys Gly Cys
                965                 970                 975

Ala Thr Thr Ala Thr Ala Ala Cys Gly Cys Ala Ala Thr Gly Gly Ala
            980                 985                 990

Ala Gly Cys Thr Ala Cys Ala Ala  Ala Gly Gly Cys Gly  Ala Thr Ala
        995                 1000                1005

Ala Ala  Gly Cys Cys Ala Ala  Thr Thr Cys Thr Gly  Gly Gly Ala
    1010                1015                1020

Gly Ala  Cys Thr Ala Thr Thr  Ala Cys Cys Ala Gly  Thr Thr Cys
    1025                1030                1035

Gly Ala  Thr Gly Gly Ala Ala  Cys Ala Cys Cys Gly  Thr Gly Gly
    1040                1045                1050

Thr Ala  Thr Gly Thr Ala Gly  Cys Gly Ala Thr Gly  Thr Ala Thr
    1055                1060                1065

Ala Gly  Gly Gly Ala Gly Gly  Cys Ala Ala Ala Gly  Gly Ala Gly
    1070                1075                1080

Thr Gly  Thr Ala Thr Cys Thr  Ala Thr Gly Thr Ala  Gly Ala Ala
    1085                1090                1095

Cys Cys  Gly Gly Ala Cys Ala  Gly Gly Gly Ala Ala  Gly Gly Thr
    1100                1105                1110

Gly Ala  Cys Ala Ala Gly Ala  Ala Ala Gly Gly Thr  Gly Thr Gly
    1115                1120                1125

Thr Ala  Cys Thr Gly Gly Thr  Ala Cys Ala Ala Cys  Ala Ala Thr
    1130                1135                1140

Ala Ala  Gly Thr Thr Ala Thr  Gly Ala
    1145                1150


<210> SEQ ID NO 23
<211> LENGTH: 383
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 23

Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser
1               5                   10                  15

Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
            20                  25                  30

Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
        35                  40                  45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
    50                  55                  60
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Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
65                  70                  75                  80

Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
                85                  90                  95

Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
            100                 105                 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
        115                 120                 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
    130                 135                 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145                 150                 155                 160

Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
                165                 170                 175

Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu
            180                 185                 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys
        195                 200                 205

His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
    210                 215                 220

Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr
225                 230                 235                 240

Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly
                245                 250                 255

Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
            260                 265                 270

Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
        275                 280                 285

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
    290                 295                 300

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
305                 310                 315                 320

Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile
                325                 330                 335

Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr
            340                 345                 350

Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
        355                 360                 365

Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu
    370                 375                 380


<210> SEQ ID NO 24
<211> LENGTH: 1161
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 24

atggttgttg ctatggacca acgcaccaat gtgaacggag atcccggcgc cggagaccgg     60

aagaaagaag aaaggtttga tccgagtgca caaccaccgt tcaagatcgg agatataagg    120

gcggcgattc ctaagcactg ttgggttaag agtcctttga gatcaatgag ttacgtcgtc    180
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agagacatta tcgccgtcgc ggctttggcc atcgctgccg tgtatgttga tagctggttc 240

ctttggcctc tttattgggc cgcccaagga acacttttct gggccatctt tgttctcggc 300

cacgactgtg gacatgggag tttctcagac attcctctac tgaatagtgt ggttggtcac 360

attcttcatt ctttcatcct cgttccttac catggttgga gaataagcca ccggacacac 420

caccagaacc atggccatgt tgaaaacgac gagtcatggg ttccgttacc agaaagggtg 480

tacaagaaat tgccccacag tactcggatg ctcagataca ctgtccctct ccccatgctc 540

gcatatcctc tctatttgtg ctacagaagt cctggaaaag aaggatcaca ttttaaccca 600

tacagtagtt tatttgctcc aagcgagaga aagcttattg caacttcaac tacttgttgg 660

tccataatgt tcgtcagtct tatcgctcta tctttcgtct tcggtccact cgcggttctt 720

aaagtctacg gtgtaccgta cattatcttt gtgatgtggt tggatgctgt cacgtatttg 780

catcatcatg gtcacgatga gaagttgcct tggtatagag gcaaggaatg gagttatcta 840

cgtggaggat taacaacaat tgatagagat tacggaatct ttaacaacat tcatcacgac 900

attggaactc acgtgatcca tcatctcttc ccacaaatcc ctcactatca cttggtcgac 960

gccacgaaag cagctaaaca tgtgttggga agatactaca gagaaccaaa gacgtcagga 1020

gcaataccga tccacttggt ggagagtttg gtcgcaagta ttaagaaaga tcattacgtc 1080

agcgacactg gtgatattgt cttctacgag acagatccag atctctacgt ttacgcttct 1140

gacaaatcta aaatcaatta a 1161

<210> SEQ ID NO 25
<211> LENGTH: 386
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 25

Met Val Val Ala Met Asp Gln Arg Thr Asn Val Asn Gly Asp Pro Gly
1 5 10 15

Ala Gly Asp Arg Lys Lys Glu Glu Arg Phe Asp Pro Ser Ala Gln Pro
20 25 30

Pro Phe Lys Ile Gly Asp Ile Arg Ala Ala Ile Pro Lys His Cys Trp
35 40 45

Val Lys Ser Pro Leu Arg Ser Met Ser Tyr Val Val Arg Asp Ile Ile
50 55 60

Ala Val Ala Ala Leu Ala Ile Ala Ala Val Tyr Val Asp Ser Trp Phe
65 70 75 80

Leu Trp Pro Leu Tyr Trp Ala Ala Gln Gly Thr Leu Phe Trp Ala Ile
85 90 95

Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser Asp Ile Pro
100 105 110

Leu Leu Asn Ser Val Val Gly His Ile Leu His Ser Phe Ile Leu Val
115 120 125

Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn His
130 135 140

Gly His Val Glu Asn Asp Glu Ser Trp Val Pro Leu Pro Glu Arg Val
145 150 155 160

Tyr Lys Lys Leu Pro His Ser Thr Arg Met Leu Arg Tyr Thr Val Pro

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               165                 170                 175

Leu Pro Met Leu Ala Tyr Pro Leu Tyr Leu Cys Tyr Arg Ser Pro Gly
            180                 185                 190

Lys Glu Gly Ser His Phe Asn Pro Tyr Ser Ser Leu Phe Ala Pro Ser
        195                 200                 205

Glu Arg Lys Leu Ile Ala Thr Ser Thr Thr Cys Trp Ser Ile Met Phe
    210                 215                 220

Val Ser Leu Ile Ala Leu Ser Phe Val Phe Gly Pro Leu Ala Val Leu
225                 230                 235                 240

Lys Val Tyr Gly Val Pro Tyr Ile Ile Phe Val Met Trp Leu Asp Ala
                245                 250                 255

Val Thr Tyr Leu His His His Gly His Asp Glu Lys Leu Pro Trp Tyr
            260                 265                 270

Arg Gly Lys Glu Trp Ser Tyr Leu Arg Gly Gly Leu Thr Thr Ile Asp
        275                 280                 285

Arg Asp Tyr Gly Ile Phe Asn Asn Ile His His Asp Ile Gly Thr His
    290                 295                 300

Val Ile His His Leu Phe Pro Gln Ile Pro His Tyr His Leu Val Asp
305                 310                 315                 320

Ala Thr Lys Ala Ala Lys His Val Leu Gly Arg Tyr Tyr Arg Glu Pro
                325                 330                 335

Lys Thr Ser Gly Ala Ile Pro Ile His Leu Val Glu Ser Leu Val Ala
            340                 345                 350

Ser Ile Lys Lys Asp His Tyr Val Ser Asp Thr Gly Asp Ile Val Phe
        355                 360                 365

Tyr Glu Thr Asp Pro Asp Leu Tyr Val Tyr Ala Ser Asp Lys Ser Lys
    370                 375                 380

Ile Asn
385
```

<210> SEQ ID NO 26
<211> LENGTH: 1521
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 26

```
atgacgtccg ttaacgttaa gctcctttac cgttacgtct taaccaactt tttcaacctc     60

tgtttgttcc cgttaacggc gttcctcgcc ggaaaagcct ctcggcttac cataaacgat    120

ctccacaact tcctttccta tctccaacac aaccttataa cagtaacttt actctttgct    180

ttcactgttt tcggtttggt tctctacatc gtaacccgac ccaatccggt ttatctcgtt    240

gactactcgt gttaccttcc accaccgcat ctcaaagtta gtgtctctaa agtcatggat    300

attttctacc aaataagaaa agctgatact tcttcacgga acgtggcatg tgatgatccg    360

tcctcgctcg atttcctgag gaagattcaa gagcgttcag gtctaggtga tgagacgtac    420

agtcctgagg gactcattca cgtaccaccg cggaagactt ttgcagcgtc acgtgaagag    480

acagagaagg ttatcatcgg tgcgctcgaa aatctattcg agaacaccaa agttaaccct    540

agagagattg gtatacttgt ggtgaactca agcatgttta atccaactcc ttcgctatcc    600

gctatggtcg ttaatacttt caagctccga agcaacatca aaagctttaa tctaggagga    660
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atgggttgta gtgctggtgt tattgccatt gatttggcta aagacttgtt gcatgttcat 720

aaaaacactt atgctcttgt ggtgagcact gagaacatca cacaaggcat ttatgctgga 780

gaaaatagat caatgatggt tagcaattgc ttgtttcgtg ttggtggggc cgcgattttg 840

ctctctaaca agtcgggaga ccggagacgg tccaagtaca agctagttca cacggtccga 900

acgcatactg gagctgatga caagtctttt cgatgtgtgc aacaagaaga cgatgagagc 960

ggcaaaatcg gagtttgtct gtcaaaggac ataaccaatg ttgcggggac aacacttacg 1020

aaaaatatag caacattggg tccgttgatt cttcctttaa gcgaaaagtt tctttttttc 1080

gctaccttcg tcgccaagaa acttctaaag gataaaatca agcattacta tgttccggat 1140

ttcaagcttg ctgttgacca tttctgtatt catgccggag gcagagccgt gatcgatgag 1200

ctagagaaga acttaggact atcgccgatc gatgtggagg catctagatc aacgttacat 1260

agatttggga atacttcatc tagctcaatt tggtatgaat tagcatacat agaggcaaag 1320

ggaagaatga agaaagggaa taaagcttgg cagattgctt taggatcagg gtttaagtgt 1380

aatagtgcgg tttgagtggc tctacgcaat gtcaaggcat cggcaaatag tccttggcaa 1440

cattgcatcg atagatatcc ggttaaaatt gattctgatt tgtcaaagtc aaagactcat 1500

gtccaaaacg gtcggtccta a 1521

<210> SEQ ID NO 27
<211> LENGTH: 464
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 27

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
1 5 10 15

Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
20 25 30

Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
35 40 45

Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50 55 60

Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65 70 75 80

Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
85 90 95

Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
100 105 110

Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
115 120 125

Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
130 135 140

Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
145 150 155 160

Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
165 170 175

Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
180 185 190

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Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
        195                 200                 205

Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
    210                 215                 220

Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225                 230                 235                 240

Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
                245                 250                 255

Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
            260                 265                 270

Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
        275                 280                 285

Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
    290                 295                 300

Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
305                 310                 315                 320

Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
                325                 330                 335

Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
            340                 345                 350

Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
        355                 360                 365

Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
    370                 375                 380

Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
385                 390                 395                 400

Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
                405                 410                 415

Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
            420                 425                 430

Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
        435                 440                 445

Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
    450                 455                 460


<210> SEQ ID NO 28
<211> LENGTH: 1149
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 28

atgagttcat cgtgtataga agaagtcagt gtaccggatg acaactggta ccgtatcgcc     60

aacgaattac ttagccgtgc cggtatagcc attaacggtt ctgccccggc ggatattcgt    120

gtgaaaaacc ccgatttttt taaacgcgtt ctgcaagaag gctctttggg gttaggcgaa    180

agttatatgg atggctggtg ggaatgtgac cgactggata tgtttttag caaagtctta    240

cgcgcaggtc tcgagaacca actcccccat catttcaaag acacgctgcg tattgccggc    300

gctcgtctct tcaatctgca gagtaaaaaa cgtgcctgga tagtcggcaa agagcattac    360

gatttgggta atgacttgtt cagccgcatg cttgatccct tcatgcaata ttcctgcgct    420

tactggaaag atgccgataa tctggaatct gcccagcagg cgaagctcaa aatgatttgt    480

gaaaaattgc agttaaaacc agggatgcgc gtactggata ttggctgcgg ctggggcgga    540
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ctggcacact acatggcatc taattatgac gtaagcgtgg tgggcgtcac catttctgcc 600

gaacagcaaa aaatggctca ggaacgctgt gaaggcctgg atgtcaccat tttgctgcaa 660

gattatcgtg acctgaacga ccagtttgat cgtattgttt ctgtggggat gttcgagcac 720

gtcggaccga aaaattacga tacctatttt gcggtggtgg atcgtaattt gaaaccggaa 780

ggcatattcc tgctccatac tatcggttcg aaaaaaaccg atctgaatgt tgatccctgg 840

attaataaat atatttttcc gaacggttgc ctgccctctg tacgccagat tgctcagtcc 900

agcgaacccc actttgtgat ggaagactgg cataacttcg gtgctgatta cgatactacg 960

ttgatggcgt ggtatgaacg attcctcgcc gcatggccag aaattgcgga taactatagt 1020

gaacgcttta aacgaatgtt tacctattat ctgaatgcct gtgcaggtgc tttccgcgcc 1080

cgtgatattc agctctggca ggtcgtgttc tcacgcggtg ttgaaaacgg ccttcgagtg 1140

gctcgctaa 1149

<210> SEQ ID NO 29
<211> LENGTH: 382
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 29

Met Ser Ser Ser Cys Ile Glu Glu Val Ser Val Pro Asp Asp Asn Trp
1 5 10 15

Tyr Arg Ile Ala Asn Glu Leu Leu Ser Arg Ala Gly Ile Ala Ile Asn
20 25 30

Gly Ser Ala Pro Ala Asp Ile Arg Val Lys Asn Pro Asp Phe Phe Lys
35 40 45

Arg Val Leu Gln Glu Gly Ser Leu Gly Leu Gly Glu Ser Tyr Met Asp
50 55 60

Gly Trp Trp Glu Cys Asp Arg Leu Asp Met Phe Phe Ser Lys Val Leu
65 70 75 80

Arg Ala Gly Leu Glu Asn Gln Leu Pro His His Phe Lys Asp Thr Leu
85 90 95

Arg Ile Ala Gly Ala Arg Leu Phe Asn Leu Gln Ser Lys Lys Arg Ala
100 105 110

Trp Ile Val Gly Lys Glu His Tyr Asp Leu Gly Asn Asp Leu Phe Ser
115 120 125

Arg Met Leu Asp Pro Phe Met Gln Tyr Ser Cys Ala Tyr Trp Lys Asp
130 135 140

Ala Asp Asn Leu Glu Ser Ala Gln Gln Ala Lys Leu Lys Met Ile Cys
145 150 155 160

Glu Lys Leu Gln Leu Lys Pro Gly Met Arg Val Leu Asp Ile Gly Cys
165 170 175

Gly Trp Gly Gly Leu Ala His Tyr Met Ala Ser Asn Tyr Asp Val Ser
180 185 190

Val Val Gly Val Thr Ile Ser Ala Glu Gln Gln Lys Met Ala Gln Glu
195 200 205

Arg Cys Glu Gly Leu Asp Val Thr Ile Leu Leu Gln Asp Tyr Arg Asp
210 215 220

Leu Asn Asp Gln Phe Asp Arg Ile Val Ser Val Gly Met Phe Glu His
225 230 235 240

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Val Gly Pro Lys Asn Tyr Asp Thr Tyr Phe Ala Val Val Asp Arg Asn
                245                 250                 255

Leu Lys Pro Glu Gly Ile Phe Leu Leu His Thr Ile Gly Ser Lys Lys
            260                 265                 270

Thr Asp Leu Asn Val Asp Pro Trp Ile Asn Lys Tyr Ile Phe Pro Asn
        275                 280                 285

Gly Cys Leu Pro Ser Val Arg Gln Ile Ala Gln Ser Ser Glu Pro His
    290                 295                 300

Phe Val Met Glu Asp Trp His Asn Phe Gly Ala Asp Tyr Asp Thr Thr
305                 310                 315                 320

Leu Met Ala Trp Tyr Glu Arg Phe Leu Ala Ala Trp Pro Glu Ile Ala
                325                 330                 335

Asp Asn Tyr Ser Glu Arg Phe Lys Arg Met Phe Thr Tyr Tyr Leu Asn
            340                 345                 350

Ala Cys Ala Gly Ala Phe Arg Ala Arg Asp Ile Gln Leu Trp Gln Val
        355                 360                 365

Val Phe Ser Arg Gly Val Glu Asn Gly Leu Arg Val Ala Arg
    370                 375                 380
```

<210> SEQ ID NO 30
<211> LENGTH: 1125
<212> TYPE: DNA
<213> ORGANISM: Crepis palaestina

<400> SEQUENCE: 30

```
atgggtgccg gcggtcgtgg tcggacatcg gaaaaatcgg tcatggaacg tgtctcagtt     60

gatccagtaa ccttctcact gagtgaattg aagcaagcaa tccctcccca ttgcttccag    120

agatctgtaa tccgctcatc ttactatgtt gttcaagatc tcattattgc ctacatcttc    180

tacttccttg ccaacacata tatccctact cttcctacta gtctagccta cttagcttgg    240

cccgtttact ggttctgtca agctagcgtc ctcactggct tatggatcct cggccacgaa    300

tgtggtcacc atgcctttag caactacaca tggtttgacg acactgtggg cttcatcctc    360

cactcatttc tcctcacccc gtatttctct tggaaattca gtcaccggaa tcaccattcc    420

aacacaagtt cgattgataa cgatgaagtt tacattccga aaagcaagtc caaactcgcg    480

cgtatctata aacttcttaa caacccacct ggtcggctgt tggttttgat tatcatgttc    540

accctaggat ttcctttata cctcttgaca aatatttccg gcaagaaata cgacaggttt    600

gccaaccact tcgaccccat gagtccaatt ttcaaagaac gtgagcggtt tcaggtcttc    660

ctttcggatc ttggtcttct tgccgtgttt tatggaatta aagttgctgt agcaaataaa    720

ggagctgctt gggtagcgtg catgtatgga gttccggtat taggcgtatt taccttttc     780

gatgtgatca ccttcttgca ccacacccat cagtcgtcgc ctcattatga ttcaactgaa    840

tggaactgga tcagaggggc cttgtcagca atcgataggg actttggatt cctgaatagt    900

gttttccatg atgttacaca cactcatgtc atgcatcatt tgttttcata cattccacac    960

tatcatgcaa aggaggcaag ggatgcaatc aagccaatct tgggcgactt ttatatgatc   1020

gacaggactc caattttaaa agcaatgtgg agagagggca gggagtgcat gtacatcgag   1080

cctgatagca agctcaaagg tgtttattgg tatcataaat tgtga                   1125
```

<210> SEQ ID NO 31
<211> LENGTH: 374

-continued

<212> TYPE: PRT
<213> ORGANISM: Crepis palaestina

<400> SEQUENCE: 31

Met Gly Ala Gly Gly Arg Gly Arg Thr Ser Glu Lys Ser Val Met Glu
1 5 10 15

Arg Val Ser Val Asp Pro Val Thr Phe Ser Leu Ser Glu Leu Lys Gln
20 25 30

Ala Ile Pro Pro His Cys Phe Gln Arg Ser Val Ile Arg Ser Ser Tyr
35 40 45

Tyr Val Val Gln Asp Leu Ile Ile Ala Tyr Ile Phe Tyr Phe Leu Ala
50 55 60

Asn Thr Tyr Ile Pro Thr Leu Pro Thr Ser Leu Ala Tyr Leu Ala Trp
65 70 75 80

Pro Val Tyr Trp Phe Cys Gln Ala Ser Val Leu Thr Gly Leu Trp Ile
85 90 95

Leu Gly His Glu Cys Gly His His Ala Phe Ser Asn Tyr Thr Trp Phe
100 105 110

Asp Asp Thr Val Gly Phe Ile Leu His Ser Phe Leu Leu Thr Pro Tyr
115 120 125

Phe Ser Trp Lys Phe Ser His Arg Asn His His Ser Asn Thr Ser Ser
130 135 140

Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ser Lys Leu Ala
145 150 155 160

Arg Ile Tyr Lys Leu Leu Asn Asn Pro Pro Gly Arg Leu Leu Val Leu
165 170 175

Ile Ile Met Phe Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn Ile
180 185 190

Ser Gly Lys Lys Tyr Asp Arg Phe Ala Asn His Phe Asp Pro Met Ser
195 200 205

Pro Ile Phe Lys Glu Arg Glu Arg Phe Gln Val Phe Leu Ser Asp Leu
210 215 220

Gly Leu Leu Ala Val Phe Tyr Gly Ile Lys Val Ala Val Ala Asn Lys
225 230 235 240

Gly Ala Ala Trp Val Ala Cys Met Tyr Gly Val Pro Val Leu Gly Val
245 250 255

Phe Thr Phe Phe Asp Val Ile Thr Phe Leu His His Thr His Gln Ser
260 265 270

Ser Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala Leu
275 280 285

Ser Ala Ile Asp Arg Asp Phe Gly Phe Leu Asn Ser Val Phe His Asp
290 295 300

Val Thr His Thr His Val Met His His Leu Phe Ser Tyr Ile Pro His
305 310 315 320

Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Ile Leu Gly Asp
325 330 335

Phe Tyr Met Ile Asp Arg Thr Pro Ile Leu Lys Ala Met Trp Arg Glu
340 345 350

Gly Arg Glu Cys Met Tyr Ile Glu Pro Asp Ser Lys Leu Lys Gly Val
355 360 365

Tyr Trp Tyr His Lys Leu
370

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<210> SEQ ID NO 32
<211> LENGTH: 1131
<212> TYPE: DNA
<213> ORGANISM: Crepis alpina

<400> SEQUENCE: 32

aagatgggtg gcggtggccg tggtcggact tcgcaaaaac ccctcatgga acgtgtctca 60

gttgatccac ccttcaccgt gagtgatctc aagcaagcaa tccctcccca ttgcttcaag 120

cgatctgtaa tccgttcctc ttactacata gtccacgatg ctattatcgc ctacatcttc 180

tacttccttg ccgacaaata cattccgatt ctccctgccc ctctagccta cctcgcttgg 240

ccccttttact ggttctgtca agctagcatc ctcaccggct tatgggtcat cggtcacgaa 300

tgcggtcacc atgccttcag cgactaccag tgggttgacg acactgtggg cttcatcctc 360

cactcgtttc tcatgacccc gtatttctcc tggaaataca gccaccggaa ccaccatgcc 420

aacacaaatt cgcttgacaa cgatgaagtt tacatcccca aaagcaaggc caaagtcgcg 480

ctttactata aagttctcaa ccacccacct ggccgactgt tgattatgtt catcaccttc 540

accctaggct tccctctata cctctttacc aatatttccg gcaagaagta tgaaaggttt 600

gccaaccatt tcgaccccat gagtccgatt ttcaaagagc gtgagcggtt tcaggtcttg 660

ctatcggatc ttggccttct tgctgtgctt tacggagtta aacttgcggt agcagcgaaa 720

ggcgccgctt gggtgacgtg catttacgga attccagttt taggcgtgtt tatctttttc 780

gatatcatca cctacttgca ccacacccat ctgtcgttgc ctcattatga ttcatctgaa 840

tggaactggc tcagaggggc tttgtcaaca atcgataggg actttgggtt cctgaatagt 900

gtgctccatg atgttacaca cactcacgtt atgcatcatc tgttttcata cattccacac 960

tatcatgcga aggaggcaag ggatgcaatc aacacagtct tgggcgactt ttataagatc 1020

gataggactc caattctgaa agcaatgtgg agagaggcca aggaatgcat cttcatcgag 1080

cctgaaaaag gtagggagtc caagggtgta tattggtaca ataaattctg a 1131

<210> SEQ ID NO 33
<211> LENGTH: 375
<212> TYPE: PRT
<213> ORGANISM: Crepis alpina

<400> SEQUENCE: 33

Met Gly Gly Gly Gly Arg Gly Arg Thr Ser Gln Lys Pro Leu Met Glu
1 5 10 15

Arg Val Ser Val Asp Pro Pro Phe Thr Val Ser Asp Leu Lys Gln Ala
20 25 30

Ile Pro Pro His Cys Phe Lys Arg Ser Val Ile Arg Ser Ser Tyr Tyr
35 40 45

Ile Val His Asp Ala Ile Ile Ala Tyr Ile Phe Tyr Phe Leu Ala Asp
50 55 60

Lys Tyr Ile Pro Ile Leu Pro Ala Pro Leu Ala Tyr Leu Ala Trp Pro
65 70 75 80

Leu Tyr Trp Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp Val Ile
85 90 95

Gly His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Val Asp
100 105 110

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Asp Thr Val Gly Phe Ile Leu His Ser Phe Leu Met Thr Pro Tyr Phe
        115                 120                 125

Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn Ser Leu
    130                 135                 140

Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ala Lys Val Ala Leu
145                 150                 155                 160

Tyr Tyr Lys Val Leu Asn His Pro Pro Gly Arg Leu Leu Ile Met Phe
                165                 170                 175

Ile Thr Phe Thr Leu Gly Phe Pro Leu Tyr Leu Phe Thr Asn Ile Ser
            180                 185                 190

Gly Lys Lys Tyr Glu Arg Phe Ala Asn His Phe Asp Pro Met Ser Pro
        195                 200                 205

Ile Phe Lys Glu Arg Glu Arg Phe Gln Val Leu Leu Ser Asp Leu Gly
    210                 215                 220

Leu Leu Ala Val Leu Tyr Gly Val Lys Leu Ala Val Ala Ala Lys Gly
225                 230                 235                 240

Ala Ala Trp Val Thr Cys Ile Tyr Gly Ile Pro Val Leu Gly Val Phe
                245                 250                 255

Ile Phe Phe Asp Ile Ile Thr Tyr Leu His His Thr His Leu Ser Leu
            260                 265                 270

Pro His Tyr Asp Ser Ser Glu Trp Asn Trp Leu Arg Gly Ala Leu Ser
        275                 280                 285

Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Ser Val Leu His Asp Val
    290                 295                 300

Thr His Thr His Val Met His His Leu Phe Ser Tyr Ile Pro His Tyr
305                 310                 315                 320

His Ala Lys Glu Ala Arg Asp Ala Ile Asn Thr Val Leu Gly Asp Phe
                325                 330                 335

Tyr Lys Ile Asp Arg Thr Pro Ile Leu Lys Ala Met Trp Arg Glu Ala
            340                 345                 350

Lys Glu Cys Ile Phe Ile Glu Pro Glu Lys Gly Arg Glu Ser Lys Gly
        355                 360                 365

Val Tyr Trp Tyr Asn Lys Phe
    370                 375


<210> SEQ ID NO 34
<211> LENGTH: 1297
<212> TYPE: DNA
<213> ORGANISM: Momordica charantia

<400> SEQUENCE: 34

aataaattag cttctttttt taagtgagtg aagggagatc tggaggcaat ggggggcaga     60

ggagctattg gagtactgag gaacggtggc ggcccaaaaa agaaaatggg gccggggcag    120

gggctggggc cgggggagcg cattacacat gccaggcctc ccttcagcat cagccagatc    180

aagaaggcca ttccccccca ctgctttcag cgatccctcc gccgctcttt ttcctacctt    240

ctttccgaca ttgccctcgt ctctgccttt tattacgttg ccgacaccta cttccaccgc    300

ctgccccacc ccctactcca ctacctggcc tggcccgttt actggttctg tcagggcgcc    360

gtactcaccg gcatgtgggg catcgctcac gactgcggcc accacgcctt cagcgactac    420

caattggtag acgacgtggt tgggttcctc atccactctt tggtttttgt cccttacttc    480

tccttcaaga tcagccaccg ccgccaccac tccaacacct catccgtgga ccgggacgag    540
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gtgttcgtcc ccaagccgaa ggccaaaatg ccctggtact tcaagtactt gacaaacccg 600

cccgccaggg tcttcattat ttttatcacg ctcactctcg ggtggccaat gtacctgacc 660

ttcaacatct ccggccggta ctacggccgg ttcaccagcc acttcgaccc gaacagcccc 720

atattcagcc caaaggagcg cgttctcgtt catatctcca acgctgggct tgtggcgacc 780

gggtatttgc tgtacaggat cgcaatggcg aaggggggtgg ggtggttgat ccgcttgtac 840

ggagtgccgc tgatcgtttt aaacgcgtgc gtagttctga tcacagcgct gcagcacacc 900

caccttcgt tcccgtatta cgactcgacg gaatgggatt ggctgagagg gaatctggtg 960

acggtggaca gagattacgg gcctataatg aatagagtgt ttcatcacat aacggacacg 1020

cacgtggttc accatttgtt tccttcgatg ccgcactaca acgggaaaga ggcgacggtt 1080

gcagcaaagc gaatactggg agagtactac cagtttgatg ggaccccaat ttggaaggcg 1140

gcctggaggg aattcagaga gtgcgtttat gtagagccag acgaagacga tggggccact 1200

tccggctcca gtagtaaggg tgttttctgg taccacaaca agctctgaat tcaataatat 1260

cctctttcac ctctcttttt cataaaaaaa aaaaaaa 1297

<210> SEQ ID NO 35
<211> LENGTH: 399
<212> TYPE: PRT
<213> ORGANISM: Momordica charantia

<400> SEQUENCE: 35

Met Gly Gly Arg Gly Ala Ile Gly Val Leu Arg Asn Gly Gly Gly Pro
1 5 10 15

Lys Lys Lys Met Gly Pro Gly Gln Gly Leu Gly Pro Gly Glu Arg Ile
20 25 30

Thr His Ala Arg Pro Pro Phe Ser Ile Ser Gln Ile Lys Lys Ala Ile
35 40 45

Pro Pro His Cys Phe Gln Arg Ser Leu Arg Arg Ser Phe Ser Tyr Leu
50 55 60

Leu Ser Asp Ile Ala Leu Val Ser Ala Phe Tyr Tyr Val Ala Asp Thr
65 70 75 80

Tyr Phe His Arg Leu Pro His Pro Leu Leu His Tyr Leu Ala Trp Pro
85 90 95

Val Tyr Trp Phe Cys Gln Gly Ala Val Leu Thr Gly Met Trp Gly Ile
100 105 110

Ala His Asp Cys Gly His His Ala Phe Ser Asp Tyr Gln Leu Val Asp
115 120 125

Asp Val Val Gly Phe Leu Ile His Ser Leu Val Phe Val Pro Tyr Phe
130 135 140

Ser Phe Lys Ile Ser His Arg Arg His His Ser Asn Thr Ser Ser Val
145 150 155 160

Asp Arg Asp Glu Val Phe Val Pro Lys Pro Lys Ala Lys Met Pro Trp
165 170 175

Tyr Phe Lys Tyr Leu Thr Asn Pro Pro Ala Arg Val Phe Ile Ile Phe
180 185 190

Ile Thr Leu Thr Leu Gly Trp Pro Met Tyr Leu Thr Phe Asn Ile Ser
195 200 205

Gly Arg Tyr Tyr Gly Arg Phe Thr Ser His Phe Asp Pro Asn Ser Pro
210 215 220

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Ile Phe Ser Pro Lys Glu Arg Val Leu Val His Ile Ser Asn Ala Gly
225                 230                 235                 240

Leu Val Ala Thr Gly Tyr Leu Leu Tyr Arg Ile Ala Met Ala Lys Gly
                245                 250                 255

Val Gly Trp Leu Ile Arg Leu Tyr Gly Val Pro Leu Ile Val Leu Asn
            260                 265                 270

Ala Cys Val Val Leu Ile Thr Ala Leu Gln His Thr His Pro Ser Phe
        275                 280                 285

Pro Tyr Tyr Asp Ser Thr Glu Trp Asp Trp Leu Arg Gly Asn Leu Val
    290                 295                 300

Thr Val Asp Arg Asp Tyr Gly Pro Ile Met Asn Arg Val Phe His His
305                 310                 315                 320

Ile Thr Asp Thr His Val Val His His Leu Phe Pro Ser Met Pro His
                325                 330                 335

Tyr Asn Gly Lys Glu Ala Thr Val Ala Ala Lys Arg Ile Leu Gly Glu
            340                 345                 350

Tyr Tyr Gln Phe Asp Gly Thr Pro Ile Trp Lys Ala Ala Trp Arg Glu
        355                 360                 365

Phe Arg Glu Cys Val Tyr Val Glu Pro Asp Glu Asp Asp Gly Ala Thr
    370                 375                 380

Ser Gly Ser Ser Ser Lys Gly Val Phe Trp Tyr His Asn Lys Leu
385                 390                 395


<210> SEQ ID NO 36
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 36

catgagtttg agtatacaca tgtcta                                          26


<210> SEQ ID NO 37
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 37

aaagaaatca tgtaaaccta atagaaacg c                                     31


<210> SEQ ID NO 38
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 38

gtgatcgatg agctagagaa gaac                                            24


<210> SEQ ID NO 39
<211> LENGTH: 41
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 39

caaggactat ttgccgatgc cttgacattg cgtagagcga c 41

<210> SEQ ID NO 40
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 40

aatatagcca tcgccgccac catt 24

<210> SEQ ID NO 41
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 41

tggcaagcaa agcgatcgta aggt 24

<210> SEQ ID NO 42
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 42

accatcactt tggaggtgga 20

<210> SEQ ID NO 43
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 43

gtcaatggtg tcggagcttt 20

<210> SEQ ID NO 44
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 44

cggtggagat tatccaacag 20

<210> SEQ ID NO 45
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 45

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ttatggtgat cctctggttg 20

<210> SEQ ID NO 46
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 46

aaaattaaaa tctcagcagt 20

1. A transgenic plant or part thereof that comprises:

a) a genomic mutation selected from the group consisting of a mutation of fad2, fad3, and fae1, or any combination of such mutations,

b) the reduced expression of one or both endogenous BADC1 and BADC3 genes, and

c) one or more transgenes that alter metabolism of a target fatty acid.

2. The transgenic plant or part thereof of claim **1**, wherein said transgenic plant part comprises wild type BADC1 gene and reduced expression of said endogenous BADC3 gene.

3. The transgenic plant or part thereof of claim **1**, wherein said transgenic plant part comprises reduced expression of said endogenous BADC1 gene and BADC3 gene.

4. The transgenic plant or part thereof of claim **1**, wherein said plant is *Camelina sativa, Brassica napus* or *Glycine max.*

5. The transgenic plant or part thereof of claim **1**, wherein said genomic mutation is fad2/fae1 or fad3/fae1.

6. The transgenic plant or part thereof of claim **1**, wherein said one or more transgenes encode *Ricinus* fatty acid hydroxylase (FAI H), *E. coli* cyclopropane fatty acid synthase, *Crepis palaestina* delta 12 fatty acid epoxygenase, *Crepis alpina* delta-12 fatty acid acetylenase, or *Momordica charantia* Conjugase (FadX).

7. The transgenic plant or part thereof of claim **1**, wherein said one or more transgenes are under control of a seed-specific promoter.

8. The transgenic plant or part thereof of claim **1**, wherein said target fatty acid comprises one or more of hydroxyl fatty acids, medium-chain fatty acids, very-long-chain fatty acids (VLCFAs), monounsaturated fatty acids (MUFAs), γ-linolenic acid, stearidonic acids, α-eleostearic acid, conjugated fatty acids, epoxy fatty acids, cyclic fatty acids and acetylenic fatty acids.

9. The transgenic plant or part thereof of claim **1**, wherein said transgenic plant part is from *Camelina sativa, Brassica napus* or *Glycine max*, said genomic mutation is fad3 fae1, and said transgene encodes acetylanase, conjugase, epoxygenase or any combinations thereof.

10. The transgenic plant or part thereof of claim **1**, wherein said transgenic plant part is from *Camelina sativa, Brassica napus* or *Glycine max*, said genomic mutation is fad2/fae1, and said transgene encodes *Ricinus* fatty acid hydroxylase.

11. The transgenic plant or part thereof of claim **1**, wherein said transgenic plant part is from *Camelina sativa, Brassica napus* or *Glycine max*, said genomic mutation is fae1, and said transgene encodes *Ricinus* fatty acid hydroxylase.

12. The transgenic plant or part of claim **1**, wherein said reduced expression comprises complete silencing.

13. The transgenic plant or part of claim **2**, wherein said reduced expression comprises complete silencing.

14. The transgenic plant or part of claim **3**, wherein said reduced expression comprises complete silencing.

15. A progeny plant of the transgenic plant of claim **1**.

16. A transgenic seed that produces the transgenic plant of claim **1**.

17. A method of producing the target fatty acid using the transgenic plant part of claim **1**.

* * * * *