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Mirkov et al.

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(45) **Date of Patent: May 5, 2020**

(54) **PATHOGEN RESISTANT CITRUS COMPOSITIONS, ORGANISMS, SYSTEMS, AND METHODS**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 163 days.

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(65) **Prior Publication Data**

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Related U.S. Application Data

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(51) **Int. Cl.**
C12N 15/82 (2006.01)
C07K 14/415 (2006.01)

(52) **U.S. Cl.**
CPC ***C12N 15/8279*** (2013.01); ***C07K 14/415*** (2013.01); ***C12N 15/8281*** (2013.01)

(58) **Field of Classification Search**
None
See application file for complete search history.

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(57) **ABSTRACT**

The present disclosure relates, according to some embodiments, to pathogen resistant citrus compositions, organisms, systems, and methods. For example, a composition may comprise a peptide (e.g., a defensin peptide) and/or a nucleic acid (e.g., a defensin nucleic acid). A pathogen resistant citrus plant may comprise, in some embodiments, a defensin peptide and/or an expressible nucleic acid encoding a defensin peptide.

23 Claims, 30 Drawing Sheets

Specification includes a Sequence Listing.

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Communication pursuant to Rule 164(1) EPC and Supplementary Partial European Search Report dated Dec. 18, 2018 in EP 16 82 5283.

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FIG. 1

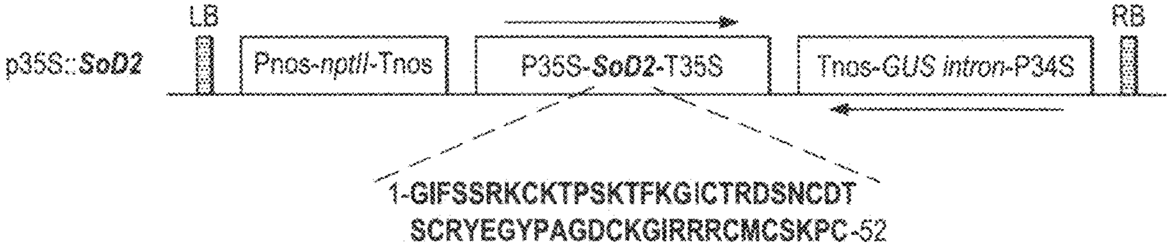
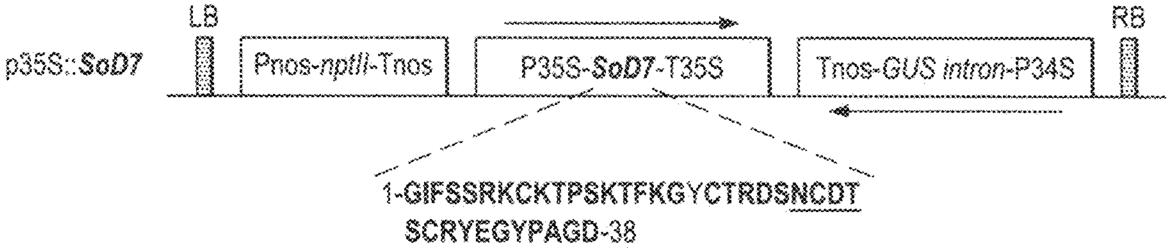

p35S::*SoD2*
LB
Pnos-*nptII*-Tnos
P35S-*SoD2*-T35S
Tnos-*GUS intron*-P34S
RB
1-GIFSSRKCKTPSKTFKGICTRDSNCDT
SCRYEGYPAGDCKGIRRRCMCSKPC-52

FIG. 2


p35S::*SoD7*
LB
Pnos-*nptII*-Tnos
P35S-*SoD7*-T35S
Tnos-*GUS intron*-P34S
RB
1-GIFSSRKCKTPSKTFKGYCTRDSNCDT
SCRYEGYPAGD-38

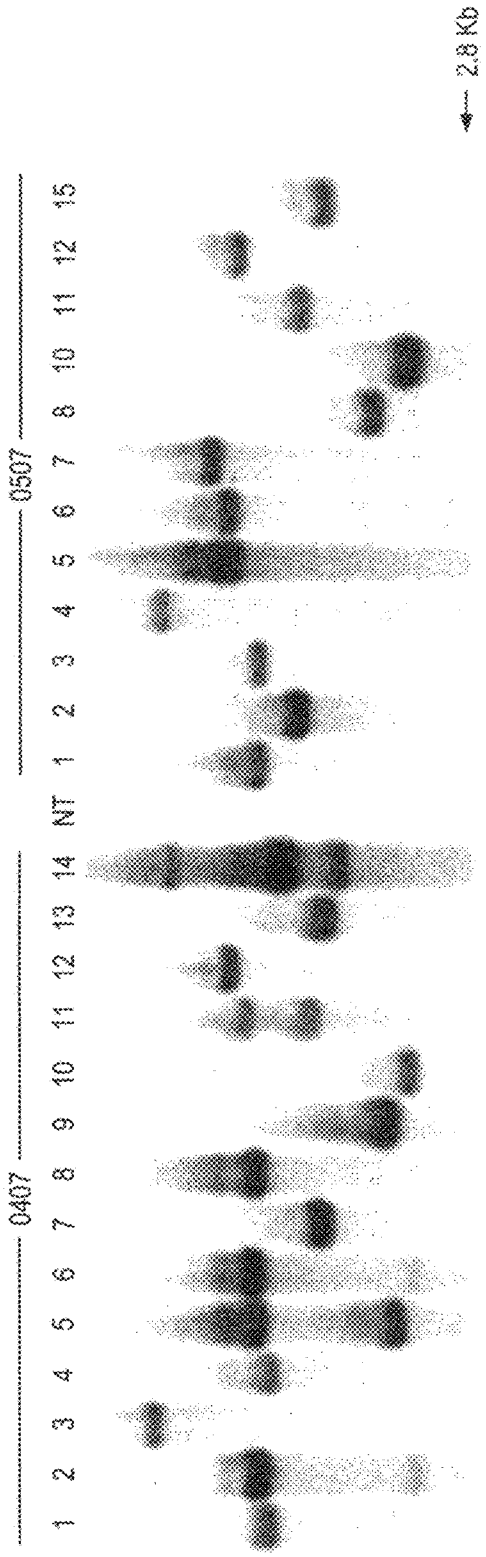

0407
1
2
3
4
5
6
7
8
9
10
11
12
13
14
NT
0507
1
2
3
4
5
6
7
8
10
11
12
15
2.8 Kb

FIG. 3

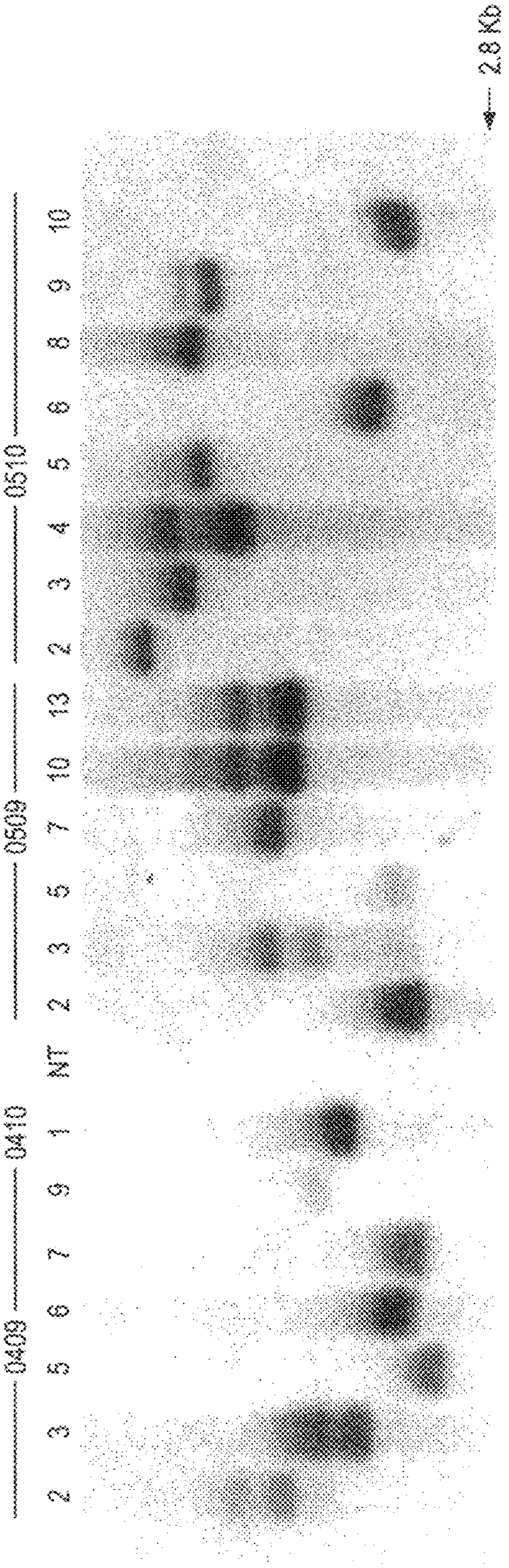

0409
2
3
5
6
7
9
0410
1
NT
0509
2
3
5
7
10
13
0510
2
3
4
5
6
8
9
10
2.8 Kb

FIG. 4

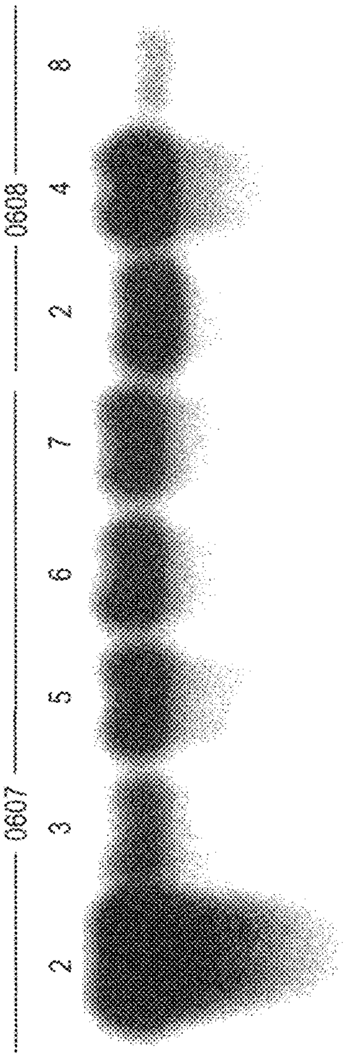
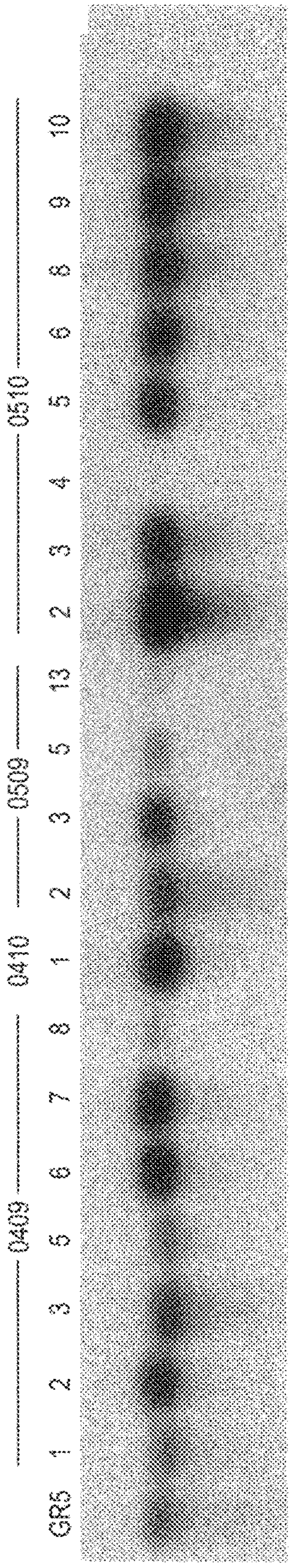

0607
2
3
5
6
7
0608
2
4
8

FIG. 5


GR5
0409
1
2
3
5
6
7
8
0410
1
2
0509
3
5
13
0510
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4
5
6
8
9
10

FIG. 6

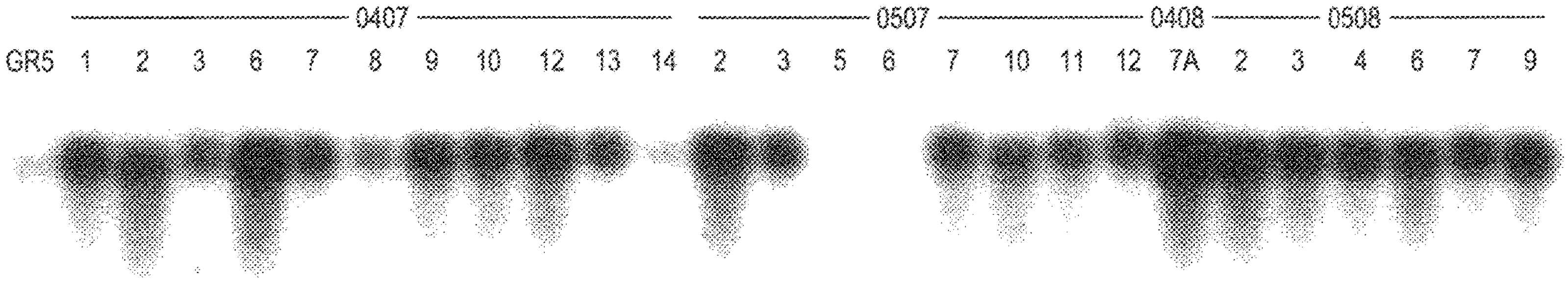

0407
0507
0408
0508
GR5
1
2
3
6
7
8
9
10
12
13
14
2
3
5
6
7
10
11
12
7A
2
3
4
6
7
9

FIG. 7

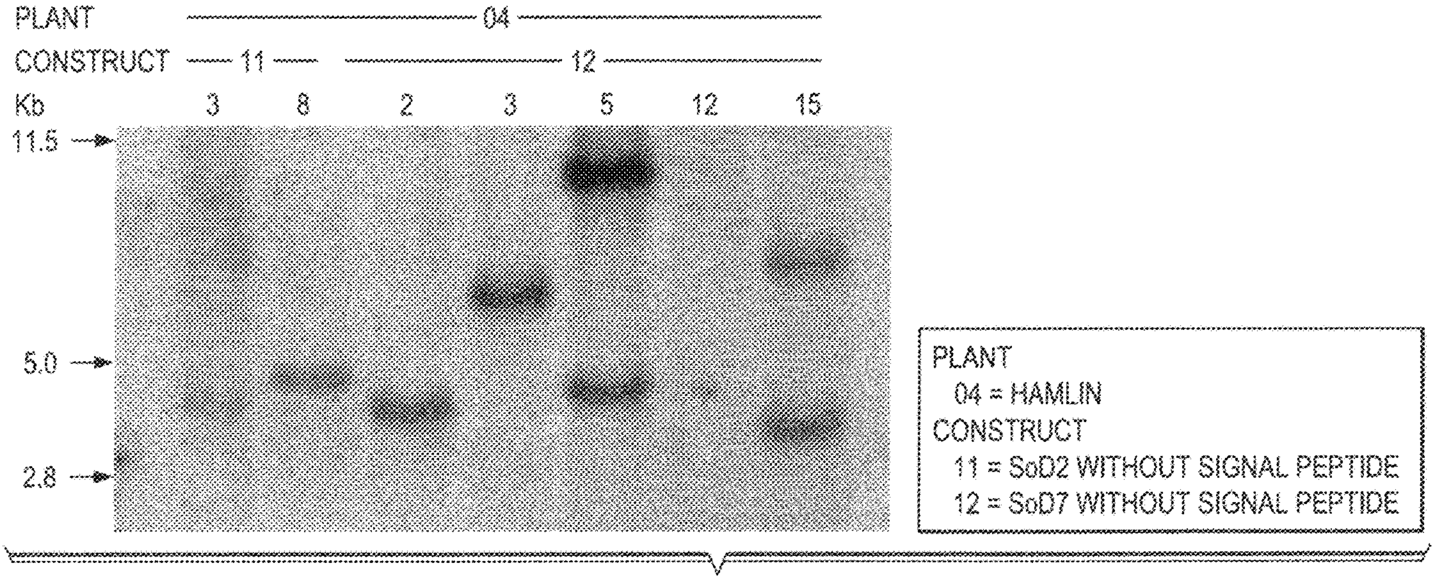

PLANT
04
CONSTRUCT
11
12
Kb
3
8
2
3
5
12
15
11.5
5.0
2.8
PLANT
04 = HAMLIN
CONSTRUCT
11 = SoD2 WITHOUT SIGNAL PEPTIDE
12 = SoD7 WITHOUT SIGNAL PEPTIDE

FIG. 8

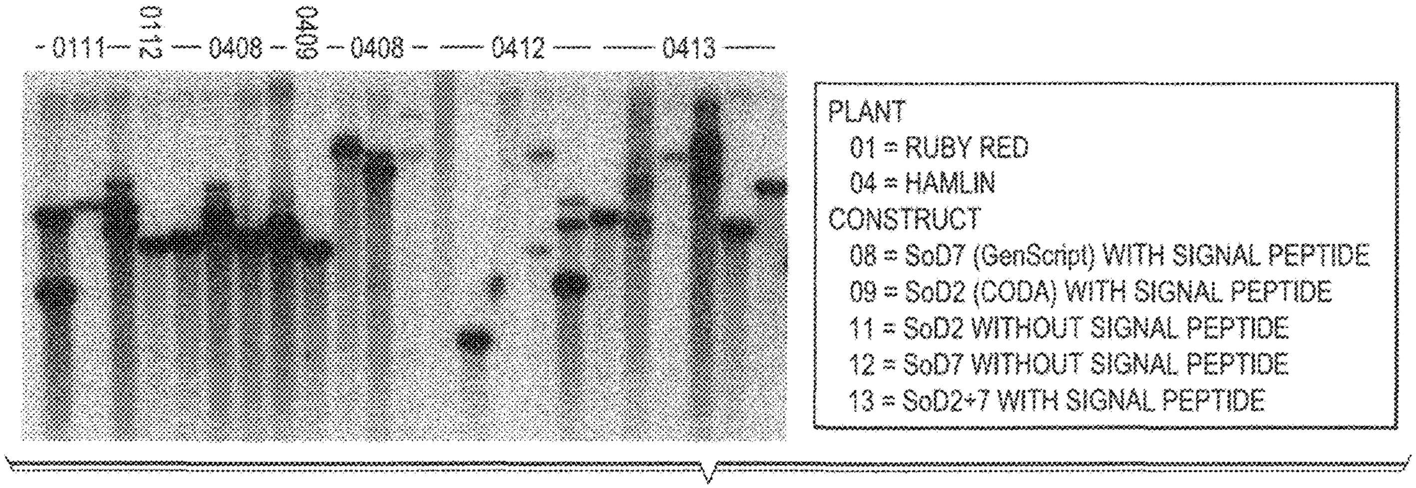

- 0111 —
0112
— 0408 —
0409
— 0408 —
— 0412 —
— 0413 —
PLANT
01 = RUBY RED
04 = HAMLIN
CONSTRUCT
08 = SoD7 (GenScript) WITH SIGNAL PEPTIDE
09 = SoD2 (CODA) WITH SIGNAL PEPTIDE
11 = SoD2 WITHOUT SIGNAL PEPTIDE
12 = SoD7 WITHOUT SIGNAL PEPTIDE
13 = SoD2+7 WITH SIGNAL PEPTIDE

FIG. 9

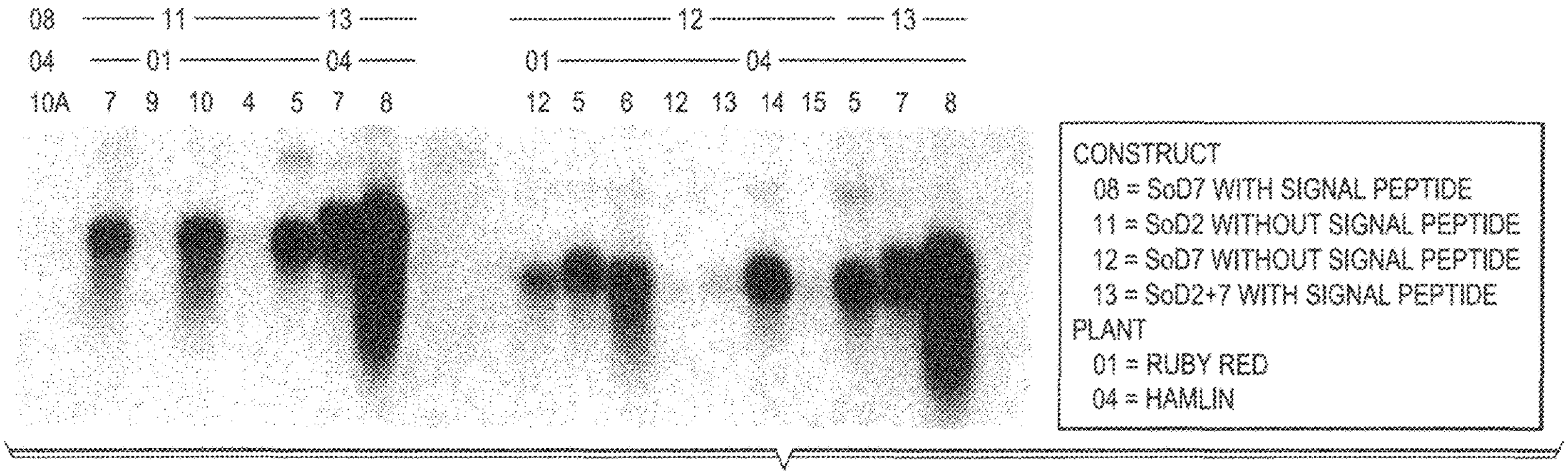

08 — 11 — 13 —
04 — 01 — 04 —
10A 7 9 10 4 5 7 8
— 12 — 13 —
01 — 04 —
12 5 6 12 13 14 15 5 7 8
CONSTRUCT
08 = SoD7 WITH SIGNAL PEPTIDE
11 = SoD2 WITHOUT SIGNAL PEPTIDE
12 = SoD7 WITHOUT SIGNAL PEPTIDE
13 = SoD2+7 WITH SIGNAL PEPTIDE
PLANT
01 = RUBY RED
04 = HAMLIN

FIG. 10

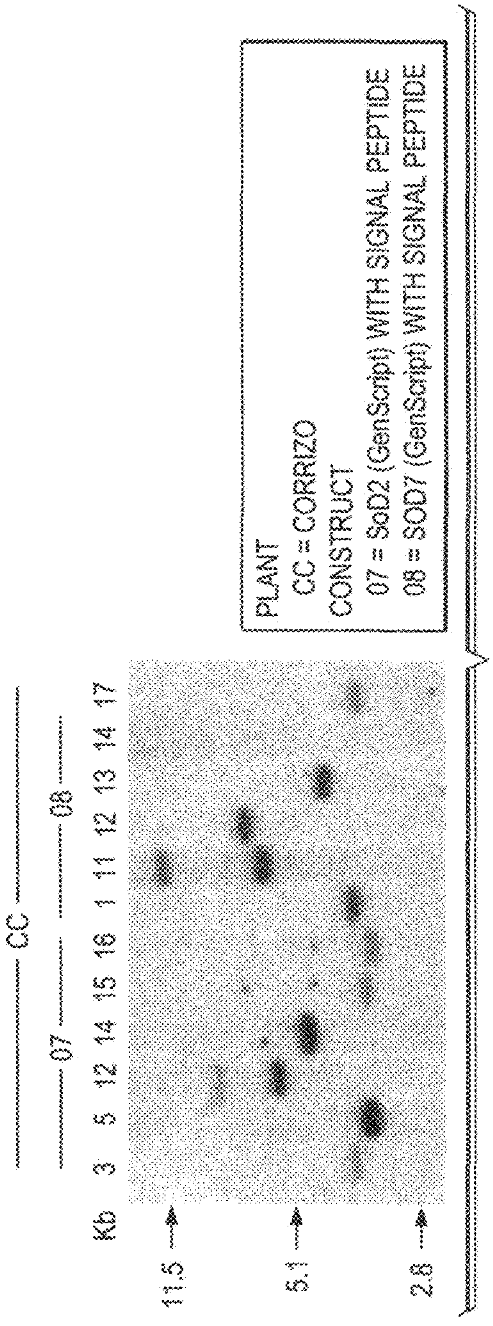

Kb
11.5
5.1
2.8
CC
07
08
3
5
12
14
15
16
1
11
12
13
14
17
PLANT
CC = CORRIZO
CONSTRUCT
07 = SoD2 (GenScript) WITH SIGNAL PEPTIDE
08 = SOD7 (GenScript) WITH SIGNAL PEPTIDE

FIG. 11

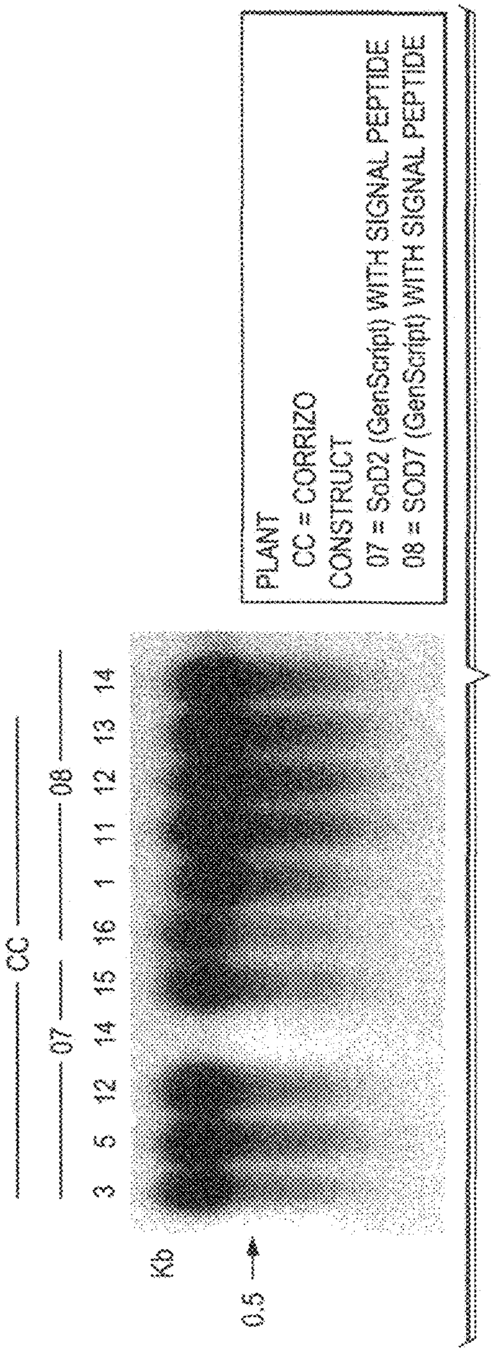

Kb
0.5
CC
07
08
3
5
12
14
15
16
1
11
12
13
14
PLANT
CC = CORRIZO
CONSTRUCT
07 = SoD2 (GenScript) WITH SIGNAL PEPTIDE
08 = SOD7 (GenScript) WITH SIGNAL PEPTIDE

FIG. 12

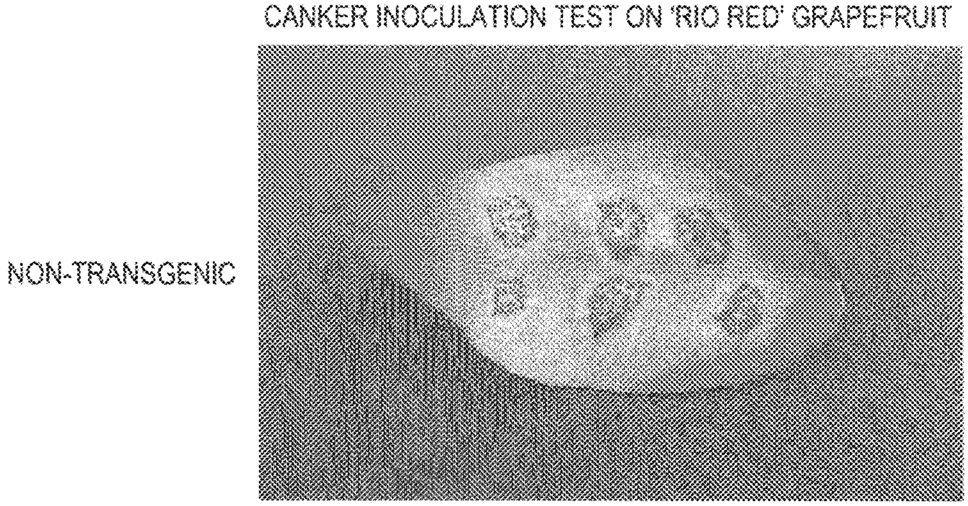


FIG. 13A

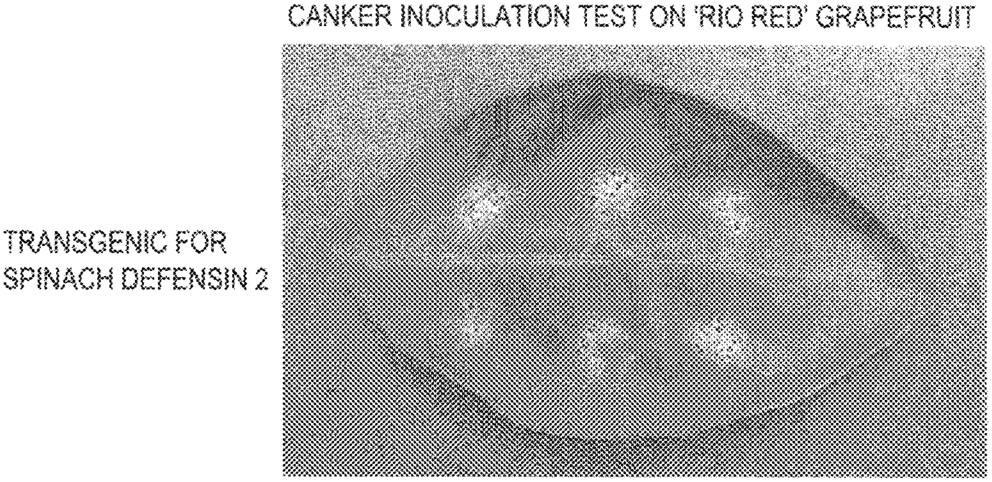


FIG. 13B

GREENING INOCULATION TEST
ON 'RIO RED' GRAPEFRUIT

FIG. 14

FIG. 15A

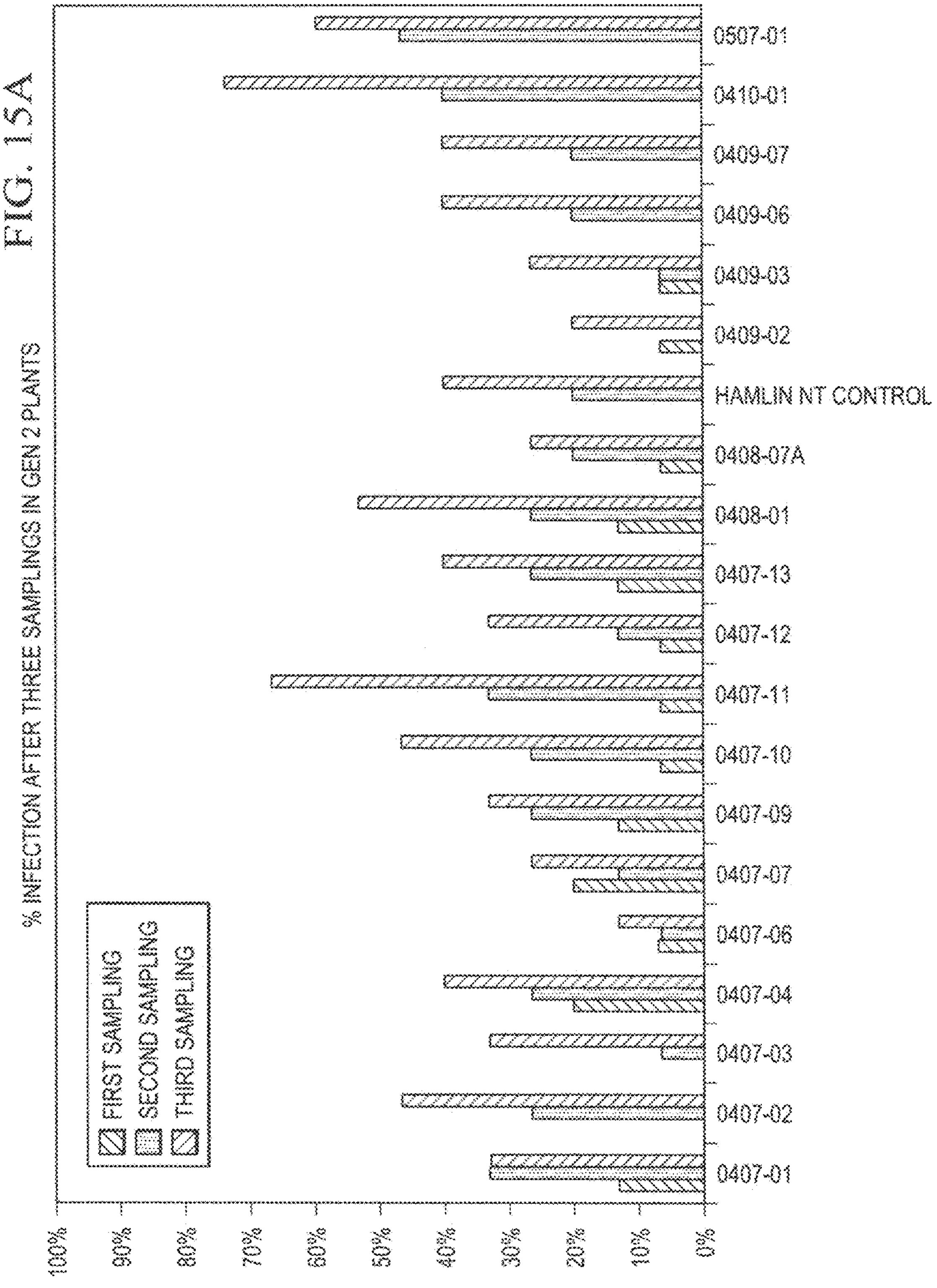

% INFECTION AFTER THREE SAMPLINGS IN GEN 2 PLANTS
FIRST SAMPLING
SECOND SAMPLING
THIRD SAMPLING
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
0507-01
0410-01
0409-07
0409-06
0409-03
0409-02
HAMLIN NT CONTROL
0408-07A
0408-01
0407-13
0407-12
0407-11
0407-10
0407-09
0407-07
0407-06
0407-04
0407-03
0407-02
0407-01

FIG. 15B

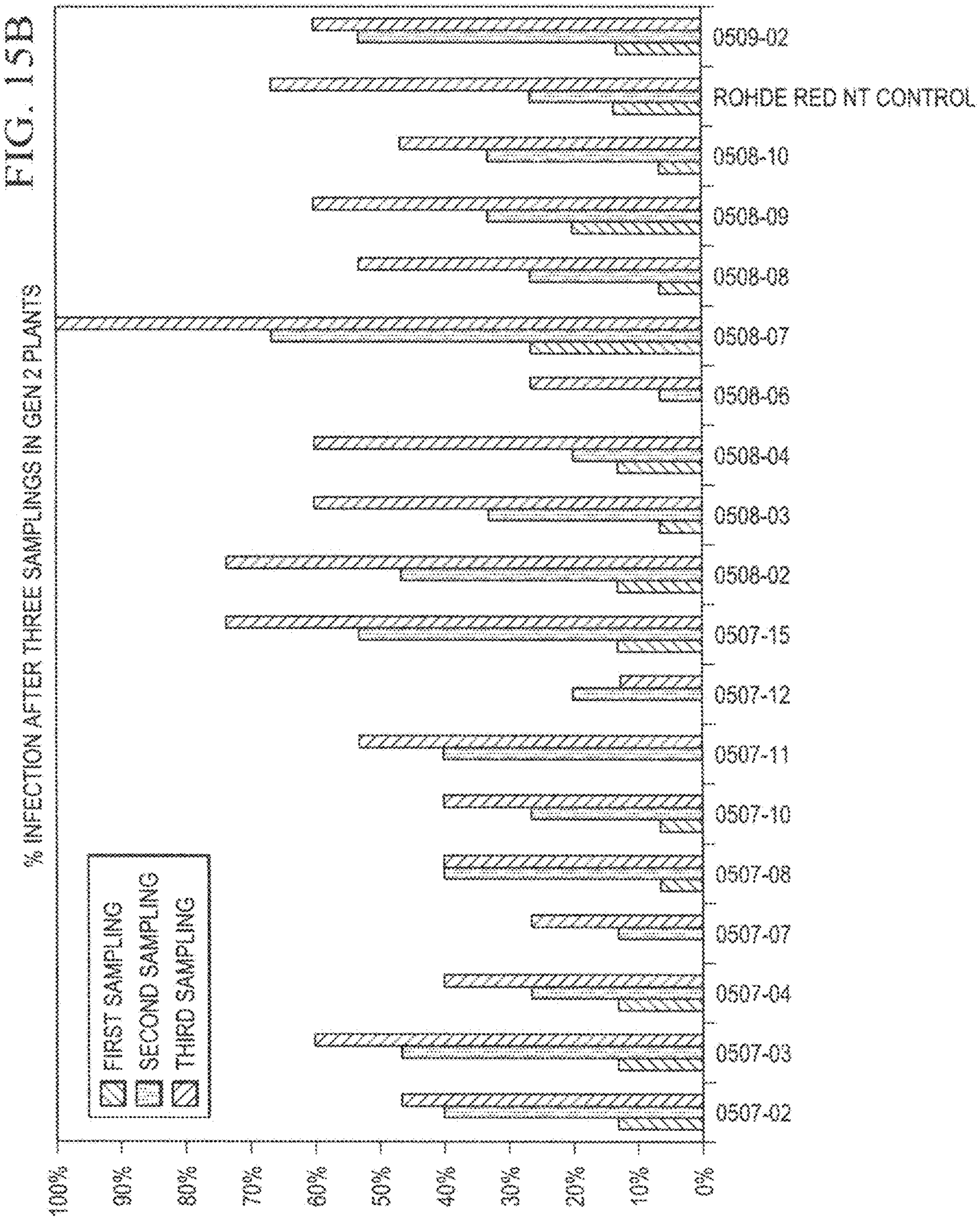

% INFECTION AFTER THREE SAMPLINGS IN GEN 2 PLANTS
▨ FIRST SAMPLING
▨ SECOND SAMPLING
▨ THIRD SAMPLING
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
0507-02
0507-03
0507-04
0507-07
0507-08
0507-10
0507-11
0507-12
0507-15
0508-02
0508-03
0508-04
0508-06
0508-07
0508-08
0508-09
0508-10
ROHDE RED NT CONTROL
0509-02

FIG. 15C

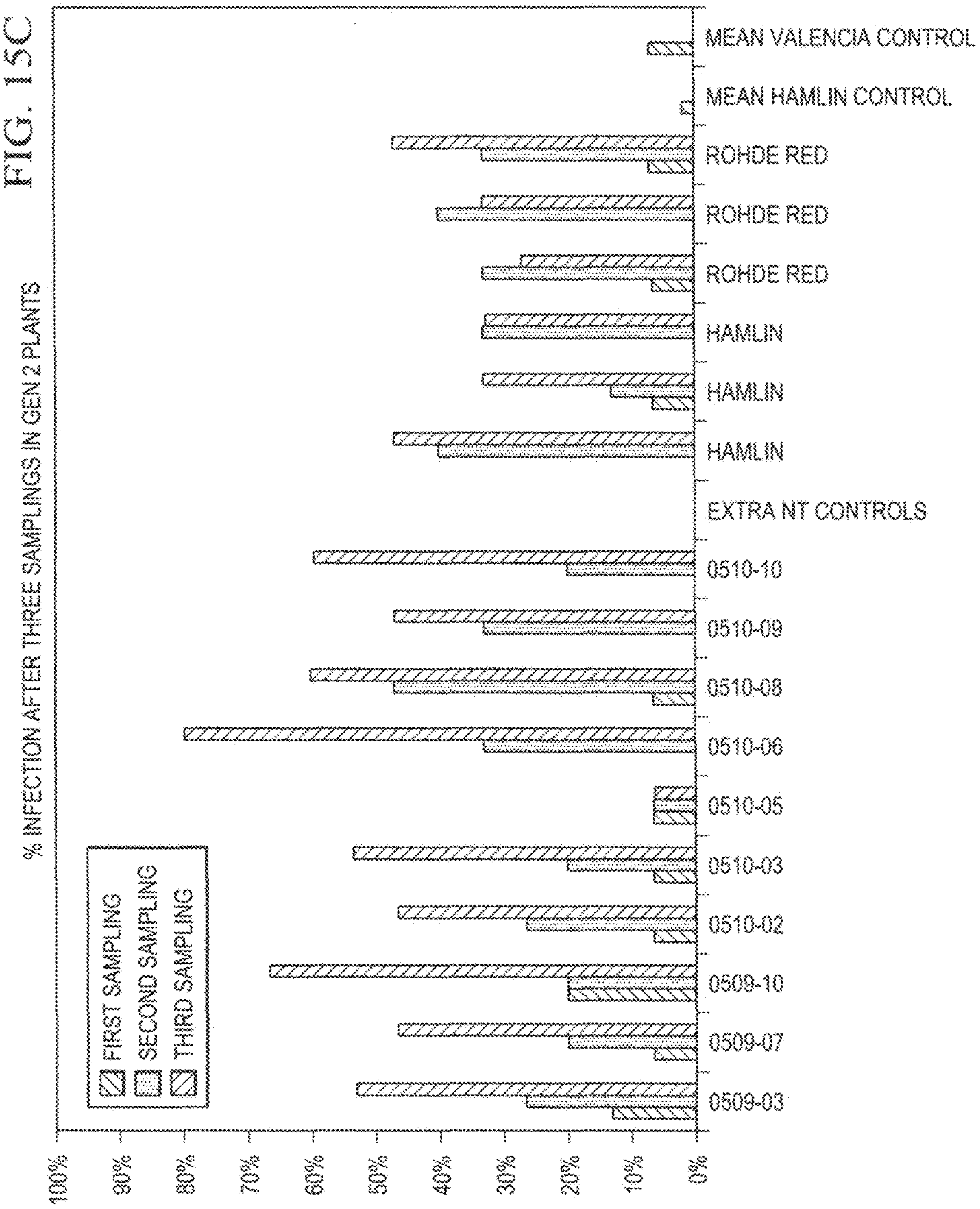

% INFECTION AFTER THREE SAMPLINGS IN GEN 2 PLANTS
FIRST SAMPLING
SECOND SAMPLING
THIRD SAMPLING
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
0509-03
0509-07
0509-10
0510-02
0510-03
0510-05
0510-06
0510-08
0510-09
0510-10
EXTRA NT CONTROLS
HAMLIN
HAMLIN
HAMLIN
ROHDE RED
ROHDE RED
ROHDE RED
MEAN HAMLIN CONTROL
MEAN VALENCIA CONTROL

FIG. 16A

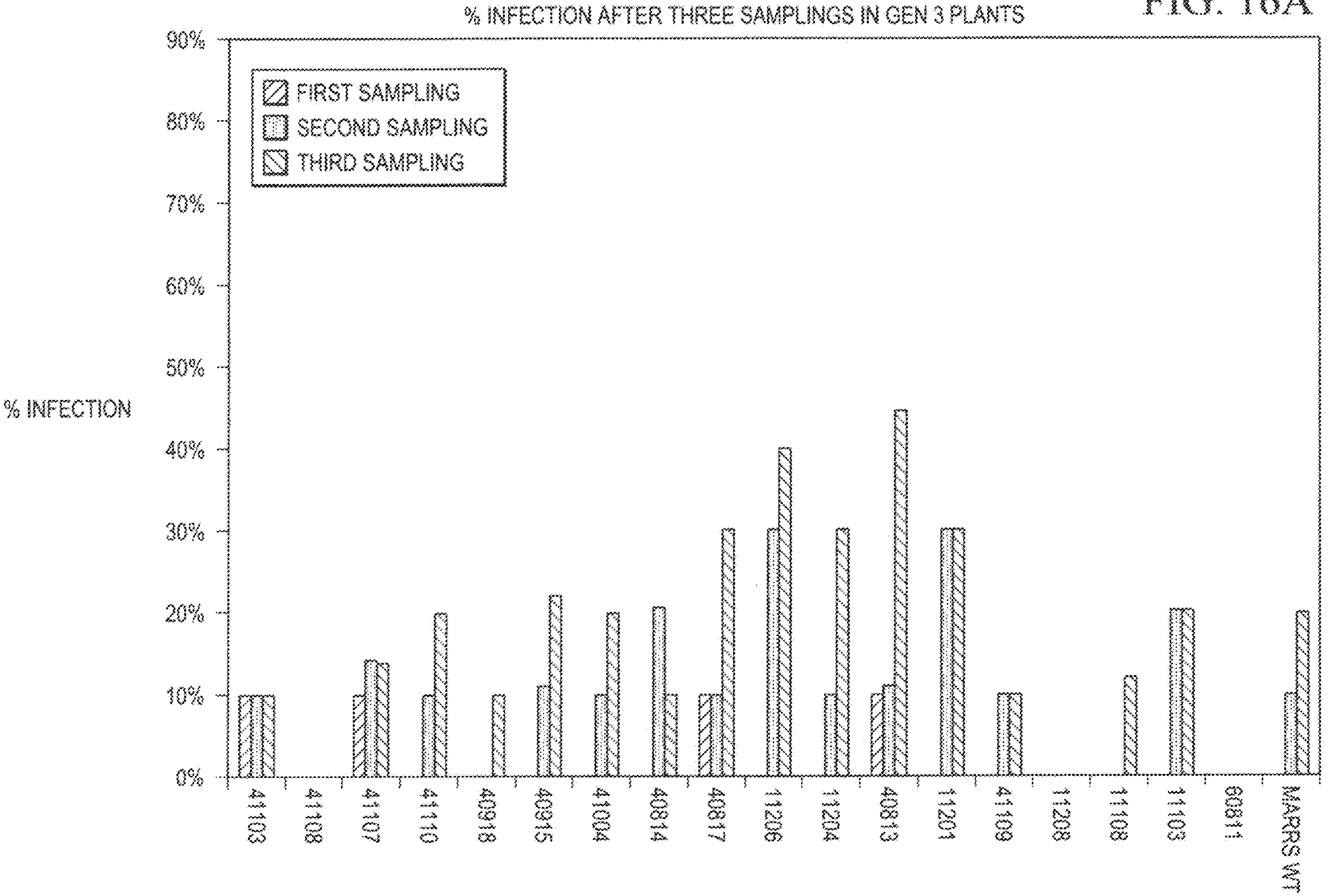

% INFECTION AFTER THREE SAMPLINGS IN GEN 3 PLANTS
FIRST SAMPLING
SECOND SAMPLING
THIRD SAMPLING
% INFECTION
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
41103
41108
41107
41110
40918
40915
41004
40814
40817
11206
11204
40813
11201
41109
11208
11108
11103
60811
MARRS WT

FIG. 16B

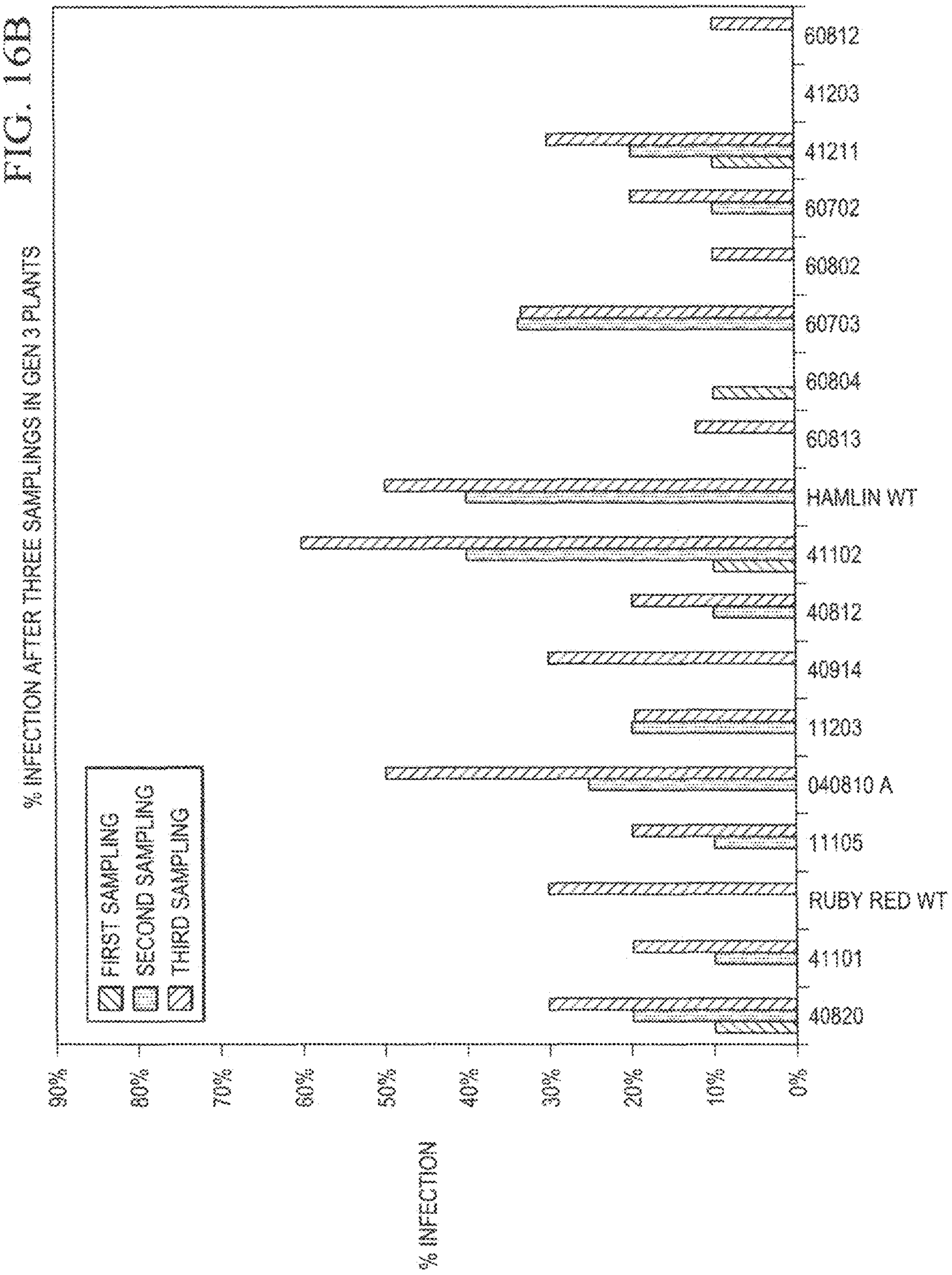
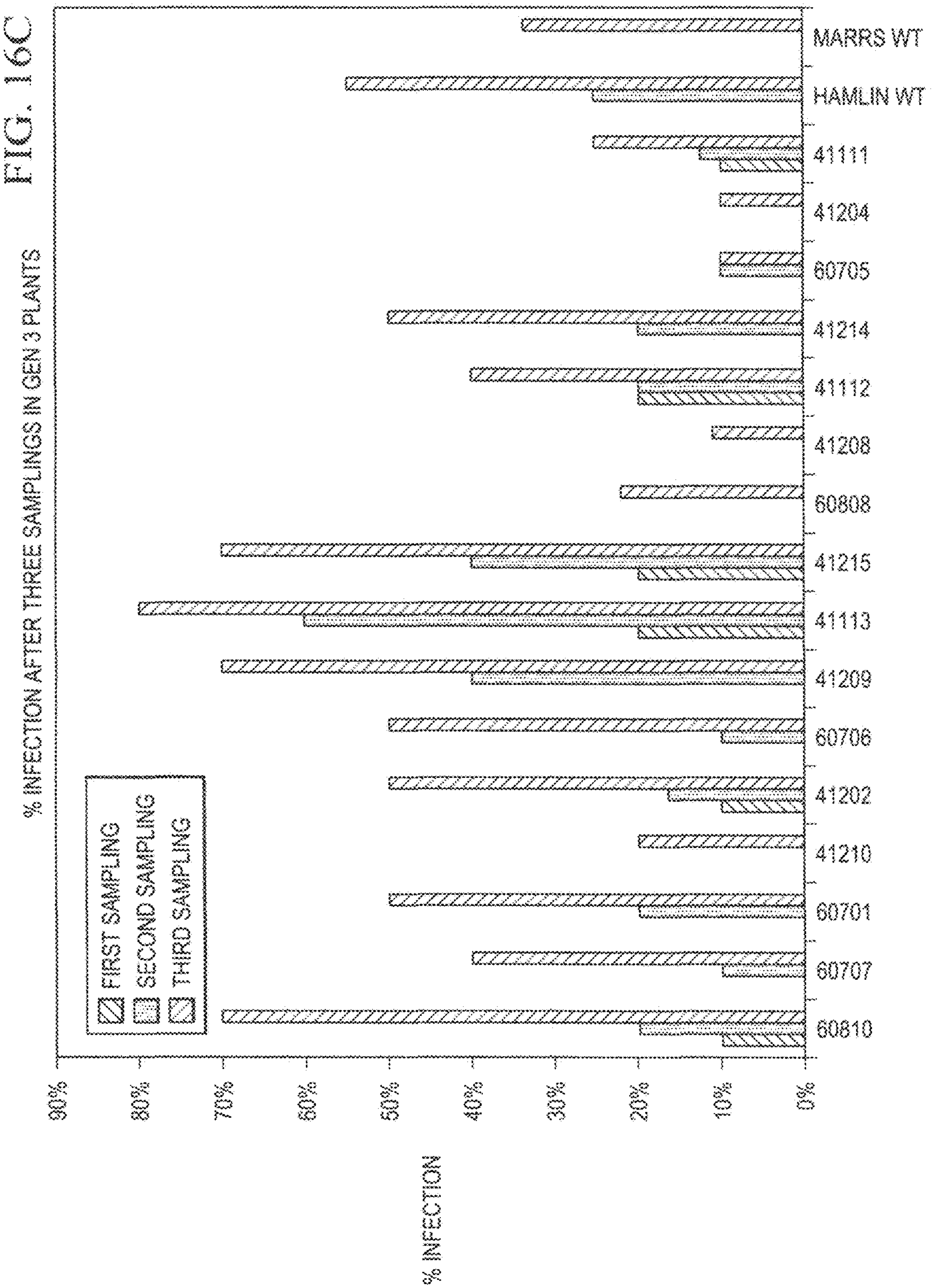

% INFECTION AFTER THREE SAMPLINGS IN GEN 3 PLANTS
FIRST SAMPLING
SECOND SAMPLING
THIRD SAMPLING
% INFECTION
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
40820
41101
RUBY RED WT
11105
040810 A
11203
40914
40812
41102
HAMLIN WT
60813
60804
60703
60802
60702
41211
41203
60812

FIG. 16C


% INFECTION AFTER THREE SAMPLINGS IN GEN 3 PLANTS
▨ FIRST SAMPLING
▨ SECOND SAMPLING
▨ THIRD SAMPLING
MARRS WT
HAMLIN WT
41111
41204
60705
41214
41112
41208
60808
41215
41113
41209
60706
41202
41210
60701
60707
60810
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
% INFECTION

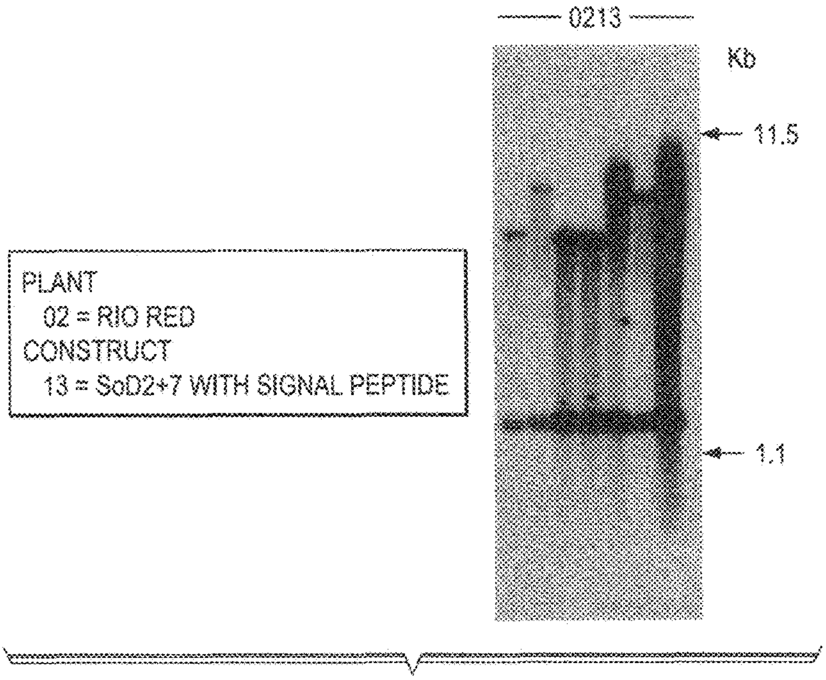

0213
Kb
11.5
1.1
PLANT
02 = RIO RED
CONSTRUCT
13 = SoD2+7 WITH SIGNAL PEPTIDE

FIG. 17

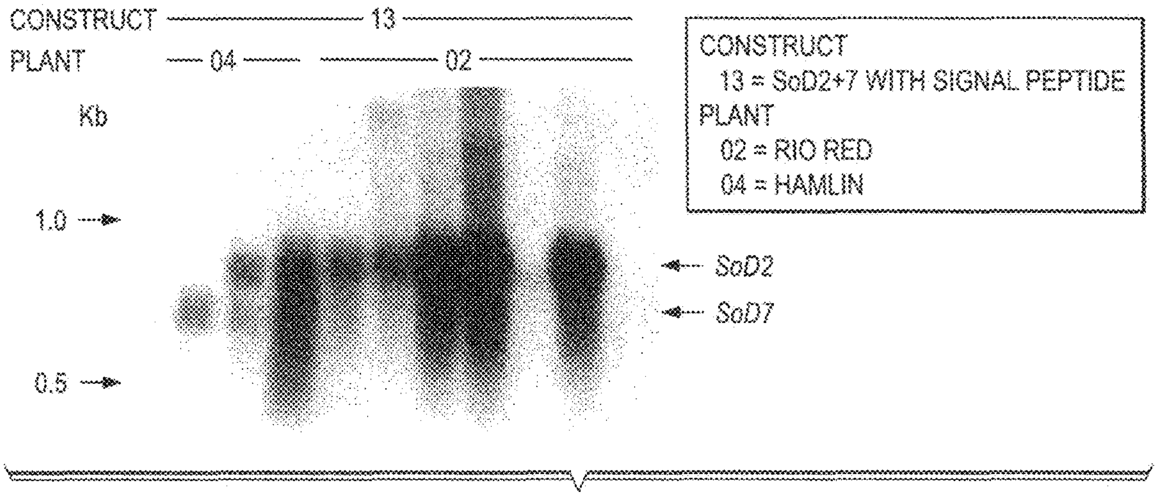
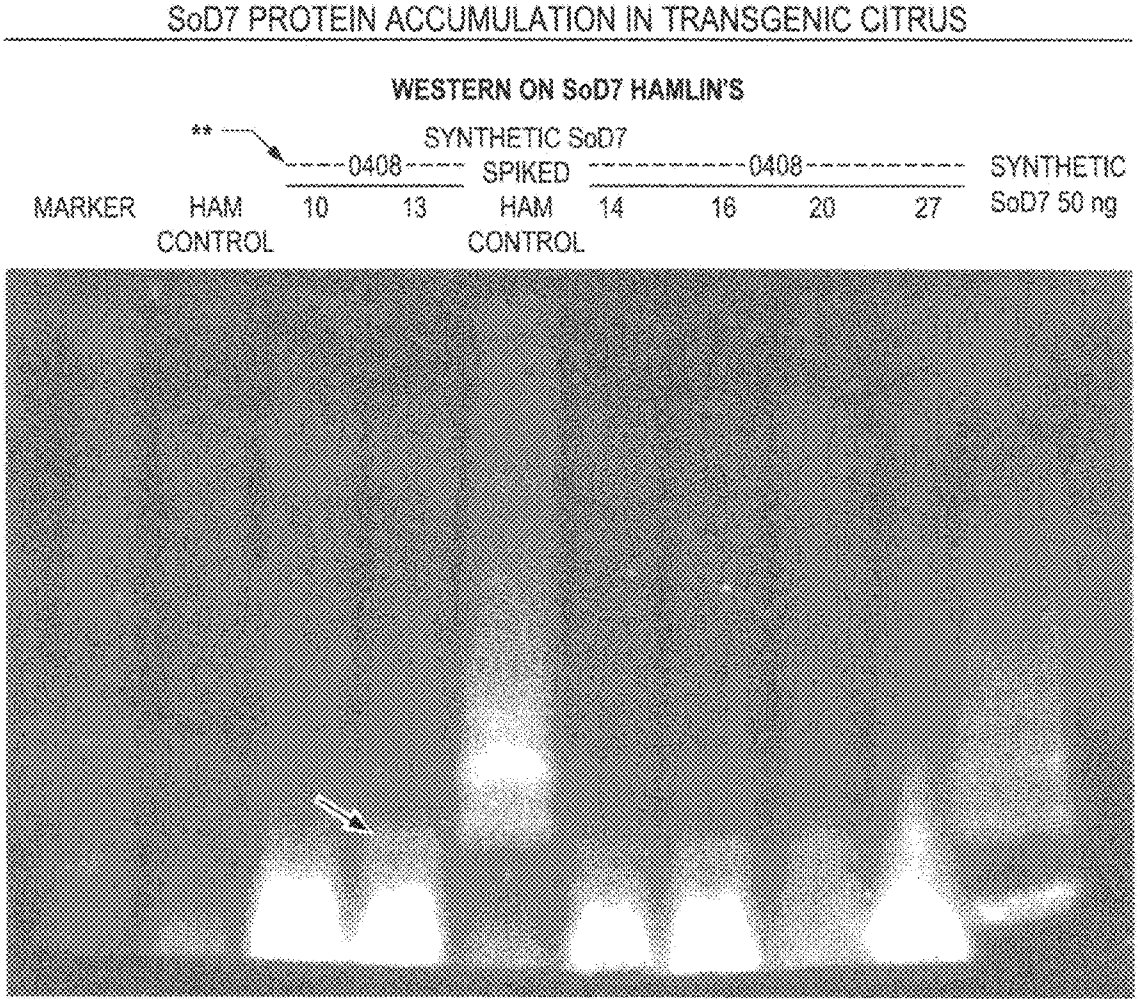
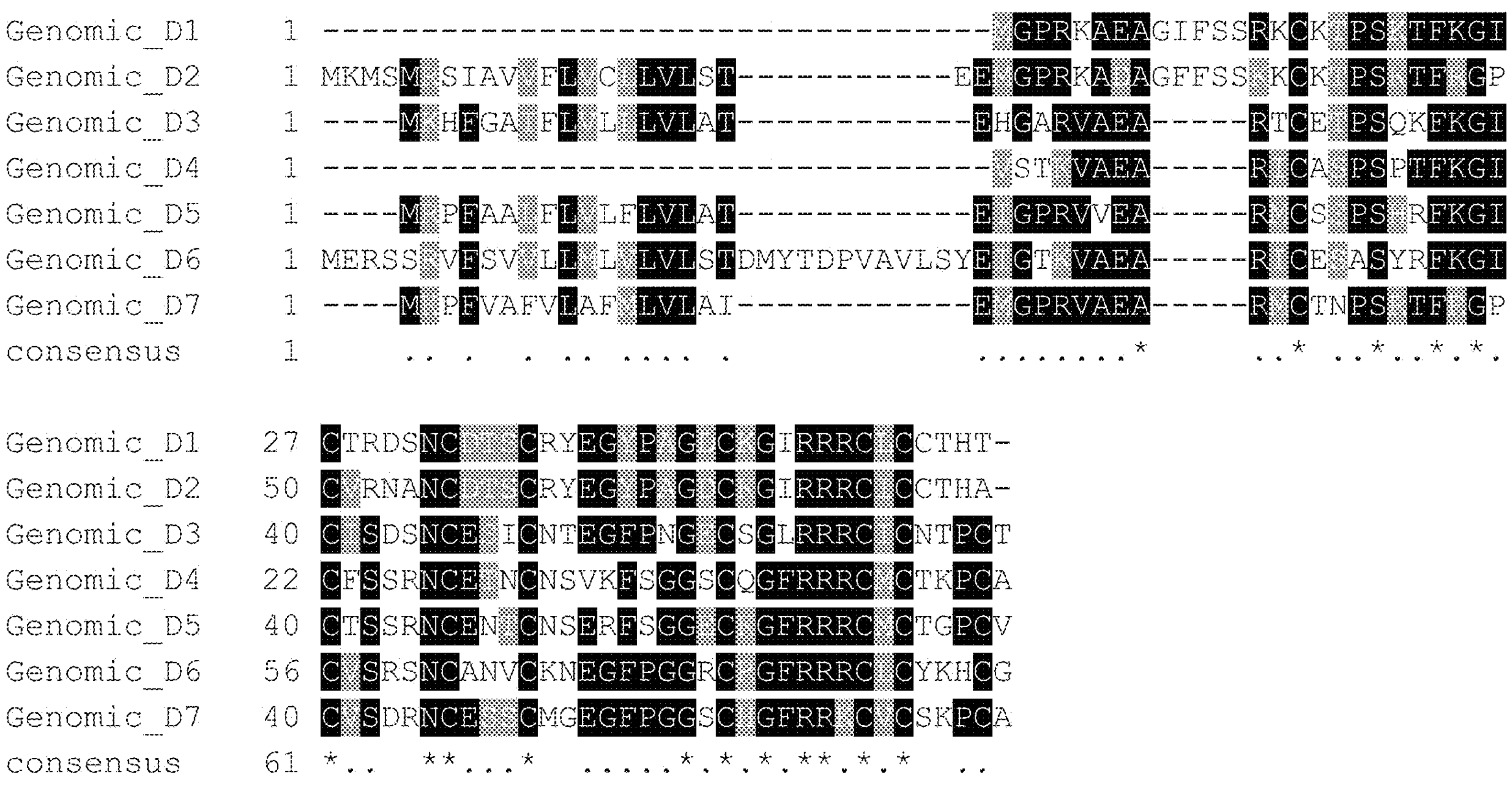

CONSTRUCT
13
PLANT
04
02
Kb
1.0
0.5
SoD2
SoD7
CONSTRUCT
13 = SoD2+7 WITH SIGNAL PEPTIDE
PLANT
02 = RIO RED
04 = HAMLIN

FIG. 18


SoD7 PROTEIN ACCUMULATION IN TRANSGENIC CITRUS

** 0408-10 IS SOUTHERN POSITIVE, BUT HAS COMPLETE RNA SILENCING DUE TO 5 INSERTIONS

FIG. 19



```
Genomic_D1    1 ---------------------------------- GPRKAEAGIFSSRKCK PS TFKGI
Genomic_D2    1 MKMSM SIAV FL C LVLST-----------EE GPRKA AGFFSS KCK PS TF GP
Genomic_D3    1 ----M HFGA FL L LVLAT------------EHGARVAEA-----RTCE PSQKFKGI
Genomic_D4    1 ---------------------------------- ST VAEA-----R CA PSPTFKGI
Genomic_D5    1 ----M PFAA FL LFLVLAT------------E GPRVVEA-----R CS PS RFKGI
Genomic_D6    1 MERSS VFSV LL L LVLSTDMYTDPVAVLSYE GT VAEA-----R CE ASYRFKGI
Genomic_D7    1 ----M PFVAFVLAF LVLAI------------E GPRVAEA-----R CTNPS TF GP
consensus     1     .. .  . .. .... .            ........*     ..* ..*..*.*.

Genomic_D1   27 CTRDSNC   CRYEG P G C GIRRRC CCTHT-
Genomic_D2   50 C RNANC   CRYEG P G C GIRRRC CCTHA-
Genomic_D3   40 C SDSNCE ICNTEGFPNG CSGLRRRC CNTPCT
Genomic_D4   22 CFSSRNCE NCNSVKFSGGSCQGFRRRC CTKPCA
Genomic_D5   40 CTSSRNCEN CNSERFSGG C GFRRRC CTGPCV
Genomic_D6   56 C SRSNCANVCKNEGFPGGRC GFRRRC CYKHCG
Genomic_D7   40 C SDRNCE  CMGEGFPGGSC GFRR C CSKPCA
consensus    61 *..  **...*  .....*.*.*.**.*.*  ..
```

FIG. 20

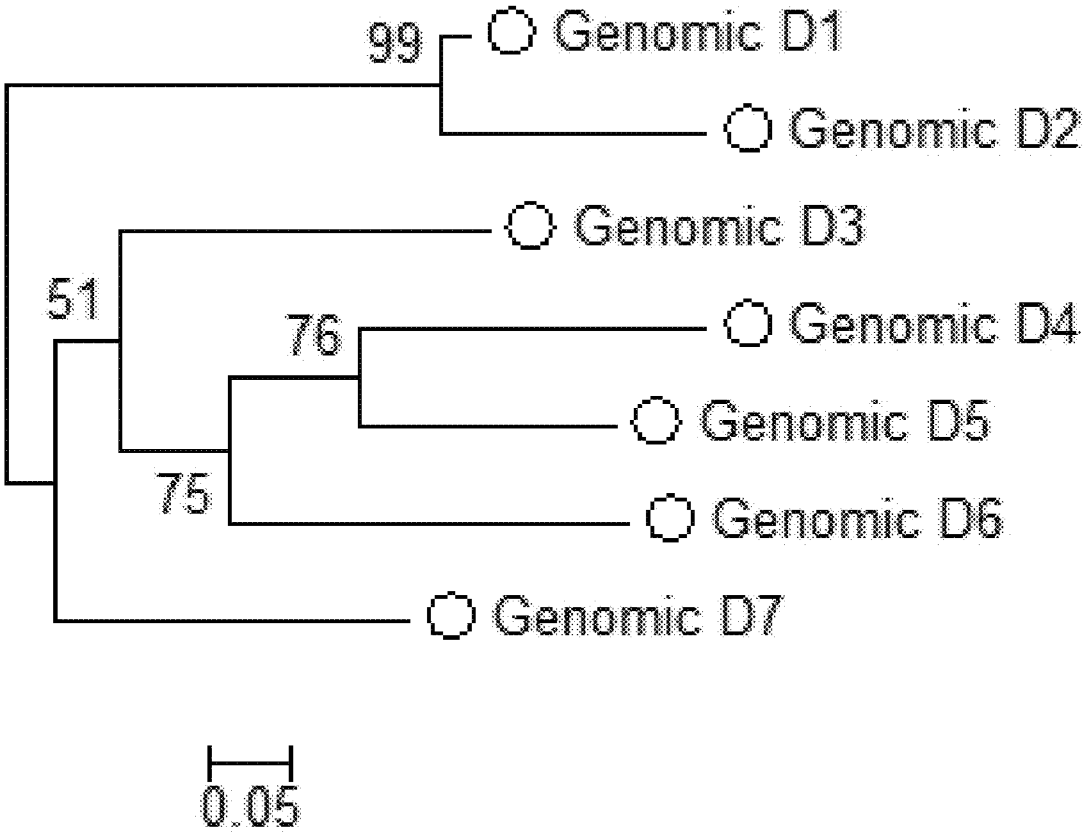

99
○ Genomic D1
○ Genomic D2
○ Genomic D3
51
76
○ Genomic D4
○ Genomic D5
75
○ Genomic D6
○ Genomic D7
0.05

FIG. 21A

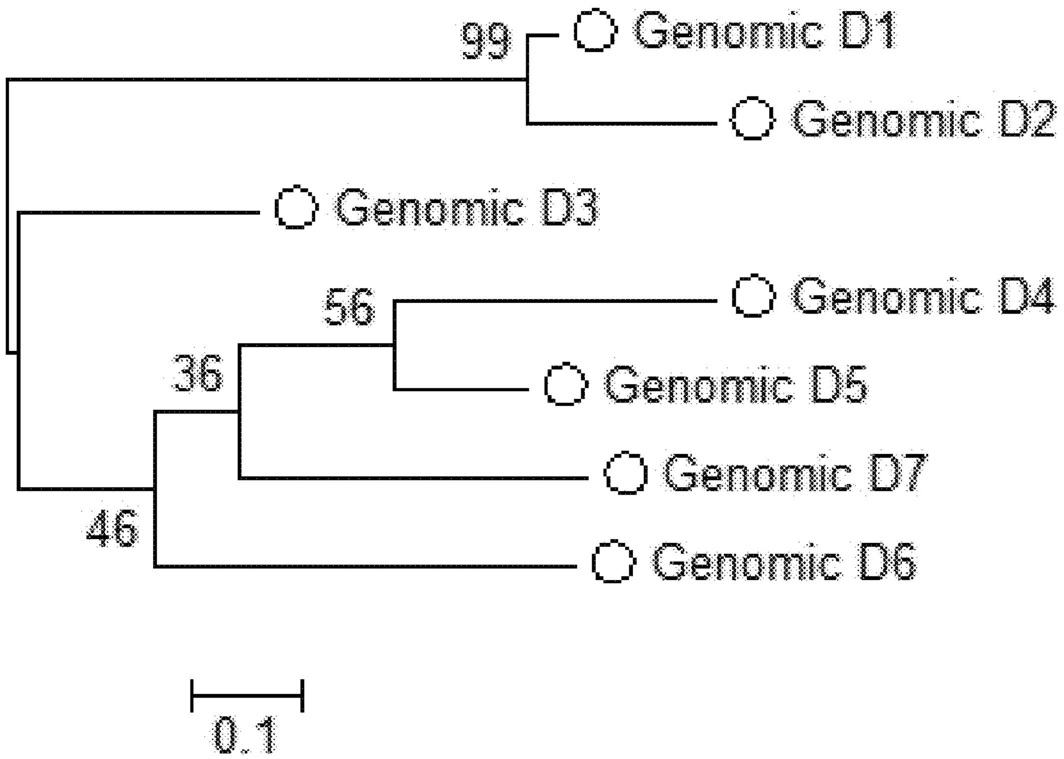

99
Genomic D1
Genomic D2
Genomic D3
56
Genomic D4
36
Genomic D5
Genomic D7
46
Genomic D6
0.1

FIG. 21B

```
Genomic_D1    1 -----------------------------MGPRKAEAG FSSRKCKTPSKTFKGICTRDS
Genomic_D2    1 ------MKMSMRSIAVVFLVCLLVLSTEEMGPRKADAGFFSS KCKTPSKTF GPCVRNA
Genomic_D3    1 ----MKHFGAIFLVLLLVLAT------------EHGAR AEARTCETPSQKFKGICISDS
Genomic_D4    1 ----------------------------------VSTK AEARICA PSPTFKGICFSSR
Genomic_D5    1 ----MRPFAALFLVLFLVLAT------------EIGPR VEARMCS PSHRFKGICTSSR
Genomic_D6    1 MERSSRVFSVVLLMLVLVLSTDMYTDPVAVLSYEIGTK AEARICE ASYRFKGICVSRS
Genomic_D7    1 ----MKPFVAFVLAFMLVLAI------------EMGPR AEARMCTNPS TF GPCVSDR
Segura_D1     1 ------------------------------------------XTCE PSHKFKGPCATNR
Segura_D2     1 -------------------------------------G FSSRKCKTPSKTFKGICTRDS
Segura_D3     1 -------------------------------------G FSSRKCKTVSKTF GICTRNA
Segura_D4     1 -----------------------------M--------FFSS KCKTVSKTF GPCVRNA
Segura_D5     1 -----------------------------M--------FFSS KCKTVXKTF GPCVRNA
Segura_D6     1 -------------------------------------G FSNMYX TPAGYF GPXGYXX
Segura_D7     1 -------------------------------------G FSSRKCKTPSKTFKGYCTRDS
consensus     1                                       .............*.*.. .

Genomic_D1   32 NC  SCRYEG P GDCKGIRRRC CCTHT-
Genomic_D2   55 NC  SCRYEG P GDCKGIRRRC CCTHA-
Genomic_D3   45 NC  ICNTEG PNGECSGLRRRC CNTPCT
Genomic_D4   27 NC  NCNSVK S GSCQGFRRRC CTKPCA
Genomic_D5   45 NC NTCNSER S GECKGFRRRC CTGPCV
Genomic_D6   61 NCANVCKNEG P GRCRGFRRRC CYKHCG
Genomic_D7   45 NC  SCMGEG P GSCHGFRR C CSKPCA
Segura_D1    19 NC  --------------------------
Segura_D2    24 NC  SCRYEG P GDCKGIRRRC CSKPC-
Segura_D3    24 NC----------------------------
Segura_D4    24 ------------------------------
Segura_D5    24 N-----------------------------
Segura_D6    24 N-----------------------------
Segura_D7    24 NC  SCRYEG P GD----------------
consensus    61 .... .  ...... . . ......
```

FIG. 22

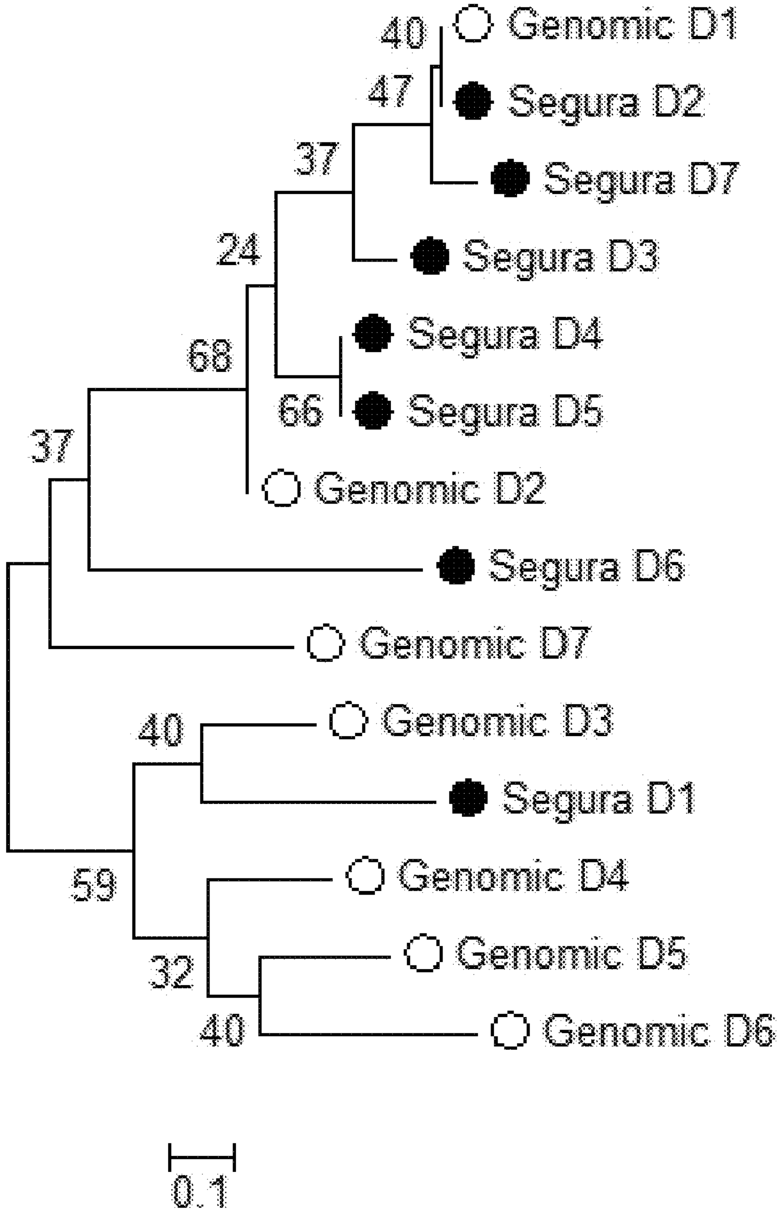

40
○ Genomic D1
47
● Segura D2
37
● Segura D7
24
● Segura D3
68
● Segura D4
66
● Segura D5
37
○ Genomic D2
● Segura D6
○ Genomic D7
40
○ Genomic D3
● Segura D1
59
○ Genomic D4
32
○ Genomic D5
40
○ Genomic D6
0.1

FIG. 23A

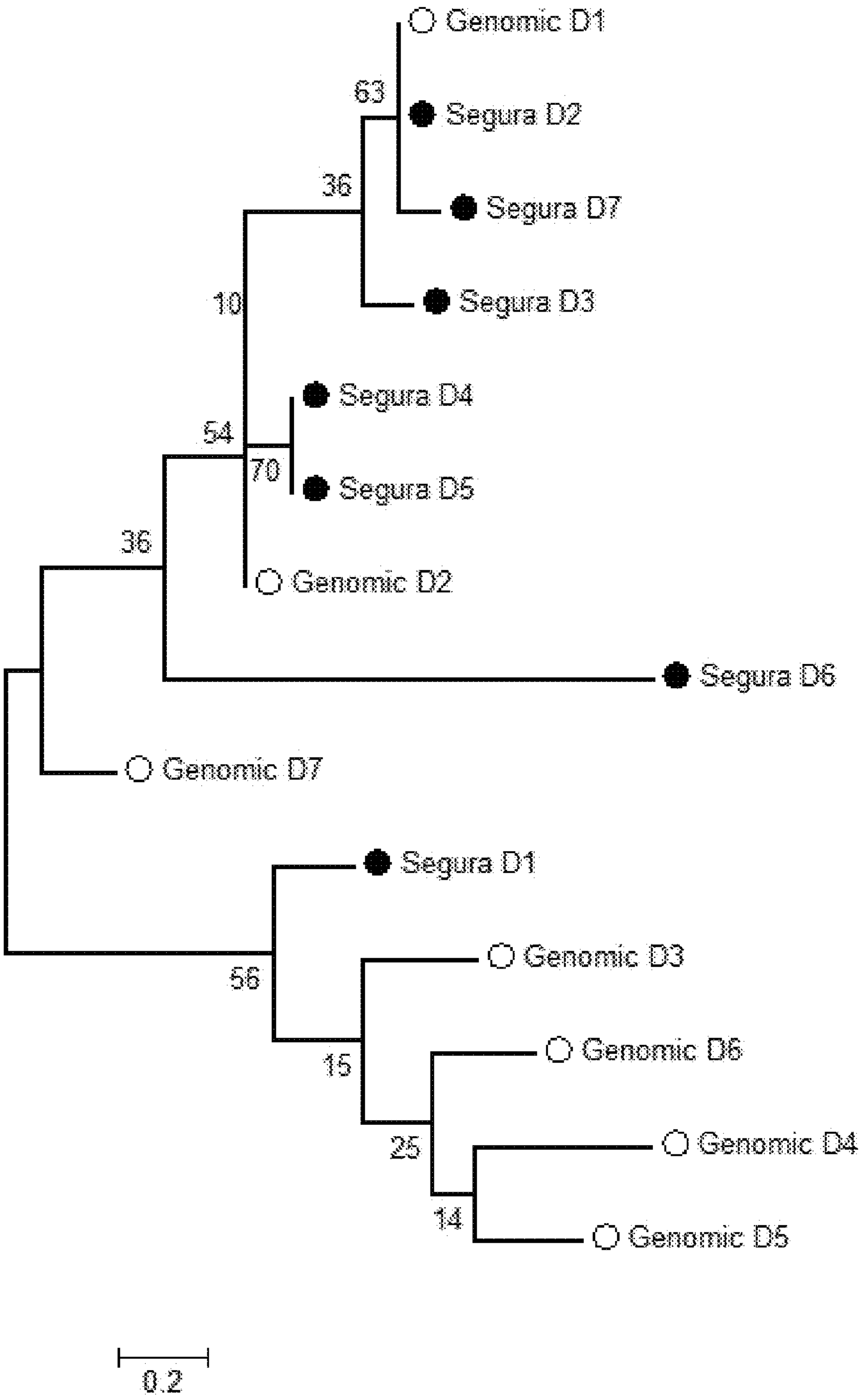
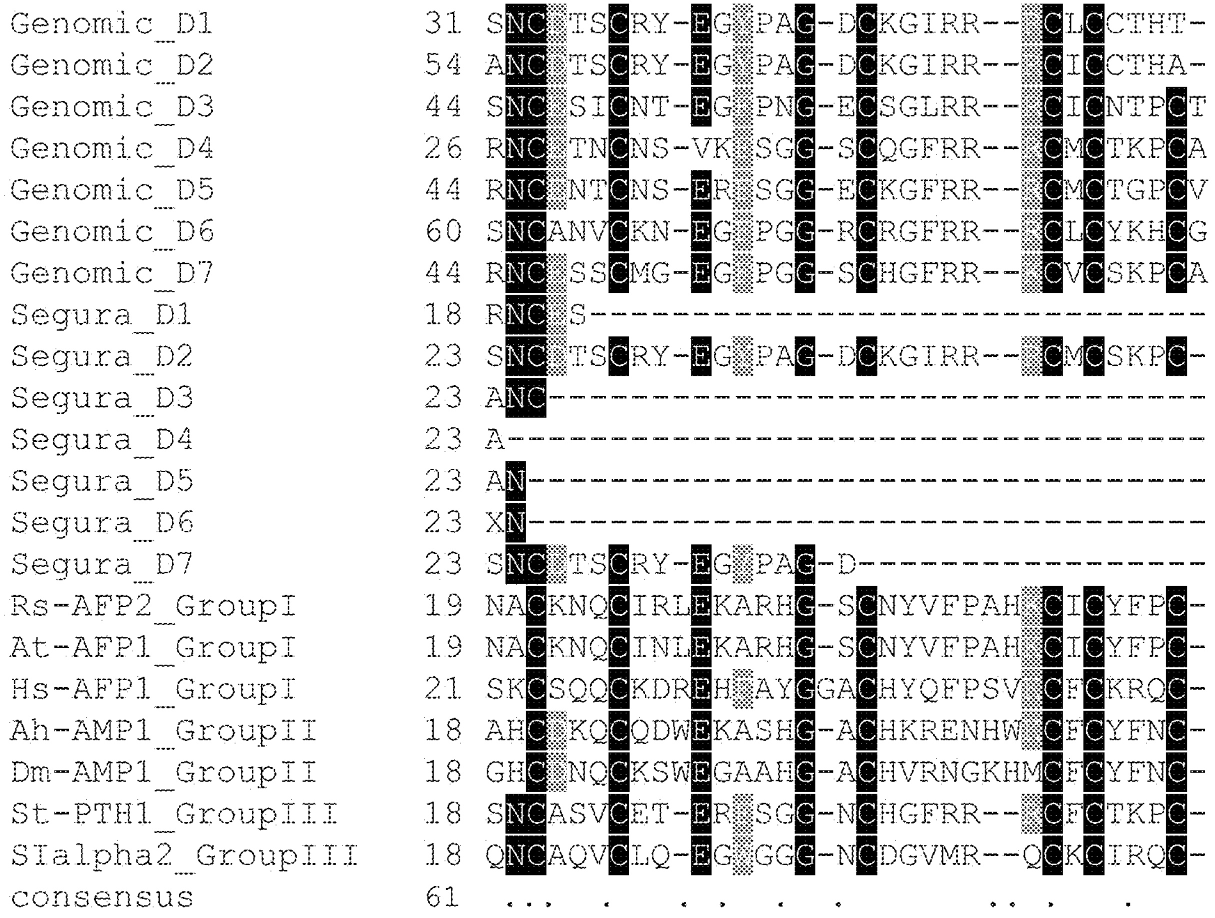

Genomic D1
63
Segura D2
36
Segura D7
10
Segura D3
Segura D4
54
70
Segura D5
36
Genomic D2
Segura D6
Genomic D7
Segura D1
Genomic D3
56
Genomic D6
15
Genomic D4
25
14
Genomic D5
0.2

FIG. 23B

```
Genomic_D1         1 -----------------------------MGPRKAEAGIFSSRKC-K PS TF GICTRD
Genomic_D2         1 ------MKMSMRSIAVVFLVCLLVLSTEEMGPRKADAGFFSS KC-K PS TF GPCVRN
Genomic_D3         1 ----MKHFGAIFLVLLLVLAT------------EHGARVAEARTC-E PSQKF GICISD
Genomic_D4         1 ----------------------------------VSTKVAEARIC-A PSPTF GICFSS
Genomic_D5         1 ----MRPFAALFLVLFLVLAT------------EIGPRVVEARMC-S PS RF GICTSS
Genomic_D6         1 MERSSRVFSVVLLMLVLVLSTDMYTDPVAVLSYEIGTKVAEARIC-E ASYRF GICVSR
Genomic_D7         1 ----MKPFVAFVLAFMLVLAI------------EMGPRVAEARMC-TNPS TF GPCVSD
Segura_D1          1 ------------------------------------------XTC-E PS KF GPCATN
Segura_D2          1 -------------------------------------GIFSSRKC-K PS TF GICTRD
Segura_D3          1 -------------------------------------GIFSSRKC-K VS TF GICTRN
Segura_D4          1 -----------------------------M--------FFSS KC-K VS TF GPCVRN
Segura_D5          1 -----------------------------M--------FFSS KC-K VX TF GPCVRN
Segura_D6          1 -------------------------------------GIFSNMYX-R PAGYF GPXGYX
Segura_D7          1 -------------------------------------GIFSSRKC-K PS TF GYCTRD
Rs-AFP2_GroupI     1 -----------------------------------------Q LC-QRPSGT SGVCGNN
At-AFP1_GroupI     1 -----------------------------------------Q LC-ERPSGT SGVCGNS
Hs-AFP1_GroupI     1 ---------------------------------------DGV LC-DVPSGT SGHCGSS
Ah-AMP1_GroupII    1 -------------------------------------------LCNERPSQT SGNCGNT
Dm-AMP1_GroupII    1 ------------------------------------------ELC-EKAS T SGNCGNT
St-PTH1_GroupIII   1 ------------------------------------------RHC-E LS RF GPCTRD
SIalpha2_GroupIII  1 ------------------------------------------RVC-MKGSAGF GLCMRD
consensus          1                                           . .  .......* .
```

FIG. 24A



```
Genomic_D1          31 SNC TSCRY-EG PAG-DCKGIRR-- CLCCTHT-
Genomic_D2          54 ANC TSCRY-EG PAG-DCKGIRR-- CICCTHA-
Genomic_D3          44 SNC SICNT-EG PNG-ECSGLRR-- CICNTPCT
Genomic_D4          26 RNC TNCNS-VK SGG-SCQGFRR-- CMCTKPCA
Genomic_D5          44 RNC NTCNS-ER SGG-ECKGFRR-- CMCTGPCV
Genomic_D6          60 SNCANVCKN-EG PGG-RCRGFRR-- CLCYKHCG
Genomic_D7          44 RNC SSCMG-EG PGG-SCHGFRR-- CVCSKPCA
Segura_D1           18 RNC S------------------------------
Segura_D2           23 SNC TSCRY-EG PAG-DCKGIRR-- CMCSKPC-
Segura_D3           23 ANC--------------------------------
Segura_D4           23 A----------------------------------
Segura_D5           23 AN---------------------------------
Segura_D6           23 XN---------------------------------
Segura_D7           23 SNC TSCRY-EG PAG-D-----------------
Rs-AFP2_GroupI      19 NACKNQCIRLEKARHG-SCNYVFPAH CICYFPC-
At-AFP1_GroupI      19 NACKNQCINLEKARHG-SCNYVFPAH CICYFPC-
Hs-AFP1_GroupI      21 SKCSQQCKDREH AYGGACHYQFPSV CFCKRQC-
Ah-AMP1_GroupII     18 AHC KQCQDWEKASHG-ACHKRENHW CFCYFNC-
Dm-AMP1_GroupII     18 GHC NQCKSWEGAAHG-ACHVRNGKHMCFCYFNC-
St-PTH1_GroupIII    18 SNCASVCET-ER SGG-NCHGFRR-- CFCTKPC-
SIalpha2_GroupIII   18 QNCAQVCLQ-EG GGG-NCDGVMR--QCKCIRQC-
consensus           61  ...  .   . .  . .       .. .  .
```

FIG. 24B

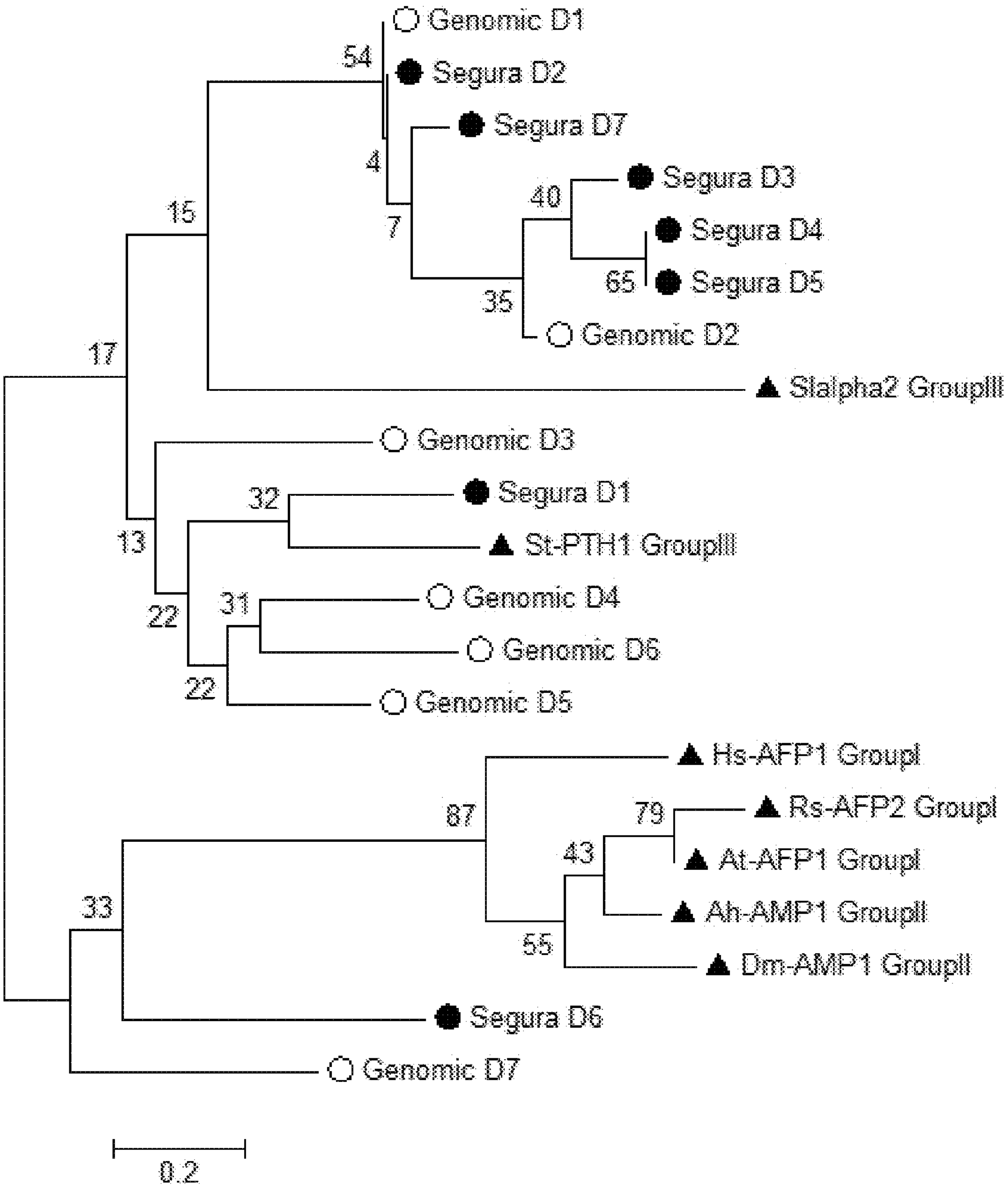

○ Genomic D1
54
● Segura D2
● Segura D7
4
7
40
● Segura D3
● Segura D4
65
● Segura D5
35
○ Genomic D2
15
17
▲ Slalpha2 GroupIII
○ Genomic D3
32
● Segura D1
▲ St-PTH1 GroupIII
13
31
○ Genomic D4
22
○ Genomic D6
22
○ Genomic D5
▲ Hs-AFP1 GroupI
87
79
▲ Rs-AFP2 GroupI
43
▲ At-AFP1 GroupI
▲ Ah-AMP1 GroupII
55
▲ Dm-AMP1 GroupII
33
● Segura D6
○ Genomic D7
0.2

FIG. 25A

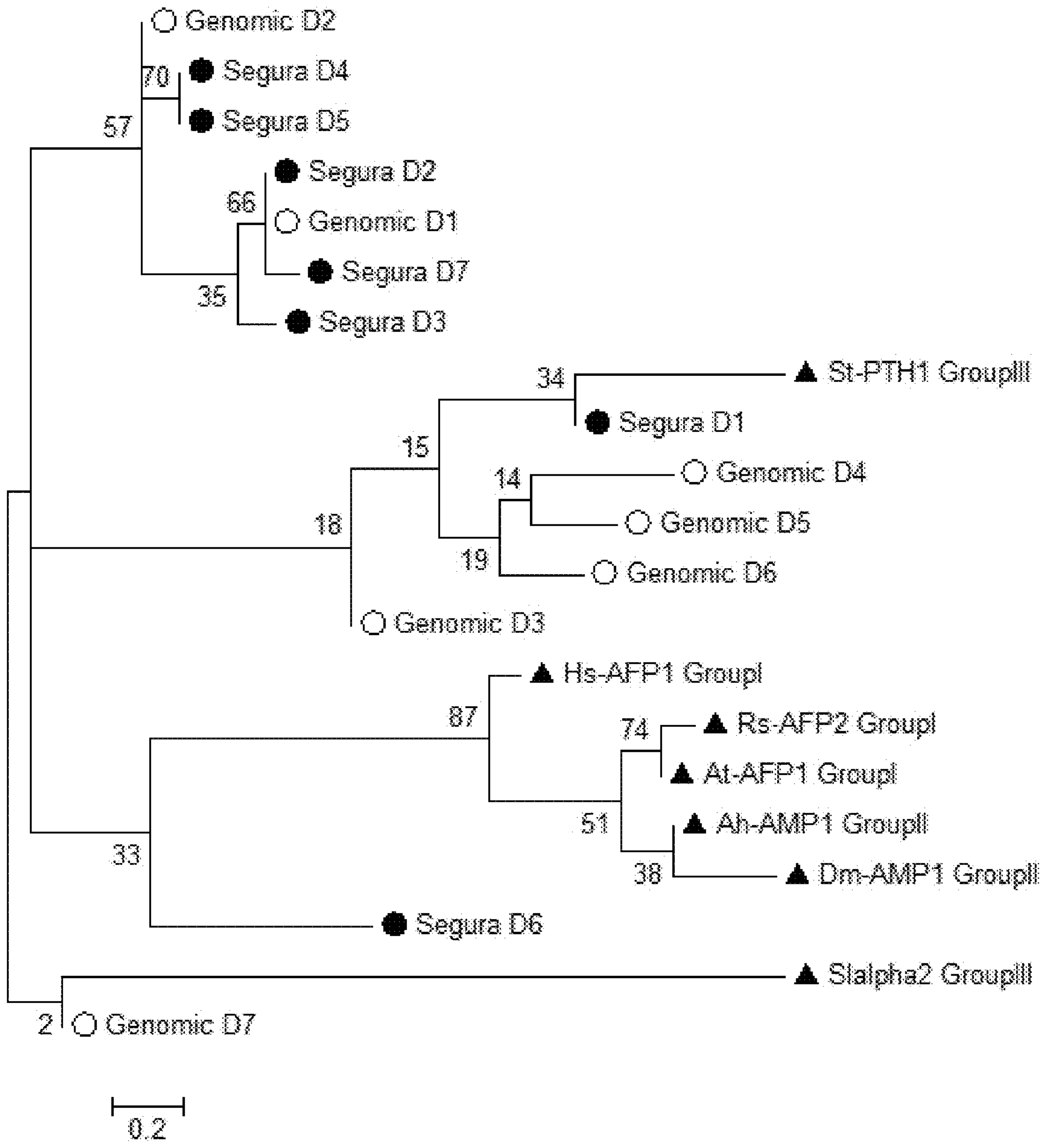

○ Genomic D2
● Segura D4
● Segura D5
● Segura D2
○ Genomic D1
● Segura D7
● Segura D3
▲ St-PTH1 GroupIII
● Segura D1
○ Genomic D4
○ Genomic D5
○ Genomic D6
○ Genomic D3
▲ Hs-AFP1 GroupI
▲ Rs-AFP2 GroupI
▲ At-AFP1 GroupI
▲ Ah-AMP1 GroupII
▲ Dm-AMP1 GroupII
● Segura D6
▲ SIalpha2 GroupIII
○ Genomic D7
70
57
66
35
34
15
14
18
19
87
74
51
38
33
2
0.2

FIG. 25B

FIG. 26A

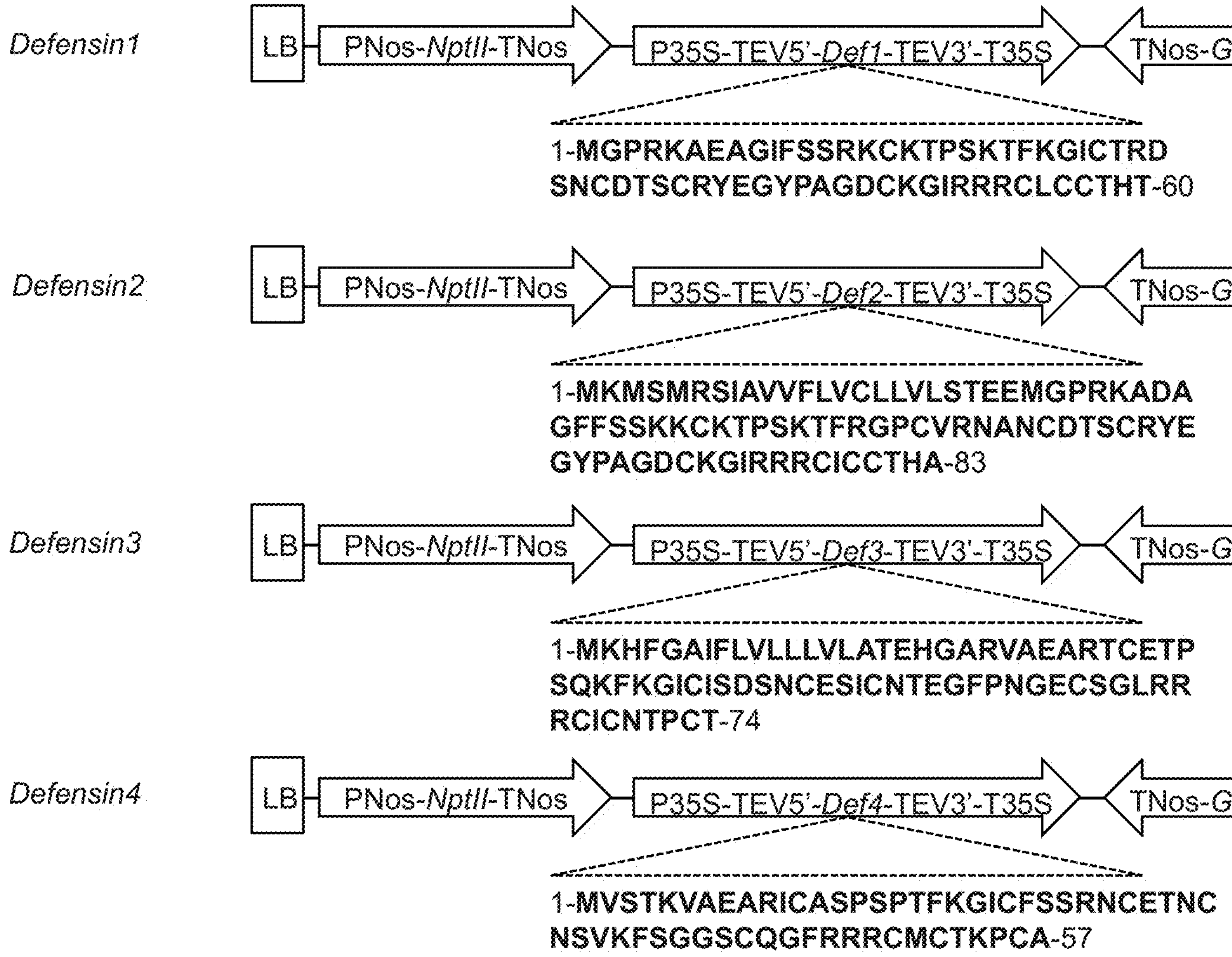

Defensin1
LB
PNos-*NptII*-TNos
P35S-TEV5'-*Def1*-TEV3'-T35S
TNos-*GUS intron*-P34S
RB
1-**MGPRKAEAGIFSSRKCKTPSKTFKGICTRD**
SNCDTSCRYEGYPAGDCKGIRRRCLCCTHT-60
Defensin2
LB
PNos-*NptII*-TNos
P35S-TEV5'-*Def2*-TEV3'-T35S
TNos-*GUS intron*-P34S
RB
1-**MKMSMRSIAVVFLVCLLVLSTEEMGPRKADA**
GFFSSKKCKTPSKTFRGPCVRNANCDTSCRYE
GYPAGDCKGIRRRCICCTHA-83
Defensin3
LB
PNos-*NptII*-TNos
P35S-TEV5'-*Def3*-TEV3'-T35S
TNos-*GUS intron*-P34S
RB
1-**MKHFGAIFLVLLLVLATEHGARVAEARTCETP**
SQKFKGICISDSNCESICNTEGFPNGECSGLRR
RCICNTPCT-74
Defensin4
LB
PNos-*NptII*-TNos
P35S-TEV5'-*Def4*-TEV3'-T35S
TNos-*GUS intron*-P34S
RB
1-**MVSTKVAEARICASPSPTFKGICFSSRNCETNC**
NSVKFSGGSCQGFRRRCMCTKPCA-57

FIG. 26B

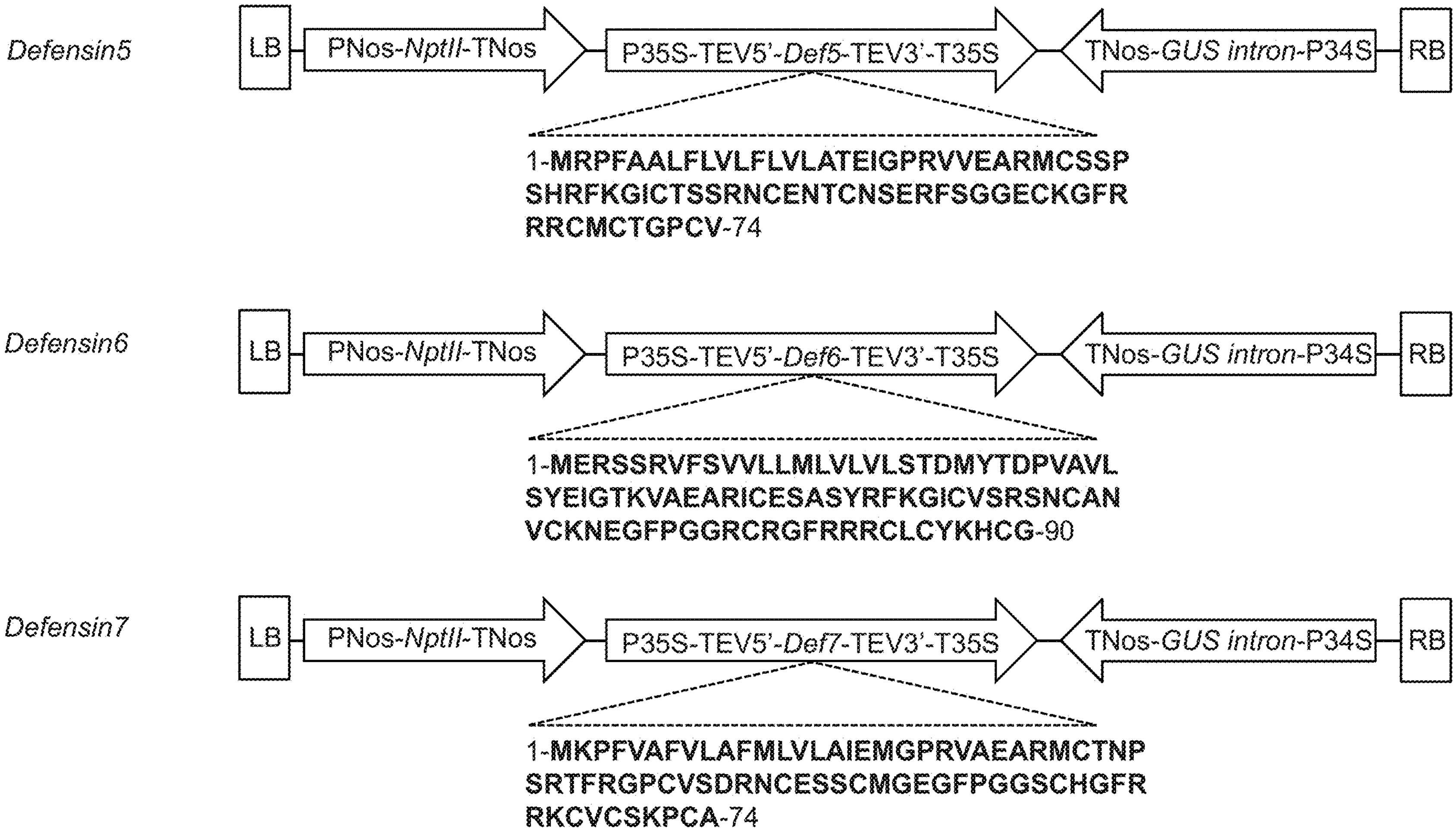
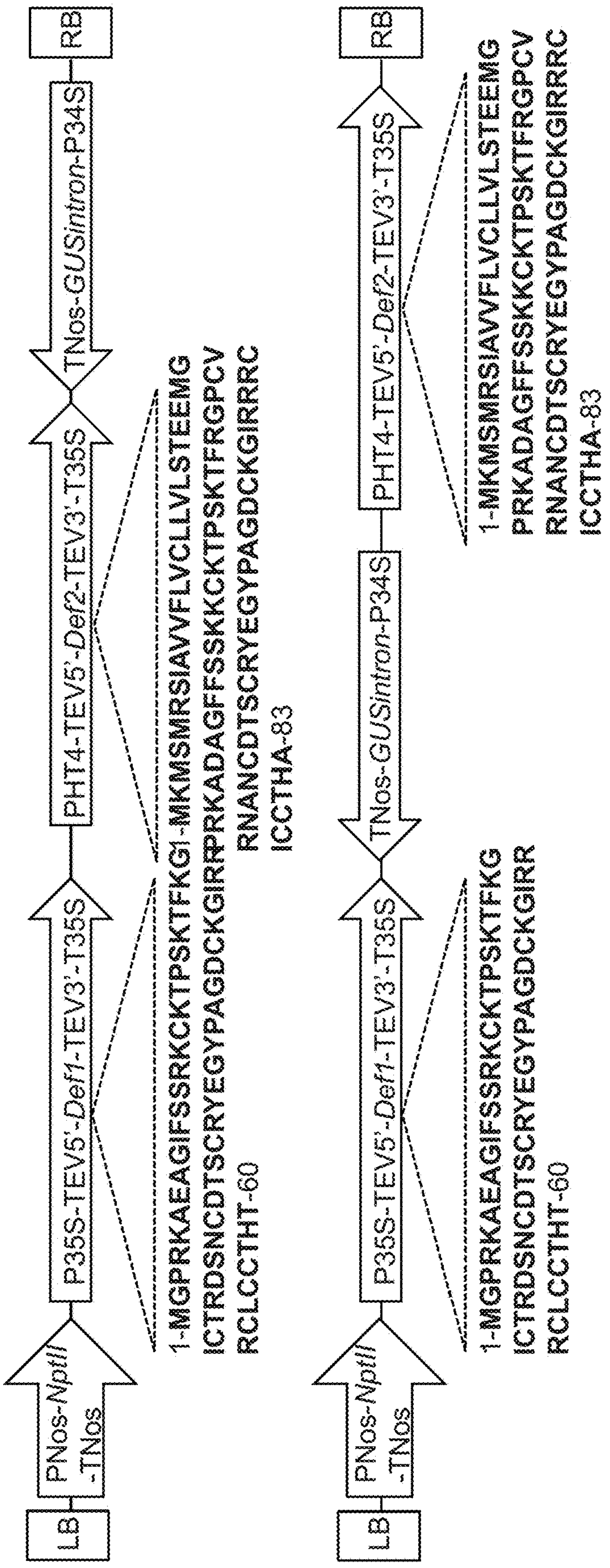

Defensin5
LB
PNos-*NptII*-TNos
P35S-TEV5'-*Def5*-TEV3'-T35S
TNos-*GUS intron*-P34S
RB
1-MRPFAALFLVLFLVLATEIGPRVVEARMCSSP
SHRFKGICTSSRNCENTCNSERFSGGECKGFR
RRCMCTGPCV-74
Defensin6
LB
PNos-*NptII*-TNos
P35S-TEV5'-*Def6*-TEV3'-T35S
TNos-*GUS intron*-P34S
RB
1-MERSSRVFSVVLLMLVLVLSTDMYTDPVAVL
SYEIGTKVAEARICESASYRFKGICVSRSNCAN
VCKNEGFPGGRCRGFRRRCLCYKHCG-90
Defensin7
LB
PNos-*NptII*-TNos
P35S-TEV5'-*Def7*-TEV3'-T35S
TNos-*GUS intron*-P34S
RB
1-MKPFVAFVLAFMLVLAIEMGPRVAEARMCTNP
SRTFRGPCVSDRNCESSCMGEGFPGGSCHGFR
RKCVCSKPCA-74

FIG. 27

Defensin1 & *Defensin2*



	Def1	Def2	Def3	Def4	Def5	Def6	Def7	SoD2	SoD7
Def1		Def1+Def2	Def1+Def3	Def1+Def4	Def1+Def5	Def1+Def6	Def1+Def7	Def1+SoD2	Def1+SoD7
Def2			Def2+Def3	Def2+Def4	Def2+Def5	Def2+Def6	Def2+Def7	Def2+SoD2	Def2+SoD7
Def3				Def3+Def4	Def3+Def5	Def3+Def6	Def3+Def7	Def3+SoD2	Def3+SoD7
Def4					Def4+Def5	Def4+Def6	Def4+Def7	Def4+SoD2	Def4+SoD7
Def5						Def5+Def6	Def5+Def7	Def5+SoD2	Def5+SoD7
Def6							Def6+Def7	Def6+SoD2	Def6+SoD7
Def7								Def7+SoD2	Def7+SoD7
SoD2									SoD2+SoD7
SoD7									

FIG. 28

PATHOGEN RESISTANT CITRUS COMPOSITIONS, ORGANISMS, SYSTEMS, AND METHODS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. Application No. 62/192,732 filed Jul. 15, 2015, the entire contents of which are hereby incorporated in this disclosure by reference.

REFERENCE TO SEQUENCE LISTING SUBMITTED VIA EFS-WEB

This application includes an electronically submitted substitute sequence listing in .txt format. The .txt file contains a sequence listing entitled "2017-02-06_10003183-50235311_ST25.txt" created on Feb. 6, 2017 and is 134,559 bytes in size. The sequence listing contained in this .txt file is part of the specification and is hereby incorporated by reference herein in its entirety.

FIELD OF THE DISCLOSURE

The present disclosure relates, in some embodiments, to pathogen resistant citrus compositions, organisms, systems, and methods.

BACKGROUND OF THE DISCLOSURE

At present, there are no *Citrus* cultivars resistant to bacterial canker (*Xanthomonas axonopodis* pv. citri) (Xac), and/or citrus Huanglongbing (ex greening) caused by *Candidatus Liberibacter asiaticus* (Las). Indeed, no genetic resistance to these microbial pathogens has ever been found within the *Citrus* genus. Conventional cross-breeding efforts to produce resistant cultivars have been hindered by the complex reproductive biology and long life cycle of *Citrus* spp.

SUMMARY

Accordingly, a need has arisen for plants (e.g., citrus) with improved resistance to disease. A further need has arisen for improved methods, compositions, and systems for preparing genetically modified plants (e.g., citrus).

The present disclosure relates, according to some embodiments, to pathogen resistant citrus compositions, organisms, systems, and methods. For example, a composition may comprise a nucleic acid (e.g., a defensin nucleic acid). In some embodiments, a nucleic acid may comprise a nucleic acid sequence (a) having from about 75% to about 100% identity (e.g., about 98% identity) to a defensin sequence (e.g., SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58) and/or (b) encoding an amino acid sequence having from about 95% to about 100% identity (e.g., 98% identity) to SEQ ID NOS: 1, 2, 7, 8, 28, 32, 33, 34, 35, 36, 37, and/or 38. A nucleic acid may comprise, in some embodiments, a nucleic acid sequence having about 98% identity to a sequence selected from the group consisting of SEQ ID NO: 3 and SEQ ID NO: 5 and encoding a peptide having an amino acid sequence having at least about 99% identity to SEQ ID NO: 1. A nucleic acid may comprise, in some embodiments, a nucleic acid sequence having about 98% identity to a sequence selected from the group consisting of SEQ ID NO: 4 and SEQ ID NO: 6 and encoding a peptide having an amino acid sequence having at least about 99% identity to SEQ ID NO: 2. According to some embodiments, a nucleic acid may comprise a nucleic acid sequence having about 98% identity to a sequence selected from the group consisting of SEQ ID NO: 9 and SEQ ID NO: 11 and encoding a peptide having an amino acid sequence having at least about 99% identity to SEQ ID NO: 7. A nucleic acid may comprise a nucleic acid sequence having about 98% identity to a sequence selected from the group consisting of SEQ ID NO: 10 and SEQ ID NO: 12 and encoding a peptide having an amino acid sequence having at least about 99% identity to SEQ ID NO: 8, in some embodiments. A nucleic acid may comprise, in some embodiments, a nucleic acid sequence having about 98% identity to a sequence selected from the group consisting of SEQ ID NO: 46 and SEQ ID NO: 52 and encoding a peptide having an amino acid sequence having at least about 99% identity to SEQ ID NO: 32. According to some embodiments, a nucleic acid may comprise a nucleic acid sequence having about 98% identity to a sequence selected from the group consisting of SEQ ID NO: 47 and SEQ ID NO: 53 and encoding a peptide having an amino acid sequence having at least about 99% identity to SEQ ID NO: 33. A nucleic acid may comprise, in some embodiments, a nucleic acid sequence having about 98% identity to a sequence selected from the group consisting of SEQ ID NO: 48 and SEQ ID NO: 54 and encoding a peptide having an amino acid sequence having at least about 99% identity to SEQ ID NO: 34. According to some embodiments, a nucleic acid may comprise a nucleic acid sequence having about 98% identity to a sequence selected from the group consisting of SEQ ID NO: 55 and encoding a peptide having an amino acid sequence having at least about 99% identity to SEQ ID NO: 35. A nucleic acid may comprise, in some embodiments, a nucleic acid sequence having about 98% identity to a sequence selected from the group consisting of SEQ ID NO: 49 and SEQ ID NO: 56 and encoding a peptide having an amino acid sequence having at least about 99% identity to SEQ ID NO: 36. According to some embodiments, a nucleic acid may comprise a nucleic acid sequence having about 98% identity to a sequence selected from the group consisting of SEQ ID NO: 50 and SEQ ID NO: 57 and encoding a peptide having an amino acid sequence having at least about 99% identity to SEQ ID NO: 37. A nucleic acid may comprise, in some embodiments, a nucleic acid sequence having about 98% identity to a sequence selected from the group consisting of SEQ ID NO: 51 and SEQ ID NO: 58 and encoding a peptide having an amino acid sequence having at least about 99% identity to SEQ ID NO: 38.

The present disclosure is related to nucleotide and amino acid sequences that are either (i) not found anywhere in nature or (ii) not found in nature in the organism into which they have been introduced. According to some embodiments, any nucleic acid sequence having less than 100% identity to a reference sequence shall differ from any naturally-occurring nucleic acid sequence of the same size by at least one nucleotide (e.g., by substitution, deletion, or insertion). Any amino acid sequence having less than 100% identity to a reference sequence shall differ from any naturally-occurring nucleic acid sequence of the same size by at least one amino acid (e.g., by substitution, deletion, or insertion).

The present disclosure relates, in some embodiments, to defensin expression vectors operable in citrus (e.g., citrus varieties, citrus rootstocks). For example, an expression vector may comprise, in a 5' to 3' direction, (a) an expression control sequence; (b) an expressible nucleic acid (e.g., a nucleic acid encoding an exogenous polypeptide) operably linked to the expression control sequence; and (c) a 3' termination sequence operably linked to the expressible nucleic acid. In some embodiments, an exogenous nucleic acid may comprise a nucleic acid sequence having at least about 75% identity (e.g., at least about 98% identity) to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 29, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID. NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, and SEQ ID NO: 58. An expression vector may be located in a bacterial cell or a plant cell according to some embodiments. An expression vector may comprise, in some embodiments, the nucleotide sequence AACAATGG at positions −4 to 4 relative to a coding sequence (e.g., encoded by an exogenous nucleic acid sequence). According to some embodiments, an expression vector may comprise a linker (e.g., 3' of the expression control sequence and/or 5' of the nucleic acid (e.g., a nucleic acid encoding an exogenous polypeptide) having a length of from about 1 to about 200 nucleotides.

The present disclosure relates, in some embodiments, to a bacterial cell comprising an expression vector. For example, a bacterial cell may comprise an expression vector comprising, in a 5' to 3' direction, (a) an expression control sequence; (b) an expressible nucleic acid (e.g., a nucleic acid encoding an exogenous polypeptide) operably linked to the expression control sequence; and (c) a 3' termination sequence operably linked to the expressible nucleic acid. A bacterial cell may comprise, for example, an expression vector comprising, in a 5' to 3' direction, (a) an expression control sequence; (b) an exogenous nucleic acid operably linked to the expression control sequence; and/or (c) a 3' termination sequence operably linked to the exogenous nucleic acid, wherein the exogenous nucleic acid comprises a nucleic acid sequence having at least about 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID. NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, and SEQ ID NO: 58.

The present disclosure relates, in some embodiments, to a plant cell (e.g., a citrus plant cell) comprising an expression vector. For example, a plant cell (e.g., a citrus plant cell) may comprise an expression vector comprising, in a 5' to 3' direction, (a) an expression control sequence; (b) an expressible nucleic acid (e.g., a nucleic acid encoding an exogenous polypeptide) operably linked to the expression control sequence; and (c) a 3' termination sequence operably linked to the expressible nucleic acid. A plant cell (e.g., a citrus plant cell) may comprise, for example, an expression vector comprising, in a 5' to 3' direction, (a) an expression control sequence; (b) an exogenous nucleic acid operably linked to the expression control sequence; and/or (c) a 3' termination sequence operably linked to the exogenous nucleic acid, wherein the exogenous nucleic acid comprises a nucleic acid sequence having at least about 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 29, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID. NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, and SEQ ID NO: 58. A plant cell (e.g., a citrus plant cell) may be located in a plant (e.g., a citrus plant) according to some embodiments. Examples of citrus plants include, without limitation, orange, grapefruit, lemon, and lime. A plant cell may comprise a defensin peptide. A defensin peptide may have, in some embodiments, an amino acid sequence having at least about 99% identity to SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 28, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, or SEQ ID NO: 38 (e.g., encoded by and/or expressed from an expression vector nucleic acid) according to some embodiments.

In some embodiments, the present disclosure relates to a citrus plant (e.g., orange and/or grapefruit and/or lemon and/or lime) comprising an expression vector. A citrus plant may comprise an expression vector in a single cell, a plurality of cells (e.g., mosaic), or in all cells. A mosaic plant may arise from a graft in some embodiments. For example, a citrus plant may comprise a graft of a transgenic plant having an expression vector in all cells (e.g., scion) and a plant having a different expression vector or no expression vector in its cells (e.g., rootstock). A citrus plant may comprise, in some embodiments, in a single cell, a plurality of cells (e.g., mosaic), or in all cells a first expression vector (e.g., encoding a first defensin peptide) and in a single cell, a plurality of cells (e.g., mosaic), or in all cells a second expression vector (e.g., encoding a second defensin peptide). For example, a citrus plant cell may comprise (a) a first expression vector, the first expression vector comprising, in a 5' to 3' direction, (i) a first expression control sequence; (ii) a first exogenous nucleic acid operably linked to the first expression control sequence; and (iii) a first 3' termination sequence operably linked to the first exogenous nucleic acid, wherein the first exogenous nucleic acid comprises a nucleic acid sequence having at least about 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID. NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, and SEQ ID NO: 58; and (b) a second expression vector, the second expression vector comprising, in a 5' to 3' direction, (iv) a second expression control sequence; (v) a second exogenous nucleic acid operably linked to the second expression control sequence; and (vi) a second 3' termination sequence operably linked to the second exogenous nucleic acid, wherein the second exogenous nucleic acid comprises a nucleic acid sequence having at least about 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, and SEQ ID NO: 12, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID. NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, and SEQ ID NO: 58. According to some embodiments, a citrus plant may comprise in a single cell, a plurality of cells (e.g., mosaic), or in all cells an expression vector comprising a first nucleic acid sequence encoding a first defensin peptide (e.g., a peptide having at least 99% identity to SEQ ID NO: 32, 33, 34, 35, 36, 37, or 38) and a second nucleic acid sequence encoding a second defensin peptide (e.g., a peptide having at least 99% identity to SEQ ID NO: 32, 33, 34, 35, 36, 37, or 38). In some embodiments, a citrus plant may comprise a defensin peptide in a single cell, a plurality of cells (e.g., mosaic), or in all cells. A citrus plant may comprise in a single cell, a plurality of cells (e.g., mosaic), or in all cells a first defensin peptide (e.g., a peptide having at least 99% identity to SEQ ID NO: 32, 33, 34, 35, 36, 37, or 38) and in a single cell, a plurality of cells (e.g., mosaic), or in all cells a second defensin peptide (e.g., a peptide having at least 99% identity to SEQ ID NO: 32, 33, 34, 35, 36, 37, or 38).

The present disclosure relates, in some embodiments, to methods of expressing in a citrus plant an exogenous nucleic acid comprising a nucleic acid sequence encoding an expressed peptide (e.g., a defensin peptide). For example, a method may comprise contacting an expression cassette comprising an exogenous nucleic acid or an expression vector comprising an exogenous nucleic acid with the cytosol of a cell of a citrus plant under conditions that permit expression of the exogenous nucleic acid and formation of the expressed peptide. In some embodiments, an exogenous nucleic acid may comprise a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 29, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID. NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, and SEQ ID NO: 58. In some embodiments, an expression vector and/or an expression cassette may comprise, in a 5' to 3' direction, an expression control sequence, the exogenous nucleic acid operably linked to the expression control sequence, and a 3' termination sequence operably linked to the exogenous nucleic acid. An expressed peptide may comprise an amino acid sequence having at least 99% identity to an amino acid sequence selected from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 28, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, and/or SEQ ID NO: 38 according to some embodiments. Contacting an expression vector or cassette may further comprise, in some embodiments, co-cultivating the cell with an *Agrobacterium* cell comprising the expression vector or expression cassette to form a co-cultivated plant cell. According to some embodiments, a plant may be regenerated from a co-cultivated plant cell.

The present disclosure relates, in some embodiments, to methods for treating a citrus plant having and/or at risk of having a microbial infection (e.g., bacterial canker (*Xanthomonas axonopodis* pv. citri) (Xac), and/or citrus Huanglongbing (ex greening) caused by *Candidatus Liberibacter asiaticus* (Las)). For example, a method may comprise forming in the citrus plant at least one defensin peptide. Forming in the citrus plant at least one defensin peptide may comprise, in some embodiments, grafting the citrus plant with a cutting (e.g., a scion or a rootstock) from a second citrus plant, the second citrus plant comprising an expression vector and/or an expression cassette comprising, in a 5' to 3' direction, an expression control sequence, a defensin nucleic acid operably linked to the expression control sequence, and a 3' termination sequence operably linked to the defensin nucleic acid, wherein the defensin nucleic acid comprises a nucleic acid sequence encoding an amino acid sequence having at least 99% identity to an amino acid sequence selected from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 28, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, and/or SEQ ID NO: 38 under conditions that permit expression of the defensin nucleic acid.

The present disclosure relates, in some embodiments, to a citrus fruit (e.g., orange, grapefruit, lemon, lime) comprising at least one defensin peptide having the amino acid sequence of SEQ ID NO:87 or SEQ ID NO: 88.

BRIEF DESCRIPTION OF THE DRAWINGS

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

Some embodiments of the disclosure may be understood by referring, in part, to the present disclosure and the accompanying drawings, wherein:

FIG. **1** illustrates an *Agrobacterium* transformation construct comprising a nucleic acid encoding SoD2 (SEQ ID NO: 1) according to specific example embodiments of the disclosure;

FIG. **2** illustrates an *Agrobacterium* transformation construct comprising a nucleic acid encoding SoD7 (SEQ ID NO: 2) according to specific example embodiments of the disclosure;

FIG. **3** is a representation of a Southern blot showing insertion number among transgenic events in Hamlin and Rhode Red transformed with a SoD2 (07) nucleic acid comprising a GenScript-optimized sequence for expression in *Citrus*, according to a specific example embodiment of the disclosure;

FIG. **4** is a representation of a Southern blot showing insertion number among transgenic events in Hamlin and Rhode Red transformed with SoD2 (09) or SoD7 (10) nucleic acids, each comprising a CODA-optimized sequence for expression in *Citrus*, according to specific example embodiments of the disclosure;

FIG. **5** is a representation of a northern blot showing RNA transcripts among transgenic events in Marrs, transformed with SoD2 (07) or SoD7 (08) nucleic acids, each comprising a GenScript-optimized sequence for expression in *Citrus*, according to a specific example embodiment of the disclosure;

FIG. **6** is a representation of a northern blot showing RNA transcripts among transgenic events in Hamlin and Rhode Red, transformed with SoD2 (09) or SoD7 (10) nucleic acids, each comprising a CODA-optimized sequence for expression in *Citrus*, according to a specific example embodiment of the disclosure;

FIG. **7** is a representation of a northern blot showing RNA transcripts among transgenic events in Hamlin and Rhode Red, transformed with SoD2 (07) or SoD7 (08) nucleic acids, each comprising a GenScript-optimized sequence for expression in *Citrus*, according to a specific example embodiment of the disclosure;

FIG. **8** is a representation of a Southern blot confirming insertion of SoD2 or SoD7 in Hamlin plants, transformed with SoD2 (11) or SoD7 (12) nucleic acids, each comprising a DNA 2.0-optimized sequence for expression in *Citrus*, according to a specific example embodiment of the disclosure;

FIG. **9** is a representation of a Southern blot confirming insertion of defensins in Ruby Red (01) or Hamlin (04) transformed with SoD2 (09, 11), SoD7 (08, 12), or both SoD2 and SoD7 (13) nucleic acids, each comprising a sequence optimized for expression in *Citrus* using a sequence optimization algorithm (GenScript for 08 and 13; Coda for 09, and DNA 2.0 for 11 and 12), according to a specific example embodiment of the disclosure;

FIG. **10** is a representation of a northern blot showing RNA transcripts among transgenic events in Ruby Red (01) or Hamlin (04), transformed with SoD2 (11), SoD7 (08, 12), or both SoD2 and SoD7 (13) nucleic acids, each comprising a GenScript-optimized sequence (08 and 13) or DNA 2.0-optimized sequence (11 and 12) for expression in *Citrus*, according to a specific example embodiment of the disclosure;

FIG. **11** is a representation of a Southern blot confirming insertion of defensins in Carrizo Citrange (CC) transformed with SoD2 (07) or SoD7 (08) nucleic acids, each comprising a GenScript-optimized sequence for expression in *Citrus*, according to a specific example embodiment of the disclosure;

FIG. **12** is a representation of a northern blot showing RNA transcripts among transgenic events in Carrizo Citrange (CC) transformed with SoD2 (07) or SoD7 (08) nucleic acids, each comprising a GenScript-optimized sequence for expression in *Citrus*, according to a specific example embodiment of the disclosure;

FIG. **13**A is a photograph of an excised leaf from a non-transgenic grapefruit tree innoculated with a citrus canker pathogen according to specific example embodiments of the disclosure;

FIG. **13**B is a photograph of an excised leaf from an SoD2 transgenic grapefruit tree innoculated with a citrus canker pathogen according to specific example embodiments of the disclosure;

FIG. **14** is a photograph of chimeric grapefruit trees resulting from the graft of uninfected, non-transgenic scions on citrus greening infected, non-transgenic rootstocks (left and center) or the graft of uninfected, SoD2 transgenic scions on citrus greening infected, non-transgenic rootstock (right), according to specific example embodiments of the disclosure;

FIG. **15**A illustrates the percentage of Generation 2 citrus plants infected upon the first, second, and third sampling of challenged material, according to specific example embodiments of the disclosure;

FIG. **15**B is a continuation of the bar graph of FIG. **15**A illustrating the percentage of Generation 2 citrus plants infected upon the first, second, and third sampling of challenged material, according to specific example embodiments of the disclosure;

FIG. **15**C is a continuation of the bar graph of FIG. **15**A illustrating the percentage of Generation 2 citrus plants infected upon the first, second, and third sampling of challenged material, according to specific example embodiments of the disclosure;

FIG. **16**A illustrates the percentage of Generations 2 and 3 citrus plants infected upon the first, second and third samplings of challenged material, according to specific example embodiments of the disclosure;

FIG. **16**B is a continuation of the bar graph of FIG. **16**A illustrating the percentage of Generations 2 and 3 citrus plants infected upon the first, second and third samplings of challenged material, according to specific example embodiments of the disclosure;

FIG. **16**C is a continuation of the bar graph of FIG. **16**A illustrating the percentage of Generations 2 and 3 citrus plants infected upon the first, second and third samplings of challenged material, according to specific example embodiments of the disclosure; and

FIG. **17** is a representation of a Southern blot confirming insertion of defensins in Rio Red (02) transformed with both SoD2 and SoD7 (13) nucleic acids, each comprising a GenScript-optimized sequence for expression in *Citrus*, according to a specific example embodiment of the disclosure;

FIG. **18** is a representation of a northern blot showing RNA transcripts among transgenic events in Rio Red (02) or Hamlin (04), transformed with both SoD2 and SoD7 (13) nucleic acids, each comprising a GenScript-optimized sequence for expression in *Citrus*, according to a specific example embodiment of the disclosure; and

FIG. **19** is a Western blot illustrating binding of an anti-SoD7 according to specific example embodiments of the disclosure to samples containing SoD7.

FIG. **20** illustrates a multiple sequence alignment of Genomic D1 (SEQ ID NO: 32), Genomic D2 (SEQ ID NO: 33), Genomic D3 (SEQ ID NO: 34), Genomic D4 (SEQ ID NO: 35), Genomic D5 (SEQ ID NO: 36, Genomic D6 (SEQ ID NO: 37), and Genomic D7 (SEQ ID NO: 38) according to a specific example embodiment of the disclosure.

FIG. **21**A is a representation of the results of phylogenetic analyses of SEQ ID NOS 32, 33, 34, 35, 36, 37, and 38 according to a specific example embodiment of the disclosure.

FIG. **21**B is a representation of the results of phylogenetic analyses of SEQ ID NOS 32, 33, 34, 35, 36, 37, and 38 according to a specific example embodiment of the disclosure.

FIG. **22** illustrates the sequence alignments of Genomic D1 (SEQ ID NO: 32), Genomic D2 (SEQ ID NO: 33), Genomic D3 (SEQ ID NO: 34), Genomic D4 (SEQ ID NO: 35), Genomic D5 (SEQ ID NO: 36, Genomic D6 (SEQ ID NO: 37), and Genomic D7 (SEQ ID NO: 38), and Segura D1 (SEQ ID NO: 89), Segura D2 (SEQ ID NO: 90), Segura D3 (SEQ ID NO: 91), Segura D4 (SEQ ID NO: 92), Segura D5 (SEQ ID NO: 93), Segura D6 (SEQ ID NO: 94), and Segura D7 (SEQ ID NO: 95) according to a specific example embodiment of the disclosure.

FIG. **23**A is a representation of the results of phylogenetic analyses of SEQ ID NOS 32, 33, 34, 35, 36, 37, 38, and group IV defensin sequences according to a specific example embodiment of the disclosure.

FIG. **23**B is a representation of the results of phylogenetic analyses of SEQ ID NOS 32, 33, 34, 35, 36, 37, 38, and group IV defensin sequences according to a specific example embodiment of the disclosure.

FIG. **24**A and FIG. **24**B illustrates the sequence alignments of Genomic D1 (SEQ ID NO: 32), Genomic D2 (SEQ ID NO: 33), Genomic D3 (SEQ ID NO: 34), Genomic D4 (SEQ ID NO: 35), Genomic D5 (SEQ ID NO: 36, Genomic D6 (SEQ ID NO: 37), and Genomic D7 (SEQ ID NO: 38), as well as, representative group I defensin sequences Rs-AFP2 (SEQ ID NO: 96), At-AFP1 (SEQ ID NO: 97), and Hs-AFP1 (SEQ ID NO: 98) as illustrated in Segura et al.; representative group II defensin sequences Ah-Amp1 (SEQ ID NO:99) and Dm-Amp1 (SEQ ID NO: 100) as illustrated in Segura et al.; and representative group III defensin sequences St-PTH1 (SEQ ID NO: 101) and Siα2 (SEQ ID NO: 102 as illustrated in Segura et. al.) according to a specific example embodiment of the disclosure. FIG. **24**A illustrates the more N-terminal portion of the alignment. FIG. **24**B illustrates the more C-terminal portion of the alignment.

FIG. **25**A is a representation of the results of phylogenetic analyses of SEQ ID NOS 32, 33, 34, 35, 36, 37, 38, and representative defensin sequences from groups I, II, III, and IV according to a specific example embodiment of the disclosure.

FIG. **25**B is a representation of the results of phylogenetic analyses of SEQ ID NOS 32, 33, 34, 35, 36, 37, 38, and representative defensin sequences from groups I, II, III, and IV according to a specific example embodiment of the disclosure.

FIG. **26**A illustrates expression cassettes encoding individual defensin genes codon optimized for citrus including Def1 (SEQ ID NO: 32), Def2 (Seq ID NO: 33), Def3 (SEQ ID NO: 34), and Def 4 (SEQ ID NO: 35), according to a specific example embodiment of the disclosure.

FIG. **26**B illustrates expression cassettes encoding individual defensin genes codon optimized for citrus, including Def5 (SEQ ID NO: 36), Def6 (Seq ID NO: 37), and Def7 (SEQ ID NO: 38), according to a specific example embodiment of the disclosure.

FIG. **27** illustrates expression cassettes for the co-expression of multiple defensin genes codon-optimized for citrus, including Def1 (SEQ ID NO: 32), Def2 (Seq ID NO: 33), according to a specific example embodiment of the disclosure.

FIG. **28** illustrates the potential combinations for co-expression of spinach defensins, according to a specific example embodiment of the disclosure.

BRIEF DESCRIPTION OF THE SEQUENCE LISTING

Some embodiments of the disclosure may be understood by referring, in part, to the present disclosure and the accompanying sequence listing, wherein:

SEQ ID NO: 1 illustrates an amino acid sequence of a spinach (*Spinacia oleracea*) defensin (SoD2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 2 illustrates an amino acid sequence of a spinach (*Spinacia oleracea*) defensin (SoD7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 3 illustrates a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 4 illustrates a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 5 illustrates a CODA-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 6 illustrates a CODA-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 7 illustrates an amino acid sequence of a chimeric peptide comprising a PR-1b signal peptide and a spinach (*Spinacia oleracea*) defensin (SoD2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 8 illustrates an amino acid sequence of a chimeric peptide comprising a PR-1b signal peptide and a spinach (*Spinacia oleracea*) defensin (SoD7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 9 illustrates a chimeric nucleic acid sequence comprising a nucleic acid sequence encoding a PR-1b signal peptide and a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 10 illustrates a chimeric nucleic acid sequence comprising a nucleic acid sequence encoding a PR-1b signal peptide and a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 11 illustrates a chimeric nucleic acid sequence comprising a nucleic acid sequence encoding a PR-1b signal peptide and a CODA-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 12 illustrates a chimeric nucleic acid sequence comprising a nucleic acid sequence encoding a PR-1b signal peptide and a CODA-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 13 illustrates an expression cassette comprising a nucleic acid sequence encoding a PR-1b signal peptide and a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 14 illustrates an expression cassette comprising a nucleic acid sequence encoding a PR-1b signal peptide and a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 15 illustrates an expression cassette comprising a nucleic acid sequence encoding a PR-1b signal peptide and a CODA-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 16 illustrates an expression cassette comprising a nucleic acid sequence encoding a PR-1b signal peptide and a CODA-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 17 illustrates an expression control sequence (CaMV 35S promoter) according to a specific example embodiment of the disclosure;

SEQ ID NO: 18 illustrates an untranslated region (TEV 5'UTR) according to a specific example embodiment of the disclosure;

SEQ ID NO: 19 illustrates an expression control sequence (CaMV 35S terminator) according to a specific example embodiment of the disclosure;

SEQ ID NO: 20 illustrates a nucleic acid sequence of a primer designated Zn5 according to a specific example embodiment of the disclosure;

SEQ ID NO: 21 illustrates a nucleic acid sequence of a primer designated Zn6 according to a specific example embodiment of the disclosure;

SEQ ID NO: 22 illustrates a nucleic acid sequence of a primer designated Fcp according to a specific example embodiment of the disclosure;

SEQ ID NO: 23 illustrates a nucleic acid sequence of a primer designated Rcp according to a specific example embodiment of the disclosure;

SEQ ID NO: 24 illustrates a nucleic acid sequence of a primer designated GUSF according to a specific example embodiment of the disclosure;

SEQ ID NO: 25 illustrates a nucleic acid sequence of a primer designated GUSR according to a specific example embodiment of the disclosure;

SEQ ID NO: 26 illustrates an amino acid sequence of a chimeric peptide comprising a modified PR-1b signal peptide and a GenScript-optimized nucleic acid sequence having a single deletion for expression of a spinach (*Spinacia oleracea*) defensin (SoD2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 27 illustrates a chimeric nucleic acid sequence comprising a nucleic acid sequence encoding a modified PR-1b signal peptide and a GenScript-optimized nucleic acid sequence having a single deletion for expression of a spinach (*Spinacia oleracea*) defensin (SoD2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 28 illustrates a core amino acid sequence of a defensin according to a specific example embodiment of the disclosure;

SEQ ID NO: 29 illustrates a nucleic acid sequence for expression of a core defensin according to a specific example embodiment of the disclosure;

SEQ ID NO: 30 illustrates a DNA 2.0-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD2) according to a specific example embodiment of the disclosure; and

SEQ ID NO: 31 illustrates a DNA 2.0-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (SoD7) according to a specific example embodiment of the disclosure.

SEQ ID NO: 32 illustrates an amino acid sequence of a spinach (*Spinacia oleracea*) defensin (Def1) according to a specific example embodiment of the disclosure;

SEQ ID NO: 33 illustrates an amino acid sequence of a spinach (*Spinacia oleracea*) defensin (Def2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 34 illustrates an amino acid sequence of a spinach (*Spinacia oleracea*) defensin (Def3) according to a specific example embodiment of the disclosure;

SEQ ID NO: 35 illustrates an amino acid sequence of a spinach (*Spinacia oleracea*) defensin (Def4) according to a specific example embodiment of the disclosure;

SEQ ID NO: 36 illustrates an amino acid sequence of a spinach (*Spinacia oleracea*) defensin (Def5) according to a specific example embodiment of the disclosure;

SEQ ID NO: 37 illustrates an amino acid sequence of a spinach (*Spinacia oleracea*) defensin (Def6) according to a specific example embodiment of the disclosure;

SEQ ID NO: 38 illustrates an amino acid sequence of a spinach (*Spinacia oleracea*) defensin (Def 7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 39 illustrates a nucleic acid sequence of a spinach (*Spinacia oleracea*) defensin (Def1) according to a specific example embodiment of the disclosure;

SEQ ID NO: 40 illustrates a nucleic acid sequence of a spinach (*Spinacia oleracea*) defensin (Def2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 41 illustrates a nucleic acid sequence of a spinach (*Spinacia oleracea*) defensin (Def3) according to a specific example embodiment of the disclosure;

SEQ ID NO: 42 illustrates a nucleic acid sequence of a spinach (*Spinacia oleracea*) defensin (Def4) according to a specific example embodiment of the disclosure;

SEQ ID NO: 43 illustrates a nucleic acid sequence of a spinach (*Spinacia oleracea*) defensin (Def5) according to a specific example embodiment of the disclosure;

SEQ ID NO: 44 illustrates a nucleic acid sequence of a spinach (*Spinacia oleracea*) defensin (Def6) according to a specific example embodiment of the disclosure;

SEQ ID NO: 45 illustrates a nucleic acid sequence of a spinach (*Spinacia oleracea*) defensin (Def7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 46 illustrates a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def1) according to a specific example embodiment of the disclosure;

SEQ ID NO: 47 illustrates a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 48 illustrates a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def3) according to a specific example embodiment of the disclosure;

SEQ ID NO: 49 illustrates a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def5) according to a specific example embodiment of the disclosure;

SEQ ID NO: 50 illustrates a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def6) according to a specific example embodiment of the disclosure;

SEQ ID NO: 51 illustrates a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 52 illustrates a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def1) according to a specific example embodiment of the disclosure;

SEQ ID NO: 53 illustrates a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Deft) according to a specific example embodiment of the disclosure;

SEQ ID NO: 54 illustrates a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def3) according to a specific example embodiment of the disclosure;

SEQ ID NO: 55 illustrates a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def4) according to a specific example embodiment of the disclosure;

SEQ ID NO: 56 illustrates a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def5) according to a specific example embodiment of the disclosure;

SEQ ID NO: 57 illustrates a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def6) according to a specific example embodiment of the disclosure;

SEQ ID NO: 58 illustrates a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 59 illustrates a chimeric nucleic acid sequence comprising a nucleic acid sequence encoding a spinach (*Spinacia oleracea*) defensin (Def2) signal peptide and a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 60 illustrates a chimeric nucleic acid sequence comprising a nucleic acid sequence encoding a spinach (*Spinacia oleracea*) defensin (Def2) signal peptide and a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 61 illustrates an expression cassette comprising a nucleic acid sequence encoding a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def1) according to a specific example embodiment of the disclosure;

SEQ ID NO: 62 illustrates an expression cassette comprising a nucleic acid sequence encoding a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 63 illustrates an expression cassette comprising a nucleic acid sequence encoding a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def3) according to a specific example embodiment of the disclosure;

SEQ ID NO: 64 illustrates an expression cassette comprising a nucleic acid sequence encoding a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def5) according to a specific example embodiment of the disclosure;

SEQ ID NO: 65 illustrates an expression cassette comprising a nucleic acid sequence encoding a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def6) according to a specific example embodiment of the disclosure;

SEQ ID NO: 66 illustrates an expression cassette comprising a nucleic acid sequence encoding a GenScript-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 67 illustrates an expression cassette comprising a nucleic acid sequence encoding a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def1) according to a specific example embodiment of the disclosure;

SEQ ID NO: 68 illustrates an expression cassette comprising a nucleic acid sequence encoding a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def2) according to a specific example embodiment of the disclosure;

SEQ ID NO: 69 illustrates an expression cassette comprising a nucleic acid sequence encoding a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def3) according to a specific example embodiment of the disclosure;

SEQ ID NO: 70 illustrates an expression cassette comprising a nucleic acid sequence encoding a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def4) according to a specific example embodiment of the disclosure;

SEQ ID NO: 71 illustrates an expression cassette comprising a nucleic acid sequence encoding a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def5) according to a specific example embodiment of the disclosure;

SEQ ID NO: 72 illustrates an expression cassette comprising a nucleic acid sequence encoding a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def6) according to a specific example embodiment of the disclosure;

SEQ ID NO: 73 illustrates an expression cassette comprising a nucleic acid sequence encoding a VGD-optimized nucleic acid sequence for expression of a spinach (*Spinacia oleracea*) defensin (Def7) according to a specific example embodiment of the disclosure;

SEQ ID NO: 74 illustrates an expression control sequence (CaMV 35S promoter) according to a specific example embodiment of the disclosure;

SEQ ID NO: 75 illustrates an untranslated region (TEV 5'UTR) according to a specific example embodiment of the disclosure;

SEQ ID NO: 76 illustrates an untranslated region (TEV 3'UTR) according to a specific example embodiment of the disclosure;

SEQ ID NO: 77 illustrates an terminator sequence (CaMV 35S terminator) according to a specific example embodiment of the disclosure;

SEQ ID NO: 78 illustrates a promoter sequence (PHT4; 6 *Arabidopsis thaliana* promoter) according to a specific example embodiment of the disclosure;

SEQ ID NO: 79 illustrates a promoter sequence (PHT4; 2 *Arabidopsis thaliana* promoter) according to a specific example embodiment of the disclosure; SEQ ID NO: 80 illustrates a promoter sequence (TPS-Cin *Arabidopsis thaliana* promoter) according to a specific example embodiment of the disclosure.

SEQ ID NO: 81 illustrates an assembled scaffold sequence of spinach (*Spinacia oleracea*) according to a specific example embodiment of the disclosure.

SEQ ID NO: 82 illustrates an assembled scaffold sequence of spinach (*Spinacia oleracea*) according to a specific example embodiment of the disclosure.

SEQ ID NO: 83 illustrates an assembled scaffold sequence of spinach (*Spinacia oleracea*) according to a specific example embodiment of the disclosure.

SEQ ID NO: 84 illustrates an assembled scaffold sequence of spinach (*Spinacia oleracea*) according to a specific example embodiment of the disclosure.

SEQ ID NO: 85 illustrates an assembled scaffold sequence of spinach (*Spinacia oleracea*) according to a specific example embodiment of the disclosure.

SEQ ID NO: 86 illustrates an assembled scaffold sequence of spinach (*Spinacia oleracea*) according to a specific example embodiment of the disclosure.

SEQ ID NO: 87 illustrates an amino acid sequence of a spinach (*Spinacia oleracea*) defensin peptide according to a specific example embodiment of the disclosure.

SEQ ID NO: 88 illustrates an amino acid sequence of a spinach (*Spinacia oleracea*) defensin peptide according to a specific example embodiment of the disclosure.

DETAILED DESCRIPTION

The present disclosure relates, in some embodiments, to compositions, organisms, systems, and methods for enhancing a plant's innate ability, if any, to respond to contact (e.g., infection) with a pathogen (e.g., bacteria, yeast, fungus, virus). In some embodiments, the present disclosure relates to compositions, organisms, systems, and methods for expressing a gene product (e.g., an antimicrobial peptide) in a plant (e.g., citrus). For example, the present disclosure relates to expression control sequences (e.g., promoters), expression cassettes, expression vectors, microorganisms, and/or plants comprising one or more antimicrobial peptides and/or one or more nucleic acids encoding one or more antimicrobial peptides.

I. Compositions

A. Antimicrobial Peptides

The present disclosure relates, according to some embodiments, to peptides and/or proteins having insecticidal activity, antimicrobial activity, and/or antiviral activity, which may include, without limitation, avidin, vegetative insecticidal proteins (e.g., Vip3A), insecticidal crystal proteins from *Bacillus thuringiensis* (e.g., Cry1, Cry1Ab, Cry2, Cry9), pea albumin (e.g., PA1b), hirsutellin A, lectins (e.g., snow drop lily lectin, garlic lectin, onion lectin), amylase inhibitors (e.g., alpha amylase inhibitor), arcelins (e.g., arcelins from beans), proteinase inhibitors, lysozymes (e.g., bovine lysozyme, human lysozyme, mollusk lysozyme), defensin (e.g., SoD2, SoD7, Def1, Def2, Def3, Def4, Def5, Def6, and/or Def7), chitinase, β-1,3-glucanase, variants thereof, and/or combinations thereof. An antimicrobial peptide may comprise, for example, one or more antimicrobial-peptides belonging to the family of plant defensins. These polypeptides were originally isolated from spinach leaves (*Spinacia oleracea*). In some embodiments, a defensin may be small (about 5 kDa), may be basic and/or may be cysteine-rich. In some embodiments, a defensin may comprise a peptide having an amino acid sequence sharing at least about 95% identity, at least about 96% identity, at least about 97% identity, at least about 98% identity, at least about 99% identity, and/or about 100% identity with SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 87, and/or SEQ ID NO: 88. In some embodiments, an antimicrobial peptide may further comprise one or more amino acids that are independently and/or collectively either neutral (e.g., do not adversely impact antibacterial functionality) and/or augment antibacterial functionality (e.g., by directing the peptide to a desired location (e.g., cellular and/or extracellular). For example, a defensin may comprise a signal peptide derived from the tobacco pathogenesis-related (PR)-1b protein that allows the transport of the peptides into the apoplast of plant cells (e.g., via the secretory pathway) and/or accumulation in the intercellular spaces of leaves, stems, flowers, fruits, seeds, and/or roots. A defensin may comprise, according to some embodiments, a peptide having an amino acid sequence sharing at least about 95% identity, at least about 96% identity, at least about 97% identity, at least about 98% identity, at least about 99% identity, and/or about 100% identity with SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 7, SEQ ID NO: 8; SEQ ID NO: 28, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, and/or SEQ ID NO: 38. Differences in peptide sequences among defensins may give rise to qualitative and/or quantitative differences in performance relative to one or more other defensins. For example, Def3, Def4, Def5, Def6, and/or Def7 (e.g., peptides having the sequence of SEQ ID NO: 34, 35, 36, 37, or 38) may perform differently than one or more other defensins within a plant cell or a plant tissue (e.g., increases or decreases in mobility, insecticidal activity, antimicrobial activity, susceptibility to processing and/or subcellular targeting, accumulation, peptide stability, degradation, and/or longevity as compared to other defensin peptides).

B. Nucleic Acids

The present disclosure relates, in some embodiments, to nucleic acids (e.g., cassettes, vectors) comprising one or more sequences encoding one or more antimicrobial peptides. For example, a nucleic acid may comprise a cassette comprising a synthetic or artificial defensin nucleic acid sequence (e.g. nucleic acid sequences SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, and/or SEQ ID NO: 73). A synthetic or artificial defensin nucleic acid may encode the same amino acid sequence as a native spinach defensin with codons modified (e.g., optimized) from the native nucleotide sequence for citrus codon usage. A nucleic acid comprising a defensin coding sequence may comprise a sequence encoding a signal peptide (e.g., SEQ ID NO: 59, SEQ ID NO: 60). In some embodiments, expression of a nucleic acid comprising a sequence encoding an antimicrobial peptide may be optimized by positioning an initiation codon in a favorable (e.g., optimal) 5' context. According to some embodiments, a nucleic acid may comprise an expression control sequence (e.g., operably linked to a coding sequence). For example, a nucleic acid may comprise a coding gene sequence under the control of a dual enhanced CaMV 35S promoter with a 5' UTR from TEV plant potyvirus (e.g., to provide a translation-enhancing activity to the defensin genes).

According to some embodiments, a nucleic acid may comprise a nucleotide sequence having at least about 75% identity to SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58; at least about 80% identity to SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58; at least about 85% identity to SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58; at least about 90% identity to SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58; at least about 95% identity to SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58; at least about 97% identity to SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58; at least about 98% identity to SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58; at least about 99% identity to SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58; and/or about 100% identity to SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58. A nucleotide sequence may encode, in some embodiments, an amino acid sequence having at least about 98% identity to SEQ ID NOS: 1, 2, 7, 8, 28, 32, 33, 34, 35, 36, 37, and/or 38, at least about 99% identity to SEQ ID NOS: 1, 2, 7, 8, 28, 32, 33, 34, 35, 36, 37, and/or 38, and/or about 100% identity to SEQ ID NOS: 1, 2, 7, 8, 28, 32, 33, 34, 35, 36, 37, and/or 38. According to some embodiments, a nucleic acid may have a first measure of sequence identity to a reference nucleic acid sequence and may encode an amino acid sequence having a second measure of sequence identity to a reference amino acid sequence. For example, a nucleic acid may have about 85% identity to SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58, and encode an amino acid sequence having about 100% identity with SEQ ID NOS: 1, 2, 7, 8, 28, 32, 33, 34, 35, 36, 37, and/or 38, according to some embodiments.

A nucleic acid sequence, according to some embodiments, may hybridize to a nucleic acid having the nucleotide sequence of SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58 under stringent conditions. Stringent conditions may include, for example, (a) 4×SSC at 65° C. followed by 0.1×SSC at 65° for 60 minutes and/or (b) 50% formamide, 4×SSC at 65° C. A nucleic acid may comprise a deletion fragment (e.g., a deletion of from about 1 to about 12 bases) of a nucleic acid having a sequence of SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58 that retains antimicrobial activity against at least one microorganism capable of infecting a citrus plant. One of ordinary skill in the art having the benefit of the present disclosure may prepare one or more deletion fragments of a nucleic acid having a sequence of SEQ ID NOS: 3, 4, 5, 6, 9, 10, 11, 12, 29, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58 and screen the resulting fragments for antimicrobial activity against at least one microorganism capable of infecting a citrus plant.

A nucleic acid sequence having a sequence like SEQ ID NOS: 3, 4, 5, 6, 30, 31, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and/or 58 may be identified by database searches using the sequence or elements thereof as the query sequence using the Gapped BLAST algorithm (Altschul et al., 1997 *Nucl. Acids Res.* 25:3389-3402) with the BLOSUM62 Matrix, a gap cost of 11 and persistence cost of 1 per residue and an E value of 10. Sequence identity may be assessed by any available method according to some embodiments. For example, two sequences may be compared with either ALIGN (Global alignment) or LALIGN (Local homology alignment) in the FASTA suite of applications (Pearson and Lipman, 1988 *Proc. Nat. Acad. Sci.* 85:2444-2448; Pearson, 1990 *Methods in Enzymology* 183: 63-98) with the BLOSUM50 matrix and gap penalties of −16, −4. Sequence similarity may be assessed according to ClustalW (Larkin et al., 2007, *Bioinformatics* 23(21): 2947-2948), BLAST, FASTA or similar algorithm.

C. Expression Cassettes and Vectors

The disclosure relates, in some embodiments, to expression vectors and/or expression cassettes for expressing a nucleic acid sequence (e.g., a coding sequence) in a cell and comprising an expression control sequence and the nucleic acid sequence operably linked to the expression control sequence. Thus, for example, an expression cassette may comprise a heterologous coding sequence, the expression of which may be desired in a plant.

1. Expression Vectors

The disclosure relates, in some embodiments, to an expression vector which may comprise, for example, a nucleic acid having an expression control sequence and a coding sequence operably linked to the expression control sequence. In some embodiments, an expression control sequence may comprise one or more promoters, one or more operators, one or more enhancers, one or more ribosome binding sites, and/or combinations thereof. An expression control sequence may comprise, for example, a nucleic acid having promoter activity. An expression control sequence, according to some embodiments, may be constitutively active or conditionally active in (a) an organ selected from root, leaf, stem, flower, seed, and/or fruit, and/or (b) active in a tissue selected from epidermis, periderm, parenchyma, collenchyma, sclerenchyma, xylem, phloem, and/or secretory structures. An expression control sequence, according to some embodiments, may be operable to drive expression of a nucleic acid sequence (e.g., a coding sequence) in a cell. Metrics for expression may include, for example, rate of appearance and/or accumulation of a gene product (e.g., RNA and/or protein) and/or total accumulation of a gene product as of one or more time points (e.g., elapsed time after a starting point and/or a stage of development). Comparative assays for gene products may be qualitative, semi-quantitative, and/or quantitative in some embodiments. Comparative assays may indirectly and/or directly assess the presence and/or amount of gene product. In some embodiments, an expression control sequence may be sensitive to one or more stimuli (e.g., one or more small molecules, one or more plant defense-inducing agents, mechanical damage, temperature, pressure). For example, activity of an expression control sequence may be enhanced or suppressed upon infection with a microorganism (e.g., a bacteria or a virus).

An expression vector may be contacted with a cell (e.g., a plant cell) under conditions that permit expression (e.g., transcription) of the coding sequence. Examples of expression vectors may include the *Agrobacterium* transformation constructs shown in FIG. **1** and FIG. **2**. An expression control sequence may be contacted with a plant cell (e.g., an embryonic cell, a stem cell, a callous cell) under conditions that permit expression of the coding sequence in the cell and/or cells derived from the plant cell according to some embodiments. An expression vector may be contacted with a cell (e.g., a plant cell), in some embodiments, under conditions that permit inheritance of at least a portion of the expression vector in the cell's progeny. According to some embodiments, an expression vector may include one or more selectable markers. For example, an expression vector may include a marker for selection when the vector is in a bacterial host, a yeast host, and/or a plant host.

2. Expression Cassettes

According to some embodiments, the disclosure relates to an expression cassette which may comprise, for example, a nucleic acid having an expression control sequence and a coding sequence operably linked to the expression control sequence. An expression cassette may be comprised in an expression vector. A coding sequence, in some embodiments, may comprise any coding sequence expressible in at least one plant cell. For example, a coding sequence may comprise a plant sequence, a yeast sequence, a bacterial sequence, a viral sequence (e.g., plant virus), an artificial sequence, an antisense sequence thereof, a fragment thereof, a variant thereof, and/or combinations thereof. A coding sequence may comprise, in some embodiments, a sequence encoding one or more gene products with insecticidal, antibacterial, antifungal, antimicrobial, and/or antiviral activity. A coding sequence may comprise, in some embodiments, a start codon, an intron, and/or a translation termination sequence. According to some embodiments, a coding sequence may comprise one or more natural or artificial coding sequences (e.g., encoding a single protein or a chimera). According to some embodiments, an expression cassette may optionally comprise a termination sequence. A coding sequence, in some embodiments, may comprise a sequence at least partially codon optimized for expression in an organism of interest (e.g., a citrus plant).

An expression control sequence may be used, in some embodiments, to construct an expression cassette comprising, in the 5' to 3' direction, (a) the expression control sequence, (b) a heterologous gene or a coding sequence, or sequence complementary to a native plant gene under control of the expression control sequence, and/or (c) a 3' termination sequence (e.g., a termination sequence comprising a polyadenylation site). Examples of expression cassettes may include, in some embodiments, the cassettes shown in SEQ ID NOS: 13-16 and SEQ ID NOS: 61-73. An expression cassette may be incorporated into a variety of autonomously replicating vectors in order to construct an expression vector. An expression cassette may be constructed, for example, by ligating an expression control sequence to a sequence to be expressed (e.g., a coding sequence).

Some techniques for construction of expression cassettes are well known to those of ordinary skill in the art. For example, a variety of strategies are available for ligating fragments of DNA, the choice of which depends on the nature of the termini of the DNA fragments. An artisan of ordinary skill having the benefit of the present disclosure, a coding sequence (e.g., having antimicrobial activity) and/or portions thereof may be provided by other means, for example chemical or enzymatic synthesis. A nucleic acid may comprise, in a 5' to 3' direction, an expression control sequence, a linker (optional), and a coding sequence according to some embodiments. A nucleic acid may comprise, in some embodiments, one or more restriction sites and/or junction sites between an expression control sequence, a linker, and/or a coding sequence.

II. Microorganisms

The present disclosure relates, in some embodiments, to a microorganism comprising an antimicrobial peptide (e.g., a heterologous antimicrobial peptide) and/or a nucleic acid (e.g., a heterologous and/or expressible nucleic acid) comprising a nucleic acid sequence encoding an antimicrobial peptide. For example, a microorganism may comprise a bacteria, a yeast, and/or a virus. Examples of microorganisms may include, without limitation, *Agrobacterium tumefaciens, Escherichia coli*, a lepidopteran cell line, a Rice tungro bacilliform virus, a Commelina yellow mosaic virus, a Banana streak virus, a Taro bacilliform virus, and/or baculovirus. According to some embodiments, an antimicrobial peptide may be tolerated by and/or innocuous to its host microorganism. A microorganism may comprise an expression control sequence and an antimicrobial peptide coding sequence operably linked to the expression control sequence. A nucleic acid (e.g., a heterologous and/or expressible nucleic acid) comprising a nucleic acid sequence encoding an antimicrobial peptide may be present, in some embodiments, on a genomic nucleic acid and/or an extragenomic nucleic acid.

III. Plants

The present disclosure relates, in some embodiments, to a plant cell (e.g., an embryonic cell, a stem cell, a callous cell), a tissue, and/or a plant comprising an antimicrobial peptide (e.g., a heterologous antimicrobial peptide) and/or a nucleic acid (e.g., a heterologous and/or expressible nucleic acid) comprising a nucleic acid sequence encoding an antimicrobial peptide. A plant and/or plant cell may be a dicot in some embodiments. Examples of a dicot may include, without limitation, coffee, tomato, pepper, tobacco, lima bean, *Arabidopsis*, rubber, orange, grapefruit, lemon, lime, tangerine, mandarin, pummelo, potato, squash, peas, and/or sugar beet. A plant cell may be included in a plant tissue, a plant organ, and/or a whole plant in some embodiments. A plant cell in a tissue, organ, and/or whole plant may be adjacent, according to some embodiments, to one or more isogenic cells and/or one or more heterogenic cells. In some embodiments, a plant may include primary transformants and/or progeny thereof. A plant comprising a nucleic acid (e.g., a heterologous and/or expressible nucleic acid) comprising a nucleic acid sequence encoding an antimicrobial peptide may further comprise an expression control sequence operably linked to the nucleic acid, in some embodiments. A nucleic acid sequence encoding an antimicrobial peptide may be expressed, according to some embodiments, in a plant in one or more up to all (e.g., substantially all) organs, tissues, and/or cell types including, without limitation, stalks, leaves, roots, seeds, flowers, fruit, meristem, parenchyma, storage parenchyma, collenchyma, sclerenchyma, epidermis, mesophyll, bundle sheath, guard cells, protoxylem, metaxylem, phloem, phloem companion, and/or combinations thereof. In some embodiments, a nucleic acid and/or its gene product (e.g., an antimicrobial peptide) may be located in and/or translocated to one or more organelles (e.g., vacuoles, chloroplasts, mitochondria, plastids).

IV. Methods

A. Transforming a Plant

The present disclosure relates, according to some embodiments, to methods for independent transformation of citrus (e.g., a native genome of a citrus plant). For example, a method may comprise independent transformation, using *Agrobacterium tumefaciens* (At), of the native genome of the orange (*Citrus sinensis*) cultivars "Rhode Red", "Hamlin", and/or "Marrs." A transformation method may comprise contacting a nucleic acid comprising a SoD2, SoD7, and/or another defensin sequence (e.g., the synthetic gene sequence SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, and/or SEQ ID NO: 58) with a citrus plant according to some embodiments. A transformed plant (e.g., a transformed genome of a new orange cultivar) may independently contain, in some embodiments a sequence of a SoD2 gene, a SoD7 gene, and/or another defensin (e.g., the synthetic gene sequence SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, and/or SEQ ID NO: 58) encoding microbial resistance not found within the native gene pool of the *Citrus* genus. According to some embodiments, a transformed orange cultivar plant may comprise a peptide encoded by a SoD2 gene, a SoD7 gene, and/or another defensin gene (e.g., the synthetic gene sequence SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, and/or SEQ ID NO: 58). A transformed plant comprising a sequence of a SoD2 gene, a SoD7 gene, and/or another defensin gene (e.g., the synthetic gene sequence SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, and/or SEQ ID NO: 58) and/or comprising a peptide encoded by a SoD2 gene, a SoD7 gene, and/or another defensin gene (e.g. SEQ ID NO: 32, SEQ ID NO. 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 86, and/or SEQ ID NO: 87) may display resistance to a range (e.g., a broad range) of bacterial and/or fungal pathogens in some embodiments. For example, a transformed plant comprising a sequence of a SoD2 gene and/or a SoD7 gene and/or comprising a peptide encoded by a SoD2 gene and/or a SoD7 gene may display resistance to bacterial canker (*Xanthomonas axonopodis* pv. citri) (Xac), and/or citrus Huanglongbing (ex greening) caused by *Candidatus Liberibacter asiaticus* (Las). See EXAMPLE section below.

B. Grafting

The present disclosure relates to grafting at least a portion of a first plant (e.g., a citrus plant) with at least a portion of a second plant (e.g., a citrus plant), according to some embodiments. A first plant may be in any desired condition including, without limitation, a healthy condition, a diseased condition, an injured condition, a stressed condition (e.g., heat, cold, water, and the like), and/or combinations thereof. A first plant may have any desired genotype including, without limitation, wild type, transgenic, mutant, and/or the like with respect to a gene and/or trait of interest.

A second plant may be in any desired condition including, without limitation, a healthy condition, a diseased condition, an injured condition, a stressed condition (e.g., heat, cold, water, and the like), and/or combinations thereof. A second plant may have any desired genotype including, without limitation, wild type, transgenic, mutant, and/or the like with respect to a gene and/or trait of interest. A first and/or a second plant may comprises at least one antimicrobial peptide and/or at least one nucleic acid comprising a sequence encoding at least one antimicrobial peptide. Where both a first plant comprises at least one antimicrobial peptide and/or at least one nucleic acid comprising a sequence encoding at least one antimicrobial peptide and a second plant comprises at least one antimicrobial peptide and/or at least one nucleic acid comprising a sequence encoding at least one antimicrobial peptide, it may be desirable for the first and second plants to have the same and/or different antimicrobial peptides and/or nucleic acids encoding antimicrobial peptides. Grafting may comprise cutting a portion of a first plant to form a fresh cut site, cutting a portion of a second plant to create a second cut site, and/or contacting a first cut site with a second cut site. A cut site may comprise at least one vascular bundle. Grafting may comprise forming a graft junction and/or, optionally, sealing the graft junction (e.g., by coating the periphery of the graft junction with one or more barrier materials).

C. Treating Plant Disease

The present disclosure relates, in some embodiments, to compositions, organisms, systems, and methods for preventing, ameliorating, and/or treating a plant disease (e.g., a citrus disease) and/or at least one symptom of a plant disease. For example, a method may comprise grafting at least a portion of a plant (e.g., a citrus plant) having a plant disease and/or expressing at least one symptom of a plant disease with at least a portion of a plant (e.g., a citrus plant) comprising an antimicrobial peptide. Examples of a plant disease include, without limitation, bacterial canker (*Xanthomonas axonopodis* pv. citri) (Xac), and/or citrus Huanglongbing (ex greening) caused by *Candidatus Liberibacter asiaticus* (Las). According to some embodiments, preventing, ameliorating, and/or treating a plant disease (e.g., a citrus disease) and/or at least one symptom of a plant disease may comprise treating and/or curing one or more devastating bacterial diseases of citrus. For example, plants comprising stably integrated SoD2 and SoD7 transgenes in expressible form may display resistance to, without limitation, bacterial canker (*Xanthomonas axonopodis* pv. citri) (Xac), and/or citrus Huanglongbing (ex greening) caused by *Candidatus Liberibacter asiaticus* (Las). Such resistance has been observed as described in the Examples below.

According to some embodiments, the present disclosure relates to compositions, organisms, systems, and methods for augmenting a plant's native resistance to and/or conferring on a plant resistance to a plant disease (e.g., a citrus disease). For example, a method may comprise contacting a plant with an antimicrobial peptide and/or an expressible nucleic acid comprising a nucleic acid sequence encoding an antimicrobial peptide. An expressible nucleic acid comprising a nucleic acid sequence encoding an antimicrobial peptide may be and/or comprise an expression cassette in some embodiments. Contacting may comprise, according to some embodiments, grafting at least a portion of a target plant with a plant comprising an antimicrobial peptide and/or an expressible nucleic acid comprising a nucleic acid sequence encoding an antimicrobial peptide. In some embodiments, contacting may comprise contacting at least a portion of a target plant with a vector (e.g., via *Agrobacterium*-mediated transformation) comprising an antimicrobial peptide and/or an expressible nucleic acid comprising a nucleic acid sequence encoding an antimicrobial peptide. Examples of a plant disease include, without limitation, bacterial canker (*Xanthomonas axonopodis* pv. citri) (Xac), and/or citrus Huanglongbing (ex greening) caused by *Candidatus Liberibacter asiaticus* (Las).

D. Making a Citrus-Expressible Antimicrobial Peptide

In some embodiments, the present disclosure relates to compositions, organisms, systems, and methods for forming a citrus-expressible nucleic acid comprising a nucleic acid sequence encoding at least one spinach-derived antimicrobial peptide. For example, a method may comprise identifying an amino acid sequence of an antimicrobial peptide of interest, reverse translating the amino acid sequence to produce a first nucleic acid sequence; codon-optimizing the first nucleic acid sequence for expression in citrus to produce a second nucleic acid sequence, and/or synthesizing a nucleic acid having the second nucleic acid sequence. A method may comprise, in some embodiments, covalently bonding a nucleic acid having the second nucleic acid sequence with one or more nucleic acids having expression control sequences that are operable in citrus in an operable orientation and/or position relative to the nucleic acid having the second nucleic acid sequence.

As will be understood by those skilled in the art who have the benefit of the instant disclosure, other equivalent or alternative pathogen resistant citrus compositions, organisms, systems, and methods can be envisioned without departing from the description contained herein. Accordingly, the manner of carrying out the disclosure as shown and described is to be construed as illustrative only.

Persons skilled in the art may make various changes in the shape, size, number, and/or arrangement of parts without departing from the scope of the instant disclosure. For example, the position and number of expression control sequences, coding sequences, linkers, and/or terminator sequences may be varied. Each disclosed method and method step may be performed in association with any other disclosed method or method step and in any order according to some embodiments. Where the verb "may" appears, it is intended to convey an optional and/or permissive condition, but its use is not intended to suggest any lack of operability unless otherwise indicated. Persons skilled in the art may make various changes in methods of preparing and using a composition, device, and/or system of the disclosure. For example, a composition, device, and/or system may be prepared and or used as appropriate for microbial and/or plant (e.g., with regard to sanitary, infectivity, safety, toxicity, biometric, and other considerations). Where desired, some embodiments of the disclosure may be practiced to the exclusion of other embodiments. For example, some polypeptide embodiments may be practiced to the exclusion of a particular amino acid sequence (e.g., SEQ ID NO: 26) and/or some nucleic acid embodiments may be practiced to the exclusion of a particular nucleic acid sequence (e.g., SEQ ID NO: 27).

Also, where ranges have been provided, the disclosed endpoints may be treated as exact and/or approximations as desired or demanded by the particular embodiment. Where the endpoints are approximate, the degree of flexibility may vary in proportion to the order of magnitude of the range. For example, on one hand, a range endpoint of about 50 in the context of a range of about 5 to about 50 may include 50.5, but not 52.5 or 55 and, on the other hand, a range endpoint of about 50 in the context of a range of about 0.5 to about 50 may include 55, but not 60 or 75. In addition, it may be desirable, in some embodiments, to mix and match range endpoints. Also, in some embodiments, each figure disclosed (e.g., in one or more of the examples, tables, and/or drawings) may form the basis of a range (e.g., depicted value+/−about 10%, depicted value+/−about 50%, depicted value+/−about 100%) and/or a range endpoint. With respect to the former, a value of 50 depicted in an example, table, and/or drawing may form the basis of a range of, for example, about 45 to about 55, about 25 to about 100, and/or about 0 to about 100.

These equivalents and alternatives along with obvious changes and modifications are intended to be included within the scope of the present disclosure. Accordingly, the foregoing disclosure is intended to be illustrative, but not limiting, of the scope of the disclosure as illustrated by the appended claims.

EXAMPLES

Some specific example embodiments of the disclosure may be illustrated by one or more of the examples provided herein.

Example 1: Plant Material

Plant materials (e.g., *Citrus sinensis*) were generally prepared for transformation as described by Yang et al., *Plant Cell Reports* (2000) 19:1203 et seq.

Example 2: Plasmid Construction and Bacterial Strains

Plasmid construction and bacterial strains were generally performed as described by Yang et al., *Plant Cell Reports* (2000) 19:1203 et seq.

Example 3*:* *Agrobacterium* Co-Culture and Plant Transformation

Agrobacterium co-culture and plant transformation were generally performed as described by Yang et al., *Plant Cell Reports* (2000) 19:1203 et seq.

Example 4: Selection and Regeneration of Transgenic Shoots

Selection and regeneration of transgenic shoots were generally performed as described by Yang et al., *Plant Cell Reports* (2000) 19:1203 et seq.

Example 5: Grafting of Transgenic Shoots

Grafting of transgenic shoots were generally performed as described by Yang et al., *Plant Cell Reports* (2000) 19:1203 et seq.

Example 6: Southern and Northern Analysis

Southern and northern analysis were generally performed as described by Yang et al., *Plant Cell Reports* (2000) 19:1203 et seq.

Example 7: Expression in *Citrus* Trees

Table 1 illustrates specific example embodiments of nucleic acid sequences codon-optimized for citrus. Signal peptides and structural gene coding sequences shown are flanked on either side by specific restriction enzyme sites. These sequences were used to construct expression cassettes, vectors, and transformed *Agrobacterium* for preparation of transgenic plants.

TABLE 1

Example embodiments of specific nucleotide sequences of antimicrobial genes. The nucleotide sequences were optimized for codon usage in Citrus.

Antimicrobial Gene	Source of the Optimized Synthetic Gene (code)	Antimicrobial genes specific nucleotide sequences. The 5' nucleotides include the cloning site and a preferred context for the start codon. The 3' nucleotides include the cloning site.
SoD2	GenScript (07)	SEQ ID NO: 9
	CODA (09)	SEQ ID NO: 11
SoD7	GenScript (08)	SEQ ID NO: 10
	CODA (10)	SEQ ID NO: 12
SoD2	DNA 2.0 (11)	SEQ ID NO: 30
SoD7	DNA 2.0 (12)	SEQ ID NO: 31
SoD2 + SoD7	GenScript (13)	SEQ ID NOS: 9 and 10
SoD2 + SoD7 no SP	DNA 2.0 (16)	SEQ ID NO: 30 and 31

The following cultivars were selected for transformation:
- Orange: Hamlin ("04"), Rhode Red ("05"), and Marrs ("06") (FIGS. **3**-**7**);
- Grapefruit: Ruby Red ("01") (FIGS. **8**-**11**) and Rio Red ("02") (Example 14 below);
- Carrizo Citrange ("CC") (FIGS. **12**-**13**);
- Flying Dragon rootstock ("13" and "16");
- Frost Eureka and Frost Lisbon (13" and "16");
- Swingle rootstock (13" and "16"); and
- C22 rootstock.

Constructs used for each cultivar are shown in Table 2.

TABLE 2

Orange, grapefruit, lemon and citrus rootstock cultivars transformed (seedling epicotyls) with three different synthetic sequences of each SoD2 and SoD7 genes encoding antimicrobial peptides from spinach (*Spinacia oleracea*) (at least 521 events in total).

Generation	Defensin Synthetic Genes	Synthetic Gene Optimized-Codon Sequence (Sequence Code)	Citrus Cultivars (Cultivar Code)	Transgenic Events Codes (Cultivar and Gene)	Number of Transgenic Events
2(141 events)	SoD2 + SP	GenScript (07)	Hamlin (04)	0407	14
			Rhode Red (05)	0507	12
			Marrs (06)	0607	6
			Carrizo Citrange (CC)	CC2	18
		CODA (09)	Hamlin (04)	0409	16
			Rhode Red (05)	0509	6
	SoD7 + SP	GenScript (08)	Hamlin (04)	0408	12
			Rhode Red (05)	0508	8
			Marrs (06)	0608	7
			Carrizo Citrange (CC)	CC7	29
		CODA (10)	Hamlin (04)	0410	5
			Rhode Red (05)	0510	8
3 (36 events)	SoD2-no SP	DNA 2.0 (11)	Hamlin (04)	0411	11
			Ruby Red (01)	0111	6
	SoD7-no SP	DNA 2.0 (12)	Hamlin (04)	0412	13
			Ruby Red (01)	0112	6
4 (187 events + 157 Swingle	SoD2 + 7 + SP	GenScript (13)	Hamlin (04)	413	15
			Rhode Red (05)	513	14
			Rio Red (02)	213	18
			Frost Eureka Lemon (10)	1013	30
			Frost Lisbon Lemon (11)	1113	33
			Swingle Rootstock (12)	1213	157
			Flying Dragon Rootstock (09)	913	46

TABLE 2-continued

Orange, grapefruit, lemon and citrus rootstock cultivars transformed (seedling epicotyls) with three different synthetic sequences of each SoD2 and SoD7 genes encoding antimicrobial peptides from spinach (*Spinacia oleracea*) (at least 521 events in total).

Generation	Defensin Synthetic Genes	Synthetic Gene Optimized-Codon Sequence (Sequence Code)	Citrus Cultivars (Cultivar Code)	Transgenic Events Codes (Cultivar and Gene)	Number of Transgenic Events
			C22(08)	813	15
			Carrizo Citrange (07)	713	16
4	SoD2 + 7	GenScript (07 + 08)	Hamlin (04)	0413	15
			Rhode Red (05)	0513	1
			Rio Red (02)	0213	7
			Carrizo Citrange (CC)	CC2 + 7	6
5	SoD2 + 7-no SP	DNA 2.0 (16)	Hamlin (04)	416	Multiple GUS positive plants
			Frost Eureka Lemon (10)	1016	Multiple GUS positive plants
			Frost Lisbon Lemon (11)	1116	Multiple GUS positive plants
			Rhode Red (05)	516	Multiple GUS positive plants

A. Transformation of Orange

Orange plants were transformed with a single construct comprising GenScript-optimized SoD2 with signal peptide (“07”), GenScript-optimized SoD7 with signal peptide (“08”), CODA-optimized SoD2 with signal peptide (“09”), or CODA-optimized SoD2 with signal peptide (“10”). FIG. **3** is a representation of a Southern blot showing insertion number among transgenic events in Hamlin transformed with GenScript-optimized SoD2 (0407) and Rhode Red transformed with GenScript-optimized SoD2 (0507). FIG. **4** is a representation of a Southern blot showing insertion number among transgenic events in Hamlin transformed with CODA-optimized SoD2 (0409) or CODA-optimized SoD7 (0410) and Rhode Red transformed with CODA-optimized SoD2 (0509) or CODA-optimized SoD7 (0510). Additional transformation events are shown for GenScript-optimized SoD7 (“08”) and CODA-optimized SoD2 (“09”) in Hamlin in FIG. **9**.

Transgenic plants of the orange cultivars Hamlin, Rhode Red, and Marrs (n=82) produce high levels of transcripts of these antimicrobial genes (Table 2 and FIGS. **5**-**7**). FIG. **5** is a representation of a northern blot showing RNA transcripts among transgenic events in Marrs, transformed with genes SoD2 (0607) or SoD7 (0608) GenScript-optimized for codon use in *Citrus*. FIG. **6** is a representation of a northern blot showing RNA transcripts among transgenic events in Hamlin transformed with CODA-optimized SoD2 (0409) or CODA-optimized SoD7 (0410) and Rhode Red transformed with CODA-optimized SoD2 (0509) or CODA-optimized SoD7 (0510). FIG. **7** is a representation of a northern blot showing RNA transcripts among transgenic events in Hamlin transformed with GenScript-optimized SoD2 (0407) or GenScript-optimized SoD7 (0408) and Rhode Red transformed with GenScript-optimized SoD2 (0507) or GenScript-optimized SoD7 (0508). For identification, Table 2 contains the transgenic event codes for cultivar and gene combination.

Orange plants (Hamlin) were also transformed with a single construct comprising DNA 2.0-optimized SoD2 without signal peptide (“11”) or DNA 2.0-optimized SoD7 without signal peptide (“12”). FIG. **8** is a representation of a Southern blot confirming insertion of SoD2 or SoD7 in these orange plants. Additional transformation events are shown for SoD7 (12) in Hamlin in FIG. **9**.

B. Transformation of Grapefruit

Ruby Red (“01”) plants were transformed with a single construct comprising DNA 2.0-optimized SoD2 without signal peptide (“11”) or DNA 2.0-optimized SoD7 without signal peptide (“12”). FIG. **9** is a representation of a Southern blot (membrane was exposed to probes for both SoD2 and SoD7) confirming insertion of SoD2 or SoD7 in these grapefruit plants. FIG. **10** is a representation of a northern blot (membrane was exposed to probes for both SoD2 and SoD7) showing RNA transcripts among transgenic events in Ruby Red transformed with SoD2 (0111) or SoD7 (0112). For identification, Table 2 contains the transgenic event codes for cultivar and gene combination.

C. Transformation of Carrizo Citrange and C22

Carrizo Citrange and C22 rootstocks have been transformed with a construct comprising uidA and either SoD2 or SoD7 or SoD2+SoD7. FIG. **11** is a representation of a Southern blot confirming insertion of SoD2 (lanes marked “07”) and SoD7 (lanes marked “08”) in these Carrizo Citrange plants. FIG. **12** is a representation of a northern blot showing RNA transcripts isolated from these Carrizo Citrange plants (marked “CC”) transformed with SoD2 (GenScript-optimized sequence with signal peptide) and SoD7 (GenScript-optimized sequence with signal peptide). For identification, Table 2 contains the transgenic event codes for cultivar and gene combination. A number of C22 transformation events have been confirmed in each by positive GUS staining.

Swingle and Flying Dragon (citrus rootstock) plants were transformed with various constructs including a single construct comprising GenScript-optimized SoD2 and SoD7 with signal peptide. Successful tranformation of C22, Flying Dragon, and Swingle plants has been at least confirmed by positive GUS staining.

D. Transformation of Lemon

Frost Lisbon and Frost Eureka (lemon) plants were transformed with various constructs including a single construct comprising GenScript-optimized SoD2 and SoD7 with signal peptide. Successful tranformation of C22, Flying Dragon, and Swingle plants has been at least confirmed by positive GUS staining.

E. Status of Transformation Events

The following cultivars of citrus and citrus rootstock have been transformed (seedling epicotyls) with synthetic sequences of SoD2 and SoD7 genes encoding antimocrobial from spinach (*Spinacia oleracea*), with the transformation even being stably maintained for between two and five years.

Orange:
- 'Hamlin' Sweet Orange
- 'Marrs' Sweet Orange
- 'Rhode Red' Valencia

Grapefruit:
- 'Rio Red' Grapefruit
- 'Ruby Red' Grapefruit

Lemon:
- 'Frost Eureka' Lemon
- 'Frost Lisbon' Lemon
- 'Limoneria 8A' Lemon

Lime:
- Key Lime

Rootstock:
- 'Carrizo'
- 'C22'
- 'Flying Dragon'
- 'Swingle'
- 'Benton Citrange'

Example 8: Canker Disease Resistance Assay

Canker disease resistance was assessed using a detached leaf assay generally as described by Francis M I et al., 2010, *Eur J Plant Pathol* 127:571-578. Briefly, detached immature leaves (~75% expanded) were triple rinsed in sterile water to remove debris, sanitized by brief immersion in 70% ethanol followed by 0.5% sodium hypochloride, and again triple rinsed in sterile water. Sanitized leaves (3-4 per replicate×3 replicates) were infiltrated on their abaxial surface with an aqueous suspension of an Xcc strain isolated in Dade County Florida. Inoculated leaves were pressed on the surface of soft water agar plates, parafilm sealed, and incubated in an environmentally-controlled growth chamber.

FIG. **13**A shows the result of inoculating a non-transgenic 'Rio Red' leaf with the citrus canker pathogen, as described above, and FIG. **13**B shows the result of inoculating a transgenic leaf from a plant of 'Rio Red' expressing SoD2 with the citrus canker pathogen, as described above. A large reduction in the size and number of lesion on the transgenic can be seen.

Example 9: *Citrus* Greening (HLB) Disease Resistance Assay by Grafting

FIG. **14** shows the result of graft inoculating non-transgenic 'Rio Red' (two trees on the left) or transgenic 'Rio Red' expressing SoD2 one tree on the right) with the citrus greening pathogen. A non-transgenic rootstock (*Cleopatra mandarin*) infected with HLB is used. Onto this rootstock several buds of transgenic 'Rio Red' are grafted and this is replicated. The same protocol is followed for non-transgenic buds of 'Rio Red'. After 8 weeks, vigorous growth can be seen from the transgenic graft, where there is no growth on the controls.

Example 10: *Citrus* Greening (HLB) Disease Resistance Assay by Psyllid Inoculation

Resistance to bacterial infection and growth was assessed by two metrics. First, resistance was evaluated by the percentage of infection, namely the number of exposed plants that were infected. Second, a PCR-based method was used to amplify bacterial sequences. In this method, the relative degree of infection influences the number of PCR cycles required to produce detectable signal. For example a heavily infested plant might only require a few cycles while a plant with a low bacterial titer may require more cycles. In general, a plant that requires 30 or more cycles to observe detectable signal is regarded to be uninfected. Since some infections of citrus progress slowly, samples were collected for testing at 5 to 11 months after the time of first exposure and thereafter over a period of 6-9 months. The frequency of sample collection may vary from about every 45 days to about every 120 days. Ten to 15 replicates of each transgenic event plus non-transgenic controls are placed haphazardly in an insect proof green house that contains thousands' of psyllids carrying the citrus greening pathogen. The first PCR testing is done about five months after continuous exposure to psyllids. DNA extraction and PCR to detect the pathogen is essentially as described by Trey M S et al., 2006, *Proc. Fla. State Hort. Soc.* 119:89-93.

Example 11: Propagation and Resistance of Generation 1

Red Grapefruit (2 varieties) and Sweet Orange (3 varieties) were transformed with *Agrobacterium* comprising an expression vector having an artificial defensin gene construct that included a 2-amino acid insertion in the signal peptide and a single amino acid deletion in the coding sequence (SEQ ID NOS: 26 and 27). A total of 6 transformation events were further tested based on having high levels of SoD2 RNA expressed. Plants were cultivated as described herein and bacterial resistance was assessed as described. A first set of samples were collected after 11 months in the field (D0). Subsequent samples were collected the indicated number of days (42-471) after the first sampling (e.g., D42=11 months+42 days). Results are shown in Table 3.

TABLE 3

Generation 1 Infection Data								
Plant Line	N	0	42	90	127	271	384	471
GR 311 Hamlin	1	0%	0%	0%	0%	100%	100%	100%
Non Transgenic Hamlin	1	0%	0%	100%	100%	100%	100%	100%
GR 420 Grapefruit	1	0%	0%	0%	0%	0%	100%	100%
GR 824 Grapefruit	2	0%	0%	50%	50%	100%	100%	100%
GR 867 Grapefruit	1	0%	0%	0%	0%	100%	100%	100%
GR 882 Grapefruit	2	0%	0%	0%	50%	50%	50%	50%
GR 890 Grapefruit	1	0%	0%	0%	0%	0%	100%	100%
Non Transgenic Grapefruit	7	0%	0%	0%	14%	0%	57%	57%
Non Transgenic Grapefruit Border	6	0%	0%	0%	0%	50%	50%	50%
Total	22	0%	0%	9%	18%	41%	68%	68%

Example 12: Propagation and Resistance of Generation 2

Sweet Orange (2 varieties) were transformed with *Agrobacterium* comprising one of the following defensin gene constructs:

(a) GenScript-optimized SoD2 with tobacco PR-1b signal peptide (SEQ ID NO: 9),

(b) CODA-optimized SoD2 with tobacco PR-1b signal peptide (SEQ ID NO: 11),
(c) GenScript-optimized SoD7 with tobacco PR-1b signal peptide (SEQ ID NO: 10), or
(d) CODA-optimized SoD7 with tobacco PR-1b signal peptide (SEQ ID NO: 12).

A total of 71 transformation events were observed. Plants were cultivated as described herein and bacterial resistance was assessed as described. A first set of samples were collected after 5 months in the psyllid house (Day 0). Subsequent samples were collected the indicated number of days after the first sampling (e.g., Day 73=5 months+73 days). Results are shown in FIG. **15**, FIG. **16**, Table 4, and Table 5.

TABLE 4

Generation 2 Infection Data

					1st Sampling		2nd Sampling		3rd Sampling		Partial 4th Sampling	
Code	Scion[1]	Genotype[2]	Rootstock[3]	Gene[4]	Day 0	Mean Ct	Day 73	Mean Ct	Day 170	Mean Ct	Day 317	Mean Ct
0407-01	H	SO	Cm	SoD2 (G)	13%	23.02	33%	26.09	33%	23.28		
0407-02	H	SO	Cm	SoD2 (G)	0%		27%	28.78	47%	26.55		
0407-03	H	SO	Cm	SoD2 (G)	0%		7%	24.84	33%	29.32		
0407-04	H	SO	Cm	SoD2 (G)	20%	25.56	27%	27.18	40%	25.28		
0407-06	H	SO	Cm	SoD2 (G)	7%	31.07	7%	26.16	13%	22.52	67%	28.81
0407-07	H	SO	Cm	SoD2 (G)	20%	27.37	13%	25.96	27%	25.85	80%	27.26
0407-09	H	SO	Cm	SoD2 (G)	13%	26.05	27%	26.83	33%	22.90		
0407-10	H	SO	Cm	SoD2 (G)	7%	23.57	27%	26.04	47%	25.32		
0407-11	H	SO	Cm	SoD2 (G)	7%	26.75	33%	26.21	67%	24.87		
0407-12	H	SO	Cm	SoD2 (G)	7%	31.66	13%	24.51	33%	23.39		
0407-13	H	SO	Cm	SoD2 (G)	13%	23.52	27%	27.89	40%	23.54		
0408-01	H	SO	Cm	SoD7 (G)	13%	24.88	27%	25.55	53%	26.15		
0408-07A	H	SO	Cm	SoD7 (G)	7%	23.40	20%	28.48	27%	22.64	80%	27.08
Hamlin NT Control	H	SO	Cm	Control	0%		20%	28.83	40%	24.59	87%	25.92
0409-02	H	SO	Cm	SoD2 (C)	7%	27.34	0%		20%	24.04	80%	26.23
0409-03	H	SO	Cm	SoD2 (C)	7%	22.28	7%	28.79	27%	22.12	93%	25.52
0409-06	H	SO	Cm	SoD2 (C)	0%		20%	26.52	40%	24.01		
0409-07	H	SO	Cm	SoD2 (C)	0%		20%	26.31	40%	23.17		
0410-01	H	SO	Cm	SoD7 (C)	0%		40%	22.96	73%	24.78		
0507-01	RR	SO	Cm	SoD2 (G)	0%		47%	26.35	60%	23.60		
0507-02	RR	SO	Cm	SoD2 (G)	13%	28.26	40%	22.18	47%	25.14		
0507-03	RR	SO	Cm	SoD2 (G)	13%	24.61	47%	26.64	60%	23.59		
0507-04	RR	SO	Cm	SoD2 (G)	13%	26.21	27%	25.25	40%	24.63		
0507-07	RR	SO	Cm	SoD2 (G)	0%		13%	27.42	27%	22.61	67%	29.19
O507-08	RR	SO	Cm	SoD2 (G)	7%	25.97	40%	26.37	40%	24.03		
0507-10	RR	SO	Cm	SoD2 (G)	7%	26.04	27%	25.71	40%	25.29		
0507-11	RR	SO	Cm	SoD2 (G)	0%		40%	26.51	53%	22.26		
0507-12	RR	SO	Cm	SoD2 (G)	0%		20%	17.61	13%	22.56	77%	27.17
0507-15	RR	SO	Cm	SoD2 (G)	13%	24.49	53%	25.65	73%	23.10		
0508-02	RR	SO	Cm	SoD7 (G)	13%	29.40	47%	26.25	73%	23.90		
0508-03	RR	SO	Cm	SoD7 (G)	7%	31.44	33%	24.53	60%	25.37		
0508-04	RR	SO	Cm	SoD7 (G)	13%	25.65	20%	28.00	60%	25.74		
0508-06	RR	SO	Cm	SoD7 (G)	0%		7%	27.72	27%	24.33	79%	25.56
0508-07	RR	SO	Cm	SoD7 (G)	27%	26.86	67%	25.30	100%	24.76	100%	21.87
0508-08	RR	SO	Cm	SoD7 (G)	7%	24.35	27%	24.55	53%	23.07		
0508-09	RR	SO	Cm	SoD7 (G)	20%	25.55	33%	24.69	60%	24.40		
0508-10	RR	SO	Cm	SoD7 (G)	7%	25.96	33%	25.94	47%	23.30		
Rhode Red NT Control	RR	SO	Cm	Control	13%	27.03	27%	25.64	67%	25.46	100%	22.32
0509-02	RR	SO	Cm	SoD2 (C)	13%	24.36	53%	23.07	60%	23.77		
0509-03	RR	SO	Cm	SoD2 (C)	13%	25.28	27%	26.60	53%	26.02		
0509-07	RR	SO	Cm	SoD2 (C)	7%	30.19	20%	24.85	47%	25.71		
0509-10	RR	SO	Cm	SoD2 (C)	20%	27.29	20%	24.93	67%	26.26		
0510-02	RR	SO	Cm	SoD7 (C)	7%	30.66	27%	23.36	47%	24.42		
0510-03	RR	SO	Cm	SoD7 (C)	7%	22.01	20%	24.70	53%	25.39		
0510-05	RR	SO	Cm	SoD7 (C)	7%	31.54	7%	31.03	7%	31.22	17%	35.78
0510-06	RR	SO	Cm	SoD7 (C)	0%		33%	26.56	80%	24.48	93%	23.67
0510-08	RR	SO	Cm	SoD7 (C)	7%	23.07	47%	25.29	60%	22.32		
0510-09	RR	SO	Cm	SoD7 (C)	0%		33%	24.63	47%	24.02		
0510-10	RR	SO	Cm	SoD7 (C)	0%		20%	27.68	60%	25.16		
Extra NT Controls												
Hamlin	H	SO	Cm	Control	0%		40%	27.29	47%	23.25		
Hamlin	H	SO	Cm	Control	7%	24.49	13%	24.87	33%	25.58		
Hamlin	H	SO	Cm	Control	0%		33%	24.44	33%	25.82		

TABLE 4-continued

Generation 2 Infection Data

					1st Sampling		2nd Sampling		3rd Sampling		Partial 4th Sampling	
Code	Scion[1]	Genotype[2]	Rootstock[3]	Gene[4]	Day 0	Mean Ct	Day 73	Mean Ct	Day 170	Mean Ct	Day 317	Mean Ct
Rhode Red	RR	SO	Cm	Control	7%	24.61	33%	26.27	27%	22.98		
Rhode Red	RR	SO	Cm	Control	0%		40%	27.07	33%	24.49		
Rhode Red	RR	SO	Cm	Control	7%	24.36	33%	29.01	47%	26.50		

[1] H = Hamlin; RR = Rhode Red

[2] SO = Sweet Orange

[3] Cm = Cleopatra mandarin

[4] (G) = GenScript-optimized sequence; (C) = CODA-optimized sequence

Example 13: Propagation and Resistance of Generation 3

One Sweet Orange variety and one grapefruit variety were transformed with *Agrobacterium* comprising one of the following defensin gene constructs:

(a) GenScript-optimized SoD2 with no signal peptide (SEQ ID NO: 3), or

(b) GenScript-optimized SoD7 with no signal peptide (SEQ ID NO: 4).

A total of 36 transformation events were observed. Plants were cultivated as described herein and bacterial resistance was assessed as described. A first set of samples were collected after 5 months in the psyllid house (Day **0**). Subsequent samples were collected the indicated number of days after the first sampling (e.g., Day 103=5 months+103 days). Results are shown in FIG. **16** and Table 5.

TABLE 5

Generations 2 and 3 Infection Data

						2nd Sampling			3rd Sampling		
Code	Scion[1]	Genotype[2]	Rootstock[3]	Gene[4]	1st Sampling Day 0	Day 103	Avg Ct	Ct of Positive	Day 215	Avg Ct	Ct of Positive
41103	H	SO	Cm	SoD2 (—P)	10%	10%	37.98	24.78	10%	36.83	19.62
41108	H	SO	Cm	SoD2 (—P)	0%	0%	40.00		0%	38.93	
41107	H	SO	Cm	SoD2 (—P)	10%	14%	37.24	23.44	14%	35.28	21.02
41110	H	SO	Cm	SoD2 (—P)	0%	10%	38.18	26.35	20%	35.24	23.33
40918	H	SO	Cm	SoD2 (C)	0%	0%	39.74		10%	36.97	21.53
40915	H	SO	Cm	SoD2 (C)	0%	11%	38.07	25.22	22%	34.31	24.44
41004	H	SO	Cm	SoD7 (C)	0%	10%	38.37	23.72	20%	35.24	25.54
40814	H	SO	Cm	SoD7 (G)	0%	20%	36.62	26.39	10%	36.85	24.35
40817	H	SO	Cm	SoD7 (G)	10%	10%	37.97	22.93	30%	34.17	23.40
11206	RR	Gf	Cm	SoD7 (—P)	0%	30%	35.18	23.93	40%	32.27	24.69
11204	RR	Gf	Cm	SoD7 (—P)	0%	10%	37.63	24.56	30%	33.49	22.16
40813	H	SO	Cm	SoD7 (G)	10%	11%	37.73	22.63	44%	31.96	22.62
11201	RR	Gf	Cm	SoD7 (—P)	0%	30%	35.87	26.76	30%	33.71	23.06
41109	H	SO	Cm	SoD2 (—P)	0%	10%	38.46	24.64	10%	37.25	22.14
11208	RR	Gf	Cm	SoD7 (—P)	0%	0%	39.82		0%	38.42	
11108	RR	Gf	Cm	SoD2 (—P)	0%	0%	38.60		13%	36.15	21.66
11103	RR	Gf	Cm	SoD2 (—P)	0%	20%	36.98	26.00	20%	33.73	19.99
60811	M	SO	Cm	SoD7 (G)	0%	0%	39.66		0%	39.03	
Marrs WT	M	SO	Cm	Control	0%	10%	38.81	28.14	20%	35.57	24.93
40820	H	SO	Cm	SoD7 (G)	10%	20%	36.99	25.96	30%	34.94	23.65
41101	H	SO	Cm	SoD2 (—P)	0%	10%	37.65	23.09	20%	34.53	21.92
Ruby Red WT	RR	Gf	Cm	Control	0%	0%	39.39		30%	34.88	26.93
11105	RR	Gf	Cm	SoD2 (—P)	0%	10%	38.64	26.38	20%	36.32	24.70
40810 A	H	SO	Cm	SoD7 (G)	0%	25%	35.46	24.94	50%	30.83	23.08
11203	RR	Gf	Cm	SoD7 (—P)	0%	20%	37.84	29.19	20%	35.55	21.51
40914	H	SO	Cm	SoD2 (C)	0%	0%	39.66		30%	35.22	26.78
40812	H	SO	Cm	SoD7 (G)	0%	10%	37.99	27.44	20%	35.67	21.75
41102	H	SO	Cm	SoD2 (—P)	10%	40%	35.03	27.58	60%	29.83	23.83
Hamlin WT	H	SO	Cm	Control	0%	40%	33.76	24.41	50%	29.52	22.14
60813	M	SO	Cm	SoD7 (G)	0%	0%	40.00		13%	37.06	24.02
60804	M	SO	Cm	SoD7 (G)	10%	0%	39.80		0%	37.74	
60703	M	SO	Cm	SoD2 (G)	0%	33%	36.35	30.88	33%	36.07	25.07
60862	M	SO	Cm	SoD7 (G)	0%	0%	39.18		10%	37.87	31.23
60702	M	SO	Cm	SoD2 (G)	0%	10%	38.30	27.16	20%	35.46	24.11
41211	H	SO	Cm	SoD7 (—P)	10%	20%	36.47	24.33	30%	34.02	21.20
41203	H	SO	Cm	SoD7 (—P)	0%	0%	39.93		0%	38.17	
60812	M	SO	Cm	SoD7 (G)	0%	0%	40.00		10%	36.79	23.40
60810	M	SO	Cm	SoD7 (G)	10%	20%	37.25	26.25	70%	27.87	23.44
60767	M	SO	Cm	SoD2 (G)	0%	10%	38.51	25.13	40%	33.77	25.40
60701	M	SO	Cm	SoD2 (G)	0%	20%	37.45	28.07	50%	30.37	23.85

TABLE 5-continued

Generations 2 and 3 Infection Data

						2nd Sampling			3rd Sampling		
Code	Scion[1]	Genotype[2]	Rootstock[3]	Gene[4]	1st Sampling Day 0	Day 103	Avg Ct	Ct of Positive	Day 215	Avg Ct	Ct of Positive
41210	H	SO	Cm	SoD7 (—P)	0%	0%	39.60		20%	34.62	22.91
41202	H	SO	Cm	SoD7 (—P)	10%	17%	35.89	23.81	50%	30.85	22.69
60706	M	SO	Cm	SoD2 (G)	0%	10%	37.64	25.23	50%	30.82	23.24
41209	H	SO	Cm	SoD7 (—P)	0%	40%	33.36	24.97	70%	27.11	22.03
41113	H	SO	Cm	SoD2 (—P)	20%	60%	31.02	25.03	80%	25.36	21.70
41215	H	SO	Cm	SoD7 (—P)	20%	40%	33.73	24.32	70%	25.95	21.94
60808	M	SO	Cm	SoD7 (G)	0%	0%	39.35		22%	36.32	22.11
41208	H	SO	Cm	SoD7 (—P)	0%	0%	39.62		11%	37.30	22.04
41112	H	SO	Cm	SoD2 (—P)	20%	20%	35.94	25.32	40%	31.22	22.22
41214	H	SO	Cm	SoD7 (—P)	0%	20%	36.57	24.47	50%	29.72	21.99
60705	M	SO	Cm	SoD2 (G)	0%	10%	37.96	23.82	10%	36.57	21.02
41204	H	SO	Cm	SoD7 (—P)	0%	0%	40.00		10%	36.50	22.28
41111	H	SO	Cm	SoD2 (—P)	10%	13%	37.98	23.82	25%	35.18	24.46
Hamlin WT	H	SO	Cm	Control	0%	25%	35.56	26.41	55%	29.82	22.51
Marrs WT	M	SO	Cm	Control	0%	0%	39.16		33%	33.11	22.73

[1] H = Hamlin; RR = Ruby Red; M = Marrs

[2] SO = Sweet Orange; Gf = Grapefruit

[3] Cm = Cleopatra mandarin

[4] (G) = GenScript-optimized sequence; (C) = CODA-optimized sequence; (—P) = DNA 2.0-optimized sequence with no signal peptide

Example 14: Propagation and Resistance of Generation 4

A first line of Sweet Orange (2 varieties), one grapefruit, and two rootstocks were prepared to co-express (i) GenScript SoD2 with tobacco PR-1b signal peptide (SEQ ID NO: 9) and (ii) GenScript SoD7 with tobacco PR-1b signal peptide (SEQ ID NO: 10). More specifically, plants were transformed with a double defensin construct comprising, in a 5' to 3' direction SoD2, uidA, and SoD7 (13). A total of 29 transformation events were observed with another 28 GUS-positive candidates in tissue culture or just out of tissue culture. Plants confirmed to co-express SoD2 and SoD7 will be cultivated and evaluated in infection assays to determine the degree to which coexpression prevents, ameliorates, and/or treats infection.

FIG. **9** is a representation of a Southern blot (membrane was exposed to probes for both SoD2 and SoD7) showing insertion number among transgenic events in Hamlin transformed with a double defensin construct comprising SoD2 and SoD7 (0413). FIG. **10** also shows insertion number among transgenic events in Hamlin transformed with a double defensin construct comprising SoD2 and SoD7 (0413).

Rio Red plants (02) were transformed with a double defensin construct (13). FIG. **17** is a representation of a Southern blot confirming insertion of both SoD2 and SoD7 in these Rio Red plants. DNA was cut with a single restriction enzyme that cut within SoD2, uidA, and SoD7 and blotted with both SoD2 and SoD7 probes simultaneously. FIG. **18** is a representation of a northern blot showing RNA transcripts isolated from Rio Red plants (marked "02") transformed with SoD2 (GenScript-optimized sequence with signal peptide) and SoD7 (GenScript-optimized sequence with signal peptide). RNA transcripts isolated from Hamlin plants (marked "04") are also shown.

Example 15: Propagation and Resistance of Generation 5

Evaluation of coexpression of SoD2 and SoD7 is underway. A line of Sweet Orange (1 variety) was prepared to co-express (i) DNA 2.0 SoD2 with no signal peptide (SEQ ID NO: 30) and (ii) DNA 2.0 SoD7 with no signal peptide (SEQ ID NO: 31). Transformation and expression may be confirmed by Southern and northern blotting analysis. Plants may be cultivated as described herein and bacterial resistance evaluated as described. Plants confirmed to co-express SoD2 and SoD7 may be cultivated and evaluated in infection assays to determine the degree to which coexpression prevents, ameliorates, and/or treats infection.

Example 16: Expression of Defensin Constructs in Various Plants

Stable expression of defensin constructs comprising nucleic acid sequences codon-optimized for citrus has been confirmed in the following:

Cultivar	Gene Code	# Events
Rio Red Grapefruit	13	18
Ruby Red Grapefruit	11 and 12	12
Hamlin Sweet Orange	07, 08, 09, 10, 11, 12, 13, and 16	over 86
Marrs Sweet Orange	07 and 08	13
Rhode Red Valencia Orange	07, 08, 09, 10, 13	over 48
Frost Eureka Lemon	13 and 16	over 30
Frost Lisbon Lemon	13 and 16	over 33
C22 and Carrizo Citrange Rootstocks	07, 08, 13	42
Flying dragon and Swingle Rootstocks	13	Multiple GUS+

For all constructs, individual transformation events have been found spanning a range of expression levels from no expression (e.g., since Southern results demonstrate the gene is present, often in multiple copies, it may be that the transgene has been silenced) to low expression to high expression.

Example 17: Antibodies to SoD2 and SoD7

Antibodies were raised to SoD2 and SoD7. Full length SoD7 peptide was synthesized by GenScript. Aliquots of synthetic SoD7 (200 ug each time) were injected into each of 2 different rabbits every three weeks for a total of 4 injections. Sera was collected 2 weeks after the third and 2 weeks after the fourth injections. IgG was purified using a Protein A column. SoD7 specific IgG was purified by passing the IgG preparation over a column of synthetic SoD7 conjugated to agarose beads and then eluting with a low pH buffer Eluate was screened for binding to a dilution series from 1 ng to 100 ng synthetic SoD7. FIG. **19** is a Western blot illustrating binding of the purified SoD7-specific IgG antibodies to about 20 ng of SoD7 peptide in either transgenic plants (lanes 3, 4, and 6-9), non-transgenic plants spiked with synthetic SoD7 peptide (lane 5), or pure synthetic SoD7 (lane 10).

Example 18: Spinach Defensin Sequences and Codon Optimization

Spinach (*Spinacea oleracea*, viroflay) defensin gene sequences were assembled using next-generation sequencing reads deposited in NCBI sequence read archive (SRA) by employing bioinformatics tools and methods (e.g., Dohm et al., 2013, *Nature,* 505, 546-549; Yao et al., 2005, *Plant Mol. Biol,* 57, 445-460). SEQ ID NOs: 81, 82, 83, 84, 85, and 86 are specific example embodiments of assembled scaffold regions that comprise nucleic acid sequences of spinach (*Spinacia oleracea*) defensin genes. Table 6 illustrates specific example embodiments of assembled scaffold regions, nucleic acid sequences, and peptide sequences of spinach defensins.

TABLE 6

Example embodiments of assembled scaffold regions, nucleic acid sequences, and peptide sequences from Spinach (*Spinacea oleracea*, viroflay) encoding defensin genes.

Spinach Scaffold Region (SEQ ID NO)	Nucleic Acid Sequence of Defensin Gene (SEQ ID NO)	Genscript Optimized Synthetic Defensin Gene (SEQ ID NO)	VGD Optimized Synthetic Defensin Gene (SEQ ID NO)	Defensin Peptide Sequence (SEQ ID NO)
81	39	46	52	32
82	40	47	53	33
83	41	48	54	34
84	42	NA	55	35
84	43	49	56	36
85	44	50	57	37
86	45	51	58	38

SEQ ID NOs: 39, 40, 41, 42, 43, 44, and 45 are specific example embodiments of nucleic acid sequences of spinach (*Spinacia oleracea*) defensin genes, Def1, Def2, Def3, Def4, Def5, Def6, and Def7, respectively.

Nucleic acid sequences encoding defensin genes (e.g. SEQ ID NOS: 39-45) were optimized using the GenScript codon-optimization algorithm available at http://www.genscript.com/codon_opt.html. Briefly, the algorithm uses a complex sorting matrix, including transcription, translation and protein folding, to sift through over 10,000 candidate sequences to identify a predicted best sequence for expression in a given organism. SEQ ID NOs 46, 47, 48, 49, 50, and 51 are specific example embodiments of Genscript codon optimized sequences of SEQ ID NOs: 39, 40, 41, 43, 44, and 45, respectively.

Nucleic acid sequences encoding defensin genes (e.g. SEQ ID NOS: 39-45) were optimized in a two-step approach using the Visual Gene Developer (VGD) platform of Jung S and McDonald K, 2011, *BMC Bioinformatics* 12: 340-353. First, the sequences were optimized for minimum mRNA secondary structure and binding energy (Gibbs free energy [G]=−0.2 to 0 kcal/base). Next, the optimized mRNA sequences were subjected to favorable synonymous codon optimization using a pre-calculated Codon Adaptation Index (CAI) for *Citrus sinensis* (Csi). The Csi-CAI was calculated from a codon usage matrix generated using data from 116 Csi codon sequences (47126 codons) available in Kazusa codon database (www.kazusa.or.jp/codon). SEQ ID NOs 52, 53, 54, 55, 56, 57, and 58 are specific example embodiments of VGD codon optimized sequences of SEQ ID NOs: 39, 40, 41, 42, 43, 44, and 45, respectively.

Predicted mRNA secondary structures of SEQ ID NOs: 39, 40, 41, 42, 43, 44, and 45, may be constructed using the Visual Gene Developer platform of Jung S and McDonald K, 2011, *BMC Bioinformatics* 12: 340-353.

Example 19: SEQ ID NOS 32, 33, 34, 35, 36, 37, and 38 Peptide Sequence Alignment

SEQ ID NOs: 32, 33, 34, 35, 36, 37, and 38 are specific example embodiments of defensin peptide sequences from spinach (*Spinacia oleracea*).

Multiple sequence alignment of SEQ ID NO: 32 (Genomic D1), SEQ ID NO: 33 (Genomic D2), SEQ ID NO: 34 (Genomic D3), SEQ ID NO: 35 (Genomic D4), SEQ ID NO: 36 (Genomic D5), SEQ ID NO: 37 (Genomic D6), and SEQ ID NO: 38 (Genomic D7) was performed using ClustalW. FIG. **20** illustrates the resulting alignment of the spinach defensin peptides. The consensus symbols are indicated below the alignments with identically conserved residues indicated by black shading and an asterisk. Amino acids with ≥50% identity are shaded gray and marked with a period.

FIG. **21**A and FIG. **21**B illustrate the results of phylogenetic analyses of SEQ ID NOs: 32, 33, 34, 35, 36, 37, and 38. Using the sequence alignment from FIG. **20**, tree construction was performed following (A) the Neighbor Joining method as illustrated in FIG. **21**A, and (B) the Maximum Likelihood method as illustrated in FIG. **21**B.

In the neighbor joining analysis shown in FIG. **21**A, optimal tree topology with a minimum sum of branch length value settings were selected. A Bootstrap test with 1000 replicates resulted in the percentage of replicate trees in which associated taxa clustered together. These values are indicated next to their respective branches in FIG. **21**A. Branch length units indicate the number of amino acid substitutions per site, and represent evolutionary distances as computed using the Poisson correction method.

FIG. **21**B illustrates a maximum likelihood tree wherein the tree topology with the highest log likelihood is shown. The heuristic search was performed using initial tree(s) generated using the Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances under the JTT substitution model, followed by selection of a tree topology with superior log likelihood value.

Example 21: Peptide Sequence Analysis of Spinach Defensins

Multiple sequence alignment of SEQ ID NO: 32 (Genomic D1), SEQ ID NO: 33 (Genomic D2), SEQ ID NO: 34 (Genomic D3), SEQ ID NO: 35 (Genomic D4), SEQ ID NO: 36 (Genomic D5), SEQ ID NO: 37 (Genomic D6), SEQ ID NO: 38 (Genomic D7), and reported spinach defensin subfamily IV sequences (Segura D1-Segura D7) as described by Segura, A. et al., 1998, *FEBS Letters* 435: 159-162 was performed using ClustalW. FIG. **22** illustrates the resulting alignment. The consensus symbols are indicated below the alignments with identically conserved residues indicated by black shading and an asterisk. Amino acids with ≥50% identity are shaded gray and marked with a period.

Phylogenetic analyses were performed using the multiple sequence alignment illustrated in FIG. **22**. Tree construction was performed using (A) the Neighbor Joining method as illustrated in FIG. **23**A, and (B) the Maximum Likelihood method as illustrated in FIG. **23**B.

In the neighbor joining analysis shown in FIG. **23**A, optimal tree topology with a minimum sum of branch length value settings were selected. A Bootstrap test with 1000 replicates resulted in the percentage of replicate trees in which associated taxa clustered together. These values are indicated next to their respective branches in FIG. **23**A. Branch length units indicate the number of amino acid substitutions per site, and represent evolutionary distances as computed using the Poisson correction method.

FIG. **23**B illustrates a maximum likelihood tree wherein the tree topology with the highest log likelihood is shown. The heuristic search was performed using initial tree(s) generated using the Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances under the JTT substitution model, followed by selection of a tree topology with superior log likelihood value.

Example 22: Peptide Sequence Analysis of Defensins

Multiple sequence alignment was performed using ClustalW to compare the following peptide sequences: SEQ ID NO: 32 (Genomic D1); SEQ ID NO: 33 (Genomic D2); SEQ ID NO: 34 (Genomic D3); SEQ ID NO: 35 (Genomic D4); SEQ ID NO: 36 (Genomic D5); SEQ ID NO: 37 (Genomic D6); SEQ ID NO: 38 (Genomic D7); reported spinach defensin subfamily IV sequences (Segura D1-Segura D7) as described by Segura, A. et al., 1998, *FEBS Letters* 435: 159-162; representative group I defensin sequences (Rs-AFP2, At-AFP1, Hs-AFP1) as illustrated in Segura et al.; representative group II defensin sequences (Ah-Amp1), Dm-AMP1) as illustrated in Segura et al.; and representative group III defensing sequences (St-PTH1, SIalpha2) as illustrated in Segura et. al. FIG. **24** illustrates the resulting alignment. The consensus symbols are indicated below the alignments with identically conserved residues indicated by black shading and an asterisk. Amino acids with ≥50% identity are shaded gray and marked with a period.

Phylogenetic analyses were performed using the multiple sequence alignment illustrated in FIG. **24**. Tree construction was performed using (A) the Neighbor Joining method as illustrated in FIG. **25**A, and (B) the Maximum Likelihood method as illustrated in FIG. **25**B.

In the neighbor joining analysis shown in FIG. **25**A, optimal tree topology with a minimum sum of branch length value settings were selected. A Bootstrap test with 1000 replicates resulted in the percentage of replicate trees in which associated taxa clustered together. These values are indicated next to their respective branches in FIG. **25**A. Branch length units indicate the number of amino acid substitutions per site, and represent evolutionary distances as computed using the Poisson correction method.

FIG. **25**B illustrates a maximum likelihood tree wherein the tree topology with the highest log likelihood is shown. The heuristic search was performed using initial tree(s) generated using the Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances under the JTT substitution model, followed by selection of a tree topology with superior log likelihood value.

Example 23: Constructs

Table 7 illustrates specific example embodiments of chimeric nucleic acid sequences encoding a signal peptide and a defensin gene codon-optimized for citrus. Signal peptides and structural gene coding sequences shown are flanked on either side by specific restriction enzyme sites. These sequences were used to construct expression cassettes, vectors, and transformed *Agrobacterium* for preparation of transgenic plants.

TABLE 7

Example embodiments of chimeric nucleotide sequences of defensin genes. The nucleotide sequences were optimized for codon usage in Citrus.

Defensin Gene	Source of the Optimized Synthetic Gene (SEQ ID NO)	A chimeric nucleotide sequence. The 5' nucleotides include the cloning site and a preferred context for the start codon. The 3' nucleotides include the cloning site.
Def2	GenScript (47)	SEQ ID NO: 59
	VGD (53)	SEQ ID NO: 60

FIG. **26**A and FIG. **26**B illustrate specific example embodiments of expression cassettes encoding a defensin gene codon-optimized for citrus. Upstream of the defensin gene coding sequences is a promoter sequence, a translational enhancer, and a XbaI restriction enzyme site. While downstream of the defensin gene coding sequence is a KpnI restriction enzyme site, a translational enhancer, and a terminator sequence. The entire construct is flanked by the left and right borders of the Ti plasmid. FIG. **27** illustrates specific example embodiments of expression cassettes encoding a multiple defensin genes, with each defensin gene codon-optimized for citrus. FIG. **28** illustrates the potential combinations for co-expression of spinach defensins.

Example 24: Constructs

Examples of successful generation of transgenic plants achieved using the compositions and methods of the disclosure are shown in Tables 8 and 9.

TABLE 8

Citrus		
Genomic Spinach Defensin Expression Construct	Number of Transgenic Events	Variety-Citrus
Defensin 1	1	Mexican Lime
Defensin 3	1	Mexican Lime
Defensin 5	4	Mexican Lime
Defensin 6	4	Mexican Lime
Defensin 3	2	Sour Orange (root stock)
Defensin 6	2	Sour Orange (root stock)
Defensin 1	8	Frost Lisbon Lemon
Defensin 2	11	Frost Lisbon Lemon

TABLE 9

Potato		
Genomic Spinach Defensin Expression Construct	Number of Transgenic Events	Variety-Potato
Defensin 1	4	Atlantic
Defensin 2	6	Atlantic
Defensin 3	2	Atlantic
Defensin 5	8	Atlantic
Defensin 6	8	Atlantic
Defensin 7	2	Atlantic

SEQUENCE LISTING

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<210> SEQ ID NO 1
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<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(52)
<223> OTHER INFORMATION: SoD2 peptide

<400> SEQUENCE: 1

Gly Ile Phe Ser Ser Arg Lys Cys Lys Thr Pro Ser Lys Thr Phe Lys
1               5                   10                  15

Gly Ile Cys Thr Arg Asp Ser Asn Cys Asp Thr Ser Cys Arg Tyr Glu
            20                  25                  30

Gly Tyr Pro Ala Gly Asp Cys Lys Gly Ile Arg Arg Arg Cys Met Cys
        35                  40                  45

Ser Lys Pro Cys
    50


<210> SEQ ID NO 2
<211> LENGTH: 38
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(38)
<223> OTHER INFORMATION: SoD7 peptide

<400> SEQUENCE: 2

Gly Ile Phe Ser Ser Arg Lys Cys Lys Thr Pro Ser Lys Thr Phe Lys
1               5                   10                  15

Gly Tyr Cys Thr Arg Asp Ser Asn Cys Asp Thr Ser Cys Arg Tyr Glu
            20                  25                  30

Gly Tyr Pro Ala Gly Asp
        35


<210> SEQ ID NO 3
<211> LENGTH: 162
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: SoD2 codon-optimized with GenScript

<400> SEQUENCE: 3

ggtattttct catctaggaa gtgcaaaact ccttcaaaga cttttaaggg aatttgcact      60

agggattcta attgcgatac ttcttgcaga tacgagggat atccagctgg cgattgcaaa     120

ggaattagga ggagatgtat gtgttcaaag ccatgttaat aa                        162


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<220> FEATURE:
<223> OTHER INFORMATION: SoD7 codon-optimized with GenScript

<400> SEQUENCE: 4

ggaattttct cttcaaggaa gtgcaagact ccatctaaga ctttcaaggg atattgtact     60

agggattcta actgcgatac atcatgcaga tacgagggct atcctgctgg cgattaataa    120


<210> SEQ ID NO 5
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<213> ORGANISM: Artificial Sequencce
<220> FEATURE:
<223> OTHER INFORMATION: SoD2 codon-optimized with CODA

<400> SEQUENCE: 5

ggtatctttt ctagtagaaa gtgtaagact ccttctaaga cttttaaagg tatttgcact     60

agagattcta attgtgacac ttcttgtaga tatgaaggtt atcctgctgg tgattgtaag    120

ggtattagaa gaagatgtat gtgttctaag ccttgttaat ag                       162


<210> SEQ ID NO 6
<211> LENGTH: 120
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: SoD7 codon-optimized with CODA

<400> SEQUENCE: 6

ggtatttttt catctcgtaa gtgtaagact ccttctaaga cttttaaggg ttattgcact     60

agagattcta attgtgatac atcttgtaga tatgaaggtt atcctgctgg tgattaatag    120


<210> SEQ ID NO 7
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric peptide comprising a signal peptide
      and SoD2
<220> FEATURE:
<221> NAME/KEY: Signal
<222> LOCATION: (1)..(30)
<223> OTHER INFORMATION: PR-1b signal peptide
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (31)..(82)
<223> OTHER INFORMATION: SoD2 peptide

<400> SEQUENCE: 7

Met Gly Phe Phe Leu Phe Ser Gln Met Pro Ser Phe Phe Leu Val Ser
-30                 -25                 -20                 -15

Thr Leu Leu Leu Phe Leu Ile Ile Ser His Ser Ser His Ala Gly Ile
               -10                 -5              -1   1

Phe Ser Ser Arg Lys Cys Lys Thr Pro Ser Lys Thr Phe Lys Gly Ile
        5                   10                  15

Cys Thr Arg Asp Ser Asn Cys Asp Thr Ser Cys Arg Tyr Glu Gly Tyr
    20                  25                  30

Pro Ala Gly Asp Cys Lys Gly Ile Arg Arg Arg Cys Met Cys Ser Lys
35                  40                  45                  50

Pro Cys

<210> SEQ ID NO 8
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<223> OTHER INFORMATION: Chimeric peptide comprising a signal peptide
      and SoD7
<220> FEATURE:
<221> NAME/KEY: Signal
<222> LOCATION: (1)..(30)
<223> OTHER INFORMATION: PR-1b signal peptide
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (31)..(68)
<223> OTHER INFORMATION: SoD7 peptide

<400> SEQUENCE: 8

Met Gly Phe Phe Leu Phe Ser Gln Met Pro Ser Phe Phe Leu Val Ser
-30                 -25                 -20                 -15

Thr Leu Leu Leu Phe Leu Ile Ile Ser His Ser Ser His Ala Gly Ile
            -10                 -5              -1   1

Phe Ser Ser Arg Lys Cys Lys Thr Pro Ser Lys Thr Phe Lys Gly Tyr
        5                   10                  15

Cys Thr Arg Asp Ser Asn Cys Asp Thr Ser Cys Arg Tyr Glu Gly Tyr
    20                  25                  30

Pro Ala Gly Asp
35


<210> SEQ ID NO 9
<211> LENGTH: 268
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding a signal peptide
      and SoD2 codon-optimized with GenScript
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(6)
<223> OTHER INFORMATION: XbaI restriction site
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (11)..(100)
<223> OTHER INFORMATION: PR-1b signal peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (101)..(256)
<223> OTHER INFORMATION: CDS of GenScript-optimized SoD2 (07)
<220> FEATURE:
<221> NAME/KEY: misc_feture
<222> LOCATION: (263)..(268)
<223> OTHER INFORMATION: XbaI restriction site

<400> SEQUENCE: 9

tctagaaaca atgggcttct tccttttctc tcaaatgcct tcatttttcc ttgtttctac     60

tcttcttctt tttcttatta tttctcattc ttctcatgct ggtattttct catctaggaa    120

gtgcaaaact ccttcaaaga cttttaaggg aatttgcact agggattcta attgcgatac    180

ttcttgcaga tacgagggat atccagctgg cgattgcaaa ggaattagga ggagatgtat    240

gtgttcaaag ccatgttaat aatctaga                                        268


<210> SEQ ID NO 10
<211> LENGTH: 226
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding a signal peptide
      and SoD7 codon-optimized with GenScript
<220> FEATURE:
<221> NAME/KEY: misc_feature
```

```
<222> LOCATION: (1)..(6)
<223> OTHER INFORMATION: XbaI restriction site
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (11)..(100)
<223> OTHER INFORMATION: PR-1b signal peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (101)..(214)
<223> OTHER INFORMATION: CDS of GenScript-optimized SoD7 (08)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (221)..(226)
<223> OTHER INFORMATION: XbaI restriction site

<400> SEQUENCE: 10

tctagaaaca atgggtttct tcttgttttc tcaaatgcct tcattctttc ttgtttcaac     60

tttgcttctt tttcttatta tttctcattc atctcatgct ggaattttct cttcaaggaa    120

gtgcaagact ccatctaaga ctttcaaggg atattgtact agggattcta actgcgatac    180

atcatgcaga tacgagggct atcctgctgg cgattaataa tctaga                  226


<210> SEQ ID NO 11
<211> LENGTH: 268
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding a signal peptide
      and SoD2 codon-optimized with CODA
<220> FEATURE:
<221> NAME/KEY: misc-feature
<222> LOCATION: (1)..(6)
<223> OTHER INFORMATION: XbaI restriction site
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (11)..(100)
<223> OTHER INFORMATION: PR-1b signal peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (101)..(256)
<223> OTHER INFORMATION: CDS of CODA-optimized SoD2 (09)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (263)..(268)
<223> OTHER INFORMATION: Sac I, SstI restriction site

<400> SEQUENCE: 11

tctagaaaca atgggtttct ttttgttttc tcaaatgcct tcatttttcc ttgtgtctac     60

tcttcttctt tttcttatta tttctcattc ttctcatgct ggtatctttt ctagtagaaa    120

gtgtaagact ccttctaaga cttttaaagg tatttgcact agagattcta attgtgacac    180

ttcttgtaga tatgaaggtt atcctgctgg tgattgtaag ggtattagaa gaagatgtat    240

gtgttctaag ccttgttaat aggagctc                                       268


<210> SEQ ID NO 12
<211> LENGTH: 226
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding a signal peptide
      and SoD7 codon-optimized with CODA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(6)
<223> OTHER INFORMATION: XbaI restriction site
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (11)..(100)
<223> OTHER INFORMATION: PR-1b signal peptide
<220> FEATURE:
```

-continued

```
<221> NAME/KEY: misc_feature
<222> LOCATION: (101)..(214)
<223> OTHER INFORMATION: CDS of CODA-optimized SoD7 (10)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (221)..(226)
<223> OTHER INFORMATION: SacI, SstI restriction site

<400> SEQUENCE: 12

tctagaaaca atgggattct ttttgttttc tcaaatgcct tctttctttc ttgtgtctac     60

tcttcttctt tttcttatta tttctcattc ttctcatgct ggtatttttt catctcgtaa    120

gtgtaagact ccttctaaga cttttaaggg ttattgcact agagattcta attgtgatac    180

atcttgtaga tatgaaggtt atcctgctgg tgattaatag gagctc                   226


<210> SEQ ID NO 13
<211> LENGTH: 1462
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: SoD2 expression cassette comprising a chimeric
      nucleic acid encoding a signal peptide and SoD2
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(780)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (781)..(923)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (924)..(929)
<223> OTHER INFORMATION: XbaI restriction site
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (934)..(1023)
<223> OTHER INFORMATION: PR-1b signal peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1024)..(1179)
<223> OTHER INFORMATION: CDS of encodes SoD2 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1186)..(1191)
<223> OTHER INFORMATION: SacI, SstI restriction site
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1192)..(1257)
<223> OTHER INFORMATION: polylinker
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1257)..(1462)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 13

atggtggagc acgacactct cgtctactcc aagaatatca aagatacagt ctcagaagac     60

caaagggcta ttgagacttt tcaacaaagg gtaatatcgg gaaacctcct cggattccat    120

tgcccagcta tctgtcactt catcaaaagg acagtagaaa aggaaggtgg cacctacaaa    180

tgccatcatt gcgataaagg aaaggctatc gttcaagatg cctctgccga cagtggtccc    240

aaagatggac ccccacccac gaggagcatc gtggaaaaag aagacgttcc aaccacgtct    300

tcaaagcaag tggattgatg tgataacatg gtggagcacg acactctcgt ctactccaag    360

aatatcaaag atacagtctc agaagaccaa agggctattg agacttttca acaaagggta    420

atatcgggaa acctcctcgg attccattgc ccagctatct gtcacttcat caaaaggaca    480

gtagaaaagg aaggtggcac ctacaaatgc catcattgcg ataaaggaaa ggctatcgtt    540
```

```
caagatgcct ctgccgacag tggtcccaaa gatggacccc cacccacgag gagcatcgtg    600

gaaaaagaag acgttccaac cacgtcttca aagcaagtgg attgatgtga tatctccact    660

gacgtaaggg atgacgcaca atcccactat ccttcgcaag accttcctct atataaggaa    720

gttcatttca tttggagagg acacgctgaa atcaccagtc tctctctaca aatctatctc    780

aaataacaaa tctcaacaca acatatacaa aacaaacgaa tctcaagcaa tcaagcattc    840

tacttctatt gcagcaattt aaatcatttc ttttaaagca aaagcaattt tctgaaaatt    900

ttcaccattt acgaacgata gcatctagaa acaatgggct tcttcctttt ctctcaaatg    960

ccttcatttt tccttgtttc tactcttctt ctttttctta ttatttctca ttcttctcat   1020

gctggtattt tctcatctag gaagtgcaaa actccttcaa agacttttaa gggaatttgc   1080

actagggatt ctaattgcga tacttcttgc agatacgagg gatatccagc tggcgattgc   1140

aaaggaatta ggaggagatg tatgtgttca aagccatgtt aataatctag aacgcgtgaa   1200

ttcgaggcct cggatccctc gaggagctcg gtacccgggg tccgcaaaaa tcaccagtct   1260

ctctctacaa atctatctct ctctattttt ctccagaata atgtgtgagt agttcccaga   1320

taagggaatt agggttctta tagggtttcg ctcatgtgtt gagcatataa gaaaccctta   1380

gtatgtattt gtatttgtaa aatacttcta tcaataaaat ttctaattcc taaaaccaaa   1440

atccagtgac ctgcaggcat gc                                            1462
```

```
<210> SEQ ID NO 14
<211> LENGTH: 1420
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: SoD7 expression cassette comprising a chimeric
      nucleic acid encoding a signal peptide and SoD7
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(780)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (781)..(923)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (924)..(929)
<223> OTHER INFORMATION: XbaI restriction site
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (934)..(1023)
<223> OTHER INFORMATION: PR-1b signal peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1024)..(1143)
<223> OTHER INFORMATION: CDS of Encodes SoD7 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1144)..(1149)
<223> OTHER INFORMATION: SacI, SstI restriction site
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1150)..(1215)
<223> OTHER INFORMATION: polylinker
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1216)..(1420)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 14

atggtggagc acgacactct cgtctactcc aagaatatca aagatacagt ctcagaagac     60

caaagggcta ttgagacttt tcaacaaagg gtaatatcgg gaaacctcct cggattccat    120
```

```
tgcccagcta tctgtcactt catcaaaagg acagtagaaa aggaaggtgg cacctacaaa    180

tgccatcatt gcgataaagg aaaggctatc gttcaagatg cctctgccga cagtggtccc    240

aaagatggac ccccacccac gaggagcatc gtggaaaaag aagacgttcc aaccacgtct    300

tcaaagcaag tggattgatg tgataacatg gtggagcacg acactctcgt ctactccaag    360

aatatcaaag atacagtctc agaagaccaa agggctattg agacttttca acaaagggta    420

atatcgggaa acctcctcgg attccattgc ccagctatct gtcacttcat caaaaggaca    480

gtagaaaagg aaggtggcac ctacaaatgc catcattgcg ataaaggaaa ggctatcgtt    540

caagatgcct ctgccgacag tggtcccaaa gatggacccc cacccacgag gagcatcgtg    600

gaaaaagaag acgttccaac cacgtcttca aagcaagtgg attgatgtga tatctccact    660

gacgtaaggg atgacgcaca atcccactat ccttcgcaag acccttcctct atataaggaa    720

gttcatttca tttggagagg acacgctgaa atcaccagtc tctctctaca aatctatctc    780

aaataacaaa tctcaacaca acatatacaa aacaaacgaa tctcaagcaa tcaagcattc    840

tacttctatt gcagcaattt aaatcatttc ttttaaagca aaagcaattt tctgaaaatt    900

ttcaccattt acgaacgata gcatctagaa acaatgggtt tcttcttgtt ttctcaaatg    960

ccttcattct ttcttgtttc aactttgctt ctttttctta ttatttctca ttcatctcat   1020

gctggaattt tctcttcaag gaagtgcaag actccatcta agactttcaa gggatattgt   1080

actagggatt ctaactgcga tacatcatgc agatacgagg gctatcctgc tggcgattaa   1140

taatctagaa cgcgtgaatt cgaggcctcg gatccctcga ggagctcggt acccggggtc   1200

cgcaaaaatc accagtctct ctctacaaat ctatctctct ctatttttct ccagaataat   1260

gtgtgagtag ttcccagata agggaattag ggttcttata gggtttcgct catgtgttga   1320

gcatataaga aacccttagt atgtatttgt atttgtaaaa tacttctatc aataaaattt   1380

ctaattccta aaaccaaaat ccagtgacct gcaggcatgc                          1420
```

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<210> SEQ ID NO 15
<211> LENGTH: 1424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding a signal peptide
      and SoD2
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(780)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (781)..(923)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (924)..(929)
<223> OTHER INFORMATION: XbaI restriction site
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (934)..(1023)
<223> OTHER INFORMATION: PR-1b signal peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1024)..(1179)
<223> OTHER INFORMATION: CDS of Encodes SoD2 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1186)..(1191)
<223> OTHER INFORMATION: SacI, SstI restriction site
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1192)..(1219)
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<223> OTHER INFORMATION: polylinker
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1220)..(1424)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 15

atggtggagc acgacactct cgtctactcc aagaatatca aagatacagt ctcagaagac 60

caaagggcta ttgagacttt tcaacaaagg gtaatatcgg gaaacctcct cggattccat 120

tgcccagcta tctgtcactt catcaaaagg acagtagaaa aggaaggtgg cacctacaaa 180

tgccatcatt gcgataaagg aaaggctatc gttcaagatg cctctgccga cagtggtccc 240

aaagatggac ccccacccac gaggagcatc gtggaaaaag aagacgttcc aaccacgtct 300

tcaaagcaag tggattgatg tgataacatg gtggagcacg acactctcgt ctactccaag 360

aatatcaaag atacagtctc agaagaccaa agggctattg agacttttca acaaagggta 420

atatcgggaa acctcctcgg attccattgc ccagctatct gtcacttcat caaaaggaca 480

gtagaaaagg aaggtggcac ctacaaatgc catcattgcg ataaaggaaa ggctatcgtt 540

caagatgcct ctgccgacag tggtcccaaa gatggacccc cacccacgag gagcatcgtg 600

gaaaaagaag acgttccaac cacgtcttca aagcaagtgg attgatgtga tatctccact 660

gacgtaaggg atgacgcaca atcccactat ccttcgcaag accttcctct atataaggaa 720

gttcatttca tttggagagg acacgctgaa atcaccagtc tctctctaca aatctatctc 780

aaataacaaa tctcaacaca acatatacaa aacaaacgaa tctcaagcaa tcaagcattc 840

tacttctatt gcagcaattt aaatcatttc ttttaaagca aaagcaattt tctgaaaatt 900

ttcaccattt acgaacgata gcatctagaa acaatgggtt tctttttgtt ttctcaaatg 960

ccttcatttt tccttgtgtc tactcttctt ctttttctta ttatttctca ttcttctcat 1020

gctggtatct tttctagtag aaagtgtaag actccttcta agacttttaa aggtatttgc 1080

actagagatt ctaattgtga cacttcttgt agatatgaag gttatcctgc tggtgattgt 1140

aagggtatta gaagaagatg tatgtgttct aagccttgtt aataggagct cggtacccgg 1200

ggtccgcaaa aatcaccagt ctctctctac aaatctatct ctctctattt ttctccagaa 1260

taatgtgtga gtagttccca gataagggaa ttagggttct tatagggttt cgctcatgtg 1320

ttgagcatat aagaaaccct tagtatgtat ttgtatttgt aaaatacttc tatcaataaa 1380

atttctaatt cctaaaacca aaatccagtg acctgcaggc atgc 1424

<210> SEQ ID NO 16
<211> LENGTH: 1388
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding a signal peptide and SoD7
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(780)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (781)..(923)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (781)..(923)
<223> OTHER INFORMATION: XbaI restriction site
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (934)..(1023)

<223> OTHER INFORMATION: PR-1b signal peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1024)..(1137)
<223> OTHER INFORMATION: CDS of Encodes SoD7 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1144)..(1149)
<223> OTHER INFORMATION: SacI, SstI restriction site
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1150)..(1177)
<223> OTHER INFORMATION: polylinker
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1178)..(1382)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 16

atggtggagc acgacactct cgtctactcc aagaatatca aagatacagt ctcagaagac 60

caaagggcta ttgagacttt tcaacaaagg gtaatatcgg gaaacctcct cggattccat 120

tgcccagcta tctgtcactt catcaaaagg acagtagaaa aggaaggtgg cacctacaaa 180

tgccatcatt gcgataaagg aaaggctatc gttcaagatg cctctgccga cagtggtccc 240

aaagatggac ccccacccac gaggagcatc gtggaaaaag aagacgttcc aaccacgtct 300

tcaaagcaag tggattgatg tgataacatg gtggagcacg acactctcgt ctactccaag 360

aatatcaaag atacagtctc agaagaccaa agggctattg agacttttca acaaagggta 420

atatcgggaa acctcctcgg attccattgc ccagctatct gtcacttcat caaaaggaca 480

gtagaaaagg aaggtggcac ctacaaatgc catcattgcg ataaaggaaa ggctatcgtt 540

caagatgcct ctgccgacag tggtcccaaa gatggacccc cacccacgag gagcatcgtg 600

gaaaaagaag acgttccaac cacgtcttca aagcaagtgg attgatgtga tatctccact 660

gacgtaaggg atgacgcaca atcccactat ccttcgcaag accttcctct atataaggaa 720

gttcatttca tttggagagg acacgctgaa atcaccagtc tctctctaca aatctatctc 780

aaataacaaa tctcaacaca acatatacaa aacaaacgaa tctcaagcaa tcaagcattc 840

tacttctatt gcagcaattt aaatcatttc ttttaaagca aaagcaattt tctgaaaatt 900

ttcaccattt acgaacgata gcatctagaa acaatgggat tctttttgtt ttctcaaatg 960

ccttctttct ttcttgtgtc tactcttctt ctttttctta ttatttctca ttcttctcat 1020

gctggtattt tttcatctcg taagtgtaag actccttcta agacttttaa gggttattgc 1080

actagagatt ctaattgtga tacatcttgt agatatgaag gttatcctgc tggtgattaa 1140

taggagctcg gtacccgggg tccgcaaaaa tcaccagtct ctctctacaa atctatctct 1200

ctctattttt ctccagaata atgtgtgagt agttcccaga taagggaatt agggttctta 1260

tagggtttcg ctcatgtgtt gagcatataa gaaaccctta gtatgtattt gtatttgtaa 1320

aatacttcta tcaataaaat ttctaattcc taaaaccaaa atccagtgac ctgcaggcat 1380

gcgagaga 1388

<210> SEQ ID NO 17
<211> LENGTH: 780
<212> TYPE: DNA
<213> ORGANISM: Cauliflower mosaic virus
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(780)
<223> OTHER INFORMATION: CaMV 35S promoter

<400> SEQUENCE: 17

```
atggtggagc acgacactct cgtctactcc aagaatatca aagatacagt ctcagaagac     60

caaagggcta ttgagacttt tcaacaaagg gtaatatcgg gaaacctcct cggattccat    120

tgcccagcta tctgtcactt catcaaaagg acagtagaaa aggaaggtgg cacctacaaa    180

tgccatcatt gcgataaagg aaaggctatc gttcaagatg cctctgccga cagtggtccc    240

aaagatggac ccccacccac gaggagcatc gtggaaaaag aagacgttcc aaccacgtct    300

tcaaagcaag tggattgatg tgataacatg gtggagcacg acactctcgt ctactccaag    360

aatatcaaag atacagtctc agaagaccaa agggctattg agacttttca acaaagggta    420

atatcgggaa acctcctcgg attccattgc ccagctatct gtcacttcat caaaaggaca    480

gtagaaaagg aaggtggcac ctacaaatgc catcattgcg ataaaggaaa ggctatcgtt    540

caagatgcct ctgccgacag tggtcccaaa gatggacccc cacccacgag gagcatcgtg    600

gaaaaagaag acgttccaac cacgtcttca aagcaagtgg attgatgtga tatctccact    660

gacgtaaggg atgacgcaca atcccactat ccttcgcaag accttcctct atataaggaa    720

gttcatttca tttggagagg acacgctgaa atcaccagtc tctctctaca aatctatctc    780


<210> SEQ ID NO 18
<211> LENGTH: 143
<212> TYPE: DNA
<213> ORGANISM: Tobacco etch virus
<220> FEATURE:
<221> NAME/KEY: enhancer
<222> LOCATION: (1)..(143)
<223> OTHER INFORMATION: TEV 5'UTR translational enhancer

<400> SEQUENCE: 18

aaataacaaa tctcaacaca acatatacaa aacaaacgaa tctcaagcaa tcaagcattc     60

tacttctatt gcagcaattt aaatcatttc ttttaaagca aaagcaattt tctgaaaatt    120

ttcaccattt acgaacgata gca                                            143


<210> SEQ ID NO 19
<211> LENGTH: 205
<212> TYPE: DNA
<213> ORGANISM: Cauliflower mosaic virus
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1)..(205)
<223> OTHER INFORMATION: CaMV 35S terminator

<400> SEQUENCE: 19

tctctctcta caaatctatc tctctctatt tttctccaga ataatgtgtg agtagttccc     60

agataaggga attagggttc ttatagggtt tcgctcatgt gttgagcata taagaaaccc    120

ttagtatgta tttgtatttg taaaatactt ctatcaataa aatttctaat tcctaaaacc    180

aaaatccagt gacctgcagg catgc                                          205


<210> SEQ ID NO 20
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Zn5 Primer

<400> SEQUENCE: 20

ccaatgcatt gatcttcaaa tgggaatgaa t                                    31


<210> SEQ ID NO 21
```

```
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Zn6 Primer

<400> SEQUENCE: 21

aactgcagtt ctaagaccag tcaaacta                                        28


<210> SEQ ID NO 22
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Fcp Primer

<400> SEQUENCE: 22

ggcctctaga gttatggacg acgagacata gtaattgaag                           40


<210> SEQ ID NO 23
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Rcp Primer

<400> SEQUENCE: 23

gcgcgagctc gatgaaactc caccatcccg atag                                 34


<210> SEQ ID NO 24
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: GUSF Primer

<400> SEQUENCE: 24

gtagaaaccc caacccgtga                                                 20


<210> SEQ ID NO 25
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: GUSR Primer

<400> SEQUENCE: 25

gcggattcac cacttgcaaa g                                               21


<210> SEQ ID NO 26
<211> LENGTH: 83
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Variant of SoD2 comprising two additional
      N-terminal amino acids and a Gly33 deletion relative to spinach
      SoD2
<220> FEATURE:
<221> NAME/KEY: signal
<222> LOCATION: (1)..(32)
<223> OTHER INFORMATION: Modified PR-1b signal peptide
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (33)..(83)
<223> OTHER INFORMATION: Putative mature SoD2 peptide with a Gly33
      deletion relative to spinach SoD2

<400> SEQUENCE: 26
```

```
Met Gly Phe Phe Leu Phe Ser Gln Met Pro Ser Phe Phe Leu Val Ser
        -30                 -25                 -20

Thr Leu Leu Leu Phe Leu Ile Ile Ser His Ser Ser His Ala Leu Glu
    -15                 -10                 -5              -1

Gly Ile Phe Ser Ser Arg Lys Cys Lys Thr Pro Ser Lys Thr Phe Lys
1               5                   10                  15

Gly Ile Cys Thr Arg Asp Ser Asn Cys Asp Thr Ser Cys Arg Tyr Glu
            20                  25                  30

Tyr Pro Ala Gly Asp Cys Lys Gly Ile Arg Arg Arg Cys Met Cys Ser
        35                  40                  45

Lys Pro Cys
    50


<210> SEQ ID NO 27
<211> LENGTH: 265
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Variant of SoD2 comprising two additional
      N-terminal amino acids and a Gly33 deletion relative to spinach
      SoD2
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (8)..(103)
<223> OTHER INFORMATION: PR-1b signal peptide fragment
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (104)..(259)
<223> OTHER INFORMATION: CDS of Putative mature SoD2 peptide with a
      Gly33 deletion relative to spinach SoD2

<400> SEQUENCE: 27

ttaattaatg ggattctttc tcttttcaca aatgccctca ttctttcttg tgtcgacact     60

tctcttattc ctaataatat ctcactcttc tcatgcgctc gagggaatat tcagctcccg    120

caagtgtaag acgccttcaa agactttcaa agggatatgt acgagagact caaactgtga    180

cacctcatgt cgttacgaat atccggcagg agactgtaaa ggaatacgtc gcagatgtat    240

gtgtagcaag ccttgttaga ggcct                                          265


<210> SEQ ID NO 28
<211> LENGTH: 38
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Core defensin based, in part, on Sod2 and Sod7
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: Any amino acid

<400> SEQUENCE: 28

Gly Ile Phe Ser Ser Arg Lys Cys Lys Thr Pro Ser Lys Thr Phe Lys
1               5                   10                  15

Gly Xaa Cys Thr Arg Asp Ser Asn Cys Asp Thr Ser Cys Arg Tyr Glu
            20                  25                  30

Gly Tyr Pro Ala Gly Asp
        35


<210> SEQ ID NO 29
<211> LENGTH: 120
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Core defensin based, in part, on Sod2 and Sod7
```

-continued

```
<220> FEATURE:
<221> NAME/KEY: variation
<222> LOCATION: (52)..(52)
<223> OTHER INFORMATION: t, any other base, or absent (e.g., if 53 and
      54 are also absent)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (52)..(54)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: variation
<222> LOCATION: (53)..(53)
<223> OTHER INFORMATION: a, any other base, or absent (e.g., if 52 and
      54 are also absent)
<220> FEATURE:
<221> NAME/KEY: variation
<222> LOCATION: (54)..(54)
<223> OTHER INFORMATION: t, any other base, or absent (e.g., if 52 and
      53 are also absent)

<400> SEQUENCE: 29

ggaattttct cttcaaggaa gtgcaagact ccatctaaga ctttcaaggg annntgtact     60

agggattcta actgcgatac atcatgcaga tacgagggct atcctgctgg cgattaataa    120


<210> SEQ ID NO 30
<211> LENGTH: 174
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: SoD2 codon-optimized with DNA 2.0

<400> SEQUENCE: 30

tctagaatgg gaatcttcag ttcgagaaag tgtaaaaccc cctcaaaaac attcaaaggt     60

atttgcacga gagattctaa ttgcgatact agctgccgtt atgagggtta ccctgctggc    120

gactgtaagg ggataaggag gagatgtatg tgctccaagc catgttaagg tacc          174


<210> SEQ ID NO 31
<211> LENGTH: 132
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: SoD7 codon-optimized with DNA 2.0

<400> SEQUENCE: 31

tctagaatgg gtatcttctc aagcagaaag tgcaaaacac cttctaaaac ctttaaggga     60

tattgtacta gggactccaa ttgtgatacg agttgccgtt acgagggcta tccagctggg    120

gattaaggta cc                                                        132


<210> SEQ ID NO 32
<211> LENGTH: 60
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(60)
<223> OTHER INFORMATION: Def1 peptide

<400> SEQUENCE: 32

Met Gly Pro Arg Lys Ala Glu Ala Gly Ile Phe Ser Ser Arg Lys Cys
1               5                   10                  15

Lys Thr Pro Ser Lys Thr Phe Lys Gly Ile Cys Thr Arg Asp Ser Asn
            20                  25                  30

Cys Asp Thr Ser Cys Arg Tyr Glu Gly Tyr Pro Ala Gly Asp Cys Lys
        35                  40                  45
```

```
Gly Ile Arg Arg Arg Cys Leu Cys Cys Thr His Thr
    50                  55                  60


<210> SEQ ID NO 33
<211> LENGTH: 83
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(83)
<223> OTHER INFORMATION: Def2 peptide

<400> SEQUENCE: 33

Met Lys Met Ser Met Arg Ser Ile Ala Val Val Phe Leu Val Cys Leu
1               5                   10                  15

Leu Val Leu Ser Thr Glu Glu Met Gly Pro Arg Lys Ala Asp Ala Gly
            20                  25                  30

Phe Phe Ser Ser Lys Lys Cys Lys Thr Pro Ser Lys Thr Phe Arg Gly
        35                  40                  45

Pro Cys Val Arg Asn Ala Asn Cys Asp Thr Ser Cys Arg Tyr Glu Gly
    50                  55                  60

Tyr Pro Ala Gly Asp Cys Lys Gly Ile Arg Arg Arg Cys Ile Cys Cys
65                  70                  75                  80

Thr His Ala


<210> SEQ ID NO 34
<211> LENGTH: 74
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(74)
<223> OTHER INFORMATION: Def3 peptide

<400> SEQUENCE: 34

Met Lys His Phe Gly Ala Ile Phe Leu Val Leu Leu Leu Val Leu Ala
1               5                   10                  15

Thr Glu His Gly Ala Arg Val Ala Glu Ala Arg Thr Cys Glu Thr Pro
            20                  25                  30

Ser Gln Lys Phe Lys Gly Ile Cys Ile Ser Asp Ser Asn Cys Glu Ser
        35                  40                  45

Ile Cys Asn Thr Glu Gly Phe Pro Asn Gly Glu Cys Ser Gly Leu Arg
    50                  55                  60

Arg Arg Cys Ile Cys Asn Thr Pro Cys Thr
65                  70


<210> SEQ ID NO 35
<211> LENGTH: 56
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(56)
<223> OTHER INFORMATION: Def4 peptide

<400> SEQUENCE: 35

Val Ser Thr Lys Val Ala Glu Ala Arg Ile Cys Ala Ser Pro Ser Pro
1               5                   10                  15

Thr Phe Lys Gly Ile Cys Phe Ser Ser Arg Asn Cys Glu Thr Asn Cys
            20                  25                  30

Asn Ser Val Lys Phe Ser Gly Gly Ser Cys Gln Gly Phe Arg Arg Arg
        35                  40                  45
```

```
Cys Met Cys Thr Lys Pro Cys Ala
    50                  55


<210> SEQ ID NO 36
<211> LENGTH: 74
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(74)
<223> OTHER INFORMATION: Def5 peptide

<400> SEQUENCE: 36

Met Arg Pro Phe Ala Ala Leu Phe Leu Val Leu Phe Leu Val Leu Ala
1               5                   10                  15

Thr Glu Ile Gly Pro Arg Val Val Glu Ala Arg Met Cys Ser Ser Pro
            20                  25                  30

Ser His Arg Phe Lys Gly Ile Cys Thr Cys Ser Arg Asn Cys Glu Asn
        35                  40                  45

Thr Cys Asn Ser Glu Arg Phe Ser Gly Gly Glu Cys Lys Gly Phe Arg
    50                  55                  60

Arg Arg Cys Met Cys Thr Gly Pro Cys Val
65                  70


<210> SEQ ID NO 37
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(90)
<223> OTHER INFORMATION: Def6 peptide

<400> SEQUENCE: 37

Met Glu Arg Ser Ser Arg Val Phe Ser Val Val Leu Leu Met Leu Val
1               5                   10                  15

Leu Val Leu Ser Thr Asp Met Tyr Thr Asp Pro Val Ala Val Leu Ser
            20                  25                  30

Tyr Glu Ile Gly Thr Lys Val Ala Glu Ala Arg Ile Cys Glu Ser Ala
        35                  40                  45

Ser Tyr Arg Phe Lys Gly Ile Cys Val Ser Arg Ser Asn Cys Ala Asn
    50                  55                  60

Val Cys Lys Asn Glu Gly Phe Pro Gly Gly Arg Cys Arg Gly Phe Arg
65                  70                  75                  80

Arg Arg Cys Leu Cys Tyr Lys His Cys Gly
                85                  90


<210> SEQ ID NO 38
<211> LENGTH: 74
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(74)
<223> OTHER INFORMATION: Def6 peptide

<400> SEQUENCE: 38

Met Lys Pro Phe Val Ala Phe Val Leu Ala Phe Met Leu Val Leu Ala
1               5                   10                  15

Ile Glu Met Gly Pro Arg Val Ala Glu Ala Arg Met Cys Thr Asn Pro
            20                  25                  30
```

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```
Ser Arg Thr Phe Arg Gly Pro Cys Val Ser Asp Arg Asn Cys Glu Ser
        35                  40                  45

Ser Cys Met Gly Glu Gly Phe Pro Gly Gly Ser Cys His Gly Phe Arg
    50                  55                  60

Arg Lys Cys Val Cys Ser Lys Pro Cys Ala
65                  70


<210> SEQ ID NO 39
<211> LENGTH: 183
<212> TYPE: DNA
<213> ORGANISM: Spinacea oleracea
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(143)
<223> OTHER INFORMATION: Def1 nucleotide

<400> SEQUENCE: 39

atgggtccaa gaaaggcaga agctggaatt tttagctcga ggaaatgcaa aactccaagt      60

aaaacgttca agggaatatg tactagggac tccaattgtg acacttcttg taggtatgag     120

ggatatccag ctggagattg caagggtatt cgtagaagat gcttatgttg tacacatact     180

taa                                                                   183


<210> SEQ ID NO 40
<211> LENGTH: 252
<212> TYPE: DNA
<213> ORGANISM: Spinacea oleracea
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(252)
<223> OTHER INFORMATION: Def2 nucleotide

<400> SEQUENCE: 40

atgaagatgt caatgaggtc gattgctgtg gttttccttg tgtgcctact tgtcttgtca      60

acagaagaaa tgggtccaag aaaggcagac gctggatttt tcagctcgaa gaaatgcaaa     120

acaccaagta aaacattcag ggaccttgt gtaaggaacg ccaactgtga cacttcttgt      180

aggtatgagg gatatccagc tggagattgc aagggtattc gtagaagatg tatttgttgt     240

acacatgctt aa                                                         252


<210> SEQ ID NO 41
<211> LENGTH: 225
<212> TYPE: DNA
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(225)
<223> OTHER INFORMATION: Def3 nucleotide

<400> SEQUENCE: 41

atgaagcact ttggggctat atttcttgtg ttgttgcttg ttctggccac agaacatgga      60

gcaagagtag cagaagcaag aacatgtgaa actccaagtc aaaagttcaa aggaatatgt     120

attagtgact ccaattgtga atcaatttgc aataccgaag gatttcctaa tggagaatgt     180

agtggccttc gcagaagatg catttgcaac acaccatgca cttaa                    225


<210> SEQ ID NO 42
<211> LENGTH: 171
<212> TYPE: DNA
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(171)
```

<223> OTHER INFORMATION: Def4 nucleotide

<400> SEQUENCE: 42

gtaagtacaa aagtagcaga agcaaggata tgtgctagtc caagtcccac gttcaaagga 60

atatgtttta gcagcaggaa ttgtgaaact aattgcaatt ctgtgaaatt ttctggagga 120

agttgtcaag gttttcgtag aagatgtatg tgcaccaagc cttgcgctta a 171

<210> SEQ ID NO 43
<211> LENGTH: 225
<212> TYPE: DNA
<213> ORGANISM: Spinacea oleracea
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(225)
<223> OTHER INFORMATION: Def5 nucleotide

<400> SEQUENCE: 43

atgaggcctt ttgctgctct tttccttgtg ctcttccttg ttttggccac agagataggg 60

ccaagagtag tagaagcaag aatgtgttca tcaccaagtc ataggttcaa gggaatttgt 120

actagcagca ggaattgtga gaacacttgc aacagcgaac gattttcagg tggtgaatgt 180

aaaggctttc gcagaagatg tatgtgcacg ggaccctgcg tttaa 225

<210> SEQ ID NO 44
<211> LENGTH: 273
<212> TYPE: DNA
<213> ORGANISM: Spinacea oleracea
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(273)
<223> OTHER INFORMATION: Def6 nucleotide

<400> SEQUENCE: 44

atggagcgtt cttcacgtgt gttttcagtt gttcttctca tgcttgttct tgtgttgtcc 60

acagatatgt acacagaccc agtggcggtt cttagttatg agattgggac aaaggtggcg 120

gaagcaagga tatgcgaatc tgcaagttac aggttcaagg gaatatgtgt gagcaggagc 180

aactgtgcta atgtttgcaa aaatgagggt ttccccggtg gccgttgccg cggtttccgt 240

cgtcgttgcc tctgttacaa acattgcggt taa 273

<210> SEQ ID NO 45
<211> LENGTH: 225
<212> TYPE: DNA
<213> ORGANISM: Spinacea oleracea
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(225)
<223> OTHER INFORMATION: Def7 nucleotide

<400> SEQUENCE: 45

atgaagccct ttgtagcttt tgttcttgct ttcatgcttg tcttggccat agagatgggt 60

ccaagagtag cagaagcaag aatgtgcaca aatccgagta gaacattcag gggaccatgc 120

gttagtgacc ggaactgcga atcgtcgtgc atgggagagg gatttcccgg tggaagttgt 180

catggctttc gtagaaaatg cgtctgcagc aagccttgtg cttag 225

<210> SEQ ID NO 46
<211> LENGTH: 186
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def1 codon-optimized with Genscript

<400> SEQUENCE: 46

atggggccaa gaaaagccga agccgggata ttcagctcaa gaaagtgcaa gacaccctcc 60

aagacattca aaggcatctg taccagggat tctaattgcg acacctcatg tagatatgag 120

ggttaccctg ctggagattg caagggtatt aggagaaggt gtctttgctg tactcataca 180

taatga 186

<210> SEQ ID NO 47
<211> LENGTH: 198
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def2 codon-optimized with Genscript

<400> SEQUENCE: 47

atgacagagg agatgggtcc aaggaaagcc gacgctgggt tcttcagttc taaaaagtgc 60

aaaacaccaa gcaaaacatt cagaggccct tgcgttagaa atgctaactg cgatacttct 120

tgtagatatg agggttaccc agcaggagac tgcaagggta ttaggagaag gtgtatctgc 180

tgtacacatg cttaatga 198

<210> SEQ ID NO 48
<211> LENGTH: 228
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def3 codon-optimized with Genscript

<400> SEQUENCE: 48

atgaaacact tcggggctat ctttttggtg ctcctgctcg tgctcgctac tgaacatggt 60

gccagagttg ctgaggctag aacctgtgaa acccccctctc aaaagtttaa aggtatctgc 120

atctctgatt caaactgcga gagcatatgt aacacagaag gtttccctaa tggtgaatgc 180

agtggcctta ggagaaggtg catctgtaac actccatgta cataatga 228

<210> SEQ ID NO 49
<211> LENGTH: 228
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def5 codon-optimized with Genscript

<400> SEQUENCE: 49

atgagaccct tcgccgcttt gtttttggtt ttgttcttgg tgctcgctac agagattgga 60

cccagagtgg tggaggccag gatgtgttct tcacctagcc ataggtttaa gggtatttgc 120

actagcagta ggaattgcga gaacacatgt aattccgaaa gattttctgg tggagagtgc 180

aaaggcttca ggagaaggtg catgtgtacc gggccatgtg tttaatga 228

<210> SEQ ID NO 50
<211> LENGTH: 276
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def6 codon-optimized with Genscript

<400> SEQUENCE: 50

atggagagat cgtcaagagt ttttagcgtt gtgctgctta tgctggtgct ggttctgtct 60

actgatatgt ataccgaccc tgtggctgtt ctttcttatg agattggtac taaggtggct 120

-continued

gaggcaagaa tctgcgaatc tgcctcatac aggtttaagg gcatttgtgt tagcagaagt 180

aattgcgcaa acgtgtgcaa gaatgagggc tttcctggtg gaagatgcag ggggttcagg 240

agaaggtgct tgtgttataa gcattgtggt taatga 276

<210> SEQ ID NO 51
<211> LENGTH: 228
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def7 codon-optimized with Genscript

<400> SEQUENCE: 51

atgaaacctt ttgtggcttt tgtgctggct tttatgctcg ttctggctat tgaaatgggt 60

ccaagagtgg ctgaggcaag gatgtgtact aatccttcta ggacttttag gggtccatgc 120

gttagtgata ggaactgcga gtcttcatgt atgggcgaag ggtttcccgg tggatcttgc 180

catggcttca ggagaaagtg cgtgtgttct aaaccttgtg cttaatga 228

<210> SEQ ID NO 52
<211> LENGTH: 186
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def1 codon-optimized with VGD

<400> SEQUENCE: 52

atgggtccta ggaaggcaga ggctggaata tttagctcga ggaagtgcaa aaccccaagt 60

aaaacgttta agggaatttg tactagagac tccaattgtg acacttcgtg taggtatgag 120

ggatacccag ctggagattg caagggtatc aggagaaggt gcttatgctg tacacataca 180

taatag 186

<210> SEQ ID NO 53
<211> LENGTH: 198
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def2 codon-optimized with VGD

<400> SEQUENCE: 53

atgacagaag agatgggccc gagaaaagca gacgctggat tttctcatc caagaaatgc 60

aagacaccct caaaaacatt caggggacct tgtgtaagga acgctaactg tgacacttct 120

tgtaggtatg agggctatcc agctggagat tgcaagggta taaggagaag atgtatttgt 180

tgtacccatg cttaatag 198

<210> SEQ ID NO 54
<211> LENGTH: 228
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def3 codon-optimized with VGD

<400> SEQUENCE: 54

atgaagcact ttggggctat attccttgtg cttttattag tcctcgcaac ggaacatgga 60

gcaagagtag cagaagcaag aacttgtgaa acgccaagtc aaaagttcaa aggcatctgt 120

atttccgact ccaattgtga aagcatttgc aataccgaag gatttccgaa tggagaatgt 180

tctggccttc gcagaagatg catttgcaac acccttgta cttaatag 228

<210> SEQ ID NO 55
<211> LENGTH: 177
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def4 codon-optimized with VGD

<400> SEQUENCE: 55

atggtaagta caaaagttgc agaagcaagg atttgtgctt caccatctcc aacgtttaag 60

ggaatatgtt ttagtagccg taattgtgaa acgaattgca attccgtaaa attttctgga 120

ggaagttgtc agggttttag gagaagatgt atgtgcacaa agccctgcgc ttgatag 177

<210> SEQ ID NO 56
<211> LENGTH: 228
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def5 codon-optimized with VGD

<400> SEQUENCE: 56

atgagaccat ttgctgctct tttccttgtg cttttccttg tgttggctac agaaataggg 60

cccagggtgg tagaagcaag aatgtgctca agtccaagtc ataggttcaa gggcatttgc 120

acttcttcga gaaattgtga aaacacttgc aacagcgaac gattttcagg tggtgagtgt 180

aaaggctttc gcagaagatg tatgtgcacg ggaccctgtg tgtaatag 228

<210> SEQ ID NO 57
<211> LENGTH: 276
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def6 codon-optimized with VGD

<400> SEQUENCE: 57

atggagaggt cttcacgtgt gttttcagtg gttctcctta tgttggttct tgtgttgagt 60

acagatatgt acacagaccc tgtagcagtt cttagttatg aaattgggac taaggtggca 120

gaagctcgca tttgtgaatc ggcaagttac aggttcaagg gaatatgtgt gtcaaggtca 180

aactgcgcta acgtttgcaa aaatgagggt ttcccaggtg gtcgttgccg gggatttaga 240

aggcggtgcc tttgctacaa acattgcggg tagtaa 276

<210> SEQ ID NO 58
<211> LENGTH: 228
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Def7 codon-optimized with VGD

<400> SEQUENCE: 58

atgaagcctt ttgtagcttt tgttctggct ttcatgcttg ttctcgccat agagatgggt 60

ccccgggtcg ctgaggcacg gatgtgcaca aatccgagca gaacattcag ggtccctgc 120

gttagcgaca ggaactgcga atcctcatgc atgggagagg gatttccggg tggtagttgc 180

catggattta gaagaaaatg cgtttgcagc aagccttgtg cttagtaa 228

<210> SEQ ID NO 59
<211> LENGTH: 271
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding a signal peptide
and Def2 codon-optimized with Genscript

<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(6)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (14)..(70)
<223> OTHER INFORMATION: Def2 signal peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (71)..(259)
<223> OTHER INFORMATION: CDS of Genscript-optimized Def2 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (266)..(271)
<223> OTHER INFORMATION: Restriction site for KpnI

<400> SEQUENCE: 59

tctagaaaca atgaagatgt caatgaggtc gatcgctgtg gttttcttgg tgtgcctatt 60

ggtgttgtca acagaggaga tgggtccaag gaaagccgac gctgggttct tcagttctaa 120

aaagtgcaaa acaccaagca aaacattcag aggcccttgc gttagaaatg ctaactgcga 180

tacttcttgt agatatgagg gttacccagc aggagactgc aagggtatta ggagaaggtg 240

tatctgctgt acacatgctt aatgaggtac c 271

<210> SEQ ID NO 60
<211> LENGTH: 267
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding a signal peptide
and Def2 codon-optimized with VGD
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(6)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (10)..(66)
<223> OTHER INFORMATION: Def2 signal peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (67)..(255)
<223> OTHER INFORMATION: CDS of VGD-optimized Def2 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (262)..(267)
<223> OTHER INFORMATION: Restriction site for KpnI

<400> SEQUENCE: 60

tctagaatga agatgtcaat gaggtcgatc gctgtggttt tcttggtgtg cctattggtg 60

ttgtcaacag aagagatggg cccgagaaaa gcagacgctg gatttttctc atccaagaaa 120

tgcaagacac cctcaaaaac attcagggga ccttgtgtaa ggaacgctaa ctgtgacact 180

tcttgtaggt atgagggcta tccagctgga gattgcaagg gtataaggag aagatgtatt 240

tgttgtaccc atgcttaata gggtacc 267

<210> SEQ ID NO 61
<211> LENGTH: 1493
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def1
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR

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<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (899)..(1084)
<223> OTHER INFORMATION: mat_peptide: Def1 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1085)..(1090)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1091)..(1277)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1278)..(1283)
<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1302)..(1493)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 61

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac     60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct    120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg    180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc    240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt    300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact    360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt    420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt    480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg    540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac    600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg    660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc    720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca    780

aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt    840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaaacaat    900

ggggccaaga aaagccgaag ccgggatatt cagctcaaga aagtgcaaga caccctccaa    960

gacattcaaa ggcatctgta ccagggattc taattgcgac acctcatgta gatatgaggg   1020

ttaccctgct ggagattgca agggtattag gagaaggtgt ctttgctgta ctcatacata   1080

atgaggtacc tagtttctgc gtgtctttgc tttccgcttt tatgcttatt gtaatatata   1140

tgaatagcta tttacagtgg gacttggtct tgtgttgaat agtatcttat atgttttaat   1200

atgtcttatt agtctcatta cttaggcgaa cgacaaagtg aggttacctc ggtctaactc   1260

tcctatgtag tgcgagaccc ggggtccgca aaaatcacca gtctctctct acaaatctat   1320

ctctctctat ttttctccag aataatgtgt gagtagttcc cagataaggg aattagggtt   1380

cttatagggt ttcgctcatg tgttgagcat ataagaaacc cttagtatgt atttgtattt   1440

gtaaaatact tctatcaata aaatttctaa ttcctaaaac caaaatccag tga          1493
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<210> SEQ ID NO 62
<211> LENGTH: 1505
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def2
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (899)..(1096)
<223> OTHER INFORMATION: mat_peptide: Def2 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1097)..(1102)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1103)..(1289)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1290)..(1295)
<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1314)..(1505)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 62

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac 60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct 120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg 180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc 240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt 300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact 360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt 420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt 480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg 540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac 600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg 660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc 720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca 780

aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt 840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaaacaat 900

gacagaggag atgggtccaa ggaaagccga cgctgggttc ttcagttcta aaaagtgcaa 960

aacaccaagc aaaacattca gaggcccttg cgttagaaat gctaactgcg atacttcttg 1020

tagatatgag ggttacccag caggagactg caagggtatt aggagaaggt gtatctgctg 1080

tacacatgct taatgaggta cctagtttct gcgtgtcttt gctttccgct tttatgctta 1140 ttgtaatata tatgaatagc tatttacagt gggacttggt cttgtgttga atagtatctt 1200

atatgtttta atatgtctta ttagtctcat tacttaggcg aacgacaaag tgaggttacc 1260

tcggtctaac tctcctatgt agtgcgagac ccggggtccg caaaaatcac cagtctctct 1320

ctacaaatct atctctctct atttttctcc agaataatgt gtgagtagtt cccagataag 1380

ggaattaggg ttcttatagg gtttcgctca tgtgttgagc atataagaaa cccttagtat 1440

gtatttgtat ttgtaaaata cttctatcaa taaaatttct aattcctaaa accaaaatcc 1500

agtga 1505

<210> SEQ ID NO 63
<211> LENGTH: 1535
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def3
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5'UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (899)..(1126)
<223> OTHER INFORMATION: mat_peptide: Def3 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1127)..(1132)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1133)..(1319)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1320)..(1325)
<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1344)..(1535)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 63

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac 60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct 120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg 180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc 240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt 300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact 360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt 420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt 480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg 540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac 600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg 660 tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc 720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca 780

aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt 840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaaacaat 900

gaaacacttc ggggctatct ttttggtgct cctgctcgtg ctcgctactg aacatggtgc 960

cagagttgct gaggctagaa cctgtgaaac cccctctcaa aagtttaaag gtatctgcat 1020

ctctgattca aactgcgaga gcatatgtaa cacagaaggt ttccctaatg gtgaatgcag 1080

tggccttagg agaaggtgca tctgtaacac tccatgtaca taatgaggta cctagtttct 1140

gcgtgtcttt gctttccgct tttatgctta ttgtaatata tatgaatagc tatttacagt 1200

gggacttggt cttgtgttga atagtatctt atatgtttta atatgtctta ttagtctcat 1260

tacttaggcg aacgacaaag tgaggttacc tcggtctaac tctcctatgt agtgcgagac 1320

ccggggtccg caaaaatcac cagtctctct ctacaaatct atctctctct attttctcc 1380

agaataatgt gtgagtagtt cccagataag ggaattaggg ttcttatagg gtttcgctca 1440

tgtgttgagc atataagaaa cccttagtat gtatttgtat ttgtaaaata cttctatcaa 1500

taaaatttct aattcctaaa accaaaatcc agtga 1535

<210> SEQ ID NO 64
<211> LENGTH: 1535
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def5
<220> FEATURE:
<221> NAME/KEY: Promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (899)..(1126)
<223> OTHER INFORMATION: mat_peptide: Def5 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1127)..(1132)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1133)..(1319)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1320)..(1325)
<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1344)..(1535)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 64

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac 60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct 120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg 180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc 240

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cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt    300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact    360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt    420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt    480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg    540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac    600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg    660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc    720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca    780

aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt    840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaaacaat    900

gagacccttc gccgctttgt ttttggtttt gttcttggtg ctcgctacag agattggacc    960

cagagtggtg gaggccagga tgtgttcttc acctagccat aggtttaagg gtatttgcac   1020

tagcagtagg aattgcgaga acacatgtaa ttccgaaaga ttttctggtg gagagtgcaa   1080

aggcttcagg agaaggtgca tgtgtaccgg gccatgtgtt taatgaggta cctagtttct   1140

gcgtgtcttt gctttccgct tttatgctta ttgtaatata tatgaatagc tatttacagt   1200

gggacttggt cttgtgttga atagtatctt atatgtttta atatgtctta ttagtctcat   1260

tacttaggcg aacgacaaag tgaggttacc tcggtctaac tctcctatgt agtgcgagac   1320

ccggggtccg caaaaatcac cagtctctct ctacaaatct atctctctct atttttctcc   1380

agaataatgt gtgagtagtt cccagataag ggaattaggg ttcttatagg gtttcgctca   1440

tgtgttgagc atataagaaa cccttagtat gtatttgtat ttgtaaaata cttctatcaa   1500

taaaatttct aattcctaaa accaaaatcc agtga                               1535


<210> SEQ ID NO 65
<211> LENGTH: 1583
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def6
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (899)..(1174)
<223> OTHER INFORMATION: mat_peptide: Def6 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1175)..(1180)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1181)..(1367)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1368)..(1373)
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<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1392)..(1583)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 65

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac     60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct    120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg    180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc    240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt    300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact    360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt    420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt    480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg    540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac    600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg    660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc    720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca    780

aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt    840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaaacaat    900

ggagagatcg tcaagagttt ttagcgttgt gctgcttatg ctggtgctgg ttctgtctac    960

tgatatgtat accgaccctg tggctgttct ttcttatgag attggtacta aggtggctga   1020

ggcaagaatc tgcgaatctg cctcatacag gtttaagggc atttgtgtta gcagaagtaa   1080

ttgcgcaaac gtgtgcaaga atgagggctt tcctggtgga agatgcaggg ggttcaggag   1140

aaggtgcttg tgttataagc attgtggtta atgaggtacc tagtttctgc gtgtctttgc   1200

tttccgcttt tatgcttatt gtaatatata tgaatagcta tttacagtgg gacttggtct   1260

tgtgttgaat agtatcttat atgttttaat atgtcttatt agtctcatta cttaggcgaa   1320

cgacaaagtg aggttacctc ggtctaactc tcctatgtag tgcgagaccc ggggtccgca   1380

aaaatcacca gtctctctct acaaatctat ctctctctat tttctccag aataatgtgt   1440

gagtagttcc cagataaggg aattagggtt cttatagggt ttcgctcatg tgttgagcat   1500

ataagaaacc cttagtatgt atttgtattt gtaaaatact tctatcaata aaatttctaa   1560

ttcctaaaac caaaatccag tga                                          1583


<210> SEQ ID NO 66
<211> LENGTH: 1535
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def7
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (899)..(1126)
<223> OTHER INFORMATION: mat_peptide: Def7 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1127)..(1132)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1133)..(1319)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1320)..(1325)
<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1344)..(1535)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 66

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac 60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct 120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg 180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc 240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt 300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact 360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt 420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt 480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg 540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac 600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg 660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc 720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca 780

aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt 840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaaacaat 900

gaaacctttt gtggcttttg tgctggcttt tatgctcgtt ctggctattg aaatgggtcc 960

aagagtggct gaggcaagga tgtgtactaa tccttctagg acttttaggg gtccatgcgt 1020

tagtgatagg aactgcgagt cttcatgtat gggcgaaggg tttcccggtg gatcttgcca 1080

tggcttcagg agaaagtgcg tgtgttctaa accttgtgct taatgaggta cctagtttct 1140

gcgtgtcttt gctttccgct tttatgctta ttgtaatata tatgaatagc tatttacagt 1200

gggacttggt cttgtgttga atagtatctt atatgtttta atatgtctta ttagtctcat 1260

tacttaggcg aacgacaaag tgaggttacc tcggtctaac tctcctatgt agtgcgagac 1320

ccggggtccg caaaaatcac cagtctctct ctacaaatct atctctctct atttttctcc 1380

agaataatgt gtgagtagtt cccagataag ggaattaggg ttcttatagg gtttcgctca 1440

tgtgttgagc atataagaaa cccttagtat gtatttgtat ttgtaaaata cttctatcaa 1500

taaaatttct aattcctaaa accaaaatcc agtga 1535

<210> SEQ ID NO 67

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<211> LENGTH: 1489
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def1
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (895)..(1080)
<223> OTHER INFORMATION: mat_peptide: Def1 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1081)..(1086)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1087)..(1273)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1274)..(1279)
<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1298)..(1489)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 67

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac 60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct 120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg 180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc 240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt 300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact 360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt 420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt 480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg 540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac 600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg 660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc 720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca 780

aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt 840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaatgggt 900

cctaggaagg cagaggctgg aatatttagc tcgaggaagt gcaaaacccc aagtaaaacg 960

tttaagggaa tttgtactag agactccaat tgtgacactt cgtgtaggta tgagggatac 1020

ccagctggag attgcaaggg tatcaggaga aggtgcttat gctgtacaca tacataatag 1080

ggtacctagt ttctgcgtgt ctttgctttc cgcttttatg cttattgtaa tatatatgaa 1140

tagctattta cagtgggact tggtcttgtg ttgaatagta tcttatatgt tttaatatgt 1200

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cttattagtc tcattactta ggcgaacgac aaagtgaggt tacctcggtc taactctcct   1260

atgtagtgcg agacccgggg tccgcaaaaa tcaccagtct ctctctacaa atctatctct   1320

ctctattttt ctccagaata atgtgtgagt agttcccaga taagggaatt agggttctta   1380

tagggtttcg ctcatgtgtt gagcatataa gaaaccctta gtatgtattt gtatttgtaa   1440

aatacttcta tcaataaaat ttctaattcc taaaaccaaa atccagtga               1489


<210> SEQ ID NO 68
<211> LENGTH: 1501
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def2
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (895)..(1092)
<223> OTHER INFORMATION: mat_peptide: Def2 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1093)..(1098)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1099)..(1285)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1286)..(1291)
<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1310)..(1501)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 68

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac     60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct    120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg    180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc    240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt    300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact    360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt    420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt    480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg    540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac    600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg    660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc    720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca    780
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aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt 840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaatgaca 900

gaagagatgg gcccgagaaa agcagacgct ggatttttct catccaagaa atgcaagaca 960

ccctcaaaaa cattcagggg accttgtgta aggaacgcta actgtgacac ttcttgtagg 1020

tatgagggct atccagctgg agattgcaag ggtataagga gaagatgtat ttgttgtacc 1080

catgcttaat agggtaccta gtttctgcgt gtctttgctt tccgctttta tgcttattgt 1140

aatatatatg aatagctatt tacagtggga cttggtcttg tgttgaatag tatcttatat 1200

gttttaatat gtcttattag tctcattact taggcgaacg acaaagtgag gttacctcgg 1260

tctaactctc ctatgtagtg cgagacccgg ggtccgcaaa aatcaccagt ctctctctac 1320

aaatctatct ctctctattt ttctccagaa taatgtgtga gtagttccca gataagggaa 1380

ttagggttct tatagggttt cgctcatgtg ttgagcatat aagaaaccct tagtatgtat 1440

ttgtatttgt aaaatacttc tatcaataaa atttctaatt cctaaaacca aaatccagtg 1500

a 1501

<210> SEQ ID NO 69
<211> LENGTH: 1531
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def3
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (895)..(1122)
<223> OTHER INFORMATION: mat_peptide: Def3 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1123)..(1128)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1129)..(1315)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1316)..(1321)
<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1340)..(1531)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 69

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac 60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct 120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg 180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc 240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt 300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact 360 tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt 420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt 480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg 540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac 600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg 660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc 720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca 780

aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt 840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaatgaag 900

cactttgggg ctatattcct tgtgctttta ttagtcctcg caacggaaca tggagcaaga 960

gtagcagaag caagaacttg tgaaacgcca agtcaaaagt tcaaaggcat ctgtatttcc 1020

gactccaatt gtgaaagcat ttgcaatacc gaaggatttc cgaatggaga atgttctggc 1080

cttcgcagaa gatgcatttg caacacccct tgtacttaat agggtaccta gtttctgcgt 1140

gtctttgctt tccgctttta tgcttattgt aatatatatg aatagctatt tacagtggga 1200

cttggtcttg tgttgaatag tatcttatat gttttaatat gtcttattag tctcattact 1260

taggcgaacg acaaagtgag gttacctcgg tctaactctc ctatgtagtg cgagacccgg 1320

ggtccgcaaa aatcaccagt ctctctctac aaatctatct ctctctattt ttctccagaa 1380

taatgtgtga gtagttccca gataagggaa ttagggttct tatagggttt cgctcatgtg 1440

ttgagcatat aagaaaccct tagtatgtat ttgtatttgt aaaatacttc tatcaataaa 1500

atttctaatt cctaaaacca aaatccagtg a 1531

<210> SEQ ID NO 70
<211> LENGTH: 1480
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def4
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (895)..(1071)
<223> OTHER INFORMATION: mat_peptide: Def4 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1072)..(1077)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1078)..(1264)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1265)..(1270)
<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1289)..(1480)

<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 70

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac 60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct 120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg 180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc 240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt 300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact 360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt 420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt 480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg 540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac 600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg 660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc 720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca 780

aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt 840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaatggta 900

agtacaaaag ttgcagaagc aaggatttgt gcttcaccat ctccaacgtt taagggaata 960

tgttttagta gccgtaattg tgaaacgaat tgcaattccg taaaattttc tggaggaagt 1020

tgtcagggtt ttaggagaag atgtatgtgc acaaagccct gcgcttgata gggtacctag 1080

tttctgcgtg tctttgcttt ccgcttttat gcttattgta atatatatga atagctattt 1140

acagtgggac ttggtcttgt gttgaatagt atcttatatg ttttaatatg tcttattagt 1200

ctcattactt aggcgaacga caaagtgagg ttacctcggt ctaactctcc tatgtagtgc 1260

gagacccggg gtccgcaaaa atcaccagtc tctctctaca aatctatctc tctctatttt 1320

tctccagaat aatgtgtgag tagttcccag ataagggaat tagggttctt atagggtttc 1380

gctcatgtgt tgagcatata agaaaccctt agtatgtatt tgtatttgta aaatacttct 1440

atcaataaaa tttctaattc ctaaaaccaa aatccagtga 1480

<210> SEQ ID NO 71
<211> LENGTH: 1531
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def5
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (895)..(1122)
<223> OTHER INFORMATION: mat_peptide: Def5 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature

<222> LOCATION: (1123)..(1128)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1129)..(1315)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1316)..(1321)
<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1340)..(1531)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 71

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cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac     60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct    120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg    180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc    240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt    300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact    360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt    420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt    480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg    540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac    600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg    660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc    720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca    780

aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt    840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaatgaga    900

ccatttgctg ctcttttcct tgtgcttttc cttgtgttgg ctacagaaat agggcccagg    960

gtggtagaag caagaatgtg ctcaagtcca agtcataggt tcaagggcat ttgcacttct   1020

tcgagaaatt gtgaaaacac ttgcaacagc gaacgatttt caggtggtga gtgtaaaggc   1080

tttcgcagaa gatgtatgtg cacgggaccc tgtgtgtaat agggtaccta gtttctgcgt   1140

gtctttgctt tccgctttta tgcttattgt aatatatatg aatagctatt tacagtggga   1200

cttggtcttg tgttgaatag tatcttatat gttttaatat gtcttattag tctcattact   1260

taggcgaacg acaaagtgag gttacctcgg tctaactctc ctatgtagtg cgagacccgg   1320

ggtccgcaaa aatcaccagt ctctctctac aaatctatct ctctctattt ttctccagaa   1380

taatgtgtga gtagttccca gataagggaa ttagggttct tatagggttt cgctcatgtg   1440

ttgagcatat aagaaaccct tagtatgtat ttgtatttgt aaaatacttc tatcaataaa   1500

atttctaatt cctaaaacca aaatccagtg a                                  1531
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<210> SEQ ID NO 72
<211> LENGTH: 1579
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def6
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)

<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (895)..(1170)
<223> OTHER INFORMATION: mat_peptide: Def6 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1171)..(1176)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1177)..(1363)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1364)..(1369)
<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1388)..(1579)
<223> OTHER INFORMATION: 5ST

<400> SEQUENCE: 72

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac 60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct 120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg 180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc 240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt 300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact 360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt 420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt 480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg 540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac 600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg 660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc 720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca 780

aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt 840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaatggag 900

aggtcttcac gtgtgttttc agtggttctc cttatgttgg ttcttgtgtt gagtacagat 960

atgtacacag accctgtagc agttcttagt tatgaaattg ggactaaggt ggcagaagct 1020

cgcatttgtg aatcggcaag ttacaggttc aagggaatat gtgtgtcaag gtcaaactgc 1080

gctaacgttt gcaaaaatga gggtttccca ggtggtcgtt gccggggatt tagaaggcgg 1140

tgcctttgct acaaacattg cgggtagtaa ggtacctagt ttctgcgtgt ctttgctttc 1200

cgcttttatg cttattgtaa tatatatgaa tagctattta cagtgggact tggtcttgtg 1260

ttgaatagta tcttatatgt tttaatatgt cttattagtc tcattactta ggcgaacgac 1320

aaagtgaggt tacctcggtc taactctcct atgtagtgcg agacccgggg tccgcaaaaa 1380

tcaccagtct ctctctacaa atctatctct ctctattttt ctccagaata atgtgtgagt 1440 agttcccaga taagggaatt agggttctta tagggtttcg ctcatgtgtt gagcatataa 1500

gaaaccctta gtatgtattt gtatttgtaa aatacttcta tcaataaaat ttctaattcc 1560

taaaaccaaa atccagtga 1579

<210> SEQ ID NO 73
<211> LENGTH: 1531
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Chimeric nucleic acid encoding Def7
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: 35SP
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (758)..(888)
<223> OTHER INFORMATION: TEV 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (889)..(894)
<223> OTHER INFORMATION: Restriction site for XbaI
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (895)..(1122)
<223> OTHER INFORMATION: mat_peptide: Def7 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1123)..(1128)
<223> OTHER INFORMATION: Restriction site for KpnI
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1129)..(1315)
<223> OTHER INFORMATION: TEV 3' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1316)..(1321)
<223> OTHER INFORMATION: Restriction site for SmaI
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1340)..(1531)
<223> OTHER INFORMATION: 35ST

<400> SEQUENCE: 73

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac 60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct 120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg 180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc 240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt 300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact 360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt 420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt 480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg 540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac 600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg 660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc 720

ctctatataa ggaagttcat ttcatttgga gaggaccctc aacacaacat atacaaaaca 780

aacgaatctc aagcaatcaa gcattctact tctattgcag caatttaaat catttctttt 840

aaagcaaaag caattttctg aaaattttca ccatttacga acgatagctc tagaatgaag 900 cctttgtag cttttgttct ggctttcatg cttgttctcg ccatagagat gggtccccgg 960

gtcgctgagg cacggatgtg cacaaatccg agcagaacat tcaggggtcc ctgcgttagc 1020

gacaggaact gcgaatcctc atgcatggga gagggatttc cgggtggtag ttgccatgga 1080

tttagaagaa aatgcgtttg cagcaagcct tgtgcttagt aaggtaccta gtttctgcgt 1140

gtctttgctt tccgctttta tgcttattgt aatatatatg aatagctatt tacagtggga 1200

cttggtcttg tgttgaatag tatcttatat gttttaatat gtcttattag tctcattact 1260

taggcgaacg acaaagtgag gttacctcgg tctaactctc ctatgtagtg cgagacccgg 1320

ggtccgcaaa aatcaccagt ctctctctac aaatctatct ctctctattt ttctccagaa 1380

taatgtgtga gtagttccca gataagggaa ttagggttct tatagggttt cgctcatgtg 1440

ttgagcatat aagaaaccct tagtatgtat ttgtatttgt aaaatacttc tatcaataaa 1500

atttctaatt cctaaaacca aaatccagtg a 1531

<210> SEQ ID NO 74
<211> LENGTH: 754
<212> TYPE: DNA
<213> ORGANISM: Cauliflower mosaic virus
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(754)
<223> OTHER INFORMATION: CaMV 35S promoter

<400> SEQUENCE: 74

cctgcaggtc aacatggtgg agcacgacac acttgtctac tccaaaaata tcaaagatac 60

agtctcagaa gaccaaaggg caattgagac ttttcaacaa agggtaatat ccggaaacct 120

cctcggattc cattgcccag ctatctgtca ctttattgtg aagatagtgg aaaaggaagg 180

tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag atgcctctgc 240

cgacagtggt cccaaagatg gacccccacc cacgaggagc atcgtggaaa aagaagacgt 300

tccaaccacg tcttcaaagc aagtggattg atgtgataac atggtggagc acgacacact 360

tgtctactcc aaaaatatca aagatacagt ctcagaagac caaagggcaa ttgagacttt 420

tcaacaaagg gtaatatccg gaaacctcct cggattccat tgcccagcta tctgtcactt 480

tattgtgaag atagtggaaa aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg 540

aaaggccatc gttgaagatg cctctgccga cagtggtccc aaagatggac ccccacccac 600

gaggagcatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag tggattgatg 660

tgatatctcc actgacgtaa gggatgacgc acaatcccac tatccttcgc aagacccttc 720

ctctatataa ggaagttcat ttcatttgga gagg 754

<210> SEQ ID NO 75
<211> LENGTH: 131
<212> TYPE: DNA
<213> ORGANISM: Tobacco etch virus
<220> FEATURE:
<221> NAME/KEY: enhancer
<222> LOCATION: (1)..(131)
<223> OTHER INFORMATION: TEV 5'UTR translational enhancer

<400> SEQUENCE: 75

ctcaacacaa catatacaaa acaaacgaat ctcaagcaat caagcattct acttctattg 60

cagcaattta aatcatttct tttaaagcaa aagcaatttt ctgaaaattt tcaccattta 120

cgaacgatag c 131

<210> SEQ ID NO 76
<211> LENGTH: 187
<212> TYPE: DNA
<213> ORGANISM: Tobacco etch virus
<220> FEATURE:
<221> NAME/KEY: enhancer
<222> LOCATION: (1)..(187)
<223> OTHER INFORMATION: TEV 3'UTR translational enhancer

<400> SEQUENCE: 76

tagtttctgc gtgtctttgc tttccgcttt tatgcttatt gtaatatata tgaatagcta 60

tttacagtgg gacttggtct tgtgttgaat agtatcttat atgttttaat atgtcttatt 120

agtctcatta cttaggcgaa cgacaaagtg aggttacctc ggtctaactc tcctatgtag 180

tgcgaga 187

<210> SEQ ID NO 77
<211> LENGTH: 192
<212> TYPE: DNA
<213> ORGANISM: Cauliflower mosaic virus
<220> FEATURE:
<221> NAME/KEY: terminator
<222> LOCATION: (1)..(192)
<223> OTHER INFORMATION: CaMV 35S terminator

<400> SEQUENCE: 77

tctctctcta caaatctatc tctctctatt tttctccaga ataatgtgtg agtagttccc 60

agataaggga attagggttc ttatagggtt tcgctcatgt gttgagcata taagaaaccc 120

ttagtatgta tttgtatttg taaaatactt ctatcaataa aatttctaat tcctaaaacc 180

aaaatccagt ga 192

<210> SEQ ID NO 78
<211> LENGTH: 1682
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(1682)
<223> OTHER INFORMATION: PHT4;6 promoter

<400> SEQUENCE: 78

caaagatgga aattctaaaa accactccct gcaatttctt atgtttcgtt tttagctcta 60

tatttttccg ttttgtattt agtatttagg gtttaaggtt tgctttttaa atgtttgatc 120

tatgagttat caaatggttg tttgatctta tgaatataag ttataagtag taaaaaaaaa 180

atttagctgt tttatctatg aatttaattc aatttatgtt tagtacgtaa tctataaatt 240

tgactcaatt tatgtgcctt acactagtct aaaaataaaa gaattaccca caaatcaaaa 300

aaaattaagc taattagatc aaaattatga ttaagtaagt gattagaaaa gataacatta 360

taatctcaac atcaaggtgc tgtggtgtag tggttatcac gtttgcctta cacgcaaaag 420

gtctccagtt cgatcctggg cagcaccata tttttttata cctattcccc tctttttttc 480

acccgttaat taataaaata agaaatggcc gttacgtgat ttatctcacg gacataaaaa 540

tatcagcatc gtcgtcgttg accctaaaaa gcgatctcca tcatcttctt ttgtttcttc 600

taaattcttt cacaaaccct aaaattctcc tccgtcactg tcgacgacca ctgcgtttca 660

cactactctc tctctcgctc tctccaccgt taaacttcaa tacccatttg tcatttcccc 720

caaatctctc cgatttctta aatctaattt ggatttactt tgcctgtaaa accattcgca 780

ttgttacgca tccgattttg cagttcgaaa ctcgagttca acttcaattt gaggtagatt 840

-continued

tcgagaaaaa gctgaagaat ttcggaacaa ctaaggtaaa gctttgtgat tttgacttcg 900

gttttcgatt tacattgtga agactgaaga agagatatag gcaacacatt ccactgtgta 960

attcggctgc ttgatgctta attttaagat ttcttcttgg gttctcgttt ctttggtact 1020

taagtttaat tgaaagaaag cttggatttt ttgcgtctgt aaaacgaaat tgagtctctg 1080

tgataacatt ggaatcgtaa ttcattagga attaggattg ttgatccttc aatttagaac 1140

caatatgatt acgttatggc ttttgggaca aattcatttg cttgatacga acttttactt 1200

cagatttatt cttatttttt aagatctgtt tatctttatc ttttgatgtc atatttagga 1260

tatgttctta tcttctgtgt tgaaggattt gacttaattt tactttctag atgccttctt 1320

gtatgattgg agaagcgtaa gattgtgtat ttttaggatg cctaattgaa aatggataaa 1380

gttgtgttac ttatacctct ctcatatata tctcaacaga ggaacgtatt gggtttgagt 1440

ctattttgtt aatgatcaga ggagaattca tcagtcatat agaatcgtcc ctgcaagttt 1500

tgtgttaaca tgtatcacaa taagcaaatt aaactgcttt gaatatgtca ttgcagattt 1560

taacggtgga attggggagt cttgaagctt atttttcctc ctggtctctt ttttcttatg 1620

tggtggtgct tgagagggtt tttgtatgat ataaatgctc tagatcagag aaaaggtcta 1680

ac 1682

<210> SEQ ID NO 79
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(1000)
<223> OTHER INFORMATION: PHT4;2 promoter

<400> SEQUENCE: 79

atatcttgag aaacacgagc aatttctcat aaatgcctaa tagtttagcc gtttaggcat 60

ctcatgatct cactgtaaac tattaggata gttacacata cacttaaata atagttacac 120

atacatctaa tattttgaaa atcctttata ttctatgaat tatccacacc aaatgacatc 180

atgtgtgact gtataaatac gactacaaat ctatgtaacc tataccaatt acaaatatgt 240

ttttctatgt ttaatagcta taccgtttgt gtgtgatata tatgattagt tacattaaga 300

tactttaaca caattctaga tttctagtgc aatgcagtta tcaaatactt ctgattttga 360

attgacaaag cgacttaaaa acgattgatt gtaaaacaac ttaccacatg gcaagcacac 420

tcctaaacgc atcgaacaaa tccataaact gcatcataca tacaacaaat ccaatggctt 480

tgtcattagg atcactaccg tagcaccagt tggggcatag tgaaatacaa atgccttttt 540

cttatgtcat tgtcttaaac agacatgacc atctctctaa tttacgacta ctttttcctt 600

tttgggcttt gaatgaatca cgctttcaaa taattgggct gcttctttct ttcccatttt 660

agaccaattt caaagacaaa aaataaaact agcaattgct aaccgaaact ccggtatccc 720

ggttaacccg ttgtaggtgg ggctgacgtg ggtgcaatca ctttgtcata tcaacacatc 780

acgtgtctcc acgtaggatg cagcagaaac tatttactac attgactaaa ataccccttca 840

ccaccaaaca ccaccagcac acgaaacttt catacgtttc tttcatggcg gattcgctct 900

ctcgctgaaa ctctctctct ctctcgttac tccaaccact cctaattatt cacatcatta 960

ttggcatgaa aagttaatct ttcctatata acaattatta 1000

<210> SEQ ID NO 80
<211> LENGTH: 2418

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<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: promoter
<222> LOCATION: (1)..(2418)
<223> OTHER INFORMATION: TPS-Cin promoter

<400> SEQUENCE: 80

tcatggcaca tcgaggagaa actgtttcct tgtggtaatc ctttataatc tctgttgcta      60

ggaggagatt tttcattaat agtctatctt tcacaaaggc agattgattt gaagagatga     120

acttgggaag aatgattttg agtctgtttg caagaatctt cgatatcacc ttatagagaa     180

cattacagca tgatatcggt ctatagtcct tcatcatcac agcttctttt ctcttgggta     240

tcaaggccaa aatagtggag tttactcctt tgggtaggaa gcctgtctta aaaaaagatt     300

ggatggctac cacaaaatcg tttcctacta tcgaccatgt ctcgttaaag aactcacaag     360

tatatccgtc agggcctggg gatttatttg aaggcattga gaagagaact ttccgcacct     420

cctctgcagt gacttctagt gtgagcttgt cttgtcattc tcatcacatc tataatccag     480

tagagtttcc agttcctccc gcgaccaatc cacgtagtct ggcggtttga gcgttaaaaa     540

gtctctgaag tatcgaactg cctctgcttt tatttgctgc tgatttgatg caatatgtcc     600

atcatcacac ttaatctctc taacattgtt acgaacctcc cgaatctttg cagcattgta     660

gaaagtttta ttattttggt ctcctatctt catccaatgc agttttgctt tttgcctaag     720

gtagctttcc tcaatacccg acagccttaa ccacttctca tatgcgtccg cttcagctac     780

cactgcctgt gaagatggcc ttgtcatagt ttctgcttgc ttttcacata aagttttata     840

ggcttctttt gctttttttg agatatcacc aagtaactgc ttccccatct ttctgaaatg     900

tggcttcaga ccttttaatt tttttgataa gcggtgcatg gctgaggtag aatgaaagag     960

aggctgagtt gtcttccaaa gctcttctgt ctcacttctg aaatccgaat acgaaattaa    1020

agcatttata aatttaaaag gcctcttgac tcgttgttcc tgctccataa tatagaatcg    1080

acatcttagg tgatctgaac aaccgcctga ttcaaagacg ctgtaggact gttcatacta    1140

ttgcatccat tgcttgctaa tcagtaccct atccagcttc ttacatatta ctccttcctt    1200

tctcttgtta caccatgtgt atctctggcc ttggtagctc atatctgtta attcacaatg    1260

tctgattaag tcttgaaaat ctctcatccc ttggagaacg aatggagatg attcatagag    1320

tgaatggtcc tctccttcta atatctcatt aaagtctcca catattaacc aagctttgtt    1380

atagaacaaa ggggaatcat gatgatattt aatatcactc cacaaatcct ttctttctgc    1440

tgcaaaattt gatgcataaa caaacgacac aaagaactct tcttgtcttc cttctaataa    1500

gacagagcaa gtgatgagtt gtgacgtctt atatattgga gatacacgca cgttatcttc    1560

tattatcttt caatagtaat ttgatataaa ttaagataat gtgcagtgaa cgagtggcga    1620

ttgttaagcc aagtgaacat tatatacttt attttatact ttctccaagc ttcgaatgga    1680

gaatttattt ccatacgact aactctacct aaaagggcca tgtttgtttg ccaacataac    1740

acgacgatca cgagatacac ataacattta gaatttggag aagatacatt ttgtttgact    1800

tcactttttg tgcgaatggc tgttctacct gaaggggcca ttagtataat ttttttgtac    1860

ataataacgt caccaaatat aacacgagaa tcacgaggta cacaaatcat ttaggcttgg    1920

acattatcta atcaaataag ctatgatatc aaatttacat acatatagtg gcctcgtggg    1980

tataattaca caaggagctt ttggagaaaa agaagtgtgt gatttaaatg acaattatac    2040

aaatgtgtac aattatcaga tccaaagttc atgttttaaa tcatcaaaaa aataataatt    2100
```

gatgagttaa atgatatttt tttcatttag atttagttag attagttgta cggttgtacc 2160

attatttaat aatttaaaag ttgaaatgat tataatgtat aaaagttgaa aatattgtaa 2220

cagatataga ttaagcattt ttgcggtcaa tatattataa aagctttttt agctattaat 2280

tgaaaaatat tttacaccct tagatctttt gatctcctaa ttatataaaa tattttcttc 2340

taccgtttgt ctatataacc atatgtgttg tctagtgcat gtattcagcc acgaataaga 2400

gaatagtcta ctaaatca 2418

<210> SEQ ID NO 81
<211> LENGTH: 2486
<212> TYPE: DNA
<213> ORGANISM: Spinacea oleracea
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1303)..(1483)
<223> OTHER INFORMATION: CDS of Def1 nucleotide
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1487)..(1768)

<400> SEQUENCE: 81

actagtacta cctgttacta gagctgtcaa aacggttatt cgagttgggt ccgggtctga 60

tcatctcgag tctcgggtca tgaactggtc gggtcgggtc gggtcatttt atcaccgggt 120

gcaggtcggg ttcaggtcgg gttcagtcag gttgaaaatt tgtcgggtta tttttacatt 180

tcggtttagg tcgggttcgg ttcgggttcg ggtcgggtct ttttctagcc gggtacaatt 240

atgggttcgg ggcttaacga gtcgggtcaa gttcggatcg gataattacc gggtcggtta 300

taattcaggt cgggttaaga ccgggtacga tagctatcgg gattagtcaa gttttaacct 360

tataattaac ttttataaat ttggttaaat ttggtttagc gtttttcact tgttctagat 420

taggtaatta taaaaaaata tattaacttg atttaagtta ttatttagtt aggtcaatga 480

caaatcggat tgtcaacaag tcgcgaaaat tcaggtaacg gattgtcacg aattgagtca 540

ataacaggtt tcatggaatt ataattggtt tcgggtttac atcgggtcgg gtgttgaatc 600

aggttcgggt catttttcgg tcgggtaagc tgactcagtt ttgttatcgg ttatatttcg 660

gtcgggtatc aggttcgggt tcgggtcttg cattaacggg tcgaaatcgg tcgtcggttt 720

taacgggttg gctacggtcg gattacgggt ttcctatttt aacaaaattt cggatctcgg 780

gttgggtccg ggtccttaaa aatacaggtc ggttcaggtc ggtttctcgg gtcgggtcag 840

tttttgacag ctctacgtgt tacggagtat gttttaattt ttttaaaaat ggctacaaat 900

aattaaatat caataattaa catgcatttt caatttgatg atttgggtat cataatagaa 960

acacagtatt atggttgaga cttgagatcg attaatcatg ggttgatagt ttgaattagt 1020

taaattttcg taattatttc attaatgtta agatctgatc cacgaaacat catattgtag 1080

ctaatgtccc aaattgataa aaagcagaat agcctaactc ctctgatctt gtaaagtgga 1140

ctatctaact aaatggccga ctaattcacc atcacaaatt aatgttctct aatatttttt 1200

ccgaccgtaa ttaagtacgt agatttgaca caaattttgg tgaaacatat agtcttgttt 1260

aattttaaca aatttgttgt gaattgtgtc atttacagaa gaaatgggtc caagaaaggc 1320

agaagctgga atttttagct cgaggaaatg caaaactcca agtaaaacgt tcaagggaat 1380

atgtactagg gactccaatt gtgacacttc ttgtaggtat gagggatatc cagctggaga 1440

ttgcaagggt attcgtagaa gatgcttatg ttgtacacat acttaaactc caaatatcaa 1500

tatcaacaaa ctcaatgtcg tgtacacctt tcgtcccaga ttagtagtca cgttagtttg 1560 aactattaag ttagggagct agtacgtaca cacatatatc aatctatgtt gcttcgtgtt 1620

gtagccatga acgtatcttg ttatcgtgtt gttgttgttg tcgtcgtcgt cagacgtccg 1680

tcgttgatga attggtgaat tctagctagc ttctatgtaa aagtatcggc aattatacgt 1740

tgtccaagtt atggtgttgt aaaataaaag tgtttggatt atgaatgaag cctagctaac 1800

tttcaggttg accttgagcc tagtcttttg agtatcctac taattactcc ctccatcccc 1860

ggaatactcg caacgttttt cttataaagt cgtcccgaat ttctcacact gtttctgtaa 1920

atgttcattt tctttttgat attatactta ctcatggacc catgggcacg acacccacct 1980

atatccctac tccttaaaaa aaacattaaa aggtgtaaag atttgtttta tactctatca 2040

cgccccctca cataaaagcc ctttggactt gaagtgtgga tgcaacatag gcctcctcat 2100

actcagcgcg aaatattcta ctttgaaatg aggggtggat gagatttgaa cccgtgacct 2160

ttgcgtcacg ctggctctga taccatgtca aatgaccaac tcaaccaaaa gcttaagctg 2220

gtggttgaag ccccaagagt agttttatac tatcactaca agaatttgtg tctttaacga 2280

caacctaatt acgacgggtc aaaaatcccg tcgcaaaagc cttttgcgac ggggctaaca 2340

accaaacaat gacgggaata accgtcgcaa atgtctttta cgacgggttt acgacaaatt 2400

tacgacggga tttctattaa cgacgacccc cttttatgac gggttcgcga caggaaaacc 2460

cgtcgttaat caacgattat tggcct 2486

<210> SEQ ID NO 82
<211> LENGTH: 3767
<212> TYPE: DNA
<213> ORGANISM: Spinacea oleracea
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (1946)..(1999)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2000)..(2060)
<223> OTHER INFORMATION: CDS of Def2 nucleotide
<220> FEATURE:
<221> NAME/KEY: Intron
<222> LOCATION: (2061)..(2579)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2579)..(2764)
<223> OTHER INFORMATION: CDS of Def2 nucleotide
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (2767)..(3126)

<400> SEQUENCE: 82

aaaatttacc tagctttcta gttttgaatt taactttcac gaaatttcat tttttttaac 60

tcaaataatg ttaaccgaat ttgattagag tcgagtttgg ttctcaagca atagcggaga 120

cagggggcgg gtgaggcgtc cacccccccca aaggaaaaaa aaagattaat atatatggta 180

ttaaatgtca ataaacattg tcaaacttgt cttgccccaa tgattgaatg atcaatattt 240

gacacaataa ccctatgatc aaatacctac attgacacat tatatacatt tcttttcttg 300

gctttttttt agttgatata aatttctcgc ccccaatctg aaatttctgg ctccaccacc 360

gttctcaagc caaatcaatt acgattattg atgggtcatg gattctacat ttatgaagca 420

aatatagcta gacttggaaa aacgaacccg gctatgaaaa tctgatccaa tttatccgac 480

ctgttaccta attttgataa gaaaagacaa ctcaaaatca acccaaagtc taaattgacc 540

tgactcgtaa cctaaatcga catggaattg atttggtctg aaatgacccg atacatgaat 600

cgttcaaaat tgaattcatt atatcgattt tcactcgaaa taaaagtaaa ccgtactgaa 660

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ataactgtaa aatttgaatc aacctaactc taatccgaaa cgaagaacaa ctcaaattta    720

cccatagctt aaacaaaata acacaaagtt tcataactaa aacaatatta ttatacttgg    780

tatatttgcc catgtcttat gtacgtctca tcttctcgat catatatagt ctcaaagagt    840

gatagagtag tatagaagac tagaatcccc taaattaact tgtaaatatg tgaaaaatgt    900

aacccttgtc aataactacc ctaacatctt tatcataatc caataaactc gatcatatcg    960

tatatgctta accctatatt aattattttg taagaaatat tgtaacaatc aacaaattaa   1020

cctaattaat cccaaaattc gaataaatcc gatttatacc caaacccgat ccaaagtaag   1080

aatgacataa aattatctga atcatgtcca taaaaaccca cttagtaggt ctaaacacat   1140

acagtgatac accatatgtt tttcttggtg tactagtcgg ttcaccttta gggcacgctt   1200

ggattgggtg taatggagta taggggtaat aaaagtcaaa ccaccataat aaaaggacaa   1260

tgaaggtgaa ttgaggtggt tgcaaggagg gtggtgtggt ggtattgtga tgagaagttg   1320

tggtagtggt ggtgttgtga ggagaaggga ggaaggggga agtacttacc ccccaaatga   1380

gggtaataat caccctagtg ggatggtggg taactattcc ctccatgatg agggtatttg   1440

ttccccctcc cctttttttt tttcttgcca acactagctt gtttcctttg ccaccacttc   1500

atcccctcat catcaccatc aattacctta gtttgacttt tattacccct ttaataaatt   1560

accctcaatc caagcatgcc cttagggtta atccggattc ggagcgagtt ctgagtggat   1620

agatttttc cccctcccaa ttgtaggtga gggtgatcga acacagggtt ctccctacta   1680

aattcagccc caatcaccac tgaaccaaca gacaattagt gatacatcat atgttaatat   1740

gttatggcgc ggtatttcca gctagtgatc taaagaccac acaaggtatg tcggtaagaa   1800

atcatttcaa acacaagccc cgtcagaaag aagcctttta gcgtcaagac aaatgcaata   1860

gtgtcccata ttatttgggc atataccctt gtcaatagtg aacattttct cctataaata   1920

atctatagtt tgtgttagtt ttgcataaca tatttacaat cttatacatt tatattcatc   1980

aataaattta aaaagaaatt atgaagatgt caatgaggtc gattgctgtg gttttccttg   2040

tgtgcctact tgtcttgtca acaggttact aatgctatcc ttacttcctt accgtctttc   2100

aaatttttat tttggaaact ttcttatata accccatatt ttattttatt ttgatgtatg   2160

attaagagca ataaatagat aaagtttgct aatgctctgt ccatgaccat actatactaa   2220

tgttgttctt tttaaacgag accatacgta cttctagaca ttaatttcct taaattggaa   2280

tcgtttatgc tttgatttta gacatatatc cctttaattt tacaacctaa ctttgatcta   2340

ataagtacgt aatatcgtac atgcatgtta ctattaagta ttgattactt ttgagtaggt   2400

cttctatgag accgccatat gcataagact gtttatgtca gctttaaagt gcacattgtt   2460

agttataagt agattacacc gtataatgtt ggcttaatca tgttttgtta gttttaatta   2520

gctaaaactc cggcaattaa attaacaaag ttgttcctaa atatgtgatt tgtttgcaga   2580

agaaatgggt ccaagaaagg cagacgctgg atttttcagc tcgaagaaat gcaaaacacc   2640

aagtaaaaca ttcaggggac cttgtgtaag gaacgccaac tgtgacactt cttgtaggta   2700

tgagggatat ccagctggag attgcaaggg tattcgtaga agatgtattt gttgtacaca   2760

tgcttaaacg aataaccctc aatgtcgtgt actctgcttg tccagaatta atagtcacgt   2820

tagtttgaac tattacgtta ctaaacctgg acgaagatag ggagtacgtg cgtgtgagtg   2880

tgtgactatc tatccagaat taatagtcac gttagtttga actattacgt tactaaacct   2940

ggacgaagat agggagtacg tgagtgtgag tgtgtgacta tctatctagc ttgctcggtc   3000

ttgtaaccgt ttcttgttat cgttttgttg ttgttgttgt tgttgttgtt ggacttgttg   3060
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tgaatttcga cctctatgta atgtattggc aattgtacgt tgtccaagtt atggttgtaa 3120

aataaaagag tttgcatgaa cggagccttt caggacttga gcctaccgta ccctttaatg 3180

aatatcctac acatcatatg ttaaattaat attcttacta gtcaatttgt tatatttata 3240

cggagtacgt atatatacat tgacgattgt aaacttgtga taatgtgaat aatgtgatgt 3300

tatattgtaa actatataat gtgagtatat agttacgttg tcggagaatt aagtgcatca 3360

tatcacaatt cacaagttta cataaaaggt ttaatcaaac acatgatatg aatttagaac 3420

attctaaact catactacat atatcaaacc tagaatttgt gaaacaatca ccccttcaaa 3480

gagttctcac tgtaatttgg gtgaggcacg tactcacaaa aaaatagagg gagaaacgta 3540

catgatacac tacaagaaat tgtactatta acgacgggaa atcccgtcgc gaaaggccaa 3600

taatcgttga ttaacgacgg gatttgttgt cgtgagcccg tcataaaagg gggccgtcgt 3660

taatagaaat cccgtcgtaa atccgtcaaa aacccgtcgt aaaagacatt tgcgacggtt 3720

attcccgtca ttgtttggtt gttagccccg tcgcaaaagg cttttac 3767

<210> SEQ ID NO 83
<211> LENGTH: 2854
<212> TYPE: DNA
<213> ORGANISM: Spinacea oleracea
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (972)..(1024)
<223> OTHER INFORMATION: CDS of Def3 nucleotide
<220> FEATURE:
<221> NAME/KEY: Intron
<222> LOCATION: (1025)..(1681)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1682)..(1851)
<223> OTHER INFORMATION: CDS of Def3 nucleotide
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (1854)..(2848)

<400> SEQUENCE: 83

aggaatagtt aaatcatgag gaaagtcaaa taaataatat caatattata aatttgtgta 60

aacatttatt ttacacgtaa gtcgtttaat attaataaat gtagattttt gtttaaactt 120

aattatgaag aatcatatca gatcagacca gaccagatca gaccagaaca gatcagatca 180

gaaaaaataa gttcagatca gatcagacca gatcagatca ggagaaataa ggtgaactaa 240

acagggcctt actccatttt tcacacacac atgaaagaaa ataccaaaaa gaaaccacac 300

aagaaagaga gtttgataca cacttcatat atgagcaagt gcaaaaggta tgccaaaaaa 360

atccatatta tttttacact atttacataa tttattttgt ttattttttta tgattgatac 420

ttcaggaaaa acatattcat ttgggatctg gttagatctg tcttaatgaa tattttgcaa 480

attttaaatt tttattattt ttaattatca ataattaaag ataataattg ttcaagttat 540

acgttaataa tcgtgaaaaa caaagtgttg caattaaaaa gaaatgaagg aagtatgatg 600

caagggtgat agttaggtag atcacagtat ttaccacgtt cttgataaaa aaaatatttg 660

gtgaaaattt attagagttt ttcaattttt tattttttgt gccgaacaat gaagtaggca 720

caactatttc ttagaagtaa attatttaga gttagaacaa ttataaggaa tagctacaat 780

tttaaattga tcatcacaaa tctttcatga caaatattcc ttcaaaaaag tcattaaaga 840

cggagatgat aatagtcgtc atcgtttagg tgacaaatta aaactacctt aaagtttttt 900

attactcgta gttcttcttc attctattga tcttctctct atattttaaa gtgcttaaac 960

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atgaaacaaa caatgaagca ctttggggct atatttcttg tgttgttgct tgttctggcc   1020

acaggtataa caaaaatttc ttccctttga attataccca gtaaatagat ctcatttgta   1080

gcaaatttta ctttgtctcc ttacactaca aaaattgtac cattaacgac gggaaatccc   1140

gtcactaaag gccaataatc attgattaat gacgagattt tctgtcgcaa acccgtcata   1200

aaagggggcg tcgttaatag aaaatcccgt cgtaaaccca tcgtaaaaga catttgcgac   1260

ggttgttccc gtctttgttt ggttgttagc cccgtcgcaa aagcctttta cgacaagatt   1320

tttgaaccgt cgtaattaga ttgtcgttaa aaatacaaat tcttatagta ttagaaaata   1380

cagagtaaat gaaaaaaata cccttattac taattcgcta tatatcgcta tcctctttac   1440

atctttatga attctaataa tactacttat tgagtatatc aaaataatat ggagtactat   1500

gtacgaagta tattattact actacttatt acggagtacg tacataaagt agtaataaaa   1560

tgacagttac ttgtaaaatg atgattgttt tgttaaaact ttttaataat ttttggatat   1620

ttattattga cctttgcttt taattttgtt gggatttaat tataccatga aaaatacaaa   1680

gaacatggag caagagtagc agaagcaaga acatgtgaaa ctccaagtca aaagttcaaa   1740

ggaatatgta ttagtgactc caattgtgaa tcaatttgca ataccgaagg atttcctaat   1800

ggagaatgta gtggccttcg cagaagatgc atttgcaaca caccatgcac ttaatgttta   1860

attatgctca taattaatta tgtttaatta ctaattgatg tgctttggaa tagaaatttc   1920

atattttatg tacgttatga attgaaatct atttgtttca gaatagctag taaaatctga   1980

aacatttttc aatacacttt gtgtgttatg ttttaaaaaa aactatcgga taagacgcgt   2040

ttcagtctaa tcgggataat aatctcatat acatatatag catgtaaaat tttggcgaca   2100

ttaatttatc tcagatttta ccaactcaaa atctgagtta tggagctctt tccaagtatt   2160

ctctccgttt tgaaataatg gttacctttg acttttaaca ctattcacaa atttcaattt   2220

gactatcatt tgttacttat gaataaggaa aaatatagcc gtgtgagatg ttgtttgatt   2280

tatttcgatg tgtacttttg taatattaac ttttttataa ttttaacgat tacaaaatta   2340

gatgtattaa tcttcaacca tttacattga caagcataaa aagatgaagt gtaatcattc   2400

aatcgaaatg gaggagaaat tccgagttaa tatcagtgat tgtaaaaaat ttccaatcaa   2460

atggcatttt cgtaaacatt atgcccgaaa aatgtatatg gtataatgtt aagtgttgac   2520

tgtacatttg taggtattga ctgtatattt gtagttattg actgcatatt actcggtgtt   2580

gattgtatac cacttgtcgt tgatgtatat tttatgattg ctgatgaatt actaaaatac   2640

aatattgttt attggtaagt gattgactgt atatttgtag ttgtagattg tttattagta   2700

gaagcttatt gtatattgtg agctgttgac tgtatattat atagttgttg atgtgttatg   2760

aaaatacaat aatgaccgta catgtggtcc acatttgatg acatgtcact atactttaac   2820

ccacatttaa tggcattttc gtaataaaat catc                                2854
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<210> SEQ ID NO 84
<211> LENGTH: 3903
<212> TYPE: DNA
<213> ORGANISM: Spinacea oleracea
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (56)..(224)
<223> OTHER INFORMATION: CDS of Def4 nucleotide
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (228)..(308)
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (2069)..(2145)

<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2146)..(2197)
<223> OTHER INFORMATION: CDS of Def5 nucleotide
<220> FEATURE:
<221> NAME/KEY: Intron
<222> LOCATION: (2198)..(2730)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2731)..(2900)
<223> OTHER INFORMATION: CDS of Def5 nucleotide
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (2904)..(3013)

<400> SEQUENCE: 84

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gtacaaaagt agcagaagca aggatatgtg ctagtccaag tcccacgttc aaaggaatat 120

gttttagcag caggaattgt gaaactaatt gcaattctgt gaaattttct ggaggaagtt 180

gtcaaggttt tcgtagaaga tgtatgtgca ccaagccttg cgcttaatta accgatggtg 240

tgccacgtgc gcgttcctcg tcatcaataa tcagcttgac attggttaaa atttgcatta 300

aaaataaaag caatttgacg cacgtgttct ctttacatca tcttcattca tccacaatcg 360

agtggatgca gtatactatg tatatctata tataatctta tatacaaagt gtgtactaat 420

acttgtatta tagttgtggt aactttgcaa tatgcaaatt aagtagtagt actatgctac 480

actaataaat taatgaaagc tacaattcat taacaaagtt gaaagtatta tttacgttta 540

tctttaattt cgttttatta acaactactt cgtgcaaatt ttagatattt gaaaagtaca 600

agttaatacg aaatatgaga attgaatagt cttcattttt aggggtataa aactcaatgc 660

gtggattatg gatatatgtg cacgatactc atgtactgcg taggaaatga acacaagtgt 720

acaacctaga ctatggacat atacacacaa atgcacacaa atgtacagcg tggaccatgg 780

acatcacgat gctcactgtg tagcaaatga atacaggtgt atagattgga atatggacat 840

atgtgtatga tactcattgt gttgcaaatt aaatgaacac aggtgtataa tccggactat 900

agacatagaa aatgaacaaa ggtgcataac aatactcatt gtttagcaaa agagcacaag 960

tgatgtcctc agttatggac atatgtgcac tatactcact atgatattat gacaaaagtg 1020

catcatatga attactttgt atattttttt aaaaaaaatc atataaaaaa aaatctcgtt 1080

tctatctact ataatcgcat gttcttttag ttacatatgc tacgtacatt tgtatacctt 1140

cattgcgtaa taattattgt gcacaatatg tccataatct aatttgcggt aaaaaattat 1200

ccaccttcta accttttttaa gggaaaatta ccttcttatt ttgatcacat gtacattcaa 1260

attctttacc aaaggtaaat gggcccggta gcaccaatta gggatgaccc gggtgagaaa 1320

aaatgtcagg gtaccctgaa tcgaaattgg aacctgttag gaacctgagg tttcggaatc 1380

ggaacctgtt gtgcaggttc tggttccgga taacgaaatc gggaacctgt tgcaacaggt 1440

tccggtttcg gttctcaatt tccggaatgg gtaccttgtt gggtaccttg tacatatcaa 1500

ttctaatatg aattgaagta cccaaaataa gggaccggga caaataaaaa tgttttctat 1560

gtccaaaata taaaacaatc caagctaatc tttggaacat ataaatatag aattacaatt 1620

taagcctaat ctataaaaca attaaagccc aaagcataaa gtacatattt tgtccaataa 1680

attatcaata ttttatttga agttttaaat gacagggtac cctgaattag aaccttagaa 1740

caggttccgg ttccggttct cattttcagg aacctgttac aacagtgttt cggtttcgat 1800

tccggttccc atttttagaa acctgttgca acaagttccg atatgattct gatttctgaa 1860

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attttaacag ggtaccgtgt tgtgctcaac cctaccgcca attaattgac aatttatgag 1920

aaagtatttt ttcttcttta tctttttaa ttggaaaaga aatagttttg atatgagcca 1980

cataaaaggg atgggtgatc acaattataa tattggaacc acaaatatct aatcctatat 2040

aagtaacctc tagtgttgtt atcttgctca ctcaccaaat acaacttcta caagttaatt 2100

tcactaaaca tcttcttaat taagagctta attatgaagc aatcaatgag gccttttgct 2160

gctcttttcc ttgtgctctt ccttgttttg gccacaggta cattttattc ctcttccttt 2220

ctaaaactta taacttataa tgtcattatt tttcgatcct tgtacgtcgt atgaagtatc 2280

aaattaaagt tcgaataata agaaaactaa tcacgtcttc tctataaatt ctaaattagt 2340

ttatatagtg tatgtcacat aattaaccac ttactttcat aaatttttaa tgcttcttcg 2400

tttcttaata tctgcatcat tttgactttt cacactattc atttagaaat atgttttaag 2460

atgatgatcg aggattttca ctggccgtac tactactaga gacattggat ctatcaaacc 2520

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catatctttt gacatcttac cgtaacttag cagtatgtga cgtagttatc taactcgtta 2700

atattttctc cttgttatga ataaaaaaag agatagggcc aagagtagta gaagcaagaa 2760

tgtgttcatc accaagtcat aggttcaagg gaatttgtac tagcagcagg aattgtgaga 2820

acacttgcaa cagcgaacga ttttcaggtg gtgaatgtaa aggctttcgc agaagatgta 2880

tgtgcacggg accctgcgtt taattaatta acataattaa tgttaattaa gtgtgtgcaa 2940

tttccatcct taaccttgta gttgagaggt ggatatatca tatatgtatg gttattagtt 3000

gaacgataat aaaattgtag catctatatg tttgaatcac tcggttgtac cattgtacgg 3060

agtatgttac tttgttaatc accactaccc caatcgatta ctattaatga aatgatgcat 3120

gtacgtgttt tttgtttgaa gttcgattgg agttatataa agatttgtga tagaagtaat 3180

ttcgtaagaa cttgatttaa ctatcttatg tatttatgta gttatgttac gtctatgttt 3240

gaacgtaatg ttcttttta acttattacg ttatttcgta tttcatatac tttaatttta 3300

gcttgttcga tctagtcact gtaacattca cattttcaat gccagcactg atcaatgaaa 3360

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ccacttgccg cctccaccgt acccaatatg tattccacaa tcattccgac tacaaaaaaa 3480

accaacttgc tttgctactt ctgtttgaga gaaaagttaa gcatgcattt tatatcaaat 3540

caagttgtga tataaaccgg ttgcttaact tttcccttga aaataaaaag taacaaggaa 3600

aaatcaatct attactatat attaaaagag acaccaggaa tgacacgtgt caatttctgg 3660

tgcgattttt tccggtcaaa aattactttc ctaaaaaaag tgtatctgtt tgattttagt 3720

tttattctct accttttta tataaactat ttatgtatgg aaacaaaata tatttagttt 3780

ataaattatg gcaataatag atacgacgta ataataatta ttctaaattg gcaatatttt 3840

agtcaatcgc tatattagta atggaaaata tatcactcaa tattttggtc aaattaccat 3900

att 3903

<210> SEQ ID NO 85
<211> LENGTH: 4294
<212> TYPE: DNA
<213> ORGANISM: Spinacea oleracea
<220> FEATURE:
<221> NAME/KEY: 5'UTR
<222> LOCATION: (1944)..(2000)
<220> FEATURE:

<221> NAME/KEY: misc_feature
<222> LOCATION: (2001)..(2064)
<223> OTHER INFORMATION: CDS of Def6 nucleotide
<220> FEATURE:
<221> NAME/KEY: Intron
<222> LOCATION: (2064)..(2653)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2654)..(2689)
<223> OTHER INFORMATION: CDS of Def6 nucleotide
<220> FEATURE:
<221> NAME/KEY: Intron
<222> LOCATION: (2690)..(3121)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3122)..(3291)
<223> OTHER INFORMATION: CDS of Def6 nucleotide
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (3294)..(4176)

<400> SEQUENCE: 85

tgtgtggggc tgataagatg aacgcgttac aattcttata atttttgcat atggtgtttt 60

caataccttc catcatatgc aagaagagtt tctctttaaa tacgacccca tttttgcttc 120

aactaggagc tttcctatta tatattcagg acacctcttt tatagaacca caaagtattt 180

gacagtttta ttttgttccc tctgttcttt cactctatta tcctttgttt tagccaaaaa 240

gttattcttc aacaagtttg gactagagca ggaatacaca ttgcttcaac caaatattag 300

ttggcccttg ggatggcctg ttagagtcta tcctggtccc caggtatgtt acacacccgc 360

atttcattaa ctttctctta aacatgacca gtatttgtgt tagagtggaa gaatgcatcc 420

attgcttaga aaattattta atctgcaatt ctgcataaga gatgtacgta ctgtataaaa 480

gtactacgta aatggtattg atatgcttac atattattga ttagtgagtg acttgaacat 540

gttgtacatg gtgtgagtac ttttgaattt gtgagtacca tctgaaatca aaacaaatta 600

ctataaattg tatcacgatt atcattttgc tagaaaggag acatgttatg aaagactggc 660

ctctcggacc tttccatatt tatcttgcag agctgtagaa tatgctaatt gaaataatat 720

aggattccct agtacattaa atctactaag atcgaaatgt tctagtgttt ttatctaagt 780

gaaggtctaa tgtcatgcat ttattttgtg tttgtccgag gatgggtatg gatgacttca 840

agtctttcca ccaagcaatg ttgctgctga tcagcgtggt ggacgtgttg gaacttgcaa 900

ccggctgtat gaggtggtcc taagattcaa aggacgagta ttggcaatgt catgttgtta 960

agttataaga cagtgaaact cttatttgat atgatagaaa tgaaattgaa tcatattatt 1020

tcagttgtta aattagcatc agctttaaaa tggttgcttt tattttttat tacatgtact 1080

ttattaacta aaaagagcta tagaataaaa aaagcccgac gaaaaatata gaatccgctt 1140

acaaatacca tcgtttttta gtttaatgct actaatttta attcatactt cgtattaaat 1200

tggttggtga gtgcactaaa gtttttgtca ttacaagaga tttgacaaca cttatatatt 1260

aaatgctgct aaatgtggca acatcaacaa cgcttattaa aagcactatt atttttttaa 1320

cagcgctagt aattcacagc ccttataaag cgctatgttt aaatgaaaaa aacgttgtta 1380

aaagcttatt gtggtgtagt gtaaaaaagc aaatcagtca ctatctctct ctagttcttt 1440

tcacttatct aatttacgta ttatatcgta caaagatctc tcagacacac tctgtgatgg 1500

tctaccgatc atataggtga tcgactaaaa ggagacaacg gtcaaacacg tcaacggtta 1560

aactaatccc caaaatatta tctttgtagt ttttcatgca gaaacatatt acaccgtaaa 1620

aaacattatg aaacaaactt aaaaaaaaaa aaaaaaaaag taaacgtcca ttataattcg 1680

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gaggtactaa tattctaata ttagaaagtg tatgtgaaca taagaacgtg taatatggca 1740

gccaacgcaa aagaaaacta cataatttga tctgagtcac tttagtgtgt tcatctatgc 1800

tttttctaga tcgatcttaa tttctttttc gtcagcagct tttctagat ctatctttaa 1860

taaacataaa attaaaagaa attaaaaata aaaaggaaaa ataccaaagt ttcggctata 1920

taaagaagtg tgttgttggt agtgataatc gtgtgccaca aaatataatc ctcgtacttt 1980

gaaattaagg agtgaataaa atggagcgtt cttcacgtgt gttttcagtt gttcttctca 2040

tgcttgttct tgtgttgtcc acaggtttat gttctttctc gtaatttcat tttatttatt 2100

tccaattaaa tcattctgct caaatattta atttgtttgt tgcttttaat taattaatct 2160

cacgccctac taatcacaaa taatgaatac tttgcatata tcacttgctc ttatttgatt 2220

tatgcaaagt gataaaagtc aaaatttgcg acaaattatt tgttttgtaa ctatattttc 2280

caaatagatt aaaaatatat aatattatta gattgtaatt tttattttt aatttacaag 2340

ataaaatgag taatatatat ggtttccttc ttttttatgg actaccttat ttaaatatat 2400

attgtcgtag taaaagtata tcgatgactg taaaaataat ttgatgagtc ttgaactacc 2460

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tttttaaaga acttgacttc atgattggcc atgaccaatt aagctaaaaa aactcataat 2580

taacttattt aaggggggc aacaaggtta gatgaatttg atgtttttt tttttcattc 2640

taaccattga tagatatgta cacagaccca gtggcggttc ttagttatgg tataaatggg 2700

ctggtgaaaa gttccataat ttatttctaa ttccaaccct aatattttaa atataattgt 2760

ataaattgca taatgtttct atagtccctc ctaaaactgt tcaaaatccg caacttcata 2820

gacagtaata agtttcttcg ttaatatgca taaagtactc cgatccacca tattaatatt 2880

gtttaatcat cctaaaatat tgaggttaca aatgacgtac tataacaagt tttcttagct 2940

aaaatacgtt gttattaaat gttatgctag aatatgtatt taatcggtta agtcccctta 3000

ctgcaacctc ccaataccc caatacgaga tatctgcatg tgaacgtaac taacatattg 3060

tttatgaatc atgttaaatc tctgtattct ttattcatgt tcttaattgt ctttcttaca 3120

gagattggga caaaggtggc ggaagcaagg atatgcgaat ctgcaagtta caggttcaag 3180

ggaatatgtg tgagcaggag caactgtgct aatgtttgca aaaatgaggg tttccccggt 3240

ggccgttgcc gcggtttccg tcgtcgttgc ctctgttaca aacattgcgg ttaattgtta 3300

tgccacggcc actttcctat gtgctagtgc ttatgacatt gatctgaagt accttcttaa 3360

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ggtttgtagt ttaattaaat tttactttca cgcgtaacta atttgaagat ttttgcacat 3540

ttacttgctt ttttgggtct atataatata gttcatctgt tccataacaa tgttctggta 3600

tatttttttt ttacgtttgt caatgcacat tttatatcat tttcatatct aatataatat 3660

taaaaattat aaaatttaat attattaaag taatcattaa gacaaatcga atcaaacatt 3720

gcgtgaatat gtttttttctt atatattgga ttagaaagaa tttagaagtt ttgcatcaac 3780

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atgctactcc gtctcaattt acttttcctt tttttatatc ctatgtactt tgcgccattt 3900

ccttttcgaa aattttctcc tctccacttt tttcttgagt taattctcac catccaccta 3960

ctcattttct tttctttagt ttttcattct cctaaaactc taccccgtga ttttagatca 4020

tttaaagttc aaaaataact ctacaaggta gagtttgagc aatatcaacc attgaatgaa 4080 aaatcaacag ctcatatatt atcttttcaa aatttcccta ttttttctca ttaatatcca 4140

ccctttttatt ttcccctcct actcatttaa aataaaggtg attttatacc ttagattcaa 4200

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<212> TYPE: DNA
<213> ORGANISM: Spinacea oleracea
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<221> NAME/KEY: 5'UTR
<222> LOCATION: (1914)..(2000)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2001)..(2052)
<223> OTHER INFORMATION: CDS of Def7 nucleotide
<220> FEATURE:
<221> NAME/KEY: Intron
<222> LOCATION: (2053)..(3353)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3354)..(3524)
<223> OTHER INFORMATION: CDS of Def7 nucleotide
<220> FEATURE:
<221> NAME/KEY: 3'UTR
<222> LOCATION: (3527)..(3661)

<400> SEQUENCE: 86

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tggtgcgaat gagccacaaa ggcggggatg agaatcgatc ccatgatcac ctggaaccgg 180

aatgaaagct ctaaccaact gagctaccca ttactctttt tgacaaccta tattaattat 240

caagtgtggg gatgtaaacg agtcgaatca aggagtatat ttaaagtttg cctactgtct 300

caaacaaaaa aagtttgtct actgttgggc tagctgatgc aagtttaagc ccaacttgat 360

tcaccatttt ttcatacttc gtatgagcct ttcttaaatc ctaatagcaa taccctatat 420

tactacggag tactacgcat tatgatctag agttaatcgc attttagata attgatcatg 480

gtgtacaagg agctataatg caccctaaaa atataagtat aacttaaaga acatacctaa 540

cgtaaaataa acatgagttt taataaaaag tgaattaaca tattgcatgt tcttttgttg 600

taattttctt ttacatgtgt atatacttcc tccgtttcga aaatatcgca ctatgattga 660

cttttacttc tctaaccttt actttgactc ttaatatcac aaaccgtgtg caagtaaaaa 720

ttataaaaag aataatatta agaaaatata tatatcgata caaatctaat ataaccccac 780

atgactaaaa ttttcttact tacgaattac aaaaaattgc caaaatcata gtgtaaatag 840

tgtaaaaaac aaatggtgcg acatttttgg aacggatgaa gtatgttatt ttaggtgctc 900

accatactca ttatgtacca ttgttcatac ttagcccaca aattagagta aattttattt 960

taaaccaaat ttgaatagaa gttccgtata aggtacataa tatacgctaa ctatgtttgt 1020

cgatgaaagg cacggggtta cctaatatgt atgaccatgt gatcagtgat ggatcttgaa 1080

caattttaag aaaaaggaca gtagaaaaat taaacaatgt agcatgtatg caatttatac 1140

aataaaacac aaaattttgg gggagctgca actaaacctg gcaaatctga cccaaacccg 1200

aaaaactgac ccgattgatc tgatctgtaa cccgaaattg atctgaagcg acgacccaaa 1260

attaacctga aaactaaaca gaaccgaccc gaaaccgaaa ctgacccaga aatgatttga 1320

cctgaaatga ccagatatcc gaatgacccg aaccaaagta cccaaaaaga tcttcacccg 1380

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aaaccgaata ttatttaaat tttttatta taattttcat tttattaatt tatactgttt 1440

tgaattatag gaaaaagatt ttgttaatat tatgatagtg accaccaaat ctaaaaagaa 1500

acaacctaat caaaactaaa aatccaaaaa atttgatcca attaacccaa aaactcgatc 1560

taaccaaaaa aatctgatat aatccgaaaa ctcgatccga tatgaacgat ctgatacgaa 1620

ttgatcctat atgacccgat ccaatattga tccgaaatca tgacgagaac cagacccggc 1680

ccgattaaaa aaaaccgaac tcacccaaaa gccgagaatt atgtttaaaa aggttgtacg 1740

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tgtaacatgt acgtgtagct tcatttaggc attggtattt gcaccaaagc accatttggc 1860

aattgccatg cacaccatct tcccttataa aagtagcttt gtgtctgttt tcatcaccaa 1920

atcaaaacaa aacaaaaaaa acacaccata tattttccta attattattg aatttttttt 1980

atcaaatagt tcaagttgca atgaagccct ttgtagcttt tgttcttgct ttcatgcttg 2040

tcttggccat aggtacaact tccttgacct tcctttgaat taagggtgtc tgtttcataa 2100

tatatgcctc attttaattg tcttcgtttt aattgtcttc gttagacgaa atgcttaaca 2160

taagtgctat tagtctagct agtactctgt actataagca taactataag cataatgtac 2220

ttcctccgag ttgattttta cactatttac atattaatta tactttaatt atactttgat 2280

aattgttggt gatttatacc taaggtaaaa catagtcgtg tgggatcttg ttaatttaat 2340

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tgatcaaagt tgttcattat gcatgaaagt gacaaacatt acagagtaaa aatgaacagt 2460

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aatgtattat ctctgttctt tgaaagtttt ttttgacgtt ttcgaatttc ttagtaagaa 3720

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aatcttgatc ataaattatc tctattatac tacctccatt tcacaatact tgtatcattt   3780

atttatttat tttcaagtat cccaacatgc ttctttgaac attaatatct ctcactgcgt   3840

ataagtaaaa attataaaaa attacggagt aatatttata atcctcacat taatacgaat   3900

ttaacaagat tttactagac tatgtttact tttacataat gtgaaagaac aattgtcaaa   3960

gttagttaat gaatagtgtc caagatgcat ctattgcgga acggaggaag tatatactag   4020

tcagaagcat gtgctatgca cgtattggct taacgtacat ttataaattt tttaaacttg   4080

catattgtaa tgcactaaac actaaggtct ttatagacca ttacaaatat taaactaaaa   4140

gtcgaattaa tatataatgc aagggtcctg tgctcgatct tcttgtaagt tttactattc   4200

gtacggagca ttaattaagt tgttttctac tatttataac ataaaagaca tttaatcaaa   4260

taaaagttta tcattcttat tcgcaagtta agaaatgtat acaccttgct ctattaaaaa   4320

tcgcatggag ttattcacat tttcaaaaaa aaatattata catgtacact ctctgttttt   4380

ttttaaatgc atcacttaaa atttcacatt gtttatattg acttagatat tttactaata   4440

tatacagagt aataatcaaa tgttattatg taaaatgttg tttcacaatg catattttct   4500

taatatcaac tttttataat atttacc                                       4527
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<210> SEQ ID NO 87
<211> LENGTH: 53
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Consensus sequence of Def3, Def4, Def5, Def6, and Def7 peptide
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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa is Arg or Lys
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: Xaa is Ala or Val
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: Xaa is Thr or Ile or Met
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: Xaa is Glu or Ser or Ala or Thr
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: Xaa is Thr or Ser or Asn
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Xaa is Pro or Ala
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Xaa is Gln or Pro or His or Tyr or Arg
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Xaa is Lys or Thr or Arg
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(16)
<223> OTHER INFORMATION: Xaa is Lys or Arg
<220> FEATURE:
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<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: Xaa is Ile or Pro
<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Ile or Phe or Thr or Val
<220> FEATURE:
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<222> LOCATION: (22)..(22)
<223> OTHER INFORMATION: Xaa is Asp or Ser or Arg
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (23)..(23)
<223> OTHER INFORMATION: Xaa is Ser or Arg
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<221> NAME/KEY: misc_feature
<222> LOCATION: (26)..(26)
<223> OTHER INFORMATION: Xaa is Glu or Ala
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<222> LOCATION: (27)..(27)
<223> OTHER INFORMATION: Xaa is Ser or Thr or Asn
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (28)..(28)
<223> OTHER INFORMATION: Xaa is Ile or Asn or Thr or Val or Ser
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa is Asn or Lys or Met
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (31)..(31)
<223> OTHER INFORMATION: Xaa is Thr or Ser or Asn or Gly
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (32)..(32)
<223> OTHER INFORMATION: Xaa is Glu or Val
<220> FEATURE:
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<222> LOCATION: (33)..(33)
<223> OTHER INFORMATION: Xaa is Gly or Lys or Arg
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (35)..(35)
<223> OTHER INFORMATION: Xaa is Pro or Ser
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(36)
<223> OTHER INFORMATION: Xaa is Asn or Gly
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (38)..(38)
<223> OTHER INFORMATION: Xaa is Glu or Ser or Arg
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (40)..(40)
<223> OTHER INFORMATION: Xaa is Ser or Gln or Lys or Arg or His
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (42)..(42)
<223> OTHER INFORMATION: Xaa is Leu or Phe
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (45)..(45)
<223> OTHER INFORMATION: Xaa is Arg or Lys
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (47)..(47)
<223> OTHER INFORMATION: Xaa is Ile or Met or Leu or Val
<220> FEATURE:
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<222> LOCATION: (49)..(49)
<223> OTHER INFORMATION: Xaa is Asn or Thr or Tyr or Ser
<220> FEATURE:
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<222> LOCATION: (50)..(50)
<223> OTHER INFORMATION: Xaa is Thr or Lys or Gly
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: Xaa is Pro or His
<220> FEATURE:
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<222> LOCATION: (53)..(53)
<223> OTHER INFORMATION: Xaa is Thr or Ala or Val or Gly

<400> SEQUENCE: 87

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            20                  25                  30

Xaa Phe Xaa Xaa Gly Xaa Cys Xaa Gly Xaa Arg Arg Xaa Cys Xaa Cys
        35                  40                  45

Xaa Xaa Xaa Cys Xaa
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<210> SEQ ID NO 88
<211> LENGTH: 53
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence of Def3, Def4, Def5, Def6,
and Def7 peptide
<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Arg or Lys
<220> FEATURE:
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<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: Xaa is Thr or Ile or Met
<220> FEATURE:
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<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: Xaa is Glu or Ser or Ala or Thr
<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Asp or Ser or Arg
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<223> OTHER INFORMATION: Xaa is Ile or Asn or Thr or Val or Ser
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<223> OTHER INFORMATION: Xaa is Asn or Lys or Met
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<223> OTHER INFORMATION: Xaa is Thr or Ser or Asn or Gly
<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Ser or Gln or Lys or Arg or His
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: Xaa is Arg or Lys
<220> FEATURE:
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<223> OTHER INFORMATION: Xaa is Ile or Met or Leu or Val
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<223> OTHER INFORMATION: Xaa is Thr or Lys or Gly
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (53)..(53)
<223> OTHER INFORMATION: Xaa is Thr or Ala or Val or Gly

<400> SEQUENCE: 88

Xaa Val Ala Glu Ala Arg Xaa Cys Xaa Xaa Pro Ser Xaa Xaa Phe Lys
1               5                   10                  15

Gly Ile Cys Xaa Ser Xaa Xaa Asn Cys Glu Xaa Xaa Cys Xaa Xaa Glu
            20                  25                  30

Xaa Phe Xaa Gly Gly Xaa Cys Xaa Gly Phe Arg Arg Arg Cys Xaa Cys
        35                  40                  45

Xaa Xaa Pro Cys Xaa
    50


<210> SEQ ID NO 89
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(22)
<223> OTHER INFORMATION: Segura SoD1 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa is Arg, Lys, or Met
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 89

Xaa Thr Cys Glu Ser Pro Ser His Lys Phe Lys Gly Pro Cys Ala Thr
1               5                   10                  15

Asn Arg Asn Cys Glu Ser
            20
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-continued

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<210> SEQ ID NO 90
<211> LENGTH: 58
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(58)
<223> OTHER INFORMATION: Segura SoD2 peptide
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 90

Gly Ile Phe Ser Ser Arg Lys Cys Lys Thr Pro Ser Lys Thr Phe Lys
1               5                   10                  15

Gly Ile Cys Thr Arg Asp Ser Asn Cys Asp Thr Ser Cys Arg Tyr Glu
            20                  25                  30

Thr Ser Cys Arg Tyr Glu Gly Tyr Pro Ala Gly Asp Cys Lys Gly Ile
        35                  40                  45

Arg Arg Arg Cys Met Cys Ser Lys Pro Cys
    50                  55


<210> SEQ ID NO 91
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(25)
<223> OTHER INFORMATION: Segura SoD3 peptide
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 91

Gly Ile Phe Ser Ser Arg Lys Cys Lys Thr Val Ser Lys Thr Phe Arg
1               5                   10                  15

Gly Ile Cys Thr Arg Asn Ala Asn Cys
            20                  25


<210> SEQ ID NO 92
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(23)
<223> OTHER INFORMATION: Segura SoD4 peptide
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 92

Met Phe Phe Ser Ser Lys Lys Cys Lys Thr Val Ser Lys Thr Phe Arg
1               5                   10                  15

Gly Pro Cys Val Arg Asn Ala
            20
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<210> SEQ ID NO 93
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(24)
<223> OTHER INFORMATION: Segura SoD5 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: Xaa is Ser or Ala
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 93

Met Phe Phe Ser Ser Lys Lys Cys Lys Thr Val Xaa Lys Thr Phe Arg
1               5                   10                  15

Gly Pro Cys Val Arg Asn Ala Asn
            20


<210> SEQ ID NO 94
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(24)
<223> OTHER INFORMATION: Segura SoD6 peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa is any amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (22)..(22)
<223> OTHER INFORMATION: Xaa is any amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (23)..(23)
<223> OTHER INFORMATION: Xaa is any amino acid
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 94

Gly Ile Phe Ser Asn Met Tyr Xaa Arg Thr Pro Ala Gly Tyr Phe Arg
1               5                   10                  15

Gly Pro Xaa Gly Tyr Xaa Xaa Asn
            20


<210> SEQ ID NO 95
<211> LENGTH: 38
<212> TYPE: PRT
<213> ORGANISM: Spinacia oleracea
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(38)
<223> OTHER INFORMATION: Segura SoD7 peptide
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
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<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 95

Gly Ile Phe Ser Ser Arg Lys Cys Lys Thr Pro Ser Lys Thr Phe Lys
1               5                   10                  15

Gly Tyr Cys Thr Arg Asp Ser Asn Cys Asp Thr Ser Cys Arg Tyr Glu
            20                  25                  30

Gly Tyr Pro Ala Gly Asp
        35


<210> SEQ ID NO 96
<211> LENGTH: 53
<212> TYPE: PRT
<213> ORGANISM: Raphanis sativus
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(53)
<223> OTHER INFORMATION: Rs-AFP2
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 96

Gly Lys Leu Cys Gln Arg Pro Ser Gly Thr Trp Ser Gly Val Cys Gly
1               5                   10                  15

Asn Asn Asn Ala Cys Lys Asn Gln Cys Ile Arg Lys Glu Lys Glu Lys
            20                  25                  30

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

Cys Tyr Phe Pro Cys
    50


<210> SEQ ID NO 97
<211> LENGTH: 51
<212> TYPE: PRT
<213> ORGANISM: Arabadopsis thaliana
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(51)
<223> OTHER INFORMATION: At-AFP1
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 97

Gln Lys Leu Cys Glu Arg Pro Ser Gly Thr Trp Ser Gly Val Cys Gly
1               5                   10                  15

Asn Ser Asn Ala Cys Lys Asn Gln Cys Ile Asn Leu Glu Lys Ala Arg
            20                  25                  30

His Gly Ser Cys Asn Tyr Val Phe Pro Ala His Lys Cys Ile Cys Tyr
        35                  40                  45

Phe Pro Cys
    50
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<210> SEQ ID NO 98
<211> LENGTH: 54
<212> TYPE: PRT
<213> ORGANISM: potato
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(54)
<223> OTHER INFORMATION: Hs-AFP1
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 98

Asp Gly Val Lys Leu Cys Asp Val Pro Ser Gly Thr Trp Ser Gly His
1               5                   10                  15

Cys Gly Ser Ser Ser Lys Cys Ser Gln Gln Cys Lys Asp Arg Glu His
            20                  25                  30

Phe Ala Tyr Gly Gly Ala Cys His Tyr Gln Phe Pro Ser Val Lys Cys
        35                  40                  45

Phe Cys Lys Arg Gln Cys
    50


<210> SEQ ID NO 99
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Aesculus hippocasastanum
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(50)
<223> OTHER INFORMATION: Ah-Amp1
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 99

Leu Cys Asn Glu Arg Pro Ser Gln Thr Trp Ser Gly Asn Cys Gly Asn
1               5                   10                  15

Thr Ala His Cys Asp Lys Gln Cys Gln Asp Trp Glu Lys Ala Ser His
            20                  25                  30

Gly Ala Cys His Lys Arg Glu Asn His Trp Lys Cys Phe Cys Tyr Phe
        35                  40                  45

Asn Cys
    50


<210> SEQ ID NO 100
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Dahlia merckii
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(50)
<223> OTHER INFORMATION: Ah-Amp1
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 100
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Glu Leu Cys Glu Lys Ala Ser Lys Thr Trp Ser Gly Asn Cys Gly Asn
1               5                   10                  15

Thr Gly His Cys Asp Asn Gln Cys Lys Ser Trp Glu Gly Ala Ala His
            20                  25                  30

Gly Ala Cys His Val Arg Asn Gly Lys His Met Cys Phe Cys Tyr Phe
        35                  40                  45

Asn Cys
    50


<210> SEQ ID NO 101
<211> LENGTH: 47
<212> TYPE: PRT
<213> ORGANISM: Solanum tuberosum
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(47)
<223> OTHER INFORMATION: St-PTH1
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 101

Arg His Cys Glu Ser Leu Ser His Arg Phe Lys Gly Pro Cys Thr Arg
1               5                   10                  15

Asp Ser Asn Cys Ala Ser Val Cys Glu Thr Glu Arg Phe Ser Gly Gly
            20                  25                  30

Asn Cys His Gly Phe Arg Arg Arg Cys Phe Cys Thr Lys Pro Cys
        35                  40                  45


<210> SEQ ID NO 102
<211> LENGTH: 47
<212> TYPE: PRT
<213> ORGANISM: Sorghum bicolor
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (1)..(47)
<223> OTHER INFORMATION: Sialpha2
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Segura, A., Moreno, M., Molina, A., &  Garcia-Olmedo, F.
<302> TITLE: Novel defensin subfamily from spinach (Spinacea oleracea)
<303> JOURNAL: FEBS Letters
<304> VOLUME: 435
<306> PAGES: 159-162
<307> DATE: 1998-07-09

<400> SEQUENCE: 102

Arg Val Cys Met Lys Gly Ser Ala Gly Phe Lys Gly Leu Cys Met Arg
1               5                   10                  15

Asp Gln Asn Cys Ala Gln Val Cys Lys Gln Glu Gly Trp Gly Gly Gly
            20                  25                  30

Asn Cys Asp Gly Val Met Arg Gln Cys Lys Cys Ile Arg Gln Cys
        35                  40                  45
```

What is claimed is:

1. A citrus plant comprising at least one defensin peptide comprising a first defensin peptide, wherein the amino acid sequence of the first defensin peptide is at least 95% identical to SEQ ID NO: 32, at least 95% identical to SEQ ID NO: 33, at least 95% identical to SEQ ID NO: 34, at least 95% identical to SEQ ID NO: 35, at least 95% identical to SEQ ID NO: 36, at least 95% identical to SEQ ID NO: 37, or at least 95% identical to SEQ ID NO: 38; wherein the peptide has antimicrobial activity in the citrus plant.

2. The citrus plant according to claim **1**, wherein the amino acid sequence of the first defensin peptide is at least 98% identical to the amino acid sequence of SEQ ID NO: 32, at least 98% identical to the amino acid sequence of SEQ ID NO: 33, at least 98% identical to the amino acid sequence of SEQ ID NO: 34, at least 98% identical to the amino acid sequence of SEQ ID NO: 35, at least 98% identical to the amino acid sequence of SEQ ID NO: 36, at least 98% identical to the amino acid sequence of SEQ ID NO: 37, or at least 98% identical to the amino acid sequence of SEQ ID NO: 38.

3. The citrus plant according to claim **1**, wherein the amino acid sequence of the first defensin peptide is 100% identical to the amino acid sequence of SEQ ID NO: 32, 100% identical to the amino acid sequence of SEQ ID NO: 33, 100% identical to the amino acid sequence of SEQ ID NO: 34, 100% identical to the amino acid sequence of SEQ ID NO: 35, 100% identical to the amino acid sequence of SEQ ID NO: 36, 100% identical to the amino acid sequence of SEQ ID NO: 37, or 100% identical to the amino acid sequence of SEQ ID NO: 38.

4. The citrus plant according to claim **1** further comprising a second defensin peptide, wherein the amino acid sequence of the second defensin peptide is at least 95% identical to SEQ ID NO: 32, at least 95% identical to SEQ ID NO: 33, at least 95% identical to SEQ ID NO: 34, at least 95% identical to SEQ ID NO: 35, at least 95% identical to SEQ ID NO: 36, at least 95% identical to SEQ ID NO: 37, or at least 95% identical to SEQ ID NO: 38.

5. The citrus plant according to claim **4**, wherein the amino acid sequence of the second defensin peptide is at least 98% identical to the amino acid sequence of SEQ ID NO: 32, at least 98% identical to the amino acid sequence of SEQ ID NO: 33, at least 98% identical to the amino acid sequence of SEQ ID NO: 34, at least 98% identical to the amino acid sequence of SEQ ID NO: 35, at least 98% identical to the amino acid sequence of SEQ ID NO: 36, at least 98% identical to the amino acid sequence of SEQ ID NO: 37, or at least 98% identical to the amino acid sequence of SEQ ID NO: 38.

6. The citrus plant according to claim **4**, wherein the amino acid sequence of the second defensin peptide is 100% identical to the amino acid sequence of SEQ ID NO: 32, 100% identical to the amino acid sequence of SEQ ID NO: 33, 100% identical to the amino acid sequence of SEQ ID NO: 34, 100% identical to the amino acid sequence of SEQ ID NO: 35, 100% identical to the amino acid sequence of SEQ ID NO: 36, 100% identical to the amino acid sequence of SEQ ID NO: 37, or 100% identical to the amino acid sequence of SEQ ID NO: 38.

7. The citrus plant according to claim **4**, wherein the amino acid sequence of the first defensin peptide and the amino acid sequence of the second defensin peptide are different.

8. The citrus plant according to claim **1**, wherein the plant is orange, grapefruit, lemon, or lime.

9. A citrus plant comprising at least one defensin nucleic acid comprising a first defensin nucleic acid, wherein the nucleic acid sequence of the first defensin nucleic acid is at least 98% identical to SEQ ID NO: 46, at least 98% identical to SEQ ID NO: 47, at least 98% identical to SEQ ID NO: 48, at least 98% identical to SEQ ID NO: 49, at least 98% identical to SEQ ID NO: 50, at least 98% identical to SEQ ID NO: 51, at least 98% identical to SEQ ID NO: 52, at least 98% identical to SEQ ID NO: 53, at least 98% identical to SEQ ID NO: 54, at least 98% identical to SEQ ID NO: 55, at least 98% identical to SEQ ID NO: 56, at least 98% identical to SEQ ID NO: 57, or at least 98% identical to SEQ ID NO: 58; wherein the first nucleic acid encodes a peptide having antimicrobial activity in the citrus plant.

10. The citrus plant according to claim **9**, wherein the nucleic acid sequence of the first defensin nucleic acid is at least 99% identical to SEQ ID NO: 46, at least 99% identical to SEQ ID NO: 47, at least 99% identical to SEQ ID NO: 48, at least 99% identical to SEQ ID NO: 49, at least 99% identical to SEQ ID NO: 50, at least 99% identical to SEQ ID NO: 51, at least 99% identical to SEQ ID NO: 52, at least 99% identical to SEQ ID NO: 53, at least 99% identical to SEQ ID NO: 54, at least 99% identical to SEQ ID NO: 55, at least 99% identical to SEQ ID NO: 56, at least 99% identical to SEQ ID NO: 57, or at least 99% identical to SEQ ID NO: 58.

11. The citrus plant according to claim **9**, wherein the nucleic acid sequence of the first defensin nucleic acid is 100% identical to the nucleic acid sequence of SEQ ID NO: 46, 100% identical to the nucleic acid sequence of SEQ ID NO: 47, 100% identical to the nucleic acid sequence of SEQ ID NO: 48, 100% identical to the nucleic acid sequence of SEQ ID NO: 49, 100% identical to the nucleic acid sequence of SEQ ID NO: 50, 100% identical to the nucleic acid sequence of SEQ ID NO: 51, 100% identical to the nucleic acid sequence of SEQ ID NO: 52, 100% identical to the nucleic acid sequence of SEQ ID NO: 53, 100% identical to the nucleic acid sequence of SEQ ID NO: 54, 100% identical to the nucleic acid sequence of SEQ ID NO: 55, 100% identical to the nucleic acid sequence of SEQ ID NO: 56, 100% identical to the nucleic acid sequence of SEQ ID NO: 57, or 100% identical to the nucleic acid sequence of SEQ ID NO: 58.

12. The citrus plant according to claim **9** further comprising a second defensin nucleic acid,

wherein the nucleic acid sequence of the second defensin nucleic acid is at least 98% identical to SEQ ID NO: 46, at least 98% identical to SEQ ID NO: 47, at least 98% identical to SEQ ID NO: 48, at least 98% identical to SEQ ID NO: 49, at least 98% identical to SEQ ID NO: 50, at least 98% identical to SEQ ID NO: 51, or at least 98% identical to SEQ ID NO: 52, at least 98% identical to SEQ ID NO: 53, at least 98% identical to SEQ ID NO: 54, at least 98% identical to SEQ ID NO: 55, at least 98% identical to SEQ ID NO: 56, at least 98% identical to SEQ ID NO: 57, or at least 98% identical to SEQ ID NO: 58.

13. The citrus plant according to claim **9** further comprising a second defensin nucleic acid,

wherein the nucleic acid sequence of the second defensin nucleic acid is at least 99% identical to SEQ ID NO: 46, at least 99% identical to SEQ ID NO: 47, at least 99% identical to SEQ ID NO: 48, at least 99% identical to SEQ ID NO: 49, at least 99% identical to SEQ ID NO: 50, at least 99% identical to SEQ ID NO: 51, or at least 99% identical to SEQ ID NO: 52, at least 99% identical to SEQ ID NO: 53, at least 99% identical to SEQ ID NO: 54, at least 99% identical to SEQ ID NO: 55, at least 99% identical to SEQ ID NO: 56, at least 99% identical to SEQ ID NO: 57, or at least 99% identical to SEQ ID NO: 58.

14. The citrus plant according to claim **9** further comprising a second defensin nucleic acid,

wherein the nucleic acid sequence of the second defensin nucleic acid is 100% identical to SEQ ID NO: 46, 100% identical to SEQ ID NO: 47, 100% identical to SEQ ID NO: 48, 100% identical to SEQ ID NO: 49, 100% identical to SEQ ID NO: 50, 100% identical to SEQ ID NO: 51, 100% identical to SEQ ID NO: 52, 100% identical to SEQ ID NO: 53, 100% identical to SEQ ID NO: 54, 100% identical to SEQ ID NO: 55, 100% identical to SEQ ID NO: 56, 100% identical to SEQ ID NO: 57, or 100% identical to SEQ ID NO: 58.

15. The citrus plant according to claim **12**, wherein the nucleic acid sequence of the first defensin nucleic acid and the nucleic acid sequence of the second defensin nucleic acid are different.

16. The citrus plant according to claim **9**, wherein the plant is orange, grapefruit, lemon, or lime.

17. A citrus composition comprising at least one defensin peptide comprising a first defensin peptide, wherein the amino acid sequence of the first defensin peptide is at least 95% identical to SEQ ID NO: 32, at least 95% identical to SEQ ID NO: 33, at least 95% identical to SEQ ID NO: 34, at least 95% identical to SEQ ID NO: 35, at least 95% identical to SEQ ID NO: 36, at least 95% identical to SEQ ID NO: 37, or at least 95% identical to SEQ ID NO: 38; wherein the peptide has antimicrobial activity in the citrus composition.

18. The citrus composition according to claim **17**, wherein the amino acid sequence of the first defensin peptide is at least 98% identical to the amino acid sequence of SEQ ID NO: 32, at least 98% identical to the amino acid sequence of SEQ ID NO: 33, at least 98% identical to the amino acid sequence of SEQ ID NO: 34, at least 98% identical to the amino acid sequence of SEQ ID NO: 35, at least 98% identical to the amino acid sequence of SEQ ID NO: 36, at least 98% identical to the amino acid sequence of SEQ ID NO: 37, or at least 98% identical to the amino acid sequence of SEQ ID NO: 38.

19. The citrus composition according to claim **17**, wherein the amino acid sequence of the first defensin peptide is 100% identical to the amino acid sequence of SEQ ID NO: 32, 100% identical to the amino acid sequence of SEQ ID NO: 33, 100% identical to the amino acid sequence of SEQ ID NO: 34, 100% identical to the amino acid sequence of SEQ ID NO: 35, 100% identical to the amino acid sequence of SEQ ID NO: 36, 100% identical to the amino acid sequence of SEQ ID NO: 37, or 100% identical to the amino acid sequence of SEQ ID NO: 38.

20. The citrus composition according to claim **17** further comprising a second defensin peptide, wherein the amino acid sequence of the second defensin peptide is at least 95% identical to SEQ ID NO: 32, at least 95% identical to SEQ ID NO: 33, at least 95% identical to SEQ ID NO: 34, at least 95% identical to SEQ ID NO: 35, at least 95% identical to SEQ ID NO: 36, at least 95% identical to SEQ ID NO: 37, or at least 95% identical to SEQ ID NO: 38.

21. The citrus composition according to claim **20**, wherein the amino acid sequence of the second defensin peptide is at least 98% identical to the amino acid sequence of SEQ ID NO: 32, at least 98% identical to the amino acid sequence of SEQ ID NO: 33, at least 98% identical to the amino acid sequence of SEQ ID NO: 34, at least 98% identical to the amino acid sequence of SEQ ID NO: 35, at least 98% identical to the amino acid sequence of SEQ ID NO: 36, at least 98% identical to the amino acid sequence of SEQ ID NO: 37, or at least 98% identical to the amino acid sequence of SEQ ID NO: 38.

22. The citrus composition according to claim **20**, wherein the amino acid sequence of the second defensin peptide is 100% identical to the amino acid sequence of SEQ ID NO: 32, 100% identical to the amino acid sequence of SEQ ID NO: 33, 100% identical to the amino acid sequence of SEQ ID NO: 34, 100% identical to the amino acid sequence of SEQ ID NO: 35, 100% identical to the amino acid sequence of SEQ ID NO: 36, 100% identical to the amino acid sequence of SEQ ID NO: 37, or 100% identical to the amino acid sequence of SEQ ID NO: 38.

23. The citrus composition according to claim **20**, wherein the amino acid sequence of the first defensin peptide and the amino acid sequence of the second defensin peptide are different.

* * * * *