

(72)

27517	102
27612	6308
27278	13 08
27712	5415
27403	214

(74)

:

(54)

가

/
/

(Fusarium), (Trichothecium) (Myrothecium)
 (F. crookwellense), (F. culmorum), (F. equiseti), (F. acuminatum),
 inearum(: Gibberella zeae)], (F. lateritium), (F. poae), [F. gram
 [F. sambucinim(: G. pulicaris)] (F. sporotrichiodes) [
 : Marasas, W.F.O., Nelson, P.E., Toussoun, T.A. 1984].

[: A. E. Desjardins and T. M Hohn, Mycotoxins in plant pathogenesis. Mol. Plant - Microbe Interac t. 10(2):147 - 152, 1997]

, 19
T - 2
(akakabi - byo)
, " DON)

가

가 가

가 (" ")

DNA

가

DON 가 C3 3 - O -
[: S. P. McCormick, N. J. Alexander, S. C. Trapp, and T. M. Hohn. Disruption of TRI101, the gene encoding trichothecene 3 - O - adetyltransferase, from *Fusarium sporotrichioides*. Applied. Environ. Microbiol. 65(12):5252 - 5256, 1999]. C3 - OH
(, " 3ADON") [: Kimura et al. infra].

3 - O -
[: Kimura et al., Biosci. Biotechnol. Biochem., 62(5) 1033 - 1036 (1998), Kimura et al., FEBS Letters, 435, 163 - 168 (1988)]
3 - O - 가
가 [: Hohn, T. M. et al., Molecular Genetics of Host - Specific Toxins in Plant Disease, 17 - 24 (1998), Kimura et al., J. Biological Chemistry, 273(3) 1654 - 1661 (1998)].

3-O-

가

3-O-

가

, DON
3ADON

, 3-O-

가

DON
3ADON

가

3-O-

, 3ADON

2

DON 3ADON

가

()

C-3

C-3

(Fusarium pseudograminearum)

가

가 1, 5 7

가 1, 5 7

1, 5 7 80 80
 , 1, 5 7 50 2
 1 50 , 1, 5 7 1, 5 2
 7 18 21 , 18 가 1, 5

3- T - 2 , HT - 2 , , 4,15 - (, " DAS"),
 , 3,15 - , ; B : 15 -
 , 4 - (- X), 4,15 - , 4,7,15 - DON

DAS DON

3 - O -

2, 6 8

(a) 가 ,

(b) ,

(c)

(d) 가 ,

가

가 , 가

C - 3

- (a) 가 ,
- (b) ,
- (c) ,
- (d) 가
- (e) , (d) 가 ,

가 ,

가

3 - 0 -

가 ,

가 ,

2

가

3,15 - (- X), 4,15 - T - 2 , HT - 2 , ; B : 15 - , DAS, 3 - , 4 -
 , 4,7,15 - DON

가

가

가

" " / .
 , DNA .
 DNA RNA / " 2 DNA " DNA " "

" " " " " DNA"
 , , DNA
 , DNA
 " " " " 가
 (,)
 () /
 [: Batzer et al., Nucleic Acid Res. 19: 5081 (1991); Ohtsuka et al., J. Biol. Chem. 260: 2605 - 2608 (1985); Rossolini et al., Mol. Cell. Probes 8: 91 - 98 (1994)]. " " " " "
 " , cDNA, mRNA 가

가 , " " , ,
 , ,
 " " , ,
 45% , 65% , 75% , 85% ,
 90% , 95% , 99% ,
 가 50 100
 , 가 150 . 가

(Smith - Waterman sequence alignment algorithm)
 [: Waterman, M.S. Introduction to Computational Biology: Maps, sequences and genomes. Chapman & Hall. London: 1995. ISBN 0 - 412 - 99391 - 0, <http://www-hto.usc.edu/software/seqaln/index.html>]. S , 1.16 : : 1, : 0.33, - : 2, - : 2 .

NA RNA " " (,) D
 가 " " ,

가 [: Tijssen (1993) Laboratory Techniques in Biochemistry and Molecular Biology - Hybridization with Nucleic Acid Probes part I chapter 2 " Overview of principles of hybridization and the strategy of nucleic acid probe assays" Elsevier, New York]

(T_m) 5 , " "

T_m 50%가 (pH) .

T_m 100

42 1mg 50%

72 15 0.15M N

aCl Sambrook, infra]. , 65 15 0.2x SSC [SSC :

100 , 100 45 15 1x SSC .

10 50) 40 15 4 - 6x SSC (

Na , 0.01 1.0M Na () , pH 7.0 8.3 1.0M

30 가 ,

2 () ,

가 , , 가

가

4, 1mM EDTA / : 50 7% (SDS), 0.5M NaPO₄, 1mM EDTA , 50 2X SSC, 0.1% SDS ,

50 7% (SDS), 0.5M NaPO₄, 1mM EDTA , 50 7%

(SDS), 0.5M NaPO₄, 1mM EDTA , 50 0.5X SSC, 0.1% SDS ,

% SDS , 50 7% (SDS), 0.5M NaPO₄, 1mM EDTA , 50 7%

1X SSC, 0.1% SDS (SDS), 0.5M NaPO₄, 1mM EDTA , 65 0.

1X SSC, 0.1% SDS , 50 21 , 18 80

6 8 45% , , 2,

3-O-

" "

BLAST

45% , 65% , 7

5% , 85% , 90% , 95% ,
 99% .
 2, 6 8 45% , , 3-
 O-

[: Smith & Waterman, Adv. Appl. Math. 2: 482 (1981)], [: Needleman & Wunsch, J. Mol. Biol. 48: 443 (1970)], [: Pearson & Lipman, Proc. Nat'l. Acad. Sci. USA 85: 2444 (1988)], [: P (GAP, BEST FIT, FASTA, TFASTA, Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), [: Ausubel et al., infra]

[: Altschul et al., J. Mol. Biol. 215: 403 - 410 (1990)] BLAST . BLAST 가 T W (HSP) . T (Altschul et al., 1999). HSP 가 가 M(: 0) N(; 0) 가 , X , BLAST W, T X가 (E) 10, 100, M=5, N= -4 (W) 3, (E) 10 BLOSUM62 (W) 11, BLASTP [: Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89: 10915 (1989)].

BLAST , 2 [: Karlin & Altschul, Proc. Nat'l, Acad. Sci. USA 90: 5873 - 5787 (1993)]. BLAST 가 (P(N)) , 2 가

가 0.1 , 0.01 가 0.001

2 가 1 2 2

2 , , " " 1 x 10⁴ M⁻¹ 1 x 10⁶ M⁻¹

: , 가 , 가

: DNA , ,

" " , " " 가 가

C - 3

3 - 0 -

3 - 0 -

RNA

RNA 65

1, 5 7 (SDS), 0.5M pH 7.0, 1mM EDTA, 10mg/mol BSA
, 65 0.5% BSA(V), 5% SDS, 40mM pH 7.0, 1mM EDTA, 0.25M
65 1% SDS, 40mM pH 7.0, 1mM EDTA, 0.125M , 65
1% SDS, 40mM pH 7.0, 1mM EDTA .

7

6

10nmol (, " TAS")/mg /15 5nmol
TAS/mg /15 , 1nmol TAS/mg /15 , 0.8nmol TAS/mg
/15 , 0.5nmol TAS/mg /15 , 0.25nmol TAS/mg /15
, 0.1nmol TAS/mg /15 , 0.05nmol TAS/mg /15

0.01nmol TAS/mg /15

15mg/ml, 20mg/ml, 5mg/ml, 25mg/ml, 10mg/ml

0%, 20%, 30%, 40%

50%, 60%, 70%, 80%, 90%

A B

(A) (B)

C - 8

DON C - 8

C - 3

HT - 2, 15 -

DAS, 3 -

4 -

3,15 -

(- X), 4,15 -

T - 2

4,7,

DON,

가

가

10%

20%

40%

50%

9

가

가

10%

20%

40%

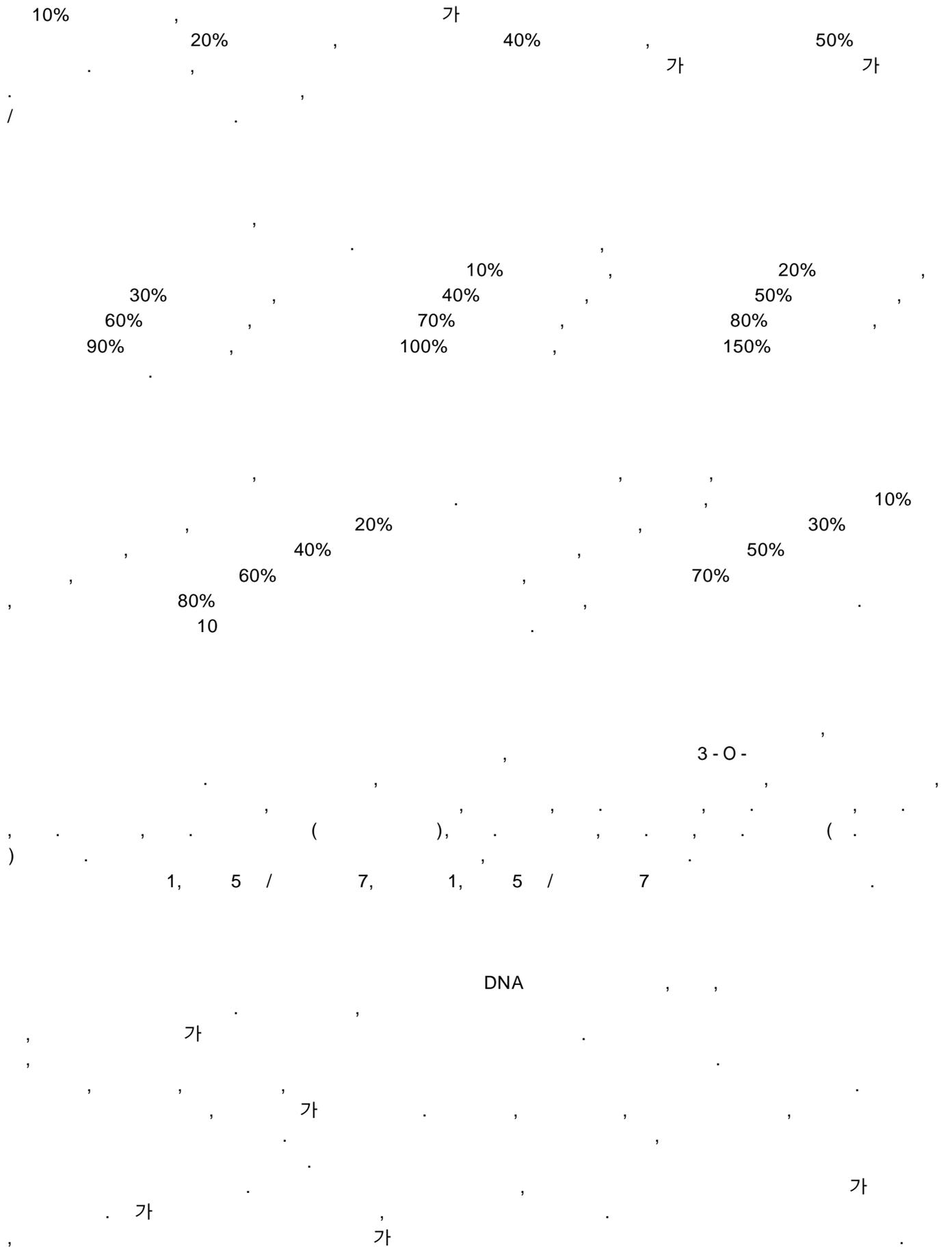
50%

가

9

가

가



가

가

, CaMV 35S
(Arabidopsis
5,689,044).

가

, CaMV 35S , tml

가 PR - 1

가

rbcS E9

Adhl

[: Perlak et al., Proc. Natl. Acad. Sci. USA 88: 3324 (1991); Koziel et al., Bio/technol. 11: 194 (1993); Fennoy and Bailey - Serres. Nucl. Acids Res. 21: 5294 - 5300 (1993)].

[: Murray et al. Nucl. Acids Res. 17: 477 - 498 (1989), table 4; Campbell and Gowri Plant Physiol. 92: 1 - 11 (1990)].

mai et al. J. Biol. Chem.263: 15104 - 15109 (1988)].

[: Unger et al. Plant Molec. Biol.13: 411 - 418 (1989)].

cDNA , DNA

ER, [: Koehler & Ho, Plant Cell2: 769 - 783 (1990)].

[: Shinshi et al. Plant Molec. Biol.14: 357 - 368 (1990)].

가

가

가

가

nptII [: Messing & Vi

erra. Gene19: 259 - 268 (1982); Bevan et al., Nature304: 184 - 187 (1983)],

bar [: White et al., Nucl. Acids Res18: 1062 (1990), Spencer et al., Theor. App

l. Genet79: 625 - 631 (1990)],

hph [: Blochinger & Di

ggelmann, Mol Cell Biol4: 2929 - 2931],

dhfr [: Bourouis et

al., EMBO J.2(7): 1099 - 1104 (1983)],

EPSPS [:

4,940,935 5,188,642],

manA[: 5,767,378 Miles & Guest, GENE, 32: 41 - 48

(1984)], BASTA PAT 가 [: Sung H. Park et al., In Vitro Cell. De

v. Biol. - Plant, 34: 117 - 121 (1998)]

가

(Agrobacterium tumefaciens)

가

T - DNA

, pBIN19[: Bevan, Nucl. Acids Res. (1984)]

pCIB10,

pCIB200 pCIB2001

[: 5,639,949].

T - DNA

T - DNA

(, PEG)

pCIB3064, pSOG19 pSOG35 [:

5,639,949].

가

, Ti

가

DNA

DNA

PCG

PEG

UC703

CG000526

WO 98/54961

09/089,111

: M. Cho, J. Wong, C. Marx, W. Jiang, P. Lemaux and

B. Buchanan (1999).

h

()

[: PNAS 96: 14641 - 14646; S. Zhang, M. Cho, T. Koprek, R. Yun, P. Bregitzer and P. Lemaux (1999)

].

(: Avena sativa L.)

(가 : Hordeum vulgare L.)

[: Plant Cell Rep.

18: 959 - 966; P. Bregitzer, S. Harlbert and P. Lemaux (1998)].

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[: Plant sci. 138: 229 - 244; P. Lemaux, M. Cho, S. Zhang, and P. Bregitzer

er (1998)].

:

가

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Improvement of Cereal Crops, Kluwer Academic Publ, Dordrecht, The Netherlands, pp 255 - 316; S. Zhang,

R. Williams - Carrier, D. Jackson, and P. Lemaux (1998)].

(

: Zea mays L.)

(

가 .)

CDC2Zm KNOTTED1

[: Planta 204: 542 - 549; D. McElroy, J. Louwerse, S. McElroy and P. Lemaux (1997)].

Ac/Ds

[: Plant J. 11: 157 - 165; S. Tingay, D. McE

Iroy, R. Kalla, S. Fieg, M. Wang, S. Thornton and R. Brettell (1997)].

-

[

: The Plant J. 11: 1369 - 1376; J. Qureshi, Z. Basri, R. Singh, R. Burton, M. Dalton, J. Kollmorgen and G.

Fincher. 1988]. (가 .) 2가

-

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onference of Australian Society for Biochemistry and Molecular Biology, September 28 - October 1, 1998,

Adelaide, Australia; J. Qureshi, R. Singh, Z. Basri, R. Stewart, R. Burton, J. kollmorgen and G. Fincher(19

97)]. [: Proc. 8th. Aust. Barley Technical symp.

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nd Y. Wan (1996)].

-

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k, R. Hansch, A. Nerlich, R. Mendel and J. Schulze (1996)].

[: Plant Sci. 119: 79 - 91; T. Hagio, T. hirabayashi, H. Machii an

d H. Tomutsune(1995)].

-

(가 .)

[: Plant Cell Rep. 14: 329 - 334; H. Funatsuki, H. Kuroda, M. Kihara, P. Lazzeri, E. Muller, H. Lorz an

d I. Kishinami (1995)].

DNA

[: TAG 91: 707 - 71

2; A. Jahne, D. Becker, R. Brettschneider and H. Lorz (1994)].

,

-

[

: TAG 89: 525 - 533; Y. Wan and P. Lemaux (1994)].

[: Plant Physiol. 104: 37 - 48]

가

/

가

가

^R), (Apron^R) - (Actellic^R) (TMTD^R)
가

가

가

가

2

S, DON T - 2

DA

가

2 DNA

, , 2, 6 8

, DAS / DON / T - 2 2, 6 8

6 8

2,

1 90µg/ml 1, 5 7

가 , DNA 2 DNA

:

1
cDNA

2 1

3 DNA

4 DNA

5

DNA

6 3

7
accharomyces cerevisiae) DNA

(S

8 5

9 pCIB9818 DNA

10 pAgroTRIr DNA

11 pNOV1704 DNA

가

, 가

1: pNOV1700, pCIB9818, pAgroTRIr pNOV1704

1. pNOV1700

pNOV1700 1999 3 19 (Agricultural Research Service, Patent Culture Collection) (NRRL), (Northern Reg
 ional Research Center: 61604 1815) ,
 NRRL B - 30117 .
 , pNOV1700 (Z. mays)
 1 .

2. pCIB9818

pCIB9818 9 DNA 6111 869
 1011 1047 1993 , 9 12 1993 .
 2090 3193 가 , 3248
 3355 PEPC #9 3357 3434 CaMV 35S

3. pAgroTRlr

pAgroTRlr 10 DNA 13,737 , pAgro
 TRlr (Arabidopsis thaliana) UBI 3 [
 : S. Norris, S. Meyer, and J. Callus, Plant Molecular Biology 22: 895 - 906 (1993)] nos
 1
 가 .

4. pNOV1704

pNOV1704 11 DNA 12949 . 11 11
 1992 (1: 895 1010 1: 1046 1992
) 2089 3192 가 3557 3688
 . pNOV1704 11234 12662
 1 3 - O - 12667 12935 nos
 9218 11218 . (1: 10110 10224 1: 1
 0225 11218) .

2: ,

(0.75 - 1.25mm) (10% X 10) , 3% ,
 3mg/ 2,4 - D (), 150mg/ 75mg/ 0.7%
 가(3MS3S) MS [: Murashige and Skoog, (1962) Physiol. Plant 15: 473 - 439]

6 7 . 4 28 5 10 (15% 가 가
) , 2.5cm .
 1 pNOV1700 PvuII XmnI , 1
 NOS 4117bp
 1 pCIB9818 AscI , UBI , 가 CaMV 35S
 4246bp
 DNA (Stanford) 0.3µm
 DNA 5µg, 2.5M CaCl₂ 50µl 0,1M 20µl 50% 50µl 3m
 가 , DNA/
 70µl /DNA 6 .
 2 3µg DNA(2 5µg) 1.
 0mg 1100psi ,
 24 , 3MS3S , 3 .

3 /
 가 NAA 2,4 - D 1mg/ GA3(A3), NAA(1 -)
 3MS3S(NG) . 10g/ 5g/ 가 (NG1M.5S).
 2 , 2 , (light room)
 (MS2S.5M). 2 , 5g/ , 20g/ 가
 4 , , 가
 가 , GA7's
 가 1/2MS 15g/
 가 , PCR

3:

1 pAgroTRIr [: Dower, W.J., Mol. Biol. Rep 1:5 (1987)
] GV3101[: Bechtold, N. et al., CR Acad. Sci. Paris, Sciences d
 e la vie, 316:1194 - 1199 (1993)] . pAgroTRIr YEB + 100
 100 GV3101 25ml 30 .
 500ml 5ml , 30 . 60
 0nm OD , GSA 15 5K . " 1M

" , 600nm O.D. 0.08 200 μ l 가 .
 4 3 500ml .
 , 15 .
 , .
 3 4 , 1 . , 1
 , 2 . , 2 4
 . 3 , .
 4:

I [: Green et al 1983, Somatic cell genetic systems in corn. A. Fazelahmad, K. Downey, J. Schultz, RW Voellmy, eds. Advances in Gene Technology: Molecular Genetics of Plants and Animals. Miami Winter Symposium Series, Vol. 20. Academic Press, NY]
 가 1.5 2.0mm . 2% 5mg/ D 14 - [: Duncan et al. (1985) Planta 165: pp322 - 332]
 14 . 2% 0.5mg/ 2,4 - D가 D
 . 6 ,
 4 12% 가

8 10mm .
 1 pNOV1700 PvuII XmnI , 1
 , NOS 4117bp .
 1 pCIB9818 AscI , 4246bp
 . DNA (DuPont Biolistics)
 . 2 3 μ g 6 .
 PDS - 1000He : 8mm, 10mm
 7cm. 650psi 2 . 200 X 200
 (McMaster - Carr, New Brunswick, NJ)
 7 ,

1% 3 5 ,
 1.5% .
 가 10 20 2
 .
 2% 1% (MS2S+1M) 0.25mg/ 0.5mg/
 MS [: Murashige and Skoog, 1962(1962) A revised medium for rapid growth and bioassays with tobacco tissue cultures. *Physiol. Plant* 15: 473 - 497] . 2 ,
 MS2S+1M . MS3S

(Magenta)

5:

1 . DNA
 , PCR
 (5' - acgaatcattcaccgaggag - 3')(3) (5' - ctcacactctcaggcttacc - 3')(4) . 2
 1 650 nt

b.

RNA
 1 RNA
 2 3 429 nt Styl . RNA

6: 3 - O -

(a) : 2 4
 3 1 x 1/8in (50mg)

(b) : 2ml ,
 24 , 0.4ml 가 . - 80
 10
 5 14,000rp
 m , 가 5 ,

, DAS 2 μ l (, pH 7.0 50mM 20%). DON .

CoA , [¹⁴ C] - CoA NEN cat. #NEC313(60mCi/mmol 0.02mCi/ml) 2 μ l.

pH 7.0 50 μ l.

가 , 30 15 .

, pH 7.0 10 μ l.

15 , 100 μ l 가 , 2 14,
 000rpm 2 . 50 μ l ,
 가 . 2

20 2 , 0.60 13.4nmol / μ g /15 .

0.1 0.2nmol / μ g /15 .

3 , 3.8 28nmol / μ g /15 5 .

0.1nmol / μ g /15 가 .

2 4 , 11.1 17.9nmol / μ g /15
 . 0.2nmol / μ g /15 -

17 183nmol/ μ g/15 , pNOV1704
 16 .

7:

CPR 250ml , KOH pH 6.5 .

½ MS 0.54g

½ MS 1.25ml

1%() 2.50g

가 1%(2.50g) 가 , . 50mg/ml 25
 ml 가 .

55 , DAS DON 가 (, 1.7ml 4, 8 16 μ l 10mg/m
 l DON 2, 4 6 μ l 50mg/ml DAS). 0.5ml 48

1/3 x 1/8in

가 . , 2
 0 2 4 . (pH) 2
 DAS DON

8:

A.

DAS DON(20mg/ml) MS3S (MS 4.3g/ , MS 100X, 30g
 / 가 8g/) 1000 1200 / (100mm) . 4

3 DAS
) . DAS (, DAS

B.

1. :

[: R. H. Proctor, T. M. Hohn, and S. P. McCormick. Reduced virulence of *Gibberella zeae* caused by disruption of a trichothecene toxin biosynthetic gene. *Mol. Plant - Microbe Interact.* 8(4): 593 - 601, 1995]

UV ml 1×10^6
 7 10 V-8 가
 , 2 2 10% 0.05
 % 15 5
 10 , 10cm (20).
 1 - 2cm $\frac{3}{4}$, 가 2 - 4cm , 1 22 16
 8 , 1 , 2 ,
 가 가 40

2 , 17%가 50% 43%가

2. :

가() 12 25
 , 2 1×10^6 /ml
 , 5 1ml / ,
 2 30 4 55
 가 14 24 14 24 12
 가 , 가
 가 가 /

9:

A.

12 V-8 가 (V-8) (가 :)
 25 , 2
 5×10^4 /ml

2
가
20 μ l (1000)
21 65 70 72
가 18

1 6
44.75% 10.40 31.20% 가 ,
0.874 29.1nm ol/ μ g/15 6

B.

V-8 가 (V-8) (: 12) 25
2 5 x 10⁵ /ml
2ml () 가 18
(0.4ml) 가 18 4
가 5 7
가 : 1 0%; 2 1 3%, 3 4 10%, 4 11 25%, 5 26 50%,
6 51 75%, 7 76 100%. 가

10:

50g (, (Retsch) ZM1 ,
: BrinkmanInstruments, Inc., Rexdale, Ontario, Romer Series3 II Mill, Union, Missouri, USA)
, DON 가 ,
, DONtest TAG™ (VICAM, LP, 313 Pleasant Street, Watertown, MA 02472)

(, Romer Kabs, Inc, Union, Missouri, USA Trilogly Ananyt
ical Laboratory, Inc., Beaufort, Missouri, USA)
. DONtest TAG™ , DON
DON

11: 가 1

A. 가

(Ashbya gossypi)
DNA

1

DAS 1.56ng/ml 196pg/ml

B. 가

3 0.1% 가 , 2 22 16 0, 5 1
0µg/ml DAS 8 DAS

5µg/ml 2 , 11 6 2 , DAS , 11 1
0 9 11 6 2 , DAS , 11 1
AS D

가가

가

(57)

1.

가

2.

1 , 가

3.

2 , C - 3

4.

1 , , C - 3

5.

4 , (Fusarium), (Fusarium graminearum)

6.

2 , 가 ,

7.

6 , 가 (Fusarium sporotrichioides)

8.

1 7 , 가 1, 5 7

9.

8 , 가 1, 5 7

10.

8 , 1, 5 7 80 80
 50 , 1, 5 7 50 21
 18 21 , 가 1, 5 7 1, 5 21
 18 18

11.

10 , 가 1, 5 7 18

12.

1 11 , T - 2 , HT - 2 , , 4,15 -
 (DAS), 3 - , 3,15 - , ; B
 : 15 - , 4 - (- X), 4,15 - , 4,7,15 -
 (DON) , DON DAS

13.

2 , 1 6 9

14.

13 ,
3 - 0 -

15.

14 , 2, 6 8

16.

2 15 , , ,

17.

2 15 .

18.

(a) 가 ,

(b) ,

(c)

(d) 가 ,

19.

18 , 가

20.

19 , .

21.

2 16 18 20 ,

22.

20 , .

23.

2 16 18 20

C - 3

24.

18 24

25.

(a) 가

(b) ,

(c) ,

(d) 가

(e) , (d) 가 ,

26.

25 , .

27.

2 가 16 25 26 ,

28.

27 , 가 .

29.

3 - 0 -

30.

29 , 가 .

31.

30 , 가 .

32.

31 , 가 .

33.

29 , T - 2 , HT - 2 , , DAS, 3 - , 3,15 -
 (-X), 4,15 - , , 4,7,15 - ; B : 15 - DON , , 4 - .

34.

18 20 가 .

35.

25 26 가 .

36.

27 28 가 .

- <110> Syngenta participations AG
- <120> Transgenic plant resistant to mycotoxins and methods
- <130> 5-2000-054004-2
- <150> US 09/282,995
- <151> 1999-03-31
- <150> US 09/502,852
- <151> 2000-02-11
- <160> 11
- <170> KOPATIN 1.71
- <210> 1
- <211> 1403
- <212> DNA
- <213> Fusarium sporotrichioides
- <400> 1

```

atcaaaatgg cgcacaag cagcacaagc agccagtctt ttgacataga gctcgacatc 60
atcggccagc aaccgectct tctttcaatc tacaccaga tcagtctcgt ttaccccgtc 120
tctgatccct cccagtatcc caccatcgtc agcacccttg aggaaggcct aaaacgcctc 180
tctcaaact tcccatgggt cgcgggccag gtcaagaccg agggcatcag cgaaggaaac 240
acaggaactt ccaagatcat tccatatgag gagacacccc gtcttgtggt gaaagacctc 300
cgtgatgatt cctcagcgcc aacgatcgag gggttgagaa aggcggggtt ccccttagag 360
atgtttgacg agaacgctgt cgtccgagg aagacattag ctatcggacc tggcaatggc 420
cccaacgacc cgaagcctgt gttgctattg cagctcaact tcattaaggg cggactcatt 480
ctcaccgtca acggacaaca tgggtgctatg gacatgacag gacaagatgc aattattcgt 540
cttctctcca aggcgtgccg caacgaatca ttcaccgagg aggaaatctc ggccatgaac 600
ctcgatcgca agacggtagt ccctctcctt gaaaactaca aagttggtcc tgagctagac 660
caccagatcg ccaaactgc gctgctggc gacgctccac ccgcaccggc caaggcaagc 720
    
```

tgggcgttct tttcattcac tcccaaggcc ctctcggagc tgaaagacgc agccacaaag 780
 actccttgacg cgtcgtccaa gtttgtgtca actgatgatg ctctttcggc gtttatctgg 840
 caatcaacct cgcgctacg tctcgcgaaga ttggatgctt ccacacctac tgaattctgc 900
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 aacatgacct accatgactc gaccgtcgcc gaaatcgcca acgaaccact tggcgcaaca 1020
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<210> 2

<211> 459

<212> PRT

<213> *Fusarium sporotrichioides*

<400> 2

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 Ser Leu Val Tyr Pro Val Ser Asp Pro Ser Gln Tyr Pro Thr Ile Val
 35 40 45
 Ser Thr Leu Glu Glu Gly Leu Lys Arg Leu Ser Gln Thr Phe Pro Trp
 50 55 60
 Val Ala Gly Gln Val Lys Thr Glu Gly Ile Ser Glu Gly Asn Thr Gly
 65 70 75 80
 Thr Ser Lys Ile Ile Pro Tyr Glu Glu Thr Pro Arg Leu Val Val Lys
 85 90 95
 Asp Leu Arg Asp Asp Ser Ser Ala Pro Thr Ile Glu Gly Leu Arg Lys
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 Ala Gly Phe Pro Leu Glu Met Phe Asp Glu Asn Val Val Ala Pro Arg
 115 120 125
 Lys Thr Leu Ala Ile Gly Pro Gly Asn Gly Pro Asn Asp Pro Lys Pro
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 Val Leu Leu Leu Gln Leu Asn Phe Ile Lys Gly Gly Leu Ile Leu Thr
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 Val Asn Gly Gln His Gly Ala Met Asp Met Thr Gly Gln Asp Ala Ile
 165 170 175
 Ile Arg Leu Leu Ser Lys Ala Cys Arg Asn Glu Ser Phe Thr Glu Glu
 180 185 190
 Glu Ile Ser Ala Met Asn Leu Asp Arg Lys Thr Val Val Pro Leu Leu
 195 200 205
 Glu Asn Tyr Lys Val Gly Pro Glu Leu Asp His Gln Ile Ala Lys Pro
 210 215 220
 Ala Pro Ala Gly Asp Ala Pro Pro Ala Pro Ala Lys Ala Ser Trp Ala
 225 230 235 240
 Phe Phe Ser Phe Thr Pro Lys Ala Leu Ser Glu Leu Lys Asp Ala Ala
 245 250 255
 Thr Lys Thr Leu Asp Ala Ser Ser Lys Phe Val Ser Thr Asp Asp Ala

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<211> 451

<212> PRT

<213> *Fusarium graminearum*

<400> 6

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 35 40 45
 Phe Ser Glu Ala Val Pro Trp Val Ala Gly Gln Val Lys Ala Glu Gly
 50 55 60
 Ile Ser Glu Gly Asn Thr Gly Thr Ser Phe Ile Val Pro Phe Glu Asp
 65 70 75 80
 Val Pro Arg Val Val Val Lys Asp Leu Arg Asp Asp Pro Ser Ala Pro
 85 90 95
 Thr Ile Glu Gly Met Arg Lys Ala Gly Tyr Pro Met Ala Met Phe Asp
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 Glu Asn Ile Ile Ala Pro Arg Lys Thr Leu Pro Ile Gly Pro Gly Thr
 115 120 125
 Gly Pro Asp Asp Pro Lys Pro Val Ile Leu Leu Gln Leu Asn Phe Ile
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 Lys Gly Gly Leu Ile Leu Thr Val Asn Gly Gln His Gly Ala Met Asp
 145 150 155 160
 Met Val Gly Gln Asp Ala Val Ile Arg Leu Leu Ser Lys Ala Cys Arg
 165 170 175
 Asn Asp Pro Phe Thr Glu Glu Glu Met Thr Ala Met Asn Leu Asp Arg
 180 185 190
 Lys Thr Ile Val Pro Tyr Leu Glu Asn Tyr Thr Ile Gly Pro Glu Val
 195 200 205

Asp His Gln Ile Val Lys Ala Asp Val Ala Gly Gly Asp Ala Val Leu
 210 215 220
 Thr Pro Val Ser Ala Ser Trp Ala Phe Phe Thr Phe Ser Pro Lys Ala
 225 230 235 240
 Met Ser Glu Leu Lys Asp Ala Ala Thr Lys Thr Leu Asp Ala Ser Thr
 245 250 255
 Lys Phe Val Ser Thr Asp Asp Ala Leu Ser Ala Phe Ile Trp Lys Ser
 260 265 270
 Ala Ser Arg Val Arg Leu Glu Arg Ile Asp Gly Ser Ala Pro Thr Glu
 275 280 285
 Phe Cys Arg Ala Val Asp Ala Arg Pro Ala Met Gly Val Ser Asn Asn
 290 295 300
 Tyr Pro Gly Leu Leu Gln Asn Met Thr Tyr His Asn Ser Thr Ile Gly
 305 310 315 320
 Glu Ile Ala Asn Glu Ser Leu Gly Ala Thr Ala Ser Arg Leu Arg Ser
 325 330 335
 Glu Leu Asp Pro Ala Ser Met Arg Gln Arg Thr Arg Gly Leu Ala Thr
 340 345 350
 Tyr Leu His Asn Asn Pro Asp Lys Ser Asn Val Ser Leu Thr Ala Asp
 355 360 365
 Ala Asp Pro Ser Thr Ser Val Met Leu Ser Ser Trp Ala Lys Val Gly
 370 375 380
 Leu Trp Asp Tyr Asp Phe Gly Leu Gly Leu Gly Lys Pro Glu Thr Val
 385 390 395 400
 Arg Arg Pro Ile Phe Glu Pro Val Glu Ser Leu Met Tyr Phe Met Pro
 405 410 415
 Lys Lys Pro Asp Gly Glu Phe Cys Ala Ala Leu Ser Leu Arg Asp Glu
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<210> 7

<211> 1425

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 7

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<210> 8

<211> 474

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 8

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Tyr Lys Leu Tyr Thr Gln Ile Cys Ser Ile Tyr Arg Val Pro Asp Pro
35 40 45
Ser Ala His Asp His Ile Val Asn Thr Leu Thr Arg Gly Leu Glu Thr
50 55 60
Leu Ala Lys Asn Phe Gln Trp Leu Ala Gly Asn Val Val Asn Glu Gly
65 70 75 80
Ala Asp Glu Gly Asn Thr Gly Thr Tyr Arg Ile Val Pro Ser Asp Lys
8 90 95
Ile Pro Leu Ile Val Gln Asp Leu Arg Glu Asp Leu Ser Ala Pro Thr
100 105 110
Met Asp Ser Leu Glu Lys Ala Asp Phe Pro Ile Tyr Met Leu Asp Glu
115 120 125
Lys Thr Phe Ala Pro Cys Met Thr Ile Asn Pro Pro Gly Asn Thr Ile
130 135 140
Gly Met Ala Ala Lys Ser Gly Pro Val Phe Ala Val Gln Ala Asn Phe
145 150 155 160
Ile Ser Gly Gly Leu Val Leu Thr Ile Val Gly Gln His Asn Ile Met
165 170 175
Asp Ile Thr Gly Gln Glu Ser Ile Ile Asn Leu Leu Asn Lys Ser Cys
180 185 190
His Gln Lys Pro Phe Ser Asp Glu Glu Leu Leu Ile Gly Asn Ile Asp
195 200 205
Lys Ser Lys Ser Ile Pro Leu Phe Asp Glu Thr Trp Glu Pro Asp Thr
210 215 220
Thr Leu Val His Glu Ile Val Glu Thr Ser Arg Asn Thr Ser Gly Glu
225 230 235 240
Glu Lys Glu Gln Ser Cys Ser Ser Asn Ser Thr Trp Ala Tyr Val Glu
245 250 255
Phe Ser Ala Ile Ser Leu Gln Asn Leu Arg Ile Leu Ala Met Gln Thr
260 265 270

Cys Thr Ser Gly Thr Lys Phe Val Ser Thr Asp Asp Ile Val Thr Ala
 275 280 285
 Phe Ile Trp Lys Ser Val Ser Arg Ala Arg Leu Ser Arg Leu Lys Pro
 290 295 300
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 305 310 315 320
 Gly Leu Pro Glu Thr Tyr Pro Gly Leu Leu Val Asn Met Thr Phe Asn
 325 330 335
 Thr Gly Ser Leu Lys Ser Leu Asp His Lys Ser Leu Gly Val Leu Ala
 340 345 350
 Ser Gln Ile Arg Arg Lys Leu Asp Pro Lys Val Phe Asp Leu Ala Tyr
 355 360 365
 Asn Thr Cys Ala Leu Ala Thr Leu Leu Ser Arg Cys Pro Asp Lys Thr
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 385 390 395 400
 Ser Ser Trp Ala Lys Val Ser Leu Tyr Asp Val Asp Phe Asn Leu Gly
 405 410 415
 Leu Gly Lys Pro Lys Ser Val Arg Arg Pro Arg Phe Ile Ser Leu Glu
 420 425 430
 Ser Leu Ile Tyr Phe Met Pro Arg Ser Ser Arg Gly Glu Met Val Val
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<210> 9

<211> 6111

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Plasmid pCIB9818, a 6111 base pair circular plasmid comprising the phosphate mannose isomerase selectable marker (base pair 2090 to 3193)

<400> 9

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<211> 13737

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Plasmid pAgroTRIr, a 13,737 base pair circular binary vector comprising a selectable marker and the polynucleotide region of SEQ ID NO: 1

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tcgtttacc cgtctctgat cctcccagt atcccacat cgtcagcacc cttgaggaag 180
gcctaaaacg cctctctcaa accttcccat gggtcgcggg ccaggtcaag accgagggca 240

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<223> Description of Artificial Sequence: Plasmid pNOV1704, a 12949 base pair circular binary vector comprising the phosphate mannose isomerase selectable marker sequence (base 2089 to 3192), and the trichothecene 3-O-acetyl transferase sequence of SEQ ID NO.1 (base 11234 to 12662)

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