US 20080295196A1

(19) United States

(12) Patent Application Publication

(10) Pub. No.: US 2008/0295196 A1

(43) Pub. Date: Nov. 27, 2008

Abad et al.

(54) **GENES AND USES FOR PLANT IMPROVEMENT**

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(21) Appl. No.: **12/001,025**

(22) Filed: **Dec. 6, 2007**

Related U.S. Application Data

(60) Provisional application No. 60/873,247, filed on Dec. 6, 2006.

Publication Classification

(51) **Int. Cl.**

A01H 1/04	(2006.01)
C12N 5/10	(2006.01)
A01H 5/00	(2006.01)
A01H 1/02	(2006.01)
C12Q 1/68	(2006.01)

(52) **U.S. Cl.** **800/275**; 435/419; 800/298; 435/6; 800/312; 800/314; 800/320; 800/320.1; 800/320.2; 800/320.3

(57) **ABSTRACT**

Transgenic seed for crops with improved traits are provided by trait-improving recombinant DNA in the nucleus of cells of the seed where plants grown from such transgenic seed exhibit one or more improved traits as compared to a control plant. Of particular interest are transgenic plants that have increased yield. The present invention also provides recombinant DNA molecules for expression of a protein, and recombinant DNA molecules for suppression of a protein.

FIG. 1

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SEQ ID NO:
10652       ------------------------------------------------------------
2928        MPPAPWPTPRTVRQAAELHAHLTTSGRLLHPPSAHHLLNSLVNCLPPSDPLHLRYALHLF
1305        ------------------------------------------------------------
17785       ------------------------------------------------------------
18398       ------------------------------------------------------------
17426       ------------------------------------------------------------
17988       ------------------------------------------------------------
5946        ------------------------------------------------------------
12948       ------------------------------------------------------------
8522        ------------------------------------------------------------
5094        ------------------------------------------------------------
2009        ------------------------------------------------------------
9559        ------------------------------------------------------------
17372       ------------------------------------------------------------
8093        ------------------------------------------------------------
761         ------------------------------------------------------------
11535       ------------------------------------------------------------
7750        ------------------------------------------------------------
13784       ------------------------------------------------------------
5527        ------------------------------------------------------------
14768       ------------------------------------------------------------
10702       ------------------------------------------------------------
2439        ------------------------------------------------------------
18735       ------------------------------------------------------------
5852        ------------------------------------------------------------
227         ------------------------------------------------------------
consensus   ------------------------------------------------------------

            ------------------------------------------------------------
            DRMPASTFLFDTALRACFRAGTSSGDPDIPFVLFRRMRRAAVRPDGFTFHFLFKCSSSSR
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ISGLAKMGMLSDARLLLAQAPVRDVISWTSLIAAYSRADRAKEAVDCFKNMLSEGIAPDD

VTVIGVLSACSQLKDLELGCSLHLLVKEKGMSMSENLVVALIDMYAKCGDFGHAREVFDA

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VGRGRRPQSWNAIIDGYCKHGHVDVARSLFDQMEVRDIITFNSMITGYIHSGQLREALL
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FMNMRRHDLRVDNFTVVSLLSACASLGALPQGRALHACIELRLVETDIYIGTALLDMYMK
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CGRVNEATIVFQRMGKRDVHAWTAMIAGLAFNGMGKAGLEYFYQMRCDGFQPNPVSYIAV
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LMEERQVKKTAGYSSVTVAGQVHKFVVSDKSHPRILEIIAMLEEISHRLKSAGYSPITSQ

VTVDVDEEEKEQTLLAHSEKLAIAFGLVSLAPNLPVHIIKNLRPTIFRPLGADDGKQKQP

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DRRVVFLLPPSRRDAPVLVRPIPSSPAPFSLRSSVTMAVRDVASLNRMITGFIRDGLADR
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ARAVYRWMVASGIRETPHTFSTILGVCSTYEALQLHGRVLALGLCCNPFVGSALVNHYMH
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VESPHAALSLFRELPLQNTAMCNVVLRGLGNLKLTEELICCFLDMRRQYLELNGLSYCYA
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GIVHKLGFSCSSVHVQTTLIDMYGKCCCFDHSLAIFNEIPSIALECCNSLITSSLGCNMF

DAALEILHCMIVEGVTPDDVTFSATMKAISLSASPSLTSCQMLHSCLVKLGFEMDMAVCS

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SLITAYACAGQLSSSHLIFEGLLDPNVICFTAIISACARYGDGARAMELFDQMVSSGLKP
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DNVTFLCAIAGCDQAGMFEEGRLVIELMRASRELDPDERHFACMVNLLSRDGFVKEAMEM
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MEQSPLRHYTKAWSSLLQSCKAHGENVLGKRAANMLIDVGRKDPATTLQVSNFFNDIGDR
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ETGDPGKLLRGHSLSRVPPASPFPRLRPQGDLVRAGDERARASGMPGEED----------
-------------------------------------------MPGGED----------
-------------------------------------------MSG-ED----------
-------------------------------------------MSG-ED----------

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--------------------------------------MRTSSDR---------------
------------------------------------------------------------
-------------------------------------THASAHASGTICFLIRVLRFLG
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-------------------------------------------xxxxxx----------

------------------MSGADVDKVQNLIHCCLQLYMDKKEVVDALSREAKIEPSVTQ
TVPLKFDLRAYSDSAILGLQCMQAHKVQNLIHCCLQLYMDKKEVVDALSREAKIEPSVTQ
-----------------AAAAFCCTQVQSLILRCLQMYMDQKEVVDALSHHSKIEPCITE
-----------------MASEEVLHKVQNLIERCLQMYMNKKEVVDALSHHSRIEPCITE
-----------------KVSREDIQLVQNLIERCLQLYMNQKEVVETLSFQAKIEPSFTE
---------------VRKVSRQDIQLVQNLIERCLQLYMNQKEVVETLSFQAKIEPSFTE
---------------VRKVSRQDIQLVQNLIERCLQLYMNQKEVVETLSFQAKLEPSFTE
---------------VRKVSRQDIQLVQNLIERCLQLYMNQKEVVETLSFQAKIEPSFTE
---------------VRKVSRQDIQLVQNLIERCLQLYMNQKEVVDTLSFQAKIEPSFTE
---------------VRKVSREDIQLVQNLIERCLQLYMNQKEVVDTLSFQAKIEPSFTE
---------------VRKVSRQDIQLVQNLIERCLQLYMNQKEVVDTLSFQAKIEPSFTE
---------------VRKVSRQDIQLVQNLIERCLQLYMNQKEVIDTLSLEAKIEPSFTE
---------------VRKVSRQDIQLVQNLIERCLQLYMNQKEVIDTLSLEAKIEPSFTE
---------MSSG-TVRRVSRQDIQLVQNLIERCLQLYMNQKEVVDTLLEQAKIEPGFTE
---------MSSG-TVRRVSRQDIQLVQNLIERCLQLYMNQKEVVDTLLEQAKIEPGFTE
---------MSSGGTVRRVSRQDIQLAQNLIERCLQLYMNQKEVVETLLEQAKIEPGFTE
---------------------------------MIVYFPS-----------------EL
---------------------------------MIVYFPS-----------------EL
----------MSSLTVRRVSREDIQLVQNLIERCLQLYMNQKEVVDTLLEQAKIEPGFTE
----------MSSLTVRRVSREDIQLVQNLIERCLQLYMNQKEVVDTLLEQAKIEPGFTE
NRIASTDISPMSSLTVRR--------VQNLIERCLQLYMNQKEVVDTLLEQAKIEPGFTE
-------------------------VQNLIERCLQLYMNQKEVVDTLLEQAKIEPGFTE
NRIASTDISPMSSLTVRRVSREDIQLVQNLIERCLQLYMNQKEVVDTLLEQAKIEPGFTE
----------MSSGTVRRVSRQDIQLVQNLIERCLQLYMNQKEVVETLLEQAKIEPGFTE
----------MSSGSVRRVSRQDIQLVQNLIERCLQLYMSQKEVVETLLAQAKIEPGFTE
----------MSSGSVRRVSRQDIQLVQNLIERCLQLYMSQKEVVETLLAQAKIEPGFTE
----------xxxxxxxxxsxxdxxxvqnlierclqlYmnqkevvxtlxxxakiepxfte

HVWQKLEENNREFFKAYYLRLMLKNQITAFNKLLEDQLRIINKEYHPGPSSMP--LPNGS
HVWQKLEENNREFFKAYYLRLMLKNQITAFNKLLEDQLRIINKEYHPGPSSMP--LPNGS
LVWRQLEHQNPLFFKAYYMRLMLKTQIMVFNKLLQDQFEVINKEFSSGIPSMS--LPNGS
LVWQQLEQQNPLFFKAYDMRLMLKNQIMVFNRLLQDQFEIMNKEFSSGIPSMS--LPNDS
LVWQKLEEENPEFFKAYYVRLMLKNQINVFNKLLAHQCRLMNKDPSGALSITPT-APNGS
LVWQKLEEENREFFKAYYVRLMLKNQIMVFNKLLEDQYRLMCKEQPSGVPSMPP-TTNGS
LVWQKLEEENREFFKAYYVRLMLKNQIMVFNKLLEDQYRLMCKEQPSGVPSMPP-TTNGS
LVWQKLEEENREFFKAYYVRLMLKNQIMVFNKLLEDQYRLMCKEQPSGVPSMPP-TTNGS
LVWQKLEEENRDFFKAYYVRLMLMNQITAFNKLLEQQYEIMTKDHPSGMPSVPSTAPNGS
IVWQRLEEENRDFFKAYYARLMLMNQIVSFNKLLEQQHQIMNKDHHYGMPAMPSTAPNGS
LVWQKLEEENRDFFKAYYVRLMLMNQITAFNKLLEQQYEIMTKDHPSGMPSVPPAAPNGS
LVWQKLEEENREFFKAYYLRLMLKNQITAFNKLLEDQFQLMNKDYXSGIPSMP--LTNGS
LVWQKLEEENREFFKAYYLRLMLKNQITXFNNFLRX-FQLMNKDYPQGS-LLS--SYQWP
LVWQKLEEENREFFKAYYLRLMVKHQIMEFNKLLEQQVHHMRQMHPTGVASVQN--TNGS
LVWQKLEEENREFFKAYYLRLMVKHQIMEFNKLLEQQVHHMRQMHPTGVASVQN--TNGS
LVWQKLEEENREFFKAYYLRLMVKHQIMEFNKLLEQQVHHMQQMHPSGVAPVQN--TNGS
TVWQKLEEENREFFKAYYLRLMVKHQIMEYNELLEQQINHMRQMHPTAGASVRN--RNGS
TVWQKLEEENREFFKAYYLRLMVKHQIMEYDELLEQQINHMRQMHPTAGASVRD--RNGS
LVWQKLEEENREFFKAYYLRLMVKHQIMEYNELLEQQINHMRQMHPTAGASVRN--RNGS
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LVWQKLEEENREFFKAYYLRLMVKHQIMEYNELLEQQINHMRQMHPTAGASVRN--RNGS
LVWQKLEEENREFFKAYYLRLMVKHQIMEYNELLEQQINHMRQMHPTAGASVRN--RNGS
LVWQKLEEENREFFKAYYLRLMVKHQIMEYNELLEQQINHMRQMHPTAGASVRN--RNGS
LVWQKLEEENREFFKAYYLRLMVKHQIMEYNELLEQQINHMRQMHPTAGASVRN--RNGS

LVWQKLEEENREFFNAYYLRLMVKHQIMEFNKLLEQQVRHMQQMHPSALTSVQN--TNGS
LVWQKLEEENEEFFKAYYARLVLKQQIMQFNKLLDQQVQLM-QLHSSAVASLPM--SNGS
LVWQKLEEENEEFFKAYYARLVLKQQIMQFNKLLDQQVQLM-QLHSSTVASLPT--SNGS
lVWqkLEeeNreFFkAYyxRLmxkxQIxxfnxlLexqxxxmxxxxxxxxxsxxx-xxngs


NSNLLK--------------QNPCFLSESTPMPAMPDDVMC----NGNSSGIVDRTQSSD
NSNLLK--------------QNPCFLSESTPMPAMPDDVMC----NGNSSGIVDRTQSSD
NSNLLK--------------QNSCFLPETAPGSAMPDGIMH----NGSSRGIINGTPSGD
NSNLLK--------------QDSCFLPETAPGNAMPDGIMH----NGSSSGIINDTPSGD
DSSTLN--------------QNTCFLQDTT-STAIPDSFLH----NGNSSGVINGAPATD
NMGTLN--------------QNACFLPDTTPSTAMPDSLLP----NGSSSGIVNGTPSSD
NMGTY-----------------------TTPSTAMPDSLLP----XGSSSGIVNGTPSSD
NMGTLN--------------QNACFLPDTTPSTAMPDSLLP----NGSSSGIVNGTPSSD
NSNMLN--------------QAVPFLPDTIPSTAMQDNLWS----NGSSSSIVNGAPSDD
NTNMLN--------------QAMPFLPDTIPSTAMQDNSLR----NGGSSSIVNGAPSDD
NSNTLN--------------QNMPFLPDTIPSTALQDNSLR----NGGSSSIVNGAPSDD
NSTTFX--------------QNLCFFTRSLGPIFC----------------------NGQ
NSTTLN--------------KTVLLQIWPFS---------------------------IQ
HLQS--------------MNQKQLCYPSEHTDQSLKSESAHHPMASSLSNAFLNGSSTLN
HLQSSK-----------ILNQKQLCYPSEHTDQSLKSESAHHPMASSLSNAFLNGSSTLN
HIQS--------------MNQKHLGYASEHTDQSLKS------IPSSLSNAYLNGSS---
HVPP--------------MNQQQLLYERKEPDQSSPN----------LSSPYLNGGSAIN
HVPP--------------MNQQQLLYERKEPDQSSPN----------LSSPYLNGGSAIN
HVPP--------------MNQQQLLYERKEPDQSSPN----------LSSPYLNGGSAIN
HVPP--------------MNQQQLLYERKEPDQSSPN----------LSSPYLNGGSAIN
HVPP--------------MNQQQLLYERKEPDQSSPN----------LSSPYLNGGSAIN
HVPP--------------MNQQQLLYERKEPDQSSPN----------LSSPYLNGGSAIN
HVPP--------------MNQQQLLYERKEPDQSSPN----------LSSPYLNGGSAIN
HIQ------------------------------------------------------------
HIPAVTSLPNSNGSHIPAIPENPACYTSDRTQTSLKPENMQHAVDSRLSNVFNNGGSSLH
HIPAVSSLPSSNGSHIPAIPENPACYTADRTQTSLKPENMQHHVDSRLSNVFNNGGSSLH
xxxxxx------------xxqxxxxxxxxxxxxxxxxxxx----xxxsxxxxngxxxxx


QLIYAGKDIQGLHSSMDASN-LLPVQNANSVLFGVENGT--TIKTESGYSSNGNFGFCGN
QLIYAGKDIQGLHSSMDASN-LLPVQNANSVLFGVENGT--TIKTESGYSSNGNFGFCGN
QLLNASKDLHGLHNGIDASTSLQSDQNAAAVLYGVDNETSATIKTESCYSSNADFAFCGN
QLLNASKDLHGLHSQIDASTSLQSDQNATAVLYGVDNETSATIKTESCYSSNADFAFCGN
QFIYGGKVVHGLPSGMDASVSLLSAHNSTGGQFNGDNGT--TIKAESSFSSNPEFAFCNE
QFIYAGKVIHGLPSSMDASSSLLAAHNSTAGRFNGDNGT--TIKTEASYSGNSDFGFCNE
QFIYAGKVIHGLPSSMDASSSLLAAHNSTAGRFNGDNGT--TIKTEASYSGNSDFGFCNE
QFIYAGKVIHGLPSSMDASSSLLAAHNSTAGRFNGDNGT--TIKTEASYSGNSDFGFCNE
QCGYSGKVAHGLPGVMDASSSLLAAHKSTVGQFNGHDGT--TTKTESDYSSNSDFGFGNE
QFMYTGKVVHGLPGVMDASSSLLAAHKSTVGQFNGHNGT--TTKTESDYSSNSDFGLGNE
QFMYTGKVVHGLPGGMDASSSLLTAHNPAVGQFNGHNGA--TIKTEFGYSSNSDFGFSNE
MVGMRQWKFHGGFK--------------------------------------------
MVIPTN----------------------------------------------------
TNVPSSINISTHARRVDASPNMLSSQTTNMPMMQGMNGG--MIKSETAFTNPASFMYGGE
TNVPSSINISTHARRVDASPNMLSSQTTNMPMMQGMNGG--MIKSETAFTNPASFMYGGE
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TNIPSYVDFSSHSRRVDPSPNSLSLQATNMPLMQG------MIKSETAYQNCAPYMYGG-
TNIPSYVDFSSHSRRVDPSPNSLXLQATNMPLMQG------MIKSETAYQNCAPYMYGG-
TNIPSYVDFSSHSRRVDPSPNSLSLQATNMPLMQG------MIKSETAYQNCAPYMYGG-
TNIPSYVDFSSHSRRVDPSPNSLSLQATNMPLMQG------MIKSETAYQNCAPYMYGG-
TNIPSYVDFSSHSRRVDPSPNSLSLQATNMPLMQG------MIKSETAYQNCAPYMYGG-
TNIPSYVDFSSHSRRVDPSPNSLSLQATNMPLMQG------MIKSETAYQNCAPYMYGG-
TNIPSYVDFSSHSRRVDPSPNSLSLQATNMPLMQG------MIKSETAYQNCAPYMYGG-
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TSMPAAVDMSVHGNRINGPASVLSAQSANMGLIQGINGGG-MIKSEPGYSGCSPYMFSTD
TSMHAAVDMSAHGNRINGPSSMLSAQSANMGLIQGINGGG-MIKSEPGYSGCSPYMFGTD
xxxxxxxxxxxxxxxxdxsxxxlxxxxxxxxxxxxxxxxx--xikxexxyxxxxxxxxxxx
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-AFLESCQSIGDASGG-SFSSSELNGQPLDDSILDIESSSFGFLSQLPRNF-FS-DLPED
-AFLESCQSIGDASGG-SFSSSELNGQPLDDSILDIESSSFGFLSQLPRNF-FS-DLPED
-TFLESCQSIGDASGGGSFSSSELNGQPLNDSILDMESSSFSFLNQMPQSFIFP-DLADD
-TFLESCQSIGDASGGGSFSSSELNGQPLNDSILDMESSSFSFLNQMPQSFMFS-DLADD

NTYLEPCQSIGDASGG-SFSSSELNGQPLGDTILDMDTSSYGFLSQIPRNFSFSXDLTED
SAFLEPCQSIGDASGG-SFSSSELNGQPLGDPIMDMDSSSFGFLSQIPRNFSFS-DLTED
SAFLEPCQSIGDASGG-SFSSSELNGQPLGDPIMDMDSSSFGFLSQIPRNFSFS-DLTED
SAFLEPCQSIGDASGG-SFSSSELNGQPLGDPIMDMDSSSFGFLSQIPRNFSFS-DLTED
TVFLE--QSVGDISGG-SFSSSELNGQP-------VGSSSYGFLSQIPCNFSLS-DWTDC
TVFLE--QSFGDISGG-SFSSSELNGQP-------VGSSSYGFLSQIPCNFSLS-DWTDC
AVFLE--QSVGDX---------------------QDSSSYGFLSQIPRNFSFS-DLTED
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RNALEGHSAVGDTSIP-NFSN-ESNNQPLSDPLLEAEASTFGFLGQIPRNFSLS-DLTAD
RNALEGHSAVGDTSIP-NFSN-ESNNQPLSDPLLEAEASTFGFLGQIPRNFSLS-DLTAD
------------------------------------------------------------
----EAQSTVGDVTIA-SFSN-DSSNQSLNDPLVDPDAPTFGSLGQIPQNFSLS-DLTAD
----EAQSTVGDVTIA-SFSN-DSSNQSLNDPLVDPDAPTFGSLGQIPQNFSLS-DLTAD
----EAQSTVGDVTIA-SFSN-DSSNQSLNDPLVDPDAPTFGSLGQIPQNFSLS-DLTAD
----EAQSTVGDVTIA-SFSN-DSSNQSLNDPLVDPDAPTFGSLGQIPQNFSLS-DLTAD
----EAQSTVGDVTIA-SFSN-DSSNQSLNDPLVDPDAPTFGSLGQIPQNFSLS-DLTAD
----EAQSTVGDVTIA-SFSN-DSSNQSLNDPLVDPDAPTFGSLGQIPQNFSLS-DLTAD
------------------------------------------------------------
GNVLETRPTIGGASVT-SFTNVESNSHSLNEAVLDPDTSSFGFLGQIPRNFSLS-DLTAD
GNVLETRPTIGGASVT-SFTNVESNSHSLNEVVLDPDTSSFGFLGQIPRNFSLS-DLTAD
xxxxexxxxxgdxxxx-sfsxxxxxxqxlxxxxxxxxxxxxgxlxqxpxnfxxs-dlxxd


FSQSTEILDNYGKSPFLPSEQNNFSDSTGGEHTG--------------------------
FSQSTEILDNYGKSPFLPSEQNNFSDSTGGEHTG--------------------------
FNQSAEIT------PFLTPETN-FSDSTGGDHTG--------------------------
FNQNAEIT------PFLTPETN-FSDSTGGDHTG--------------------------
FSHSTEILENYGSSPFIPSETNTFSESTAGGHTEI-------------------------
FSQSAEILENYGRSPFIPSEPNNFSESTPGDHAEI-------------------------
FSQSAEILENYGRSPFIPSEPNNFSESTPGDHAG--------------------------
FSQSAEILENYGRSPFIPSEPNNFSESTPGDHAEI-------------------------
FSQSSEIFENYGGSPFIPSDANNIPESSARENTG--------------------------
FSQSSEILENYGRSPFIPSDANNFPESTAEEHTG--------------------------
FSQSAEILENYGRSPFIPSDANNFPESTAGEHTEI-------------------------
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FSQSSEILESYDRSPFLVPNAENFLDSRDRGEYQG--------------------------
FSQSSEILESYDRSPFLVPNAENFLDSRDRGEYQG--------------------------
------------------------------------------------------------
FSQSSDILESYEGSPFLLADAENFLDSSERVEHQG--------------------------
FSQSSDILESYEGSPFLLADAENFLDSSERVEHQG--------------------------
FSQSSDILESYEGSPFLLADAENFLDSSERVEHQDFMECLAHLSYNGKNLKLNHSGTRDT
FSQSSDILESYEGSPFLLADAENFLDSSERVEHQG--------------------------
FSQSSDILESYEGSPFLLADAENFLDSSERVEHQG--------------------------
FSQSSDILESYEGSPFLLADAENFLDSSERVEHQG--------------------------
FSQSSDILESYEGSPFLLADAENFLDSSERVEHQG--------------------------
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FSQSSDILETYSRSPFLATDNENFLDRGEQ------------------------------
FSQSSDILETYSRSPFLATDNENFLDRGEQ------------------------------
fsqsxxilxxyxxspfxxxxxxnfxxsxxxxxxxx-------------------------


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-GNIRLDSISEGVSYEDFGSD*
-GNRRLDTISEGVSYEDFGSD*
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-GNRRLDTISEGVSYEDFGSD*
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-GNRRLDTISEGIHFEDFGSD*
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-DNKRLDTISEGFSYDNIGSE*

-DNKRLDTISEGFSYDNIGSE*
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-DHERLRTISSGFSYENFRSN*
-DHERLRTISSGFSYENFRSN*
RDHERLRTISSGFSYENFRSN*
-DHERLRTISSGFSYENFRSN*
-EHLKLC----------*
-EHLKLC----------*
-DHERLRTISSGFSYENFRSN*
----------*
-DNNRLDSISEGLSYEDFGSE*
-DNNRLDSISEGLSYEDFGSE*
-xxxxxxxxxxxxxxxxxxxxxx*

FIG. 2

pMON93039
SEQ ID NO: 19940
11722 bp
E-Os.Act1 + E-CaMV.35S.2xA1-B3 + P-Os.Act1
B-AGRtu.right border
T-Ec.aadA-SPC/STR
CR-Ec.aadA-SPC/STR
P-Ec.aadA-SPC/STR
OR-Ec.ori-ColE1
CR-Ec.rop
I-Os.Act1
L-Ta.Lhcb1
P-Os.Act1
E-CaMV.35S
E-Os.Act1
T-StPis4
P-Os.Act1
L-Os.Act1
I-Os.Act1
TS-At.ShkG-CTP2
CR-AGRtu.aroA-CP4.nat
T-AGRtu.nos
B-AGRtu.left border
OR-Ec.oriV-RK2

FIG 3.

T-AGRtu.nos
P-CaMV.35S-enh
T-Gb.E6-3b
CR-AGRtu.aroA-CP4.nno
B-AGRtu.rightborder
T-Ec.aadA-SPC/STR
TS-At.ShkG-CTP2
CR-Ec.aadA-SPC/STR
I-At.Act7
pMON82053
Soybean transformation base vector
SEQ ID NO:19941
P-Ec.aadA-SPC/STR
L-At.Act7
P-At.Act7
ORI-322
OR-Ec.ori-ColE1
B-AGRtu.leftborder
CR-Ec.rop
OR-Ec.oriV-RK2

FIG 4.

Exp-CaMV.35S-enh+Ph.DnaK
T-Ps.RbcS2-E9
B-AGRtu.right border
EXP-CaMV.35S
T-Ec.aadA-SPC/STR
CR-Ec.nptII-Tn5
CR-Ec.aadA-SPC/STR
pMON99053
Cotton transformation base vetor
T-AGRtu.nos
P-Ec.aadA-SPC/STR
SEQ ID NO: 19942.
8504 bp
B-AGRtu.left border
ORI-322
OR-Ec.oriV-RK2
CR-Ec.rop

GENES AND USES FOR PLANT IMPROVEMENT

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims benefit under 35USC § 119 (e) of U.S. provisional application Ser. No. 60/873,247, filed Dec. 6, 2006, herein incorporated by reference.

INCORPORATION OF SEQUENCE LISTING

[0002] Two copies of the sequence listing (Copy 1 and Copy 2) and a computer readable form (CRF) of the sequence listing, all on CD-Rs, each containing the file named 38-21 (53949)B_seqListing.txt, which is 67,317,760 bytes (measured in MS-WINDOWS) and was created on Dec. 4, 2007, are incorporated herein by reference in their entirety.

INCORPORATION OF COMPUTER PROGRAM LISTING

[0003] A Computer Program Listing with folders "hmmer-2.3.2" and "161pfamDir" is contained on a CD-R and is incorporated herein by reference in their entirety. Folder hmmer-2.3.2 contains the source code and other associated file for implementing the HMMer software for Pfam analysis. Folder 161pfamDir contains 161 profile Hidden Markov Models. Both folders were created on the disk on Dec. 4, 2007 having a total size of 15,534,080 bytes when measured in MS-WINDOWS® operating system.

FIELD OF THE INVENTION

[0004] Disclosed herein are transgenic plant cells, plants and seeds comprising recombinant DNA and methods of making and using such plant cells, plants and seeds

BACKGROUND OF THE INVENTION

[0005] Transgenic plants with enhanced traits such as improved yield, environmental stress tolerance, pest resistance, herbicide tolerance, modified seed compositions, and the like are desired by both farmers and consumers. Although considerable efforts in plant breeding have provided significant gains in desired traits, the ability to introduce specific DNA into plant genomes provides further opportunities for generation of plants with improved and/or unique traits. The ability to develop transgenic plants with improved traits depends in part on the identification of useful recombinant DNA for production of transformed plants with improved properties, e.g. by actually selecting a transgenic plant from a screen for such improved property. An object of this invention is to provide transgenic plant cell nuclei, plant cells, plants and seeds by screening transgenic crop plants for one of more enhanced agronomic traits where the nucleus in cells of the plant or seed has recombinant DNA that was identified as imparting an improved trait in a model plant, e.g. *Arabidopsis thaliana*. In some cases the model plant may exhibit an improved trait that corresponds to an enhanced agronomic trait, e.g. cold stress tolerance, water deficit stress tolerance, low nitrogen stress tolerance and the like. In other cases the model plant may exhibit an improved trait that is a surrogate to an enhanced agronomic trait, e.g. salinity stress tolerance being a surrogate to drought tolerance or improvement in plant growth and development being a surrogate to enhanced yield. A further object of the invention is to provide screening methods requiring routine experimentation by which such transgenic plant cell nuclei, cells, plants and seeds can be identified by making a reasonable number of transgenic events and engaging in screening identified in this specification and illustrated in the examples.

SUMMARY OF THE INVENTION

[0006] This invention provides plant cell nuclei with recombinant DNA that imparts enhanced agronomic traits in transgenic plants having the nuclei in their cells. Recombinant DNA in this invention is provided in a construct comprising a promoter that is functional in plant cells and that is operably linked to DNA that encodes a protein having at least one amino acid domain in a sequence that exceeds the Pfam gathering cutoff for amino acid sequence alignment with a protein domain family identified by a Pfam name in the group of Pfam domain names identified in Table 17. In more specific embodiments of the invention plant cells are provided which express a protein having amino acid sequence with at least 90% identity to a consensus amino acid sequence in the group of consensus amino acid sequences consisting of the consensus amino acid sequence constructed for SEQ ID NO: 198 and homologs thereof listed in Table 2 through the consensus amino acid sequence constructed for SEQ ID NO: 394 and homologs thereof listed in Table 2. Amino acid sequences of homologs are SEQ ID NO: 395 through 19,938. In even more specific embodiments of the invention the protein expressed in plant cells is a protein selected from the group of proteins identified in Table 1 by annotation to a related protein in Genbank and alternatively identified in Table 16 by identification of protein domain family.

[0007] Other aspects of the invention are specifically directed to transgenic plant cells, and transgenic plants comprising a plurality of plant cells with such nuclei, progeny transgenic seed, embryo and transgenic pollen from such plants. Such plant cell nuclei are selected from a population of transgenic plants regenerated from plant cells with a nucleus transformed with recombinant DNA by screening the transgenic plants in the population for an enhanced trait as compared to control plants that do not have the recombinant DNA in their nucleus, where the enhanced trait is enhanced water use efficiency, enhanced cold tolerance, enhanced heat tolerance, enhanced shade tolerance, enhanced tolerance to salt exposure, increased yield, enhanced nitrogen use efficiency, enhanced seed protein or enhanced seed oil. In some aspects of the invention the recombinant DNA expresses a protein that imparts the enhanced trait; in other aspects of the invention the recombinant DNA expresses RNA for suppressing the level of an endogenous protein. In yet another aspect of the invention the nucleus of plant cells in plants, seeds, embryo and pollen further comprise DNA expressing a protein that provides tolerance from exposure to an herbicide applied at levels that are lethal to a wild type plant cell. Such tolerance is especially useful not only as an advantageous trait in such plants but is also useful in a selection step in the methods of the invention. In aspects of the invention the agent of such herbicide is a glyphosate, dicamba, or glufosinate compound.

[0008] Yet other aspects of the invention provide nuclei in cells of transgenic plants which are homozygous for the recombinant DNA and transgenic seed of the invention from corn, soybean, cotton, canola, alfalfa, wheat or rice plants.

[0009] In other embodiments for practice of various aspects of the invention in Argentina the recombinant DNA in the

nucleus is provided in plant cells derived from corn lines that are and maintain resistance to a virus such as the Mal de Rio Cuarto virus or a fungus such as the *Puccina sorghi* fungus or to both.

[0010] This invention also provides methods for manufacturing non-natural, transgenic seed that can be used to produce a crop of transgenic plants with an enhanced trait resulting from expression of stably-integrated, recombinant DNA in the nucleus of the plant cells. In some aspects of the invention the recombinant DNA can express a protein having at least one domain of amino acids in a sequence that exceeds the Pfam gathering cutoff for amino acid sequence alignment with a protein domain family identified by a Pfam name in the group of Pfam names identified in Table 17; in other aspects the recombinant DNA suppresses the level of such a protein. More specifically the method comprises (a) screening a population of plants for an enhanced trait and recombinant DNA, where individual plants in the population can exhibit the trait at a level less than, essentially the same as or greater than the level that the trait is exhibited in control plants which do not express the recombinant DNA; (b) selecting from the population one or more plants that exhibit the trait at a level greater than the level that said trait is exhibited in control plants; (c) verifying that the recombinant DNA is stably integrated in said selected plants; (d) analyzing tissue of a selected plant to determine the production of a protein having the function of a protein encoded by nucleotides in a sequence of one of SEQ ID NO: 1-197; and (e) collecting seed from a selected plant. In one aspect of the invention the plants in the population further comprise DNA expressing a protein that provides tolerance to exposure to an herbicide applied at levels that are lethal to wild type plant cells and where the selecting is effected by treating the population with the herbicide, e.g. a glyphosate, dicamba, or glufosinate compound. In another aspect of the invention the plants are selected by identifying plants with the enhanced trait. The methods are especially useful for manufacturing corn, soybean, cotton, alfalfa, wheat or rice seed selected as having at least one of the enhanced traits described above.

[0011] Another aspect of the invention provides a method of producing hybrid corn seed comprising acquiring hybrid corn seed from a herbicide tolerant corn plant which also has a nucleus of this invention with stably-integrated, recombinant DNA The method further comprises producing corn plants from said hybrid corn seed, where a fraction of the plants produced from said hybrid corn seed is homozygous for said recombinant DNA, a fraction of the plants produced from said hybrid corn seed is hemizygous for said recombinant DNA, and a fraction of the plants produced from said hybrid corn seed has none of said recombinant DNA; selecting corn plants which are homozygous and hemizygous for said recombinant DNA by treating with an herbicide; collecting seed from herbicide-treated-surviving corn plants and planting said seed to produce further progeny corn plants; repeating the selecting and collecting steps at least once to produce an inbred corn line; and crossing the inbred corn line with a second corn line to produce hybrid seed.

[0012] Another aspect of the invention provides a method of selecting a plant comprising a nucleus of this invention in its plant cells by using an immunoreactive antibody to detect the presence of protein expressed by recombinant DNA in seed or plant tissue. Another aspect of the invention provides anti-counterfeit milled seed having, as an indication of origin, a nucleus of this invention with unique recombinant DNA.

[0013] Aspects of the invention relating to nucleus in plant cells having recombinant DNA for suppressing the expression of a protein are identified in Table 1 and Table 16. More specific aspects of the invention provide plant cells having recombinant DNA for suppressing the expression of a protein having the function in a plant of the protein with amino acid sequence of SEQ ID NO: 200, 201, 205, 207, 211 and 394 or the corresponding Pfam identified in Table 16, i.e. SNF5, LMBR1, TFIIS_M, TFIIS_C, Glyco_transf__8, respectively. Such suppression can be effected by any of a number of ways known in the art, e.g. anti-sense suppression, RNAi or mutation knockout and the like.

[0014] Another aspect of this invention relates to growing transgenic plants with enhanced water use efficiency or enhanced nitrogen use efficiency. For instance, this invention provides methods of growing a corn, cotton or soybean crop without irrigation water comprising planting seed having plant cells of the invention which are selected for enhanced water use efficiency. Alternatively methods comprise applying reduced irrigation water, e.g. providing up to 300 millimeters of ground water during the production of a corn crop. This invention also provides methods of growing a corn, cotton or soybean crop without added nitrogen fertilizer comprising planting seed having plant cells of the invention which are selected for enhanced nitrogen use efficiency. Alternatively methods comprise applying reduced amount of nitrogen input as compared to the conventional input during the production of a corn crop.

[0015] The various aspects of this invention are especially useful for transgenic plant cells in seeds and transgenic plants having any of the above-described enhanced traits in crop plants such as corn (maize), soybean, cotton, canola (rape), wheat, sunflower, sorghum, alfalfa, barley, millet, rice, tobacco, fruit and vegetable crops, and turfgrass.

[0016] The invention also provides recombinant DNA constructs comprising the DNA useful in the nuclei in plant cells for imparting enhanced traits in plants having those cells.

BRIEF DESCRIPTION OF THE DRAWINGS

[0017] FIG. **1** illustrates a consensus amino acid sequence of SEQ ID NO: 227 and its homologs.

[0018] FIGS. **2**, **3** and **4** illustrate plasmid maps.

DETAILED DESCRIPTION OF THE INVENTION

[0019] In the attached sequence listing:

[0020] SEQ ID NO: 1-197 are nucleotide sequences of the coding strand of DNA for "genes" used in the recombinant DNA imparting an enhanced trait in plant cells, i.e. each represents a coding sequence for a protein;

[0021] SEQ ID NO: 198-394 are amino acid sequences of the cognate protein of the "genes" with nucleotide coding sequence 1-197;

[0022] SEQ ID NO: 395-19938 are amino acid sequences of homologous proteins;

[0023] SEQ ID NO: 19939 is a consensus amino acid sequence.

[0024] SEQ ID NO: 19940 is a nucleotide sequence of a plasmid base vector useful for corn transformation; and

[0025] SEQ ID NO: 19941 is a DNA sequence of a plasmid base vector useful for soybean or canola transformation.

[0026] SEQ ID NO: 19942 is a DNA sequence of a plasmid base vector useful for cotton transformation.

[0027] The nuclei of this invention are identified by screening transgenic plants for one or more traits including improved drought stress tolerance, improved heat stress tolerance, improved cold stress tolerance, improved high salinity stress tolerance, improved low nitrogen availability stress tolerance, improved shade stress tolerance, improved plant growth and development at the stages of seed imbibition through early vegetative phase, and improved plant growth and development at the stages of leaf development, flower production and seed maturity.

[0028] "Gene" refers to chromosomal DNA, plasmid DNA, cDNA, synthetic DNA, or other DNA that encodes a peptide, polypeptide, protein, or RNA molecule, and regions flanking the coding sequences involved in the regulation of expression. In aspects of the invention where an improved trait is provided by expression of a protein, "gene" refers at least to coding nucleotide sequence for a protein or a functional polypeptide fragment of a protein that imparts the trait. In aspects of the invention where an improved trait is provided by suppression of expression of an endogenous protein, "gene" refers to any part of the gene that can be a target for suppression.

[0029] "Transgenic seed" means a plant seed whose nucleus has been altered by the incorporation of recombinant DNA, e.g., by transformation as described herein. The term "transgenic plant" is used to refer to the plant produced from an original transformation event, or progeny from later generations or crosses of a plant to a transformed plant, so long as the progeny contains a nucleus with the recombinant DNA in its genome.

[0030] "Recombinant DNA" means a polynucleotide having a genetically engineered modification introduced through combination of endogenous and/or exogenous elements in a transcription unit, manipulation via mutagenesis, restriction enzymes, and the like or simply by inserting multiple copies of a native transcription unit. Recombinant DNA may comprise DNA segments obtained from different sources, or DNA segments obtained from the same source, but which have been manipulated to join DNA segments which do not naturally exist in the joined form. A recombinant polynucleotide may exist outside of the cell, for example as a PCR fragment, or integrated into a genome, such as a plant genome.

[0031] "Trait" means a physiological, morphological, biochemical, or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by biochemical techniques, such as detecting the protein, starch, or oil content of seed or leaves, or by observation of a metabolic or physiological process, e.g., by measuring uptake of carbon dioxide, or by the observation of the expression level of a gene or genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays, or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield, or pathogen tolerance.

[0032] A "control plant" is a plant without trait-improving recombinant DNA in its nucleus. A control plant is used to measure and compare trait improvement in a transgenic plant with such trait-improving recombinant DNA. A suitable control plant may be a non-transgenic plant of the parental line used to generate a transgenic plant herein. Alternatively, a control plant may be a transgenic plant that comprises an empty vector or marker gene, but does not contain the recombinant DNA that produces the trait improvement. A control plant may also be a negative segregant progeny of hemizygous transgenic plant. In certain demonstrations of trait improvement, the use of a limited number of control plants can cause a wide variation in the control dataset. To minimize the effect of the variation within the control dataset, a "reference" is used. As use herein a "reference" is a trimmed mean of all data from both transgenic and control plants grown under the same conditions and at the same developmental stage. The trimmed mean is calculated by eliminating a specific percentage, e.g., 20%, of the smallest and largest observation from the data set and then calculating the average of the remaining observation.

[0033] "Trait enhancement" means a detectable and desirable difference in a characteristic in a transgenic plant relative to a control plant or a reference. In some cases, the trait enhancement can be measured quantitatively. For example, the trait improvement can entail at least a 2% desirable difference in an observed trait, at least a 5% desirable difference, at least about a 10% desirable difference, at least about a 20% desirable difference, at least about a 30% desirable difference, at least about a 50% desirable difference, at least about a 70% desirable difference, or at least about a 100% difference, or an even greater desirable difference. In other cases, the trait enhancement is only measured qualitatively. It is known that there can be a natural variation in a trait. Therefore, the trait enhancement observed entails a change of the normal distribution of the trait in the transgenic plant compared with the trait distribution observed in a control plant or a reference, which is evaluated by statistical methods provided herein. Trait enhancement includes, but is not limited to, yield increase, including increased yield under non-stress conditions and increased yield under environmental stress conditions. Stress conditions may include, for example, drought, shade, fungal disease, viral disease, bacterial disease, insect infestation, nematode infestation, cold temperature exposure, heat exposure, osmotic stress, reduced nitrogen nutrient availability, reduced phosphorus nutrient availability and high plant density.

[0034] Many agronomic traits can affect "yield", including without limitation, plant height, pod number, pod position on the plant, number of internodes, incidence of pod shatter, grain size, efficiency of nodulation and nitrogen fixation, efficiency of nutrient assimilation, resistance to biotic and abiotic stress, carbon assimilation, plant architecture, resistance to lodging, percent seed germination, seedling vigor, and juvenile traits. Other traits that can affect yield include, efficiency of germination (including germination in stressed conditions), growth rate (including growth rate in stressed conditions), ear number, seed number per ear, seed size, composition of seed (starch, oil, protein) and characteristics of seed fill. Also of interest is the generation of transgenic plants that demonstrate desirable phenotypic properties that may or may not confer an increase in overall plant yield. Such properties include enhanced plant morphology, plant physiology or improved components of the mature seed harvested from the transgenic plant.

[0035] "Yield-limiting environment" means the condition under which a plant would have the limitation on yield including environmental stress conditions.

[0036] "Stress condition" means a condition unfavorable for a plant, which adversely affect plant metabolism, growth and/or development. A plant under the stress condition typically shows reduced germination rate, retarded growth and development, reduced photosynthesis rate, and eventually leading to reduction in yield. Specifically, "water deficit

stress" used herein preferably refers to the sub-optimal conditions for water and humidity needed for normal growth of natural plants. Relative water content (RWC) can be used as a physiological measure of plant water deficit. It measures the effect of osmotic adjustment in plant water status, when a plant is under stress conditions. Conditions that may result in water deficit stress include heat, drought, high salinity and PEG induced osmotic stress.

[0037] "Cold stress" means the exposure of a plant to a temperatures below (two or more degrees Celsius below) those normal for a particular species or particular strain of plant.

[0038] "Nitrogen nutrient" means any one or any mix of the nitrate salts commonly used as plant nitrogen fertilizer, including, but not limited to, potassium nitrate, calcium nitrate, sodium nitrate, ammonium nitrate. The term ammonium as used herein means any one or any mix of the ammonium salts commonly used as plant nitrogen fertilizer, e.g., ammonium nitrate, ammonium chloride, ammonium sulfate, etc.

[0039] "Low nitrogen availability stress" means a plant growth condition that does not contain sufficient nitrogen nutrient to maintain a healthy plant growth and/or for a plant to reach its typical yield under a sufficient nitrogen growth condition. For example, a low nitrogen condition can refers to a growth condition with 50% or less of the conventional nitrogen inputs. "Sufficient nitrogen growth condition" means a growth condition where the soil or growth medium contains or receives optimal amounts of nitrogen nutrient to sustain a healthy plant growth and/or for a plant to reach its typical yield for a particular plant species or a particular strain. One skilled in the art would recognize what constitute such soil, media and fertilizer inputs for most plant species.

[0040] "Shade stress" means a growth condition that has limited light availability that triggers the shade avoidance response in plant. Plants are subject to shade stress when localized at lower part of the canopy, or in close proximity of neighboring vegetation. Shade stress may become exacerbated when the planting density exceeds the average prevailing density for a particular plant species. The average prevailing densities per acre of a few examples of crop plants in the USA in the year 2000 were: wheat 1,000,000-1,500,000; rice 650,000-900,000; soybean 150,000-200,000, canola 260,000-350,000, sunflower 17,000-23,000 and cotton 28,000-55,000 plants per acre (Cheikh, e.g., (2003) U.S. Patent Application No. 20030101479).

[0041] "Increased yield" of a transgenic plant of the present invention is evidenced and measured in a number of ways, including test weight, seed number per plant, seed weight, seed number per unit area (i.e., seeds, or weight of seeds, per acre), bushels per acre, tons per acre, tons per acre, kilo per hectare. For example, maize yield can be measured as production of shelled corn kernels per unit of production area, e.g., in bushels per acre or metric tons per hectare, often reported on a moisture adjusted basis, e.g., at 15.5% moisture. Increased yield can result from improved utilization of key biochemical compounds, such as nitrogen, phosphorous and carbohydrate, or from improved tolerance to environmental stresses, such as cold, heat, drought, salt, and attack by pests or pathogens. Trait-improving recombinant DNA can also be used to provide transgenic plants having improved growth and development, and ultimately increased yield, as the result of modified expression of plant growth regulators or modification of cell cycle or photosynthesis pathways.

[0042] "Expression" means transcription of DNA to produce RNA. The resulting RNA may be without limitation mRNA encoding a protein, antisense RNA, or a double-stranded RNA for use in RNAi technology. Expression also refers to production of encoded protein from mRNA.

[0043] A "plant promoter" is a promoter capable of initiating transcription in plant cells whether or not its origin is a plant cell. Exemplary plant promoters include, but are not limited to, those that are obtained from plants, plant viruses, and bacteria which comprise genes expressed in plant cells such *Agrobacterium* or *Rhizobium*. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as leaves, roots, or seeds. Such promoters are referred to as "tissue preferred". Promoters which initiate transcription only in certain tissues are referred to as "tissue specific". A "cell type" specific promoter primarily drives expression in certain cell types in one or more organs, for example, vascular cells in roots or leaves. An "inducible" or "repressible" promoter is a promoter which is under environmental control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions, or certain chemicals, or the presence of light. Tissue specific, tissue preferred, cell type specific, and inducible promoters constitute the class of "non-constitutive" promoters. A "constitutive" promoter is a promoter which is active under most conditions. As used herein, "antisense orientation" includes reference to a polynucleotide sequence that is operably linked to a promoter in an orientation where the antisense strand is transcribed. The antisense strand is sufficiently complementary to an endogenous transcription product such that translation of the endogenous transcription product is often inhibited.

[0044] As used herein, "operably linked" refers to the association of two or more nucleic acid fragments on a single nucleic acid fragment so that the function of one is affected by the other. For example, a promoter is operably linked with a coding sequence when it is capable of affecting the expression of that coding sequence (i.e., that the coding sequence is under the transcriptional control of the promoter). Coding sequences can be operably linked to regulatory sequences in sense or antisense orientation.

[0045] A "consensus sequence" refers to an artificial, amino acid sequence of conserved parts of the proteins encoded by homologous genes, e.g., as determined by a CLUSTALW alignment of amino acid sequence of homolog proteins.

[0046] Homologous genes are genes which encode proteins with the same or similar biological function to the protein encoded by the second gene. Homologous genes may be generated by the event of speciation (see ortholog) or by the event of genetic duplication (see paralog). "Orthologs" refer to a set of homologous genes in different species that evolved from a common ancestral gene by specification. Normally, orthologs retain the same function in the course of evolution; and "paralogs" refer to a set of homologous genes in the same species that have diverged from each other as a consequence of genetic duplication. Thus, homologous genes can be from the same or a different organism. As used herein, "homolog" means a protein that performs the same biological function as a second protein including those identified by sequence identity search.

[0047] Percent identity refers to the extent to which two optimally aligned DNA or protein segments are invariant

throughout a window of alignment of components, e.g., nucleotide sequence or amino acid sequence. An "identity fraction" for aligned segments of a test sequence and a reference sequence is the number of identical components which are shared by sequences of the two aligned segments divided by the total number of sequence components in the reference segment over a window of alignment which is the smaller of the full test sequence or the full reference sequence. "Percent identity" ("% identity") is the identity fraction times 100. "% identity to a consensus amino acid sequence" is 100 times the identity fraction in a window of alignment of an amino acid sequence of a test protein optimally aligned to consensus amino acid sequence of this invention.

[0048] "*Arabidopsis*" means plants of *Arabidopsis thaliana*.

[0049] "Pfam" refers to a large collection of multiple sequence alignments and hidden Markov models covering many common protein families, e.g. Pfam version 18.0 (August 2005) contains alignments and models for 7973 protein families and is based on the Swissprot 47.0 and SP-TREMBL 30.0 protein sequence databases. See S. R. Eddy, "Profile Hidden Markov Models", *Bioinformatics* 14:755-763, 1998. Pfam is currently maintained and updated by a Pfam Consortium. The alignments represent some evolutionary conserved structure that has implications for the protein's function. Profile hidden Markov models (profile HMMs) built from the Pfam alignments are useful for automatically recognizing that a new protein belongs to an existing protein family even if the homology by alignment appears to be low. Once one DNA is identified as encoding a protein which imparts an enhanced trait when expressed in transgenic plants, other DNA encoding proteins in the same protein family are identified by querying the amino acid sequence of protein encoded by candidate DNA against the Hidden Markov Model which characterizes the Pfam domain using HMMER software, a current version of which is provided in the appended computer listing. Candidate proteins meeting the gathering cutoff for the alignment of a particular Pfam are in the protein family and have cognate DNA that is useful in constructing recombinant DNA for the use in the plant cells of this invention. Hidden Markov Model databases for use with HMMER software in identifying DNA expressing protein in a common Pfam for recombinant DNA in the plant cells of this invention are also included in the appended computer listing. The HMMER software and Pfam databases are version 18.0 and were used to identify known domains in the proteins corresponding to amino acid sequence of SEQ ID NO: 198 through SEQ ID NO: 394. All DNA encoding proteins that have scores higher than the gathering cutoff disclosed in Table 17 by Pfam analysis disclosed herein can be used in recombinant DNA of the plant cells of this invention, e.g. for selecting transgenic plants having enhanced agronomic traits. The relevant Pfams for use in this invention, as more specifically disclosed below, are L51_S25_CI-B8, iPGM_N, WD40, BPL_LipA_LipB, DUF676, AAA, S_locus_glycop, ArfGap, Rotamase, Metallophos, CMAS, Sugar_tr, LMBR1, RmaAD, NAF, BolA, Pkinase, C2, FA_hydroxylase, p450, Complex1__30 kDa, Histone, DUF822, PEP-utilizers, PCI, ETC_C1_NDUFA5, 2-Hacid_dh, Tryp_alpha_amyl, PK_C, MAP65_ASE1, FBPase, SWIB, Ank, Ribosomal_S8e, 2-Hacid_dh_C, SMC_N, GTP_cyclohydro2, PfkB, ORMDL, ADH_zinc_N, SWIM, TrkA_N, HLH, GH3, SNF5, Ceramidase_alk, Ribonuclease_T2, Complex1__49 kDa, Gp_dh_C, Aldo_ket_red, zf-AN1, TFIIS_C, MFS__1, Thioredoxin, DUF1005, LEA__3, Sterol_MT_C, Gp_dh_N, TFIIS_M, PAN__2, BPL_C, DUF26, Aa_trans, ACT, ADH_N, NAD_binding__1, Auxin_inducible, B_lectin, Anti-silence, Response_reg, 14-3-3, LRRNT__2, GDC-P, zf-CCHC, NPH3, TPR__1, TFIIA, DHBP_synthase, UQ_con, TPR__2, TPT, F-box, adh_short, Cyclin_C, Na_H_Exchanger, AA_permease, MtN3_slv, TIM, NDK, Pantoate_transf, Allene_ox_cyc, Cyclin_N, Methyltransf__1, CBM__20, Methyltransf__12, Rhodanese, Glycolytic, Actin, Usp, eIF-4B, Glyco_transf__8, BURP, Alpha-amylase, F420_oxidored, EGF_CA, Kelch__1, PGAM, Aminotran__1__2, Kelch__2, UPF0261, CoA_binding, DUF868, Peptidase_S10, Lung__7-TM_R, Oleosin, Sad1_UNC, Gln-synt_C, LSM, NTP_transferase, Metalloenzyme, Prenylcys_lyase, Subtilisin_N, SAM__1, DUF298, ESCRT-III, DNA_pol_E_B, Aminotran__3, NAD_Gly3P_dh_N, Gln-synt_N, MMR_HSR1, DUF588, zf-CCCH, DnaJ, Pkinase_Tyr, Cupin__2, LRR__1, Cupin__3, zf-CSL, FAR1, HD, FH2, APC8, PTR2, MannoseP_isomer, Rib__5-P_isom_A, DUF1336, Phosphorylase, DUF1191, Asp, Mit_rib_S27, PAP_fibrillin, DUF1195, Aldedh, zf-C3HC4, PPR, PK, PurA, RMMBL, HTH__11, Tim17, and PBD.

Recombinant DNA Constructs

[0050] The present invention provides recombinant DNA constructs comprising one or more polynucleotides disclosed herein for imparting one or more improved traits to transgenic plant when incorporated into the nucleus of the plant cells. Such constructs also typically comprise a promoter operatively linked to said polynucleotide to provide for expression in the plant cells. Other construct components may include additional regulatory elements, such as 5' or 3' untranslated regions (such as polyadenylation sites), intron regions, and transit or signal peptides. Such recombinant DNA constructs can be assembled using methods known to those of ordinary skill in the art.

[0051] In a preferred embodiment, a polynucleotide of the present invention is operatively linked in a recombinant DNA construct to a promoter functional in a plant to provide for expression of the polynucleotide in the sense orientation such that a desired protein or polypeptide fragment of a protein is produced. Also provided are embodiments wherein a polynucleotide is operatively linked to a promoter functional in a plant to provide for expression of gene suppression RNA to suppress the level of an endogenous protein.

[0052] Recombinant constructs prepared in accordance with the present invention also generally include a 3' untranslated DNA region (UTR) that typically contains a polyadenylation sequence following the polynucleotide coding region. Examples of useful 3' UTRs include those from the nopaline synthase gene of *Agrobacterium tumefaciens* (nos), a gene encoding the small subunit of a ribulose-1,5-bisphosphate carboxylase-oxygenase (rbcS), and the T7 transcript of *Agrobacterium tumefaciens*.

[0053] Constructs and vectors may also include a transit peptide for targeting of a gene target to a plant organelle, particularly to a chloroplast, leucoplast or other plastid organelle. For descriptions of the use of chloroplast transit peptides, see U.S. Pat. No. 5,188,642 and U.S. Pat. No. 5,728,925, incorporated herein by reference.

[0054] Table 1 provides a list of genes that provided recombinant DNA that was expressed in a model plant and identified from screening as imparting an improved trait. When the stated orientation is "sense", the expression of the gene or a

homolog in a crop plant provides the means to identify transgenic events that provide an enhanced trait in the crop plant. When the stated orientation is "antisense", the suppression of the native homolog in a crop plant provides the means to identify transgenic events that provide an enhanced trait in the crop plant. In some cases the expression/suppression in the model plant exhibited an improved trait that corresponds to an enhanced agronomic trait, e.g. cold stress tolerance, water deficit stress tolerance, low nitrogen stress tolerance and the like. In other cases the expression/suppression in the model plant exhibited an improved trait that is a surrogate to an enhance agronomic trait, e.g. salinity stress tolerance being a surrogate to drought tolerance or improvement in plant growth and development being a surrogate to enhanced yield. Even when expression of a transgene or suppression of a native gene imparts an improved trait in a model plant, not every crop plant expressing the same transgene or suppressing the same native gene will necessarily demonstrate an indicated enhanced agronomic trait. For instance, it is well known that multiple transgenic events are required to identify a transgenic plant that can exhibit an enhanced agronomic trait. However, by with routine experimentation a transgenic plant cell nuclei, cell, plant or seed of this invention can be identified by making a reasonable number of transgenic events and engaging in screening process identified in this specification and illustrated in the examples. An understanding of Table 1 is facilitated by the following description of the headings:

[0055] "NUC SEQ ID NO" refers to a SEQ ID NO. for particular DNA sequence in the Sequence Listing.

[0056] "PEP SEQ ID NO" refers to a SEQ ID NO. in the Sequence Listing for the amino acid sequence of a protein cognate to a particular DNA

[0057] "construct_id" refers to an arbitrary number used to identify a particular recombinant DNA construct comprising the particular DNA.

[0058] "Gene ID" refers to an arbitrary name used to identify the particular DNA.

[0059] "orientation" refers to the orientation of the particular DNA in a recombinant DNA construct relative to the promoter.

TABLE 1

NUC Seq ID No.	PEP SEQ ID No	Gene ID	Construct ID	Orientation
1	198	CGPG106	11029	SENSE
2	199	CGPG1133	12223	SENSE
3	200	CGPG117	10422	ANTI-SENSE
4	201	CGPG1226	13485	ANTI-SENSE
5	202	CGPG1288	13235	SENSE
6	203	CGPG1301	13411	SENSE
7	204	CGPG1458	73944	SENSE
8	205	CGPG1542	13846	ANTI-SENSE
9	206	CGPG170	12602	SENSE
10	207	CGPG1828	74065	ANTI-SENSE
11	208	CGPG2206	72783	SENSE
12	209	CGPG2217	17210	SENSE
13	210	CGPG2292	72724	SENSE
14	211	CGPG2457	17805	ANTI-SENSE
15	212	CGPG2499	16610	SENSE
16	213	CGPG2653	76602	SENSE
17	214	CGPG2813	18456	SENSE
18	215	CGPG3002	18414	SENSE
19	216	CGPG3154	71538	SENSE
20	217	CGPG3235	76532	SENSE

TABLE 1-continued

NUC Seq ID No.	PEP SEQ ID No	Gene ID	Construct ID	Orientation
21	218	CGPG3274	18231	SENSE
22	219	CGPG3275	18232	SENSE
23	220	CGPG3363	18256	SENSE
24	221	CGPG3367	18258	SENSE
25	222	CGPG3375	19193	SENSE
26	223	CGPG3528	71301	SENSE
27	224	CGPG3534	18354	SENSE
28	225	CGPG3638	77334	SENSE
29	226	CGPG3918	19767	SENSE
30	227	CGPG3920	19774	SENSE
31	228	CGPG3962	70992	SENSE
32	229	CGPG3972	19956	SENSE
33	230	CGPG3990	70948	SENSE
34	231	CGPG3994	70201	SENSE
35	232	CGPG4026	19973	SENSE
36	233	CGPG4048	70987	SENSE
37	234	CGPG4052	70950	SENSE
38	235	CGPG4057	70962	SENSE
39	236	CGPG4058	70915	SENSE
40	237	CGPG4069	19947	SENSE
41	238	CGPG4087	70969	SENSE
42	239	CGPG4088	70985	SENSE
43	240	CGPG4102	70971	SENSE
44	241	CGPG4121	70963	SENSE
45	242	CGPG4122	70994	SENSE
46	243	CGPG4140	70956	SENSE
47	244	CGPG4154	70995	SENSE
48	245	CGPG4311	73306	SENSE
49	246	CGPG4363	70657	SENSE
50	247	CGPG4369	70660	SENSE
51	248	CGPG442	74536	SENSE
52	249	CGPG4454	71328	SENSE
53	250	CGPG4456	71329	SENSE
54	251	CGPG4473	70755	SENSE
55	252	CGPG4588	70684	SENSE
56	253	CGPG4765	73330	SENSE
57	254	CGPG4788	76202	SENSE
58	255	CGPG4912	72807	SENSE
59	256	CGPG4926	72811	SENSE
60	257	CGPG4967	73235	SENSE
61	258	CGPG4977	72813	SENSE
62	259	CGPG5001	72825	SENSE
63	260	CGPG5025	73628	SENSE
64	261	CGPG5041	76105	SENSE
65	262	CGPG5116	73242	SENSE
66	263	CGPG5144	74217	SENSE
67	264	CGPG5171	73735	SENSE
68	265	CGPG5194	73256	SENSE
69	266	CGPG5200	73260	SENSE
70	267	CGPG5210	75822	SENSE
71	268	CGPG5221	72001	SENSE
72	269	CGPG5269	72056	SENSE
73	270	CGPG5404	77308	SENSE
74	271	CGPG5432	73766	SENSE
75	272	CGPG5518	72774	SENSE
76	273	CGPG5535	72788	SENSE
77	274	CGPG5540	72753	SENSE
78	275	CGPG5568	72709	SENSE
79	276	CGPG5577	73954	SENSE
80	277	CGPG5587	73137	SENSE
81	278	CGPG5594	73161	SENSE
82	279	CGPG5633	73057	SENSE
83	280	CGPG5640	73127	SENSE
84	281	CGPG5646	73033	SENSE
85	282	CGPG5656	73105	SENSE
86	283	CGPG5659	73141	SENSE
87	284	CGPG5661	73165	SENSE
88	285	CGPG5684	73155	SENSE
89	286	CGPG5694	73026	SENSE
90	287	CGPG5704	73120	SENSE
91	288	CGPG5714	73133	SENSE
92	289	CGPG5721	73134	SENSE

TABLE 1-continued

NUC Seq ID No.	PEP SEQ ID No	Gene ID	Construct ID	Orientation
93	290	CGPG5728	73123	SENSE
94	291	CGPG5757	73981	SENSE
95	292	CGPG5764	73136	SENSE
96	293	CGPG5783	73172	SENSE
97	294	CGPG5791	73020	SENSE
98	295	CGPG5799	72946	SENSE
99	296	CGPG5856	74746	SENSE
100	297	CGPG5927	77312	SENSE
101	298	CGPG5941	75237	SENSE
102	299	CGPG5957	75240	SENSE
103	300	CGPG5967	74349	SENSE
104	301	CGPG6040	76422	SENSE
105	302	CGPG607	70812	SENSE
106	303	CGPG6178	77322	SENSE
107	304	CGPG6185	74662	SENSE
108	305	CGPG6306	76527	SENSE
109	306	CGPG6318	77020	SENSE
110	307	CGPG6326	77609	SENSE
111	308	CGPG6370	73485	SENSE
112	309	CGPG6429	73433	SENSE
113	310	CGPG6440	73411	SENSE
114	311	CGPG6516	73568	SENSE
115	312	CGPG6653	74688	SENSE
116	313	CGPG6712	74420	SENSE
117	314	CGPG6737	74435	SENSE
118	315	CGPG6747	74460	SENSE
119	316	CGPG6796	74566	SENSE
120	317	CGPG6805	77610	SENSE
121	318	CGPG6810	77618	SENSE
122	319	CGPG6952	77517	SENSE
123	320	CGPG6953	77518	SENSE
124	321	CGPG7121	76460	SENSE
125	322	CGPG7163	77069	SENSE
126	323	CGPG7168	76161	SENSE
127	324	CGPG7206	76171	SENSE
128	325	CGPG7225	76178	SENSE
129	326	CGPG7267	76467	SENSE
130	327	CGPG7272	77536	SENSE
131	328	CGPG7281	76576	SENSE
132	329	CGPG7308	74862	SENSE
133	330	CGPG7316	74863	SENSE
134	331	CGPG7371	74858	SENSE
135	332	CGPG7457	74933	SENSE
136	333	CGPG7520	75379	SENSE
137	334	CGPG7529	77816	SENSE
138	335	CGPG7636	75434	SENSE
139	336	CGPG7737	77821	SENSE
140	337	CGPG7767	75685	SENSE
141	338	CGPG7804	75654	SENSE
142	339	CGPG7823	75692	SENSE
143	340	CGPG7828	75657	SENSE
144	341	CGPG7833	75622	SENSE
145	342	CGPG7933	77549	SENSE
146	343	CGPG7986	77917	SENSE
147	344	CGPG8012	77568	SENSE
148	345	CGPG8015	77570	SENSE
149	346	CGPG8055	77338	SENSE
150	347	CGPG8062	77580	SENSE
151	348	CGPG8082	77928	SENSE
152	349	CGPG8083	77349	SENSE
153	350	CGPG8106	77357	SENSE
154	351	CGPG8107	77587	SENSE
155	352	CGPG8136	77933	SENSE
156	353	CGPG8152	77619	SENSE
157	354	CGPG8166	77621	SENSE
158	355	CGPG8377	77629	SENSE
159	356	CGPG8976	77832	SENSE
160	357	CGPG8987	76802	SENSE
161	358	CGPG9013	76829	SENSE
162	359	CGPG9080	76961	SENSE
163	360	CGPG9081	76973	SENSE
164	361	CGPG9130	77150	SENSE

TABLE 1-continued

NUC Seq ID No.	PEP SEQ ID No	Gene ID	Construct ID	Orientation
165	362	CGPG9133	77186	SENSE
166	363	CGPG9134	77103	SENSE
167	364	CGPG9137	77139	SENSE
168	365	CGPG9141	77187	SENSE
169	366	CGPG9145	77140	SENSE
170	367	CGPG9147	77164	SENSE
171	368	CGPG9148	77176	SENSE
172	369	CGPG9155	77165	SENSE
173	370	CGPG9163	77166	SENSE
174	371	CGPG9170	77155	SENSE
175	372	CGPG9180	77180	SENSE
176	373	CGPG9183	77121	SENSE
177	374	CGPG9186	77157	SENSE
178	375	CGPG9205	77195	SENSE
179	376	CGPG9207	77124	SENSE
180	377	CGPG9219	77261	SENSE
181	378	CGPG9220	77273	SENSE
182	379	CGPG9230	77203	SENSE
183	380	CGPG9236	77275	SENSE
184	381	CGPG9238	77204	SENSE
185	382	CGPG9259	77266	SENSE
186	383	CGPG9271	77220	SENSE
187	384	CGPG9275	77268	SENSE
188	385	CGPG9278	77209	SENSE
189	386	CGPG9283	77269	SENSE
190	387	CGPG9309	77451	SENSE
191	388	CGPG9311	77452	SENSE
192	389	CGPG9322	77430	SENSE
193	390	CGPG9335	77432	SENSE
194	391	CGPG9341	77433	SENSE
195	392	CGPG9344	77444	SENSE
196	393	CGPG9345	77409	SENSE
197	394	CGPG976	12313	ANTI-SENSE
10	207	CGPG1828	16322	SENSE

Recombinant DNA

[0060] DNA for use in the present invention to improve traits in plants have a nucleotide sequence of SEQ ID NO:1 through SEQ ID NO:197, as well as the homologs of such DNA molecules. A subset of the DNA for gene suppression aspects of the invention includes fragments of the disclosed full polynucleotides consisting of oligonucleotides of 21 or more consecutive nucleotides. Oligonucleotides the larger molecules having a sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:197 are useful as probes and primers for detection of the polynucleotides used in the invention. Also useful in this invention are variants of the DNA. Such variants may be naturally occurring, including DNA from homologous genes from the same or a different species, or may be non-natural variants, for example DNA synthesized using chemical synthesis methods, or generated using recombinant DNA techniques. Degeneracy of the genetic code provides the possibility to substitute at least one base of the protein encoding sequence of a gene with a different base without causing the amino acid sequence of the polypeptide produced from the gene to be changed. Hence, a DNA useful in the present invention may have any base sequence that has been changed from the sequences provided herein by substitution in accordance with degeneracy of the genetic code.

[0061] Homologs of the genes providing DNA demonstrated as useful in improving traits in model plants disclosed

herein will generally have significant identity with the DNA disclosed herein. DNA is substantially identical to a reference DNA if, when the sequences of the polynucleotides are optimally aligned there is about 60% nucleotide equivalence; more preferably 70%; more preferably 80% equivalence; more preferably 85% equivalence; more preferably 90%; more preferably 95%; and/or more preferably 98% or 99% equivalence over a comparison window. A comparison window is preferably at least 50-100 nucleotides, and more preferably is the entire length of the polynucleotide provided herein. Optimal alignment of sequences for aligning a comparison window may be conducted by algorithms; preferably by computerized implementations of these algorithms (for example, the Wisconsin Genetics Software Package Release 7.0-10.0, Genetics Computer Group, 575 Science Dr., Madison, Wis.). The reference polynucleotide may be a full-length molecule or a portion of a longer molecule. Preferentially, the window of comparison for determining polynucleotide identity of protein encoding sequences is the entire coding region.

[0062] Proteins useful for imparting improved traits are entire proteins or at least a sufficient portion of the entire protein to impart the relevant biological activity of the protein. Proteins useful for generation of transgenic plants having improved traits include the proteins with an amino acid sequence provided herein as SEQ ID NO: 198 through SEQ ID NO: 394, as well as homologs of such proteins.

[0063] Homologs of the proteins useful in the invention are identified by comparison of the amino acid sequence of the protein to amino acid sequences of proteins from the same or different plant sources, e.g., manually or by using known homology-based search algorithms such as those commonly known and referred to as BLAST, FASTA, and Smith-Waterman. As used herein, a homolog is a protein from the same or a different organism that performs the same biological function as the polypeptide to which it is compared. An orthologous relation between two organisms is not necessarily manifest as a one-to-one correspondence between two genes, because a gene can be duplicated or deleted after organism phylogenetic separation, such as speciation. For a given protein, there may be no ortholog or more than one ortholog. Other complicating factors include alternatively spliced transcripts from the same gene, limited gene identification, redundant copies of the same gene with different sequence lengths or corrected sequence. A local sequence alignment program, e.g., BLAST, can be used to search a database of sequences to find similar sequences, and the summary Expectation value (E-value) used to measure the sequence base similarity. As a protein hit with the best E-value for a particular organism may not necessarily be an ortholog or the only ortholog, a reciprocal BLAST search is used in the present invention to filter hit sequences with significant E-values for ortholog identification. The reciprocal BLAST entails search of the significant hits against a database of amino acid sequences from the base organism that are similar to the sequence of the query protein. A hit is a likely ortholog, when the reciprocal BLAST's best hit is the query protein itself or a protein encoded by a duplicated gene after speciation. Thus, homolog is used herein to describe proteins that are assumed to have functional similarity by inference from sequence base similarity. The relationship of homologs with amino acid sequences of SEQ ID NO: 395 to SEQ ID NO: 19,938 to the proteins with amino acid sequences of SEQ ID NO: to 198 to SEQ ID NO: 394 are found in the listing of Table 2.

[0064] Other functional homolog proteins differ in one or more amino acids from those of a trait-improving protein disclosed herein as the result of one or more of the well-known conservative amino acid substitutions, e.g., valine is a conservative substitute for alanine and threonine is a conservative substitute for serine. Conservative substitutions for an amino acid within the native sequence can be selected from other members of a class to which the naturally occurring amino acid belongs. Representative amino acids within these various classes include, but are not limited to: (1) acidic (negatively charged) amino acids such as aspartic acid and glutamic acid; (2) basic (positively charged) amino acids such as arginine, histidine, and lysine; (3) neutral polar amino acids such as glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; and (4) neutral nonpolar (hydrophobic) amino acids such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine. Conserved substitutes for an amino acid within a native amino acid sequence can be selected from other members of the group to which the naturally occurring amino acid belongs. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Naturally conservative amino acids substitution groups are: valine-leucine, valine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, aspartic acid-glutamic acid, and asparagine-glutamine. A further aspect of the invention comprises proteins that differ in one or more amino acids from those of a described protein sequence as the result of deletion or insertion of one or more amino acids in a native sequence.

[0065] Homologs of the trait-improving proteins provided herein will generally demonstrate significant sequence identity. Of particular interest are proteins having at least 50% sequence identity, more preferably at least about 70% sequence identity or higher, e.g., at least about 80% sequence identity with an amino acid sequence of SEQ ID NO:198 through SEQ ID NO: 394. Of course useful proteins also include those with higher identity, e.g., 90% to 99% identity. Identity of protein homologs is determined by optimally aligning the amino acid sequence of a putative protein homolog with a defined amino acid sequence and by calculating the percentage of identical and conservatively substituted amino acids over the window of comparison. The window of comparison for determining identity can be the entire amino acid sequence disclosed herein, e.g., the full sequence of any of SEQ ID NO: 198 through SEQ ID NO: 394.

[0066] Genes that are homologous to each other can be grouped into families and included in multiple sequence alignments. Then a consensus sequence for each group can be derived. This analysis enables the derivation of conserved and class- (family) specific residues or motifs that are functionally important. These conserved residues and motifs can be further validated with 3D protein structure if available. The consensus sequence can be used to define the full scope of the invention, e.g., to identify proteins with a homolog relationship. Thus, the present invention contemplates that protein

homologs include proteins with an amino acid sequence that has at least 90% identity to such a consensus amino acid sequence sequences.

Promoters

[0067] Numerous promoters that are active in plant cells have been described in the literature. These include promoters present in plant genomes as well as promoters from other sources, including nopaline synthase (NOS) promoter and octopine synthase (OCS) promoters carried on tumor-inducing plasmids of *Agrobacterium tumefaciens*, caulimovirus promoters such as the cauliflower mosaic virus or Figwort mosaic virus promoters. For instance, see U.S. Pat. Nos. 5,858,742 and 5,322,938 which disclose versions of the constitutive promoter derived from cauliflower mosaic virus (CaMV35S), U.S. Pat. No. 5,378,619 which discloses a Figwort Mosaic Virus (FMV) 35S promoter, U.S. Pat. No. 6,437,217 which discloses a maize RS81 promoter, U.S. Pat. No. 5,641,876 which discloses a rice actin promoter, U.S. Pat. No. 6,426,446 which discloses a maize RS324 promoter, U.S. Pat. No. 6,429,362 which discloses a maize PR-1 promoter, U.S. Pat. No. 6,232,526 which discloses a maize A3 promoter, U.S. Pat. No. 6,177,611 which discloses constitutive maize promoters, U.S. Pat. No. 6,433,252 which discloses a maize L3 oleosin promoter, U.S. Pat. No. 6,429,357 which discloses a rice actin 2 promoter and intron, U.S. Pat. No. 5,837,848 which discloses a root specific promoter, U.S. Pat. No. 6,084,089 which discloses cold inducible promoters, U.S. Pat. No. 6,294,714 which discloses light inducible promoters, U.S. Pat. No. 6,140,078 which discloses salt inducible promoters, U.S. Pat. No. 6,252,138 which discloses pathogen inducible promoters, U.S. Pat. No. 6,175,060 which discloses phosphorus deficiency inducible promoters, U.S. Patent Application Publication 2002/0192813A1 which discloses 5', 3' and intron elements useful in the design of effective plant expression vectors, U.S. patent application Ser. No. 09/078,972 which discloses a coixin promoter, U.S. patent application Ser. No. 09/757,089 which discloses a maize chloroplast aldolase promoter, and U.S. patent application Ser. No. 10/739,565 which discloses water-deficit inducible promoters, all of which are incorporated herein by reference. These and numerous other promoters that function in plant cells are known to those skilled in the art and available for use in recombinant polynucleotides of the present invention to provide for expression of desired genes in transgenic plant cells.

[0068] Furthermore, the promoters can include multiple "enhancer sequences" to assist in elevating gene expression. Such enhancers are known in the art. By including an enhancer sequence with such constructs, the expression of the selected protein may be enhanced. These enhancers often are found 5' to the start of transcription in a promoter that functions in eukaryotic cells, but can often be inserted in the forward or reverse orientation 5' or 3' to the coding sequence. In some instances, these 5' enhancing elements are introns. Deemed to be particularly useful as enhancers are the 5' introns of the rice actin 1 and rice actin 2 genes. Examples of other enhancers that can be used in accordance with the invention include elements from the CaMV 35S promoter, octopine synthase genes, the maize alcohol dehydrogenase gene, the maize shrunken 1 gene and promoters from non-plant eukaryotes.

[0069] In some aspects of the invention it is preferred that the promoter element in the DNA construct be capable of causing sufficient expression to result in the production of an effective amount of a polypeptide in water deficit conditions. Such promoters can be identified and isolated from the regulatory region of plant genes that are over expressed in water deficit conditions. Specific water-deficit-inducible promoters for use in this invention are derived from the 5' regulatory region of genes identified as a heat shock protein 17.5 gene (HSP17.5), an HVA22 gene (HVA22), a Rab17 gene and a cinnamic acid 4-hydroxylase (CA4H) gene (CA4H) of *Zea maize*. Such water-deficit-inducible promoters are disclosed in U.S. application Ser. No. 10/739,565, incorporated herein by reference.

[0070] In some aspects of the invention, sufficient expression in plant seed tissues is desired to effect improvements in seed composition. Exemplary promoters for use for seed composition modification include promoters from seed genes such as napin (U.S. Pat. No. 5,420,034), maize L3 oleosin (U.S. Pat. No. 6,433,252), zein Z27 (Russell et al., (1997) *Transgenic Res.* 6(2):157-166), globulin 1 (Belanger et al., (1991) Genetics 129:863-872), glutelin 1 (Russell (1997) supra), and peroxiredoxin antioxidant (Per1) (Stacy et al., (1996) *Plant Mol. Biol.* 31(6):1205-1216).

[0071] In some aspects of the invention, preferential expression in plant green tissues is desired. Promoters of interest for such uses include those from genes such as SSU (Fischhoff, et al., (1992) Plant Mol. Biol. 20:81-93), aldolase and pyruvate orthophosphate dikinase (PPDK) (Taniguchi, et al., (2000) *Plant Cell Physiol.* 41(1):42-48).

[0072] Gene suppression includes any of the well-known methods for suppressing transcription of a gene or the accumulation of the mRNA corresponding to that gene thereby preventing translation of the transcript into protein. Posttranscriptional gene suppression is mediated by transcription of RNA that forms double-stranded RNA (dsRNA) having homology to a gene targeted for suppression. Suppression can also be achieved by insertion mutations created by transposable elements may also prevent gene function. For example, in many dicot plants, transformation with the T-DNA of *Agrobacterium* may be readily achieved and large numbers of transformants can be rapidly obtained. Also, some species have lines with active transposable elements that can efficiently be used for the generation of large numbers of insertion mutations, while some other species lack such options. Mutant plants produced by *Agrobacterium* or transposon mutagenesis and having altered expression of a polypeptide of interest can be identified using the polynucleotides of the present invention. For example, a large population of mutated plants may be screened with polynucleotides encoding the polypeptide of interest to detect mutated plants having an insertion in the gene encoding the polypeptide of interest.

Gene Stacking

[0073] The present invention also contemplates that the trait-improving recombinant DNA provided herein can be used in combination with other recombinant DNA to create plants with multiple desired traits or a further enhanced trait. The combinations generated can include multiple copies of any one or more of the recombinant DNA constructs. These stacked combinations can be created by any method, including but not limited to cross breeding of transgenic plants, or multiple genetic transformation.

[0074] In particular embodiments, the inventors contemplate the use of antibodies, either monoclonal or polyclonal which bind to the proteins disclosed herein. Means for preparing and characterizing antibodies are well known in the art

(See, e.g., Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988; incorporated herein by reference). The methods for generating monoclonal antibodies (mAbs) generally begin along the same lines as those for preparing polyclonal antibodies. Briefly, a polyclonal antibody is prepared by immunizing an animal with an immunogenic composition in accordance with the present invention and collecting antisera from that immunized animal. A wide range of animal species can be used for the production of antisera. Typically the animal used for production of anti-antisera is a rabbit, a mouse, a rat, a hamster, a guinea pig or a goat. Because of the relatively large blood volume of rabbits, a rabbit is a preferred choice for production of polyclonal antibodies.

[0075] As is well known in the art, a given composition may vary in its immunogenicity. It is often necessary therefore to boost the host immune system, as may be achieved by coupling a peptide or polypeptide immunogen to a carrier. Exemplary and preferred carriers are keyhole limpet hemocyanin (KLH) and bovine serum albumin (BSA). Other albumins such as ovalbumin, mouse serum albumin or rabbit serum albumin can also be used as carriers. Means for conjugating a polypeptide to a carrier protein are well known in the art and include using glutaraldehyde, m-maleimidobencoyl-N-hydroxysuccinimide ester, carbodiimide and bis-biazotized benzidine.

[0076] As is also well known in the art, the immunogenicity of a particular immunogen composition can be enhanced by the use of non-specific stimulators of the immune response, known as adjuvants. Exemplary and preferred adjuvants include complete Freund's adjuvant (a non-specific stimulator of the immune response containing killed *Mycobacterium tuberculosis*), incomplete Freund's adjuvants and aluminum hydroxide adjuvant.

[0077] The amount of immunogen composition used in the production of polyclonal antibodies varies upon the nature of the immunogen as well as the animal used for immunization. A variety of routes can be used to administer the immunogen (subcutaneous, intramuscular, intradermal, intravenous and intraperitoneal). The production of polyclonal antibodies may be monitored by sampling blood of the immunized animal at various points following immunization. A second, booster, injection may also be given. The process of boosting and titering is repeated until a suitable titer is achieved. When a desired level of immunogenicity is obtained, the immunized animal can be bled and the serum isolated and stored, and/or the animal can be used to generate mAbs.

[0078] mAbs may be readily prepared through use of well-known techniques, such as those exemplified in U.S. Pat. No. 4,196,265, incorporated herein by reference. Typically, this technique involves immunizing a suitable animal with a selected immunogen composition, e.g., a purified or partially purified antifungal protein, polypeptide or peptide. The immunizing composition is administered in a manner effective to stimulate antibody producing cells. Rodents such as mice and rats are preferred animals, however, the use of rabbit, sheep, or frog cells is also possible. The use of rats may provide certain advantages (Goding, 1986, pp. 60-61), but mice are preferred, with the BALB/c mouse being most preferred as this is most routinely used and generally gives a higher percentage of stable fusions.

[0079] Following immunization, somatic cells with the potential for producing antibodies, specifically B lymphocytes (B cells), are selected for use in the mAb generating protocol. These cells may be obtained from biopsied spleens, tonsils or lymph nodes, or from a peripheral blood sample. Spleen cells and peripheral blood cells are preferred, the former because they are a rich source of antibody-producing cells that are in the dividing plasmablast stage, and the latter because peripheral blood is easily accessible. Often, a panel of animals will have been immunized and the spleen of animal with the highest antibody titer will be removed and the spleen lymphocytes obtained by homogenizing the spleen with a syringe. Typically, a spleen from an immunized mouse contains approximately 5×10^7 to 2×10^8 lymphocytes.

[0080] The antibody-producing B lymphocytes from the immunized animal are then fused with cells of an immortal myeloma cell, generally one of the same species as the animal that was immunized. Myeloma cell lines suited for use in hybridoma-producing fusion procedures preferably are non-antibody-producing, have high fusion efficiency, and enzyme deficiencies that render them incapable of growing in certain selective media which support the growth of only the desired fused cells (hybridomas).

[0081] Any one of a number of myeloma cells may be used, as are known to those of skill in the art (Goding, 1986, pp. 65-66; Campbell, 1984, pp. 75-83). For example, where the immunized animal is a mouse, one may use P3-X63/Ag8, X63-Ag8.653, NS1/1.Ag 4 1, Sp210-Ag14, FO, NSO/U, MPC-11, MPC11-X45-GTG 1.7 and S194/5XX0 Bul; for rats, one may use R210.RCY3, Y3-Ag 1.2.3, IR983F and 4B210; and U-266, GM1500-GRG2, LICR-LON-HMy2 and UC729-6 are all useful in connection with human cell fusions.

[0082] One preferred murine myeloma cell is the NS-1 myeloma cell line (also termed P3-NS-1-Ag-4-1), which is readily available from the NIGMS Human Genetic Mutant Cell Repository by requesting cell line repository number GM3573. Another mouse myeloma cell line that may be used is the 8-azaguanine-resistant mouse murine myeloma SP2/0 non-producer cell line.

[0083] Methods for generating hybrids of antibody-producing spleen or lymph node cells and myeloma cells usually comprise mixing somatic cells with myeloma cells in a 2:1 ratio, though the ratio may vary from about 20:1 to about 1:1, respectively, in the presence of an agent or agents (chemical or electrical) that promote the fusion of cell membranes. Fusion methods using Spend virus have been described (Kohler and Milstein, 1975; 1976), and those using polyethylene glycol (PEG), such as 37% (v/v) PEG, (Gefter et al., 1977). The use of electrically induced fusion methods is also appropriate (Goding, 1986, pp. 71-74).

[0084] Fusion procedures usually produce viable hybrids at low frequencies, about 1×10^{-6} to 1×10^{-8}. However, this does not pose a problem, as the viable, fused hybrids are differentiated from the parental, unfused cells (particularly the unfused myeloma cells that would normally continue to divide indefinitely) by culturing in a selective medium. The selective medium is generally one that contains an agent that blocks the de novo synthesis of nucleotides in the tissue culture media. Exemplary and preferred agents are aminopterin, methotrexate, and azaserine. Aminopterin and methotrexate block de novo synthesis of both purines and pyrimidines, whereas azasenne blocks only purine synthesis. Where aminopterin or methotrexate is used, the media is supplemented with hypoxanthine and thymidine as a source of nucleotides (HAT medium). Where azaserine is used, the media is supplemented with hypoxanthine.

[0085] The preferred selection medium is HAT. Only cells capable of operating nucleotide salvage pathways are able to survive in HAT medium. The myeloma cells are defective in key enzymes of the salvage pathway, e.g., hypoxanthine phosphoribosyl transferase (HPRT), and they cannot survive. The B-cells can operate this pathway, but they have a limited life span in culture and generally die within about two weeks. Therefore, the only cells that can survive in the selective media are those hybrids formed from myeloma and B-cells.

[0086] This culturing provides a population of hybridomas from which specific hybridomas are selected. Typically, selection of hybridomas is performed by culturing the cells by single-clone dilution in microtiter plates, followed by testing the individual clonal supernatants (after about two to three weeks) for the desired reactivity. The assay should be sensitive, simple and rapid, such as radioimmunoassays, enzyme immunoassays, cytotoxicity assays, plaque assays, dot immunobinding assays, and the like.

[0087] The selected hybridomas would then be serially diluted and cloned into individual antibody-producing cell lines, which clones can then be propagated indefinitely to provide mAbs. The cell lines may be exploited for mAb production in two basic ways. A sample of the hybridoma can be injected (often into the peritoneal cavity) into a histocompatible animal of the type that was used to provide the somatic and myeloma cells for the original fusion. The injected animal develops tumors secreting the specific monoclonal antibody produced by the fused cell hybrid. The body fluids of the animal, such as serum or ascites fluid, can then be tapped to provide mAbs in high concentration. The individual cell lines could also be cultured in vitro, where the mAbs are naturally secreted into the culture medium from which they can be readily obtained in high concentrations. mAbs produced by either means may be further purified, if desired, using filtration, centrifugation and various chromatographic methods such as HPLC or affinity chromatography.

Transformation Methods

[0088] Numerous methods for producing plant cell nuclei with recombinant DNA are known in the art and may be used in the present invention. Two commonly used methods for plant transformation are *Agrobacterium*-mediated transformation and microprojectile bombardment. Microprojectile bombardment methods are illustrated in U.S. Pat. Nos. 5,015,580 (soybean); 5,550,318 (corn); 5,538,880 (corn); 5,914,451 (soybean); 6,160,208 (corn); 6,399,861 (corn) and 6,153,812 (wheat) and *Agrobacterium*-mediated transformation is described in U.S. Pat. Nos. 5,159,135 (cotton); 5,824,877 (soybean); 5,591,616 (corn); and 6,384,301 (soybean), all of which are incorporated herein by reference. For *Agrobacterium tumefaciens* based plant transformation system, additional elements present on transformation constructs will include T-DNA left and right border sequences to facilitate incorporation of the recombinant polynucleotide into the plant genome.

[0089] In general it is preferred to introduce heterologous DNA randomly, i.e., at a non-specific location, in the genome of a target plant line. In special cases it may be useful to target heterologous DNA insertion in order to achieve site-specific integration, e.g., to replace an existing gene in the genome, to use an existing promoter in the plant genome, or to insert a recombinant polynucleotide at a predetermined site known to be active for gene expression. Several site specific recombination systems exist which are known to function implants include cre-lox as disclosed in U.S. Pat. No. 4,959,317 and FLP-FRT as disclosed in U.S. Pat. No. 5,527,695, both incorporated herein by reference.

[0090] Transformation methods of this invention are preferably practiced in tissue culture on media and in a controlled environment. "Media" refers to the numerous nutrient mixtures that are used to grow cells in vitro, that is, outside of the intact living organism. Recipient cell targets include, but are not limited to, meristem cells, callus, immature embryos and gametic cells such as microspores, pollen, sperm and egg cells. It is contemplated that any cell from which a fertile plant may be regenerated is useful as a recipient cell. Callus may be initiated from tissue sources including, but not limited to, immature embryos, seedling apical meristems, microspores and the like. Cells capable of proliferating as callus are also recipient cells for genetic transformation. Practical transformation methods and materials for making transgenic plants of this invention, e.g., various media and recipient target cells, transformation of immature embryos and subsequent regeneration of fertile transgenic plants are disclosed in U.S. Pat. Nos. 6,194,636 and 6,232,526 and U.S. patent application Ser. No. 09/757,089, which are incorporated herein by reference.

[0091] In practice DNA is introduced into only a small percentage of target cell nuclei in any one experiment. Marker genes are used to provide an efficient system for identification of those cells with nuclei that are stably transformed by receiving and integrating a transgenic DNA construct into their genomes. Preferred marker genes provide selective markers that confer resistance to a selective agent, such as an antibiotic or herbicide. Potentially transformed cells with a nucleus of the invention are exposed to the selective agent. In the population of surviving cells will be those cells where, generally, the resistance-conferring gene has been integrated and expressed at sufficient levels to permit cell survival. Cells may be tested further to confirm stable integration of the exogenous DNA in the nucleus. Useful selective marker genes include those conferring resistance to antibiotics such as kanamycin (nptII), hygromycin B (aph IV) and gentamycin (aac3 and aacC4) or resistance to herbicides such as glufosinate (bar or pat) and glyphosate (EPSPS). Examples of such selectable are illustrated in U.S. Pat. Nos. 5,550,318; 5,633,435; 5,780,708 and 6,118,047, all of which are incorporated herein by reference. Screenable markers which provide an ability to visually identify transformants can also be employed, e.g., a gene expressing a colored or fluorescent protein such as a luciferase or green fluorescent protein (GFP) or a gene expressing a beta-glucuronidase or uidA gene (GUS) for which various chromogenic substrates are known. It is also contemplated that combinations of screenable and selectable markers will be useful for identification of transformed cells. See PCT publication WO 99/61129 which discloses use of a gene fusion between a selectable marker gene and a screenable marker gene, e.g., an NPTII gene and a GFP gene.

[0092] Cells that survive exposure to the selective agent, or cells that have been scored positive in a screening assay, may be cultured in regeneration media and allowed to mature into plants. Developing plantlets can be transferred to soil less plant growth mix, and hardened off, e.g., in an environmentally controlled chamber at about 85% relative humidity, 600 ppm CO_2, and 25-250 microeinsteins m^{-2} s^{-1} of light, prior to

transfer to a greenhouse or growth chamber for maturation. Plants are preferably matured either in a growth chamber or greenhouse. Plants are regenerated from about 6 wk to 10 months after a transformant is identified, depending on the initial tissue. During regeneration, cells are grown to plants on solid media at about 19 to 28° C. After regenerating plants have reached the stage of shoot and root development, they may be transferred to a greenhouse for further growth and testing. Plants may be pollinated using conventional plant breeding methods known to those of skill in the art and seed produced.

[0093] Progeny may be recovered from transformed plants and tested for expression of the exogenous recombinant polynucleotide. Useful assays include, for example, "molecular biological" assays, such as Southern and Northern blotting and PCR; "biochemical" assays, such as detecting the presence of RNA, e.g., double stranded RNA, or a protein product, e.g., by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of the whole regenerated plant.

Discovery of Trait-Improving Recombinant DNA

[0094] To identify nuclei with recombinant DNA that confer improved traits to plants, *Arabidopsis thaliana* was transformed with a candidate recombinant DNA construct and screened for an improved trait.

[0095] *Arabidopsis thaliana* is used a model for genetics and metabolism in plants. *Arabidopsis* has a small genome, and well-documented studies are available. It is easy to grow in large numbers and mutants defining important genetically controlled mechanisms are either available, or can readily be obtained. Various methods to introduce and express isolated homologous genes are available (see Koncz, e.g., Methods in *Arabidopsis* Research e.g., (1992), World Scientific, New Jersey, New Jersey, in "Preface").

[0096] A two-step screening process was employed which comprised two passes of trait characterization to ensure that the trait modification was dependent on expression of the recombinant DNA, but not due to the chromosomal location of the integration of the transgene. Twelve independent transgenic lines for each recombinant DNA construct were established and assayed for the transgene expression levels. Five transgenic lines with high transgene expression levels were used in the first pass screen to evaluate the transgene's function in T2 transgenic plants. Subsequently, three transgenic events, which had been shown to have one or more improved traits, were further evaluated in the second pass screen to confirm the transgene's ability to impart an improved trait. The following Table 3 summarizes the improved traits that have been confirmed as provided by a recombinant DNA construct.

[0097] In particular, Table 3 reports:

[0098] "PEP SEQ ID" which is the amino acid sequence of the protein cognate to the DNA in the recombinant DNA construct corresponding to a protein sequence of a SEQ ID NO. in the Sequence Listing.

[0099] "construct_id" is an arbitrary name for the recombinant DNA describe more particularly in Table 1.

[0100] "annotation" refers to a description of the top hit protein obtained from an amino acid sequence query of each PEP SEQ ID NO to GenBank database of the National Center for Biotechnology Information (ncbi). More particularly, "gi" is the GenBank ID number for the top BLAST hit.

[0101] "description" refers to the description of the top BLAST hit.

[0102] "e-value" provides the expectation value for the BLAST hit.

[0103] "% id" refers to the percentage of identically matched amino acid residues along the length of the portion of the sequences which is aligned by BLAST between the sequence of interest provided herein and the hit sequence in GenBank.

[0104] "traits" identify by two letter codes the confirmed improvement in a transgenic plant provided by the recombinant DNA. The codes for improved traits are:

[0105] "CK" which indicates cold tolerance improvement identified under a cold shock tolerance screen;

[0106] "CS" which indicates cold tolerance improvement identified by a cold germination tolerance screen;

[0107] "DS" which indicates drought tolerance improvement identified by a soil drought stress tolerance screen;

[0108] "PEG" which indicates osmotic stress tolerance improvement identified by a PEG induced osmotic stress tolerance screen;

[0109] "HS" which indicates heat stress tolerance improvement identified by a heat stress tolerance screen;

[0110] "SS" which indicates high salinity stress tolerance improvement identified by a salt stress tolerance screen;

[0111] "LN" which indicates nitrogen use efficiency improvement identified by a limited nitrogen tolerance screen;

[0112] "LL" which indicates attenuated shade avoidance response identified by a shade tolerance screen under a low light condition;

[0113] "PP" which indicates improved growth and development at early stages identified by an early plant growth and development screen;

[0114] "SP" which indicates improved growth and development at late stages identified by a late plant growth and development screen provided herein.

TABLE 3

PEP		Annotation			
SEQ ID	Construct ID	e value	% id	description	trait
198	11029	1.00E−170	85	gb|AAD02882.1|gamma-tocopherol methyltransferase [*Arabidopsis thaliana*]	DS LN
199	12223	/	/	/	CK PEG
200	10422	1.00E−133	100	gb|AAB47766.1|SNF5 homolog BSH [*Arabidopsis thaliana*]	LN

TABLE 3-continued

PEP SEQ ID	Construct ID	Annotation e value	% id	description	trait		
201	13485	4.00E−39	55	emb|CAB79347.1|hypothetical protein [*Arabidopsis thaliana*]	LN		
202	13235	7.00E−76	100	emb|CAB78153.1|putative protein [*Arabidopsis thaliana*]	LN		
203	13411	3.00E−29	100	ref|NP_179638.1|unknown protein [*Arabidopsis thaliana*]	LN	CK	
204	73944	0	95	ref|NP_189578.1|phosphorylase/ transferase, transferring glycosyl groups [*Arabidopsis thaliana*]	CS		
205	13846	0	91	gb|AAN60291.1|unknown [*Arabidopsis thaliana*]	LN		
206	12602	0	100	ref|NP_565974.1|PP2A-4; hydrolase/ protein phosphatase type 2A/protein serine/threonine phosphatase [*Arabidopsis thaliana*]	LN		
207	74065	0	94	ref|NP_181390.1|DNA binding/ transcription factor [*Arabidopsis thaliana*] gb|AAN13033.1|putative elongation	CS	DS	
208	72783	0	83	ref|NP_564690.1|unknown protein [*Arabidopsis thaliana*]	CK	PEG	HS
209	17210	1.00E−92	100	ref|NP_563622.1|unknown protein [*Arabidopsis thaliana*]	CS	CK	PEG
210	72724	1.00E−128	90	ref|NP_190525.1|protein translocase/ protein transporter [*Arabidopsis thaliana*	LL		
211	17805	1.00E−172	80	ref|NP_563761.1|unknown protein [*Arabidopsis thaliana*]	LN		
212	16610	0	100	gb|AAL44550.1|fructose bisphosphate aldolase [*Agrobacterium tumefaciens* str. C58]	LN	HS	
213	76602	0	78	ref|NP_566515.1|signal transducer [*Arabidopsis thaliana*]	CS	HS	
214	18456	1.00E−135	81	ref|NP_176820.1|DNA binding/ transcription factor [*Arabidopsis thaliana*]	CK	SS	PEG
215	18414	1.00E−169	70	ref|NP_195583.1|translation initiation factor [*Arabidopsis thaliana*]	CK		
216	71538	1.00E−137	90	emb|CAE85115.1|synaptotagmin [*Arabidopsis thaliana*]	SP		
217	76532	0	99	ref|NP_564775.1|ATP binding/ carbohydrate binding/kinase/protein kinase/protein serine/threonine kinase/protein-tyrosine kinase/sugar binding [*Arabidopsis thaliana*]	CK	CS	
218	18231	1.00E−142	100	emb|CAC83762.1|allene oxide cyclase [*Arabidopsis thaliana*]	CK	LN	
219	18232	6.00E−85	89	ref|NP_191628.1|unknown protein [*Arabidopsis thaliana*]	CS		
220	18256	1.00E−102	100	dbj|BAD44508.1|putative zinc finger protein (PMZ) [*Arabidopsis thaliana*]	SS	CK	HS
221	18258	1.00E−175	83	emb|CAA11525.1|transcription factor IIA large subunit [*Arabidopsis thaliana*]	SP		
222	19193	1.00E−103	100	ref|NP_564682.1|lipid binding [*Arabidopsis thaliana*] dbj|BAE73268.1|xylogen like protein 12 [*Arabidopsis thaliana*]	SP	HS	
223	71301	0	84	ref|NP_568393.1|nucleic acid binding [*Arabidopsis thaliana*]	LN		
224	18354	0	96	ref|NP_567568.1|ATP binding/ kinase/protein kinase/protein serine/threonine kinase/protein-tyrosine kinase [*Arabidopsis thaliana*]	LN		
225	77334	1.00E−117	100	ref|NP_178399.1|RNS1 (RIBONUCLEASE 1); endoribonuclease [*Arabidopsis thaliana*]	LL		
226	19767	1.00E−180	95	gb|AAO69665.1|serine threonine protein phosphatase [*Phaseolus acutifolius*]	CS	DS	

TABLE 3-continued

PEP SEQ ID	Construct ID	Annotation e value	% id	description	trait				
227	19774	1.00E−100	57	ref|NP_974271.1|unknown protein [*Arabidopsis thaliana*]	CS	PP			
228	70992	1.00E−108	65	gb|ABE87200.1|hypothetical protein MtrDRAFT_AC151668g4v1 [*Medicago truncatula*]	CS	PEG			
229	19956	1.00E−146	100	gb|AAF64040.1|14-3-3-like protein [*Glycine max*]	PP				
230	70948	3.00E−59	45	ref|NP_201297.1|CIP8 (COP1-INTERACTING PROTEIN 8); protein binding/zinc ion binding [*Arabidopsis thaliana*]	PP	HS			
231	70201	0	68	ref|NP_567072.1|ATP binding/ kinase/protein kinase/protein serine/threonine kinase/protein-tyrosine kinase [*Arabidopsis thaliana*]	CS	SS			
232	19973	0	96	gb|AAB04057.1|S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase	PP	SS			
233	70987	0	93	gb|AAM83095.1|SOS2-like protein kinase [*Glycine max*]	CK	CS	HS	SS	PEG
234	70950	1.00E−116	77	dbj|BAD38167.1|putative leucine zipper protein [*Oryza sativa* (*japonica* cultivar-group)]	PP	PEG			
235	70962	1.00E−179	78	gb|ABE93200.1|conserved hypothetical protein [*Medicago truncatula*]	PP	HS			
236	70915	0	76	dbj|BAE71210.1|hypothetical protein [Trifolium pratense] dbj|BAE71208.1| hypothetical protein [*Trifolium pratense*]	CS	PP			
237	19947	1.00E−116	65	gb|AAS38575.1|short-chain dehydrogenase Tic32 [*Pisum sativum*]	CS	DS	SS		
238	70969	1.00E−144	76	ref|NP_174321.2|unknown protein [*Arabidopsis thaliana*]	SS				
239	70985	0	69	dbj|BAB08296.1|unnamed protein product [*Arabidopsis thaliana*] sp|Q9FMT4|Y5417_ARATH Protein At5g14170	CS	HS	PEG		
240	70971	1.00E−92	63	gb|ABE80664.1|GNS1/SUR4 membrane protein [*Medicago truncatula*] gb|ABE78502.1| GNS1/SUR4 membrane protein [*Medicago truncatula*]	SS				
241	70963	1.00E−96	56	ref|NP_177178.1|CYCD1; 1; cyclin-dependent protein kinase regulator [*Arabidopsis thaliana*]	CS	PP	HS		
242	70994	2.00E−33	44	ref|NP_172962.1|RHA2A; protein binding/ubiquitin-protein ligase/zinc ion binding [*Arabidopsis thaliana*]	PP	DS	HS	SS	
243	70956	0	85	gb|AAO23063.1|ent-kaurenoic acid oxidase [*Pisum sativum*]	CS	SS	HS		
244	70995	1.00E−132	66	dbj|BAD73789.1|putative uncharacterized hypothalamus protein HT010 [*Oryza sativa* (*japonica* cultivar-group)]	CK	CS	PP	LL	PEG
245	73306	0	93	ref|NP_201243.1|phosphoric ester hydrolase [*Arabidopsis thaliana*]	SS	PEG			
246	70657	9.00E−31	73	emb|CAB78150.1|probable wound-induced protein [*Arabidopsis thaliana*]	SP	LL			
247	70660	2.00E−32	79	ref|NP_568217.1|transcription regulator [*Arabidopsis thaliana*]	SP				
248	74536	0	91	ref|NP_001031061.1|PGDH; phosphoglycerate dehydrogenase [*Arabidopsis thaliana*]]	CS				
249	71328	0	99	gb|AAD46022.1|Strong simlarity to gb|286426 F10M6.190 cytochrome p450 homolog from *Arabidopsis thaliana* BAC	PP				

TABLE 3-continued

PEP SEQ ID	Construct ID	Annotation e value	% id	description	trait				
250	71329	0	94	ref|NP_177477.1|heme binding/iron ion binding/monooxygenase/oxygen binding [*Arabidopsis thaliana*]	LN				
251	70755	1.00E−142	100	ref|NP_188925.1|unknown protein [*Arabidopsis thaliana*]	LL				
252	70684	3.00E−53	100	emb|CAB80194.1|putative protein [*Arabidopsis thaliana*]	CS	LN	HS	PP	
253	73330	1.00E−158	72	emb|CAB96855.1|putative protein [*Arabidopsis thaliana*]	CK	CS	SS		
254	76202	3.00E−83	67	emb|CAA16586.1|putative protein [*Arabidopsis thaliana*]	LL				
255	72807	0	100	ref|NP_173478.2|nucleotide binding [*Arabidopsis thaliana*]	PEG	CK	HS	SS	
256	72811	1.00E−176	100	ref|NP_565782.1|nucleotide binding [*Arabidopsis thaliana*]	CK	SS	PEG		
257	73235	0	89	ref|NP_564867.1|pepsin A [*Arabidopsis thaliana*]	SS	HS			
258	72813	2.00E−79	93	ref|NP_850506.1|unknown protein [*Arabidopsis thaliana*]	LL	LN			
259	72825	1.00E−154	95	ref|NP_563635.1|oxidoreductase [*Arabidopsis thaliana*]	CK	PEG	HS		
260	73628	1.00E−163	92	ref|NP_849428.1|oxidoreductase [*Arabidopsis thaliana*]	CS	DS	LL	HS	PEG
261	76105	0	93	emb|CAB79123.1|receptor kinase-like protein [*Arabidopsis thaliana*]	DS				
262	73242	0	100	ref|NP_567292.1|unknown protein [*Arabidopsis thaliana*]	SP	PEG			
263	74217	0	100	emb|CAB93726.1|cytochrome P450-like protein [*Arabidopsis thaliana*]	DS	CK			
264	73735	0	97	gb|AAU94404.1|At3g48520 [*Arabidopsis thaliana*]	CK				
265	73256	1.00E−114	77	ref|NP_566329.1|unknown protein [*Arabidopsis thaliana*] gb|AAL06975.1|	CS	PP	PEG		
266	73260	4.00E−37	100	ref|NP_566488.1|unknown protein [*Arabidopsis thaliana*]	CS				
267	75822	1.00E−90	88	emb|CAB63015.1|putative protein [*Arabidopsis thaliana*]	LL				
268	72001	0	96	ref|NP_200045.1|CYP96A4; heme binding/iron ion binding/ monooxygenase/oxygen binding [*Arabidopsis thaliana*]	CS	PP	HS		
269	72056	0	92	ref|NP_010186.1|Essential, non-ATPase regulatory subunit of the 26S proteasome lid required for the assembly and activity of the 26S proteasome;	SP				
270	77308	0	100	ref|NP_178642.1|SCPL38; serine carboxypeptidase [*Arabidopsis thaliana*]	PEG				
271	73766	1.00E−163	100	emb|CAB62363.1|MTN3-like protein [*Arabidopsis thaliana*]	LL				
272	72774	1.00E−139	95	ref|NP_011052.1|Constituent of 66S pre-ribosomal particles, involved in 60S ribosomal subunit biogenesis;	LL	CK	HS		
273	72788	0	81	ref|NP_010007.1|General repressor of transcription, forms complex with Cyc8p, involved in the establishment of repressive chromatin structure through interactions with histones H3 and H4, appears to enhance expression of some genes	CK	CS	SS		
274	72753	1.00E−105	85	ref|NP_013125.1|One of four subunits of the endosomal sorting complex required for transport III (ESCRT-III);	CS	PP	HS	PEG	
275	72709	0	94	ref|NP_011827.1|Low affinity methionine permease, similar to Mup1p;	LL				
276	73954	0	98	ref|NP_200954.1|MIM; ATP binding [*Arabidopsis thaliana*]	HS				

TABLE 3-continued

PEP SEQ ID	Construct ID	Annotation e value	% id	description	trait		
277	73137	1.00E−110	94	gb|AAD32800.1|putative thioredoxin H [*Arabidopsis thaliana*]	CS		
278	73161	1.00E−36	65	emb|CAB85993.1|putative protein [*Arabidopsis thaliana*]	CS	PEG	
279	73057	1.00E−133	95	ref|NP_012770.1|Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis;	SP		
280	73127	0	99	dbj|BAB05414.1|aspartate aminotransferase [*Bacillus halodurans* C-125] ref|NP_242561.1|aspartate aminotransferase [*Bacillus halodurans* C-125]	SS	HS	
281	73033	0	96	dbj|BAB07276.1|2,3-bisphosphoglycerate-independent phosphoglycerate mutase [*Bacillus halodurans* C-125]	CK		
282	73105	0	99	emb|CAB13630.1|glutamine synthetase [*Bacillus subtilis* subsp. *subtilis* str. 168]	PP	PEG	
283	73141	0	95	ref|NP_414696.1|glutamate-1-semialdehyde aminotransferase [*Escherichia coli* K12]	CS		
284	73165	0	99	ref|NP_288110.1|pyruvate kinase [*Escherichia coli* O157:H7 EDL933]	DS	PEG	
285	73155	1.00E−173	92	emb|CAC47346.1|PROBABLE FRUCTOSE-BISPHOSPHATE ALDOLASE CLASS I PROTEIN [*Sinorhizobium meliloti*]]	CS		
286	73026	1.00E−116	87	emb|CAG77169.1|triosephosphate isomerase [*Erwinia carotovora* subsp. *atroseptica* SCRI1043]	PEG		
287	73120	8.00E−82	100	ref|NP_441918.1|nucleoside diphosphate kinase [*Synechocystis* sp. PCC 6803]	CS	SS	HS
288	73133	2.00E−63	90	gb|ABA76342.1|Nucleoside diphosphate kinase [*Pseudomonas fluorescens* PfO-1]	LL		
289	73134	9.00E−98	81	emb|CAE15979.1|ribose 5-phosphate isomerase A (phosphoriboisomerase A) [*Photorhabdus luminescens* subsp. *laumondii* TTO1]	SS	CK	
290	73123	0	95	ref|NP_180412.2|nucleic acid binding [*Arabidopsis thaliana*]	CS	PEG	
291	73981	0	93	ref|NP_014797.1|hypothetical protein; Slp1p [*Saccharomyces cerevisiae*]	DS	PEG	
292	73136	0	91	ref|NP_012454.1|Nuclear actin-related protein involved in chromatin remodeling	DS	PP	
293	73172	0	100	ref|NP_04952.1|Protein involved in ER-to-Golgi transport; Sly41p [*Saccharomyces cerevisiae*]	CK	PEG	HS
294	73020	0	93	ref|NP_014993.1|Proline permease, required for high-affinity transport of proline	LL		
295	72946	0	95	ref|NP_012534.1|Vacuolar transporter, imports large neutral amino acids into the vacuole	PEG	LL	
296	74746	0	93	ref|NP_566298.1|ATP binding/kinase/protein kinase/protein serine/threonine kinase/protein-tyrosine kinase [*Arabidopsis thaliana*]	CK		
297	77312	0	90	ref|NP_178463.1|CDC48B; ATP binding/ATP-dependent peptidase/ATPase/nucleoside-triphosphatase/nucleotide binding/serine-type endopeptidase [*Arabidopsis thaliana*]	PP	SS	HS

TABLE 3-continued

PEP SEQ ID	Construct ID	Annotation e value	% id	description	trait				
298	75237	0	100	ref|NP_173390.1|kinase [*Arabidopsis thaliana*] gb|AAF98405.1|Unknown protein [*Arabidopsis thaliana*]	LN				
299	75240	0	100	emb|CAB69854.1|putative protein [*Arabidopsis thaliana*]	CK				
300	74349	1.00E−148	79	ref|NP_565187.1|transcription regulator [*Arabidopsis thaliana*]	LN				
301	76422	5.00E−44	100	ref|NP_171781.1|unknown protein [*Arabidopsis thaliana*]	LN				
302	70812	1.00E−152	92	ref|NP_850182.1|PUR ALPHA-1; nucleic acid binding [*Arabidopsis thaliana*]	PP	PEG			
303	77322	1.00E−172	100	gb|AAW38983.1|At5g10750 [*Arabidopsis thaliana*]	LN	LL			
304	74662	4.00E−89	100	ref|NP_001031939.1|ubiquitin conjugating enzyme/ubiquitin-like activating enzyme [*Arabidopsis thaliana*]	PP	HS			
305	76527	0	96	emb|CAB51062.1|cell division cycle protein 23 homolog [*Arabidopsis thaliana*]	CS				
306	77020	0	98	emb|CAB75781.1|putative transporter protein [*Arabidopsis thaliana*] ref|NP_190154.1|transporter [*Arabidopsis thaliana*]	CS				
307	77609	0	96	gb|AAU95452.1|At5g04420 [*Arabidopsis thaliana*]	LL	SS			
308	73485	0	100	emb|CAD84238.1|Glyceraldehyde 3-phosphate dehydrogenase	PEG				
309	73433	1.00E−132	65	ref|ZP_00819153.1|putative alcohol dehydrogenase [*Marinobacter aquaeolei* VT8]	SP	LN	PP		
310	73411	0	99	emb|CAB14878.1|pyruvate kinase [*Bacillus subtilis* subsp. *subtilis* str. 168]	CS	HS	PP	PEG	
311	73568	0	97	emb|CAC41401.1|PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE [NADP+] PROTEIN [*Sinorhizobium meliloti*]	SP				
312	74688	0	98	emb|CAA16688.1|receptor protein kinase - like protein [*Arabidopsis thaliana*]	CS	PP	SS	PEG	
313	74420	1.00E−142	99	emb|CAD85691.1|Phosphoglycerate mutase family [*Nitrosomonas europaea* ATCC 19718]	PP	LN	SS		
314	74435	1.00E−117	100	emb|CAC41549.1|PROBABLE PHOSPHOGLYCERATE MUTASE 1 PROTEIN [*Sinorhizobium meliloti*]	LL				
315	74460	0	95	ref|NP_441738.1|fructose-1,6-bisphosphatase [*Synechocystis* sp. PCC 6803]	CK				
316	74566	0	93	emb|CAC48499.1|Putative trehalose synthase protein [*Sinorhizobium meliloti* 1021]	SP	PP	SS	PEG	HS
317	77610	0	94	gb|AAC23406.1|hypothetical protein [*Arabidopsis thaliana*]	CS	HS			
318	77618	0	100	ref|NP_850453.1|JAR1 (JASMONATE RESISTANT 1) [*Arabidopsis thaliana*]	PP	HS			
319	77517	7.00E−77	100	emb|CAB75802.1|putative protein [*Arabidopsis thaliana*]	CS	LL			
320	77518	1.00E−49	100	ref|NP_199600.1|oxidoreductase, acting on NADH or NADPH, quinone or similar compound as acceptor [*Arabidopsis thaliana*]	SS	LL	HS		
321	76460	/	/	/	CS	PEG			
322	77069	0	85	ref|NP_201196.1|unknown protein [*Arabidopsis thaliana*]	PP				
323	76161	1.00E−161	100	ref|NP_851282.1|unknown protein [*Arabidopsis thaliana*]	CK				

TABLE 3-continued

PEP SEQ ID	Construct ID	Annotation e value	% id	description	trait				
324	76171	1.00E−178	95	ref|NP__176204.1|oxidoreductase [*Arabidopsis thaliana*]	LL				
325	76178	5.00E−60	86	ref|NP__565029.1|unknown protein [*Arabidopsis thaliana*]	CS	PP	HS	LL	PEG
326	76467	6.00E−86	89	ref|NP__565671.1|unknown protein [*Arabidopsis thaliana*]	LL				
327	77536	1.00E−119	83	gb|AAS99692.1|At1g10020 [*Arabidopsis thaliana*]	SP	CS	DS	PP	LN
328	76576	1.00E−145	100	ref|NP__181023.1|FAH1 (FATTY ACID HYDROXYLASE 1); catalytic [*Arabidopsis thaliana*]	DS				
329	74862	1.00E−145	100	gb|ABA77057.1|Delta 1-pyrroline-5-carboxylate reductase [*Pseudomonas fluorescens* PfO-1]	PP				
330	74863	1.00E−93	100	ref|NP__012420.1|Nucleosome assembly factor, involved in chromatin assembly after DNA replication]	LL	PEG	CK	SS	
331	74858	5.00E−50	68	gb|AAK14395.1|response regulator protein [*Dianthus caryophyllus*]	LL				
332	74933	1.00E−177	95	gb|AAK85899.1|AGR__C__118p [*Agrobacterium tumefaciens* str. C58]	LL				
333	75379	1.00E−105	76	dbj|BAD73205.1|unknown protein [*Oryza sativa* (*japonica* cultivar-group)]	LN				
334	77816	4.00E−41	89	gb|ABA98984.1|expressed protein [*Oryza sativa* (*japonica* cultivar-group)]	SP	PP	HS		
335	75434	3.00E−52	79	ref|XP__472650.1|OSJNBa0027P08.15 [*Oryza sativa* (*japonica* cultivar-group)]	LN				
336	77821	0	71	gb|ABE84883.1|conserved hypothetical protein [*Medicago truncatula*]	PP	SS	HS	PEG	
337	75685	0	82	ref|XP__475937.1|unknown protein [*Oryza sativa* (*japonica* cultivar-group)]	LL				
338	75654	0	100	ref|NP__563865.1|unknown protein [*Arabidopsis thaliana*]	SP	CK	HS		
339	75692	1.00E−119	87	dbj|BAD30296.1|peptidyl-prolyl cis-trans isomerase-like protein [*Oryza sativa* (*japonica* cultivar-group)]	CK	LN			
340	75657	6.00E−57	67	dbj|BAD38392.1|DNAJ heat shock N-terminal domain-containing protein-like [*Oryza sativa* (*japonica* cultivar-group)]	CS	LL	HS		
341	75622	1.00E−30	78	dbj|BAD45825.1|unknown protein [*Oryza sativa* (*japonica* cultivar-group)]	LN				
342	77549	1.00E−132	89	emb|CAB80891.1|AT4g00820 [*Arabidopsis thaliana*]]	PP	HS			
343	77917	0	91	ref|NP__197917.1|EBF2 (EIN3-BINDING F BOX PROTEIN 2) [*Arabidopsis thaliana*]	PP	PEG			
344	77568	9.00E−99	76	ref|NP__849792.1|nucleic acid binding [*Arabidopsis thaliana*]	PP				
345	77570	7.00E−54	100	gb|AAS75309.1|multidomain cyclophilin type peptidyl-prolyl cis-trans isomerase [*Arabidopsis thaliana*]]	CK	SS			
346	77338	4.00E−24	65	gb|AAM61454.1|unknown [*Arabidopsis thaliana*]	PEG				
347	77580	3.00E−45	100	dbj|BAB01457.1|unnamed protein product [*Arabidopsis thaliana*]	PEG	CS	HS	SS	
348	77928	4.00E−38	100	ref|NP__196244.1|unknown protein [*Arabidopsis thaliana*]	HS				
349	77349	1.00E−81	93	emb|CAC05463.1|putative lipid transfer protein [*Arabidopsis thaliana*]	LL	SS			
350	77357	1.00E−155	95	ref|NP__175357.1|unknown protein [*Arabidopsis thaliana*]	PEG				

TABLE 3-continued

PEP SEQ ID	Construct ID	Annotation e value	% id	description	trait				
351	77587	/	/	/	CS	PP	HS	SS	
352	77933	/	/	/	SS				
353	77619	3.00E−40	98	dbj|BAB09403.1|unnamed protein product [*Arabidopsis thaliana*]	CK	SS	PEG	HS	
354	77621	4.00E−58	74	ref|NP_197632.1|Rac GTPase activator [*Arabidopsis thaliana*] [*Arabidopsis thaliana*]	CK				
355	77629	5.00E−36	100	ref|NP_196372.1|GRP19 [*Arabidopsis thaliana*]	SS	HS			
356	77832	0	83	ref|NP_917762.1|P0501G01.24 [*Oryza sativa* (*japonica* cultivar-group)]	CS	SS	PEG	HS	LN
357	76802	0	76	ref|NP_181908.1|actin binding [*Arabidopsis thaliana*] gb|AAB64026.1|unknown protein [*Arabidopsis thaliana*]	CK				
358	76829	0	89	ref|NP_909912.1|ferredoxin-NADP+ reductase [*Oryza sativa*]	CK				
359	76961	0	65	ref|XP_473189.1|OSJNBa0073E02.11 [*Oryza sativa* (*japonica* cultivar-group)]	LL	LN			
360	76973	1.00E−151	76	ref|XP_480055.1|unknown protein [*Oryza sativa* (*japonica* cultivar-group)]	LL				
361	77150	0	76	dbj|BAD61385.1|putative nucleostemin [*Oryza sativa* (*japonica* cultivar-group)]	SP	HS	PEG		
362	77186	0	85	dbj|BAD27898.1|putative pentatricopeptide (PPR) repeat-containing protein [*Oryza sativa* (*japonica* cultivar-group)]	PP				
363	77103	1.00E−174	66	ref|NP_568580.1|catalytic [*Arabidopsis thaliana*]	LL	DS			
364	77139	2.00E−93	58	ref|NP_171690.1|PFC1 (PALEFACE 1) [*Arabidopsis thaliana*]	CS	SS			
365	77187	1.00E−160	83	ref|NP_913437.1|3-methyl-2-oxobutanoate hydroxy-methyl-transferase-like protein [*Oryza sativa* (*japonica* cultivar-group)]	CS	PP	LL	PEG	
366	77140	0	77	dbj|BAD36145.1|membrane protein PTM1-like [*Oryza sativa* (*japonica* cultivar-group)]	CK	PEG	SS		
367	77164	0	91	gb|ABF93778.1|DNA polymerase delta small subunit, putative, expressed [*Oryza sativa* (*japonica* cultivar-group)]	PP	HS			
368	77176	0	76	ref|NP_914476.1|putative phytochrome P450 [*Oryza sativa* (*japonica* cultivar-group)]	LL				
369	77165	1.00E−139	75	ref|NP_914949.1|serine/threonine protein kinase-like protein [*Oryza sativa* (*japonica* cultivar-group)]	CK	LL	LN		
370	77166	0	85	dbj|BAB75233.1|all3534 [*Nostoc* sp. PCC 7120]	CK	PP			
371	77155	0	97	emb|CAA35550.1|hycE [*Escherichia coli*]	PP				
372	77180	2.00E−62	61	gb|ABA99663.1|expressed protein [*Oryza sativa* (*japonica* cultivar-group)]	CS	PP	HS	PEG	
373	77121	1.00E−166	93	dbj|BAB05404.1|transcriptional repressor of the biotin operon [*Bacillus halodurans* C-125]	CK				
374	77157	0	100	ref|NP_531453.1|3,4-dihydroxy-2-butanone-4-phoshate synthase/GTP cyclohydrolase II [*Agrobacterium tumefaciens* str. C58]	CK	LL			
375	77195	0	94	gb|AAM71555.1|mannose-6-phosphate isomerase/mannose-1-phosphate guanylyl transferase [*Chlorobium tepidum* TLS]	PP	SS	PEG	LL	

TABLE 3-continued

PEP SEQ ID	Construct ID	Annotation e value	% id	description			trait
376	77124	1.00E−180	100	ref|NP_418404.1|biotin--protein ligase [*Escherichia coli* K12]	PP	SS	PEG
377	77261	0	100	ref|NP_416982.1|hydrogenase 4, subunit [*Escherichia coli* K12]	PEG		
378	77273	0	93	dbj|BAB06534.1|glycine dehydrogenase subunit 1 [*Bacillus halodurans* C-125]	PP	PEG	
379	77203	1.00E−176	60	dbj|BAD33942.1|putative serine carboxypeptidase precursor [*Oryza sativa* (*japonica* cultivar-group)]	PEG	CK	
380	77275	4.00E−37	55	gb|ABA91490.1|expressed protein [*Oryza sativa* (*japonica* cultivar-group)]	SS	HS	PEG
381	77204	2.00E−27	44	ref|XP_469963.1|putative protease inhibitor [*Oryza sativa* (*japonica* cultivar-group)]	CK	CS	
382	77266	7.00E−25	73	gb|AAT93978.1|unknown protein [*Oryza sativa* (*japonica* cultivar-group)]	CS	PP	PEG
383	77220	1.00E−169	78	dbj|BAD52854.1|putative non-phototropic hypocotyl 3 [*Oryza sativa* (*japonica* cultivar-group)]	LL		
384	77268	4.00E−71	85	gb|ABF95596.1|ETC complex I subunit conserved region family protein, expressed [*Oryza sativa* (*japonica* cultivar-group)]	PP	SS	
385	77209	9.00E−86	85	ref|XP_479456.1|putative 60S ribosome subunit biogenesis protein [*Oryza sativa* (*japonica* cultivar-group)]	PP	LL	
386	77269	2.00E−56	70	dbj|BAD32031.1|unknown protein [*Oryza sativa* (*japonica* cultivar-group)]	SS		
387	77451	0	71	ref|XP_475231.1|putative microtubule-associated protein [*Oryza sativa* (*japonica* cultivar-group)]	PP	SS	
388	77452	1.00E−106	69	dbj|BAD69045.1|unknown protein [*Oryza sativa* (*japonica* cultivar-group)]	PP		
389	77430	1.00E−160	83	dbj|BAD33328.1|putative protein serine/threonine kinase [*Oryza sativa* (*japonica* cultivar-group)]	CS	PP	SS
390	77432	0	86	ref|NP_849565.1|carbohydrate transporter/nucleoside transporter/ sugar porter [*Arabidopsis thaliana*] gb|AAM19835.1| AT4g35300/F23E12_140 [*Arabidopsis thaliana*]	PP	HS	PEG
391	77433	0	100	gb|AAK59487.1|putative cleavage and polyadenylation specificity factor [*Arabidopsis thaliana*]	CK	PP	
392	77444	0	96	ref|NP_199947.1|unknown protein [*Arabidopsis thaliana*]	CS	PP	
393	77409	0	91	ref|NP_001032163.1|unknown protein [*Arabidopsis thaliana*]	PP		
394	12313	0	94	ref|NP_189150.1|QUA1 (QUASIMODO1); transferase, transferring glycosyl groups/ transferase, transferring hexosyl groups [*Arabidopsis thaliana*]	SP		

Trait Improvement Screens

[0115] DS-Improvement of drought tolerance identified by a soil drought stress tolerance screen: Drought or water deficit conditions impose mainly osmotic stress on plants. Plants are particularly vulnerable to drought during the flowering stage. The drought condition in the screening process disclosed in Example 1B started from the flowering time and was sustained to the end of harvesting. The present invention provides recombinant DNA that can improve the plant survival rate under such sustained drought condition. Exemplary recombinant DNA for conferring such drought tolerance are identified as such in Table 3. Such recombinant DNA may find particular use in generating transgenic plants that are tolerant to the drought condition imposed during flowering

time and in other stages of the plant life cycle. As demonstrated from the model plant screen, in some embodiments of transgenic plants with trait-improving recombinant DNA grown under such sustained drought condition can also have increased total seed weight per plant in addition to the increased survival rate within a transgenic population, providing a higher yield potential as compared to control plants.

[0116] PEG-Improvement of drought tolerance identified by PEG induced osmotic stress tolerance screen: Various drought levels can be artificially induced by using various concentrations of polyethylene glycol (PEG) to produce different osmotic potentials (Pilon-Smits e.g., (1995) Plant Physiol. 107:125-130). Several physiological characteristics have been reported as being reliable indications for selection of plants possessing drought tolerance. These characteristics include the rate of seed germination and seedling growth. The traits can be assayed relatively easily by measuring the growth rate of seedling in PEG solution. Thus, a PEG-induced osmotic stress tolerance screen is a useful surrogate for drought tolerance screen. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in the PEG-induced osmotic stress tolerance screen can survive better drought conditions providing a higher yield potential as compared to control plants.

[0117] SS-Improvement of drought tolerance identified by high salinity stress tolerance screen: Three different factors are responsible for salt damages: (1) osmotic effects, (2) disturbances in the mineralization process, and (3) toxic effects caused by the salt ions, e.g., inactivation of enzymes. While the first factor of salt stress results in the wilting of the plants that is similar to drought effect, the ionic aspect of salt stress is clearly distinct from drought. The present invention provides genes that help plants maintain biomass, root growth, and/or plant development in high salinity conditions, which are identified as such in Table 3. Since osmotic effect is one of the major components of salt stress, which is common to the drought stress, trait-improving recombinant DNA identified in a high salinity stress tolerance screen can also provide transgenic crops with improved drought tolerance. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in a high salinity stress tolerance screen can survive better drought conditions and/or high salinity conditions providing a higher yield potential as compared to control plants.

[0118] HS-Improvement of drought tolerance identified by heat stress tolerance screen: Heat and drought stress often occur simultaneously, limiting plant growth. Heat stress can cause the reduction in photosynthesis rate, inhibition of leaf growth and osmotic potential in plants. Thus, genes identified by the present invention as heat stress tolerance conferring genes may also impart improved drought tolerance to plants. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in a heat stress tolerance screen can survive better heat stress conditions and/or drought conditions providing a higher yield potential as compared to control plants.

[0119] CK and CS-Improvement of tolerance to cold stress: Low temperature may immediately result in mechanical constraints, changes in activities of macromolecules, and reduced osmotic potential. In the present invention, two screening conditions, i.e., cold shock tolerance screen (CK) and cold germination tolerance screen (CS), were set up to look for transgenic plants that display visual growth advantage at lower temperature. In cold germination tolerance screen, the transgenic *Arabidopsis* plants were exposed to a constant temperature of 8° C. from planting until day 28 post plating. The trait-improving recombinant DNA identified by such screen are particular useful for the production of transgenic plant that can germinate more robustly in a cold temperature as compared to the wild type plants. In cold shock tolerance screen, the transgenic plants were first grown under the normal growth temperature of 22° C. until day 8 post plating, and subsequently were placed under 8° C. until day 28 post plating. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in a cold shock stress tolerance screen and/or a cold germination stress tolerance screen can survive better cold conditions providing a higher yield potential as compared to control plants.

[0120] Improvement of tolerance to multiple stresses: Different kinds of stresses often lead to identical or similar reaction in the plants. Genes that are activated or inactivated as a reaction to stress can either act directly in a way the genetic product reduces a specific stress, or they can act indirectly by activating other specific stress genes. By manipulating the activity of such regulatory genes, i.e., multiple stress tolerance genes, the plant can be enabled to react to different kinds of stresses. For examples, PEP SEQ ID NO: 231 can be used to improve both salt stress tolerance and cold stress tolerance in plants. Of particular interest, plants transformed with PEP SEQ ID NO: 233 can resist heat stress, salt stress and cold stress. In addition to these multiple stress tolerance genes, the stress tolerance conferring genes provided by the present invention may be used in combinations to generate transgenic plants that can resist multiple stress conditions.

[0121] PP-Improvement of early plant growth and development: It has been known in the art that to minimize the impact of disease on crop profitability, it is important to start the season with healthy and vigorous plants. This means avoiding seed and seedling diseases, leading to increased nutrient uptake and increased yield potential. Traditionally early planting and applying fertilizer are the methods used for promoting early seedling vigor. In early development stage, plant embryos establish only the basic root-shoot axis, a cotyledon storage organ(s), and stem cell populations, called the root and shoot apical meristems, that continuously generate new organs throughout post-embryonic development. "Early growth and development" used herein encompasses the stages of seed imbibition through the early vegetative phase. The present invention provides genes that are useful to produce transgenic plants that have advantages in one or more processes including, but not limited to, germination, seedling vigor, root growth and root morphology under non-stressed conditions. The transgenic plants starting from a more robust seedling are less susceptible to the fungal and bacterial pathogens that attach germinating seeds and seedling. Furthermore, seedlings with advantage in root growth are more resistant to drought stress due to extensive and deeper root architecture. Therefore, it can be recognized by those skilled in the art that genes conferring the growth advantage in early stages to plants may also be used to generate transgenic plants that are more resistant to various stress conditions due to improved early plant development. The present invention provides such exemplary recombinant DNA that confer both the stress tolerance and growth advantages to plants, identified as such in Table 3, e.g., PEP SEQ ID NO: 268 which can improve the plant early growth and development, and impart

heat and cold tolerance to plants. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in the early plant development screen can grow better under non-stress conditions and/or stress conditions providing a higher yield potential as compared to control plants.

[0122] SP-Improvement of late plant growth and development: "Late growth and development" used herein encompasses the stages of leaf development, flower production, and seed maturity. In certain embodiments, transgenic plants produced using genes that confer growth advantages to plants provided by the present invention, identified as such in Table 3, exhibit at least one phenotypic characteristics including, but not limited to, increased rosette radius, increased rosette dry weight, seed dry weight, silique dry weight, and silique length. On one hand, the rosette radius and rosette dry weight are used as the indexes of photosynthesis capacity, and thereby plant source strength and yield potential of a plant. On the other hand, the seed dry weight, silique dry weight and silique length are used as the indexes for plant sink strength, which are considered as the direct determinants of yield. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in the late development screen can grow better and/or have improved development during leaf development and seed maturation providing a higher yield potential as compared to control plants.

[0123] LL-Improvement of tolerance to shade stress identified in a low light screen: The effects of light on plant development are especially prominent at the seedling stage. Under normal light conditions with unobstructed direct light, a plant seeding develops according to a characteristic photomorphogenic pattern, in which plants have open and expanded cotyledons and short hypocotyls. Then the plant's energy is devoted to cotyledon and leaf development while longitudinal extension growth is minimized. Under low light condition where light quality and intensity are reduced by shading, obstruction or high population density, a seedling displays a shade-avoidance pattern, in which the seedling displays a reduced cotyledon expansion, and hypocotyls extension is greatly increased. As the result, a plant under low light condition increases significantly its stem length at the expanse of leaf, seed or fruit and storage organ development, thereby adversely affecting of yield. The present invention provides recombinant DNA that enable plants to have an attenuated shade avoidance response so that the source of plant can be contributed to reproductive growth efficiently, resulting higher yield as compared to the wild type plants. As demonstrated from the model plant screen, embodiments of transgenic plants with trait-improving recombinant DNA identified in a shade stress tolerance screen can have attenuated shade response under shade conditions providing a higher yield potential as compared to control plants. The transgenic plants generated by the present invention may be suitable for a higher density planting, thereby resulting increased yield per unit area.

[0124] LN-Improvement of Tolerance to Low Nitrogen Availability Stress

[0125] Nitrogen is a key factor in plant growth and crop yield. The metabolism, growth and development of plants are profoundly affected by their nitrogen supply. Restricted nitrogen supply alters shoot to root ratio, root development, activity of enzymes of primary metabolism and the rate of senescence (death) of older leaves. All field crops have a fundamental dependence on inorganic nitrogenous fertilizer. Since fertilizer is rapidly depleted from most soil types, it must be supplied to growing crops two or three times during the growing season. Enhanced nitrogen use efficiency by plants should enable crops cultivated under low nitrogen availability stress condition resulted from low fertilizer input or poor soil quality.

[0126] According to the present invention, transgenic plants generated using the recombinant nucleotides, which confer enhanced nitrogen use efficiency, identified as such in Table 3, exhibit one or more desirable traits including, but not limited to, increased seedling weight, greener leaves, increased number of rosette leaves, increased or decreased root length. One skilled in the art may recognize that the transgenic plants provided by the present invention with enhanced nitrogen use efficiency may also have altered amino acid or protein compositions, increased yield and/or better seed quality. The transgenic plants of the present invention may be productively cultivated under low nitrogen growth conditions, i.e., nitrogen-poor soils and low nitrogen fertilizer inputs, which would cause the growth of wild type plants to cease or to be so diminished as to make the wild type plants practically useless. The transgenic plants also may be advantageously used to achieve earlier maturing, faster growing, and/or higher yielding crops and/or produce more nutritious foods and animal feedstocks when cultivated using nitrogen non-limiting growth conditions.

[0127] Stacked Traits: The present invention also encompasses transgenic plants with stacked engineered traits, e.g., a crop having an improved phenotype resulting from expression of a trait-improving recombinant DNA, in combination with herbicide and/or pest resistance traits. For example, genes of the current invention can be stacked with other traits of agronomic interest, such as a trait providing herbicide resistance, for example a RoundUp Ready® trait, or insect resistance, such as using a gene from *Bacillus thuringensis* to provide resistance against lepidopteran, coliopteran, homopteran, hemiopteran, and other insects. Herbicides for which resistance is useful in a plant include glyphosate herbicides, phosphinothricin herbicides, oxynil herbicides, imidazolinone herbicides, dinitroaniline herbicides, pyridine herbicides, sulfonylurea herbicides, bialaphos herbicides, sulfonamide herbicides and gluphosinate herbicides. To illustrate that the production of transgenic plants with herbicide resistance is a capability of those of ordinary skill in the art, reference is made to U.S. patent application publications 2003/0106096A1 and 2002/0112260A1 and U.S. Pat. Nos. 5,034,322; 5,776,760, 6,107,549 and 6,376,754, all of which are incorporated herein by reference. To illustrate that the production of transgenic plants with pest resistance is a capability of those of ordinary skill in the art reference is made to U.S. Pat. Nos. 5,250,515 and 5,880,275 which disclose plants expressing an endotoxin of *Bacillus thuringiensis* bacteria, to U.S. Pat. No. 6,506,599 which discloses control of invertebrates which feed on transgenic plants which express dsRNA for suppressing a target gene in the invertebrate, to U.S. Pat. No. 5,986,175 which discloses the control of viral pests by transgenic plants which express viral replicase, and to U.S. Patent Application Publication 2003/0150017 A1 which discloses control of pests by a transgenic plant which express a dsRNA targeted to suppressing a gene in the pest, all of which are incorporated herein by reference.

[0128] Once one recombinant DNA has been identified as conferring an improved trait of interest in transgenic *Arabi-*

dopsis plants, several methods are available for using the sequence of that recombinant DNA and knowledge about the protein it encodes to identify homologs of that sequence from the same plant or different plant species or other organisms, e.g., bacteria and yeast. Thus, in one aspect, the invention provides methods for identifying a homologous gene with a DNA sequence homologous to any of SEQ ID NO: 1 through SEQ ID NO: 197, or a homologous protein with an amino acid sequence homologous to any of SEQ ID NO: 198 through SEQ ID NO: 394. In another aspect, the present invention provides the protein sequences of identified homologs for a sequence listed as SEQ ID NO: 395 through SEQ ID NO: 19938. In yet another aspect, the present invention also includes linking or associating one or more desired traits, or gene function with a homolog sequence provided herein.

[0129] The trait-improving recombinant DNA and methods of using such trait-improving recombinant DNA for generating transgenic plants with improved traits provided by the present invention are not limited to any particular plant species. Indeed, the plants according to the present invention may be of any plant species, i.e., may be monocotyledonous or dicotyledonous. Preferably, they will be agricultural useful plants, i.e., plants cultivated by man for purposes of food production or technical, particularly industrial applications. Of particular interest in the present invention are corn and soybean plants. The recombinant DNA constructs optimized for soybean transformation and recombinant DNA constructs optimized for corn transformation are provided by the present invention. Other plants of interest in the present invention for production of transgenic plants having improved traits include, without limitation, cotton, canola, wheat, sunflower, sorghum, alfalfa, barley, millet, rice, tobacco, fruit and vegetable crops, and turfgrass.

[0130] In certain embodiments, the present invention contemplates to use an orthologous gene in generating the transgenic plants with similarly improved traits as the transgenic *Arabidopsis* counterpart. Improved physiological properties in transgenic plants of the present invention may be confirmed in responses to stress conditions, for example in assays using imposed stress conditions to detect improved responses to drought stress, nitrogen deficiency, cold growing conditions, or alternatively, under naturally present stress conditions, for example under field conditions. Biomass measures may be made on greenhouse or field grown plants and may include such measurements as plant height, stem diameter, root and shoot dry weights, and, for corn plants, ear length and diameter.

[0131] Trait data on morphological changes may be collected by visual observation during the process of plant regeneration as well as in regenerated plants transferred to soil. Such trait data includes characteristics such as normal plants, bushy plants, taller plants, thicker stalks, narrow leaves, striped leaves, knotted phenotype, chlorosis, albino, anthocyanin production, or altered tassels, ears or roots. Other enhanced traits may be identified by measurements taken under field conditions, such as days to pollen shed, days to silking, leaf extension rate, chlorophyll content, leaf temperature, stand, seedling vigor, internode length, plant height, leaf number, leaf area, tillering, brace roots, stay green, stalk lodging, root lodging, plant health, barreness/prolificacy, green snap, and pest resistance. In addition, trait characteristics of harvested grain may be confirmed, including number of kernels per row on the ear, number of rows of kernels on the ear, kernel abortion, kernel weight, kernel size, kernel density and physical grain quality.

[0132] To confirm hybrid yield in transgenic corn plants expressing genes of the present invention, it may be desirable to test hybrids over multiple years at multiple locations in a geographical location where maize is conventionally grown, e.g., in Iowa, Illinois or other locations in the Midwestern United States, under "normal" field conditions as well as under stress conditions, e.g., under drought or population density stress.

[0133] Transgenic plants can be used to provide plant parts according to the invention for regeneration or tissue culture of cells or tissues containing the constructs described herein. Plant parts for these purposes can include leaves, stems, roots, flowers, tissues, epicotyl, meristems, hypocotyls, cotyledons, pollen, ovaries, cells and protoplasts, or any other portion of the plant which can be used to regenerate additional transgenic plants, cells, protoplasts or tissue culture. Seeds of transgenic plants are provided by this invention can be used to propagate more plants containing the trait-improving recombinant DNA constructs of this invention. These descendants are intended to be included in the scope of this invention if they contain a trait-improving recombinant DNA construct of this invention, whether or not these plants are selfed or crossed with different varieties of plants.

[0134] The various aspects of the invention are illustrated by means of the following examples which are in no way intended to limit the full breath and scope of claims.

EXAMPLES

Example 1

Identification of Recombinant DNA that Confers Improved Trait(s) to Plants

A. Plant Expression Constructs for *Arabidopsis* Transformation

[0135] Each gene of interest was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. Transformation vectors were prepared to constitutively transcribe DNA in either sense orientation (for enhanced protein expression) or anti-sense orientation (for endogenous gene suppression) under the control of an enhanced Cauliflower Mosaic Virus 35S promoter (U.S. Pat. No. 5,359,142) directly or indirectly (Moore, e.g., PNAS 95:376-381, 1998; Guyer, e.g., Genetics 149: 633-639, 1998; International patent application NO. PCT/EP98/07577). The transformation vectors also contain a bar gene as a selectable marker for resistance to glufosinate herbicide. The transformation of *Arabidopsis* plants was carried out using the vacuum infiltration method known in the art (Bethtold, e.g., Methods Mol. Biol. 82:259-66, 1998). Seeds harvested from the plants, named as T1 seeds, were subsequently grown in a glufosinate-containing selective medium to select for plants which were actually transformed and which produced T2 transgenic seed.

B. Soil Drought Tolerance Screen

[0136] This example describes a soil drought tolerance screen to identify *Arabidopsis* plants transformed with recombinant DNA that wilt less rapidly and/or produce higher seed yield when grown in soil under drought conditions

[0137] T2 seeds were sown in flats filled with Metro/Mix® 200 (The Scotts® Company, USA). Humidity domes were added to each flat and flats were assigned locations and placed in climate-controlled growth chambers. Plants were grown under a temperature regime of 22° C. at day and 20° C. at night, with a photoperiod of 16 hours and average light intensity of 170 μmol/m^2/s. After the first true leaves appeared, humidity domes were removed. The plants were sprayed with glufosinate herbicide and put back in the growth chamber for 3 additional days. Flats were watered for 1 hour the week following the herbicide treatment. Watering was continued every seven days until the flower bud primordia became apparent, at which time plants were watered for the last time.

[0138] To identify drought tolerant plants, plants were evaluated for wilting response and seed yield. Beginning ten days after the last watering, plants were examined daily until 4 plants/line had wilted. In the next six days, plants were monitored for wilting response. Five drought scores were assigned according to the visual inspection of the phenotypes: 1 for healthy, 2 for dark green, 3 for wilting, 4 severe wilting, and 5 for dead. A score of 3 or higher was considered as wilted.

[0139] At the end of this assay, seed yield measured as seed weight per plant under the drought condition was characterized for the transgenic plants and their controls and analyzed as a quantitative response according to example 1M.

[0140] Two approaches were used for statistical analysis on the wilting response. First, the risk score was analyzed for wilting phenotype and treated as a qualitative response according to the example 1L. Alternatively, the survival analysis was carried out in which the proportions of wilted and non-wilted transgenic and control plants were compared over each of the six days under scoring and an overall log rank test was performed to compare the two survival curves using S-PLUS statistical software (S-PLUS 6, Guide to statistics, Insightful, Seattle, Wash., USA). A list of recombinant DNA constructs which improve drought tolerance in transgenic plants is illustrated in Table 4.

[0141] If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait improvement as compared to the reference (p value, of the delta of a quantitative response or of the risk score of a qualitative response, is the probability that the observed difference between the transgenic plants and the reference occur by chance)

If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait improvement as compared to the reference.

[0142] Transgenic plants comprising recombinant DNA expressing a protein as set forth in SEQ ID NO: 226, 237, 242, or 363 showed improved drought tolerance evidenced by the second criteria as illustrated in Example 1L and 1M.

C. Heat Stress Tolerance Screen

[0143] Under high temperatures, *Arabidopsis* seedlings become chlorotic and root growth is inhibited. This example sets forth the heat stress tolerance screen to identify *Arabidopsis* plants transformed with the gene of interest that are more resistant to heat stress based on primarily their seedling weight and root growth under high temperature. T2 seeds were plated on ½×MS salts, 1% phytagel, with 10 μg/ml BASTA (7 per plate with 2 control seeds; 9 seeds total per plate). Plates were placed at 4° C. for 3 days to stratify seeds. Plates were then incubated at room temperature for 3 hours and then held vertically for 11 additional days at temperature of 34° C. at day and 20° C. at night. Photoperiod was 16 h. Average light intensity was ~140 μmol/m^2/s. After 14 days of growth, plants were scored for glufosinate resistance, root length, final growth stage, visual color, and seedling fresh weight. A photograph of the whole plate was taken on day 14.

[0144] The seedling weight and root length were analyzed as quantitative responses according to example 1M. The final grow stage at day 14 was scored as success if 50% of the plants had reached 3 rosette leaves and size of leaves are greater than 1 mm (Boyes, e.g., (2001) The Plant Cell 13, 1499-1510). The growth stage data was analyzed as a qualitative response according to example 1L. A list of recombinant DNA constructs that improve heat tolerance in transgenic plants illustrated in Table 5.

TABLE 4

PEP				Drought score		Seed yield		Time to wilting Risk	
SEQ ID NO	Construct ID	Nomination ID	Orientation	Delta mean	P-value	Delta mean	P-value	score mean	P-value
198	11029	CGPG106	SENSE	0.109	0.381	0.072	0.717	0.119	1.000
292	73136	CGPG5764	SENSE	0.030	0.090	0.136	0.067	0.104	1.000
284	73165	CGPG5661	SENSE	−0.031	0.504	0.526	0.018	−0.075	1.000
260	73628	CGPG5025	SENSE	0.342	0.038	−0.474	0.022	0.208	1.000
291	73981	CGPG5757	SENSE	0.517	0.026	−0.096	0.000	0.573	1.000
207	74065	CGPG1828	ANTI-SENSE	−0.078	0.164	0.646	0.027	0.048	1.000
263	74217	CGPG5144	SENSE	−0.026	0.414	0.418	0.032	0.071	1.000
261	76105	CGPG5041	SENSE	0.288	0.029	−1.780	0.027	0.173	1.000
328	76576	CGPG7281	SENSE	0.241	0.032	−0.555	0.442	0.212	1.000
327	77536	CGPG7272	SENSE	0.089	0.194	1.059	0.001	0.042	1.000
226	19767	CGPG3918	SENSE	0.117	0.038	0.164	0.296	/	/
237	19947	CGPG4069	SENSE	−0.009	0.852	−0.104	0.504	/	/
242	70994	CGPG4122	SENSE	0.040	0.021	−0.131	0.447	/	/
363	77103	CGPG9134	SENSE	0.145	0.023	−0.499	0.096	/	/

TABLE 5

				Root length at day 14		Growth stage at day 14		Seedling weight at day 14	
PEP SEQ ID	Construct ID	Nomination ID	Orientation	Delta mean	P-value	Risk score mean	P-value	Delta mean	P-value
239	70985	CGPG4088	SENSE	0.480	0.036	1.176	0.196	1.333	0.018
233	70987	CGPG4048	SENSE	0.228	0.021	−0.036	0.670	1.214	0.002
268	72001	CGPG5221	SENSE	0.273	0.004	0.210	0.330	1.393	0.009
274	72753	CGPG5540	SENSE	0.434	0.006	0.414	0.258	1.100	0.006
276	73954	CGPG5577	SENSE	0.406	0.002	0.455	0.282	1.274	0.000
325	76178	CGPG7225	SENSE	0.714	0.001	1.093	0.145	1.537	0.000
361	77150	CGPG9130	SENSE	0.219	0.032	0.178	0.237	1.159	0.002
367	77164	CGPG9147	SENSE	0.317	0.026	0.651	0.099	1.152	0.002
390	77432	CGPG9335	SENSE	0.581	0.001	0.457	0.124	1.551	0.000
351	77587	CGPG8107	SENSE	0.488	0.006	0.628	0.072	1.328	0.001
348	77928	CGPG8082	SENSE	0.462	0.032	0.191	0.301	1.498	0.004
212	16610	CGPG2499	SENSE	0.055	0.640	0.109	0.609	0.983	0.020
220	18256	CGPG3363	SENSE	0.070	0.138	0.071	0.541	1.021	0.004
222	19193	CGPG3375	SENSE	0.255	0.094	0.267	0.368	1.023	0.003
252	70684	CGPG4588	SENSE	0.010	0.781	0.003	0.979	1.002	0.045
230	70948	CGPG3990	SENSE	0.282	0.095	0.351	0.335	1.045	0.023
243	70956	CGPG4140	SENSE	0.155	0.313	0.091	0.320	1.129	0.018
235	70962	CGPG4057	SENSE	0.469	0.085	0.267	0.508	1.410	0.007
241	70963	CGPG4121	SENSE	−0.002	0.979	−0.131	0.311	0.976	0.005
242	70994	CGPG4122	SENSE	0.140	0.574	1.204	0.096	1.207	0.030
244	70995	CGPG4154	SENSE	0.374	0.112	1.640	0.171	1.328	0.013
208	72783	CGPG2206	SENSE	0.387	0.057	0.053	0.509	1.013	0.019
255	72807	CGPG4912	SENSE	0.357	0.071	0.443	0.020	1.099	0.009
259	72825	CGPG5001	SENSE	0.171	0.349	0.213	0.234	1.118	0.012
287	73120	CGPG5704	SENSE	0.096	0.490	0.193	0.364	1.080	0.033
280	73127	CGPG5640	SENSE	−0.220	0.077	−0.194	0.030	0.643	0.014
293	73172	CGPG5783	SENSE	0.283	0.197	0.887	0.162	1.154	0.007
310	73411	CGPG6440	SENSE	0.198	0.389	0.631	0.345	1.320	0.003
260	73628	CGPG5025	SENSE	0.406	0.149	1.475	0.365	1.169	0.016
316	74566	CGPG6796	SENSE	0.627	0.092	0.777	0.466	1.714	0.014
338	75654	CGPG7804	SENSE	0.292	0.237	0.804	0.315	0.940	0.017
340	75657	CGPG7828	SENSE	0.390	0.067	1.222	0.307	1.521	0.011
213	76602	CGPG2653	SENSE	0.036	0.748	0.092	0.670	0.752	0.025
372	77180	CGPG9180	SENSE	0.068	0.555	−0.045	0.177	0.871	0.022
380	77275	CGPG9236	SENSE	0.282	0.125	0.971	0.285	1.027	0.013
297	77312	CGPG5927	SENSE	0.201	0.344	0.710	0.372	1.039	0.032
320	77518	CGPG6953	SENSE	0.238	0.344	0.069	0.655	1.188	0.015
342	77549	CGPG7933	SENSE	0.184	0.180	−0.012	/	0.978	0.007
347	77580	CGPG8062	SENSE	0.157	0.143	−0.074	/	0.891	0.049
317	77610	CGPG6805	SENSE	0.023	0.937	−0.063	/	1.207	0.029
318	77618	CGPG6810	SENSE	0.002	0.942	−0.074	/	1.015	0.006
353	77619	CGPG8152	SENSE	0.213	0.316	−0.076	0.457	0.956	0.019
355	77629	CGPG8377	SENSE	0.095	0.124	−0.063	/	1.133	0.005
334	77816	CGPG7529	SENSE	0.033	0.705	0.856	0.385	0.611	0.038

[0145] If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait improvement as compared to the reference. If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait improvement as compared to the reference.

[0146] Transgenic plants comprising recombinant DNA expressing a protein as set forth in SEQ ID NO: 237, 307, 313, 327, 330, 349, 366, or 387 showed improved heat stress tolerance evidenced by the second criteria as illustrated in Example 1L and 1M.

D. Salt Stress Tolerance Screen

[0147] This example sets forth the high salinity stress screen to identify *Arabidopsis* plants transformed with the gene of interest that are tolerant to high levels of salt based on their rate of development, root growth and chlorophyll accumulation under high salt conditions.

[0148] T2 seeds were plated on glufosinate selection plates containing 90 mM NaCl and grown under standard light and temperature conditions. All seedlings used in the experiment were grown at a temperature of 22° C. at day and 20° C. at night, a 16-hour photoperiod, an average light intensity of approximately 120 umol/m^2. On day 11, plants were measured for primary root length. After 3 more days of growth (day 14), plants were scored for transgenic status, primary root length, growth stage, visual color, and the seedlings were pooled for fresh weight measurement. A photograph of the whole plate was also taken on day 14.

[0149] The seedling weight and root length were analyzed as quantitative responses according to example 1M. The final growth stage at day 14 was scored as success if 50% of the plants reached 3 rosette leaves and size of leaves are greater than 1 mm (Boyes, D. C., et al., (2001), The Plant Cell 13, 1499/1510). The growth stage data was analyzed as a qualitative response according to example 1L. A list of recombinant DNA constructs that improve high salinity tolerance in transgenic plants illustrated in Table 6.

TABLE 6

			Root length at day 11		Root length at day 14		Growth stage at day 14		Seedling weight at day 14	
PEP SEQ ID	Construct ID	Orientation	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
220	18256	SENSE	0.192	0.232	0.236	0.080	1.291	0.151	0.598	0.039
214	18456	SENSE	0.213	0.089	0.209	0.197	2.062	0.197	0.476	0.046
232	19973	SENSE	0.289	0.012	0.299	0.002	0.976	0.054	1.002	0.013
231	70201	SENSE	0.363	0.030	0.403	0.052	2.083	0.229	1.057	0.014
243	70956	SENSE	0.006	0.923	0.128	0.016	−0.045	NA	−0.364	0.371
238	70969	SENSE	0.435	0.091	0.471	0.027	0.653	0.473	0.994	0.058
240	70971	SENSE	0.337	0.063	0.257	0.041	1.418	0.226	0.593	0.030
233	70987	SENSE	0.363	0.030	0.284	0.044	1.434	0.380	0.865	0.012
273	72788	SENSE	0.484	0.019	0.456	0.016	1.813	0.314	0.929	0.008
256	72811	SENSE	0.385	0.024	0.409	0.002	2.968	0.031	0.805	0.004
287	73120	SENSE	0.341	0.001	0.244	0.019	0.613	0.103	0.755	0.015
280	73127	SENSE	0.501	0.028	0.395	0.055	0.212	0.175	0.739	0.023
289	73134	SENSE	0.226	0.134	0.266	0.045	0.152	0.487	0.378	0.056
257	73235	SENSE	0.431	0.020	0.360	0.018	1.618	0.327	0.650	0.009
245	73306	SENSE	0.228	0.046	0.219	0.018	0.249	0.217	0.708	0.008
253	73330	SENSE	0.196	0.225	0.186	0.029	0.000	NA	0.543	0.045
316	74566	SENSE	0.331	0.001	0.076	0.422	0.597	0.031	0.716	0.003
312	74688	SENSE	0.480	0.076	0.415	0.031	0.000	NA	0.808	0.062
376	77124	SENSE	0.340	0.034	0.322	0.015	2.306	0.137	0.411	0.168
364	77139	SENSE	0.339	0.096	0.287	0.041	1.683	0.294	0.602	0.039
375	77195	SENSE	0.445	0.009	0.345	0.010	0.367	0.185	0.582	0.022
384	77268	SENSE	0.495	0.047	0.468	0.102	1.906	0.079	0.992	0.042
386	77269	SENSE	0.454	0.038	0.426	0.004	1.996	0.065	1.136	0.001
380	77275	SENSE	0.457	0.008	0.487	0.040	2.119	0.154	1.070	0.010
297	77312	SENSE	0.335	0.086	0.361	0.013	0.960	0.208	0.723	0.063
389	77430	SENSE	0.303	0.030	0.360	0.004	0.131	0.495	0.894	0.022
320	77518	SENSE	0.171	0.017	0.185	0.026	−0.134	0.443	0.339	0.109
345	77570	SENSE	0.326	0.091	0.241	0.134	1.396	0.090	0.862	0.026
351	77587	SENSE	0.178	0.083	0.096	0.665	0.995	0.426	0.632	0.036
353	77619	SENSE	0.389	0.058	0.398	0.011	1.913	0.257	0.857	0.040
355	77629	SENSE	0.404	0.043	0.389	0.019	2.523	0.083	0.826	0.040
336	77821	SENSE	0.393	0.063	0.444	0.033	0.196	0.228	0.619	0.015
356	77832	SENSE	0.134	0.238	0.304	0.011	0.914	0.156	0.413	0.050
352	77933	SENSE	0.112	0.044	0.165	0.009	0.749	0.482	0.517	0.171
347	77580	SENSE	−0.019	0.814	0.087	0.018	−0.158	0.151	0.124	0.204

[0150] If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait improvement as compared to the reference. If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait improvement as compared to the reference.

[0151] Transgenic plants comprising recombinant DNA expressing a protein as set forth in SEQ ID NO: 237, 242, 255, 307, 313, 327, 330, 349, 366, or 387 showed improved salt stress tolerance evidenced by the second criteria as illustrated in Example 1L.

E. Polyethylene Glycol (PEG) Induced Osmotic Stress Tolerance Screen

[0152] There are numerous factors, which can influence seed germination and subsequent seedling growth, one being the availability of water. Genes, which can directly affect the success rate of germination and early seedling growth, are potentially useful agronomic traits for improving the germination and growth of crop plants under drought stress. In this assay, PEG was used to induce osmotic stress on germinating transgenic lines of *Arabidopsis thaliana* seeds in order to screen for osmotically resistant seed lines.

[0153] T2 seeds were plated on BASTA selection plates containing 3% PEG and grown under standard light and temperature conditions. Seeds were plated on each plate containing 3% PEG, ½×MS salts, 1% phytagel, and 10 μg/ml glufosinate. Plates were placed at 4° C. for 3 days to stratify seeds. On day 11, plants were measured for primary root length. After 3 more days of growth, i.e., at day 14, plants were scored for transgenic status, primary root length, growth stage, visual color, and the seedlings were pooled for fresh weight measurement. A photograph of the whole plate was taken on day 14.

[0154] Seedling weight and root length were analyzed as quantitative responses according to example 1M. The final growth stage at day 14 was scored as success or failure based on whether the plants reached 3 rosette leaves and size of leaves are greater than 1 mm. The growth stage data was analyzed as a qualitative response according to example 1L. A list of recombinant DNA constructs that improve osmotic stress tolerance in transgenic plants illustrated in Table 7.

TABLE 7

			Root length at day 11		Root length at day 14		Growth stage at day 14		Seedling weight at day 14	
PEP SEQ ID	Construct ID	Orientation	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
199	12223	SENSE	/	/	/	/	/	/	0.353	0.024
214	18456	SENSE	0.320	0.018	0.274	0.033	3.109	0.073	0.553	0.006
302	70812	SENSE	0.195	0.078	0.078	0.296	4	0.000	0.363	0.016
234	70950	SENSE	0.322	0.056	0.427	0.016	4	0.000	0.381	0.127
239	70985	SENSE	0.270	0.066	0.221	0.005	4	0.000	0.372	0.007
233	70987	SENSE	0.227	0.205	0.128	0.470	4	0.000	0.495	0.000
228	70992	SENSE	0.369	0.002	0.370	0.013	4	0.000	0.574	0.027
244	70995	SENSE	0.379	0.049	0.320	0.065	4	0.000	0.491	0.003
208	72783	SENSE	0.154	0.084	0.043	0.553	4	0.000	0.264	0.044
255	72807	SENSE	0.165	0.080	0.158	0.150	4	0.000	0.333	0.047
256	72811	SENSE	0.489	0.052	0.491	0.050	4	0.000	0.784	0.016
259	72825	SENSE	0.423	0.055	0.388	0.080	2.741	0.161	0.608	0.020
295	72946	SENSE	0.345	0.053	0.473	0.050	0.898	0.632	0.415	0.181
286	73026	SENSE	0.636	0.021	0.619	0.028	2.741	0.161	0.752	0.045
290	73123	SENSE	0.460	0.048	0.445	0.007	NA	NA	0.609	0.069
278	73161	SENSE	0.510	0.024	0.506	0.006	2.624	0.246	0.626	0.073
284	73165	SENSE	0.304	0.101	0.285	0.044	2.499	0.270	0.643	0.077
293	73172	SENSE	0.197	0.056	0.137	0.204	2.374	0.293	0.660	0.081
262	73242	SENSE	0.305	0.029	0.332	0.022	2.249	0.317	0.677	0.085
265	73256	SENSE	0.325	0.084	0.182	0.178	2.124	0.341	0.694	0.089
308	73485	SENSE	0.133	0.070	0.039	0.583	1.999	0.365	0.711	0.093
291	73981	SENSE	0.239	0.147	0.238	0.281	1.874	0.389	0.728	0.096
316	74566	SENSE	0.451	0.004	0.248	0.118	1.749	0.412	0.745	0.100
312	74688	SENSE	0.190	0.191	0.102	0.520	1.624	0.436	0.762	0.104
330	74863	SENSE	0.174	0.164	0.216	0.109	1.499	0.460	0.779	0.108
366	77140	SENSE	0.644	0.005	0.572	0.015	1.374	0.484	0.796	0.112
361	77150	SENSE	0.313	0.047	0.359	0.044	1.249	0.508	0.813	0.116
365	77187	SENSE	0.273	0.084	0.032	0.763	1.124	0.532	0.830	0.120
375	77195	SENSE	0.319	0.021	0.256	0.041	NA	NA	0.847	0.124
379	77203	SENSE	0.113	0.485	0.019	0.829	0.999	0.555	0.864	0.127
377	77261	SENSE	0.115	0.230	0.085	0.315	0.874	0.579	0.881	0.131
270	77308	SENSE	0.174	0.321	0.074	0.700	0.749	0.603	0.898	0.135
346	77338	SENSE	0.227	0.158	0.196	0.272	0.624	0.627	0.915	0.139
350	77357	SENSE	0.169	0.300	0.259	0.066	2.715	0.169	0.303	0.020
390	77432	SENSE	0.306	0.043	0.122	0.270	2.570	0.214	0.734	0.019
347	77580	SENSE	0.300	0.107	0.240	0.009	2.288	0.119	0.500	0.179
353	77619	SENSE	0.142	0.216	0.139	0.002	4	0.000	0.129	0.582
356	77832	SENSE	0.236	0.006	0.266	0.001	1.333	0.435	0.286	0.037
343	77917	SENSE	0.174	0.163	0.160	0.006	4	0.000	0.330	0.009

[0155] If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait improvement as compared to the reference.

If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait improvement as compared to the reference.

[0156] Transgenic plants comprising recombinant DNA expressing a protein as set forth in SEQ ID NO: 209, 245, 260, 274, 282, 310, 321, 325, 336, 372, 376, 378, 380, or 382 showed improved osmotic stress tolerance evidenced by the second criteria as illustrated in Example 1L and 1M.

F. Cold Shock Tolerance Screen

[0157] This example set forth a screen to identify *Arabidopsis* plants transformed with the genes of interest that are more tolerant to cold stress subjected during day 8 to day 28 after seed planting. During these crucial early stages, seedling growth and leaf area increase were measured to assess tolerance when *Arabidopsis* seedlings were exposed to low temperatures. Using this screen, genetic alterations can be found that enable plants to germinate and grow better than wild type plants under sudden exposure to low temperatures.

[0158] Eleven seedlings from T2 seeds of each transgenic line plus one control line were plated together on a plate containing ½× Gamborg Salts with 0.8 Phytagel™, 1% Phytagel, and 0.3% Sucrose. Plates were then oriented horizontally and stratified for three days at 4° C. At day three, plates were removed from stratification and exposed to standard conditions (16 hr photoperiod, 22° C. at day and 20° C. at night) until day 8. At day eight, plates were removed from standard conditions and exposed to cold shock conditions (24 hr photoperiod, 8° C. at both day and night) until the final day of the assay, i.e., day 28. Rosette areas were measured at day 8 and day 28, which were analyzed as quantitative responses according to example 1M. A list of recombinant nucleotides that improve cold shock stress tolerance in plants illustrated in Table 8.

TABLE 8

				Rosette area at day 8		Rosette area at day 28		Rosette area difference	
PEP SEQ ID	Construct ID	Nomination ID	Orientation	Delta mean	P-alue	Risk score mean	P-value	Delta mean	P-value
199	12223	CGPG1133	SENSE	0.112	0.617	0.334	0.014	0.273	0.143
218	18231	CGPG3274	SENSE	−0.131	0.269	1.144	0.002	1.179	0.003
215	18414	CGPG3002	SENSE	0.997	0.034	1.665	0.001	1.895	0.001
214	18456	CGPG2813	SENSE	0.099	0.757	0.799	0.001	0.684	0.001
233	70987	CGPG4048	SENSE	0.864	0.136	1.213	0.010	1.146	0.002
244	70995	CGPG4154	SENSE	1.088	0.008	1.262	0.023	1.407	0.025
208	72783	CGPG2206	SENSE	0.814	0.023	0.957	0.018	0.899	0.052
273	72788	CGPG5535	SENSE	0.262	0.058	1.090	0.016	1.212	0.021
256	72811	CGPG4926	SENSE	0.880	0.058	0.669	0.002	0.715	0.018
259	72825	CGPG5001	SENSE	0.032	0.887	0.338	0.071	0.357	0.027
281	73033	CGPG5646	SENSE	0.322	0.394	1.311	0.012	1.480	0.017
293	73172	CGPG5783	SENSE	0.395	0.209	1.065	0.030	1.099	0.074
253	73330	CGPG4765	SENSE	0.347	0.515	0.835	0.065	1.043	0.007
264	73735	CGPG5171	SENSE	0.624	0.076	0.655	0.001	0.718	0.005
315	74460	CGPG6747	SENSE	0.452	0.005	0.542	0.043	0.455	0.154
296	74746	CGPG5856	SENSE	0.304	0.346	0.978	0.001	1.061	0.007
299	75240	CGPG5957	SENSE	0.479	0.153	0.652	0.143	0.875	0.039
338	75654	CGPG7804	SENSE	0.531	0.140	1.712	0.010	1.979	0.015
339	75692	CGPG7823	SENSE	0.526	0.063	2.027	0.001	2.246	0.001
323	76161	CGPG7168	SENSE	0.768	0.000	1.810	0.004	2.146	0.003
217	76532	CGPG3235	SENSE	0.921	0.008	1.216	0.001	1.324	0.002
357	76802	CGPG8987	SENSE	0.468	0.097	1.578	0.000	1.872	0.000
358	76829	CGPG9013	SENSE	−0.434	0.329	0.709	0.010	0.314	0.118
373	77121	CGPG9183	SENSE	0.081	0.385	0.757	0.023	0.698	0.014
366	77140	CGPG9145	SENSE	−0.221	0.165	0.896	0.007	1.043	0.005
374	77157	CGPG9186	SENSE	0.190	0.566	1.110	0.016	1.176	0.015
369	77165	CGPG9155	SENSE	1.573	0.043	0.683	0.038	0.699	0.022
370	77166	CGPG9163	SENSE	0.777	0.011	1.432	0.016	1.570	0.025
381	77204	CGPG9238	SENSE	0.545	0.139	1.313	0.003	1.436	0.006
391	77433	CGPG9341	SENSE	1.054	0.103	0.895	0.027	0.659	0.084
345	77570	CGPG8015	SENSE	0.538	0.215	0.866	0.025	0.898	0.023
353	77619	CGPG8152	SENSE	−0.589	0.322	0.503	0.068	0.558	0.049
354	77621	CGPG8166	SENSE	0.053	0.863	0.716	0.044	0.792	0.040
203	13411	CGPG1301	SENSE	0.183	0.427	0.577	0.033	0.573	0.031
209	17210	CGPG2217	SENSE	−0.244	0.685	0.162	0.038	0.156	0.104
220	18256	CGPG3363	SENSE	0.272	0.400	0.639	0.008	0.719	0.020
289	73134	CGPG5721	SENSE	0.014	0.947	1.053	0.000	1.062	0.025
263	74217	CGPG5144	SENSE	0.168	0.390	0.261	0.043	0.206	0.075
379	77203	CGPG9230	SENSE	0.606	0.051	0.620	0.032	0.778	0.039

[0159] If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait improvement as compared to the reference (p value, of the delta of a quantitative response or of the risk score of a qualitative response, is the probability that the observed difference between the transgenic plants and the reference occur by chance)

If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait improvement as compared to the reference.

[0160] Transgenic plants comprising recombinant DNA expressing a protein as set forth in SEQ ID NO: 255, 272, or 330 showed improved cold stress tolerance evidenced by the second criterial as illustrated in Example 1L.

G. Cold Germination Tolerance Screen

[0161] This example sets forth a screen to identify *Arabidopsis* plants transformed with the genes of interests are resistant to cold stress based on their rate of development, root growth and chlorophyll accumulation under low temperature conditions.

T2 seeds were plated and all seedlings used in the experiment were grown at 8° C. Seeds were first surface disinfested using chlorine gas and then seeded on assay plates containing an aqueous solution of ½× Gamborg's B/5 Basal Salt Mixture (Sigma/Aldrich Corp., St. Louis, Mo., USA G/5788), 1% Phytagel™ (Sigma-Aldrich, P-8169), and 10 ug/ml glufosinate with the final pH adjusted to 5.8 using KOH. Test plates were held vertically for 28 days at a constant temperature of 8° C., a photoperiod of 16 hr, and average light intensity of approximately 100 umol/m^2/s. At 28 days post plating, root length was measured, growth stage was observed, the visual color was assessed, and a whole plate photograph was taken.

[0162] The root length at day 28 was analyzed as a quantitative response according to example 1M. The growth stage at day 7 was analyzed as a qualitative response according to example 1L. A list of recombinant DNA constructs that improve cold stress tolerance in transgenic plants illustrated in Table 9.

TABLE 9

PEP SEQ ID	Construct ID	Nomination ID	Orientation	Root length at day 28 Delta mean	Root length at day 28 P-value	Growth stage at day 28 Delta mean	Growth stage at day 28 P-value
209	17210	CGPG2217	SENSE	0.164	0.089	4.000	0.000
219	18232	CGPG3275	SENSE	−0.081	0.613	4.000	0.000
226	19767	CGPG3918	SENSE	0.212	0.007	4.000	0.000
227	19774	CGPG3920	SENSE	0.140	0.011	4.000	0.000
237	19947	CGPG4069	SENSE	/	/	4.000	0.000
231	70201	CGPG3994	SENSE	0.311	0.010	4.000	0.000
252	70684	CGPG4588	SENSE	0.335	0.209	4.000	0.000
236	70915	CGPG4058	SENSE	0.231	0.258	4.000	0.000
243	70956	CGPG4140	SENSE	0.113	0.525	4.000	0.000
241	70963	CGPG4121	SENSE	0.210	0.252	4.000	0.000
239	70985	CGPG4088	SENSE	0.283	0.063	4.000	0.000
233	70987	CGPG4048	SENSE	0.392	0.202	4.000	0.000
228	70992	CGPG3962	SENSE	0.008	0.959	4.000	0.000
244	70995	CGPG4154	SENSE	0.426	0.002	4.000	0.000
268	72001	CGPG5221	SENSE	0.070	0.728	4.000	0.000
274	72753	CGPG5540	SENSE	0.189	0.010	2.889	0.121
273	72788	CGPG5535	SENSE	0.548	0.009	4.000	0.000
287	73120	CGPG5704	SENSE	0.401	0.146	4.000	0.000
290	73123	CGPG5728	SENSE	0.171	0.166	4.000	0.000
277	73137	CGPG5587	SENSE	0.382	0.019	4.000	0.000
283	73141	CGPG5659	SENSE	0.348	0.029	1.891	0.219
285	73155	CGPG5684	SENSE	0.194	0.105	4.000	0.000
278	73161	CGPG5594	SENSE	0.327	0.018	2.889	0.121
265	73256	CGPG5194	SENSE	0.176	0.473	4.000	0.000
266	73260	CGPG5200	SENSE	0.256	0.047	4.000	0.000
253	73330	CGPG4765	SENSE	0.229	0.016	4.000	0.000
310	73411	CGPG6440	SENSE	0.232	0.213	4.000	0.000
260	73628	CGPG5025	SENSE	0.304	0.040	1.330	0.467
204	73944	CGPG1458	SENSE	0.426	0.026	4.000	0.000
207	74065	CGPG1828	ANTI-SENSE	0.215	0.026	2.599	0.205
248	74536	CGPG442	SENSE	−0.054	0.431	4.000	0.000
312	74688	CGPG6653	SENSE	0.645	0.006	4.000	0.000
340	75657	CGPG7828	SENSE	0.394	0.017	2.680	0.180
325	76178	CGPG7225	SENSE	0.334	0.107	4.000	0.000
321	76460	CGPG7121	SENSE	0.136	0.381	4.000	0.000
305	76527	CGPG6306	SENSE	0.238	0.001	0.335	0.421
217	76532	CGPG3235	SENSE	0.250	0.331	4.000	0.000
213	76602	CGPG2653	SENSE	0.283	0.387	4.000	0.000
306	77020	CGPG6318	SENSE	0.507	0.038	0.000	0.000
364	77139	CGPG9137	SENSE	0.445	0.005	0.000	0.000
372	77180	CGPG9180	SENSE	0.370	0.046	4.000	0.000
365	77187	CGPG9141	SENSE	0.456	0.036	4.000	0.000
381	77204	CGPG9238	SENSE	0.314	0.002	4.000	0.000
382	77266	CGPG9259	SENSE	0.017	0.948	4.000	0.000
389	77430	CGPG9322	SENSE	0.095	0.233	4.000	0.000
392	77444	CGPG9344	SENSE	0.171	0.292	4.000	0.000
319	77517	CGPG6952	SENSE	0.132	0.001	2.507	0.235
327	77536	CGPG7272	SENSE	−0.084	0.675	4.000	0.000
351	77587	CGPG8107	SENSE	0.415	0.112	4.000	0.000
317	77610	CGPG6805	SENSE	0.267	0.180	4.000	0.000
356	77832	CGPG8976	SENSE	0.153	0.579	4.000	0.000

[0163] If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait improvement as compared to the reference. If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait improvement as compared to the reference.

[0164] Transgenic plants comprising recombinant DNA expressing a protein as set forth in SEQ ID NO: 347 showed improved cold stress tolerance evidenced by the second criteria as illustrated in Example 1L and 1M.

H. Shade Tolerance Screen

[0165] Plants undergo a characteristic morphological response in shade that includes the elongation of the petiole, a change in the leaf angle, and a reduction in chlorophyll content. While these changes may confer a competitive advantage to individuals, in a monoculture the shade avoidance response is thought to reduce the overall biomass of the population. Thus, genetic alterations that prevent the shade avoidance response may be associated with higher yields. Genes that favor growth under low light conditions may also promote yield, as inadequate light levels frequently limit yield. This protocol describes a screen to look for *Arabidopsis* plants that show an attenuated shade avoidance response and/or grow better than control plants under low light intensity. Of particular interest, we were looking for plants that didn't extend their petiole length, had an increase in seedling weight relative to the reference and had leaves that were more close to parallel with the plate surface.

[0166] T2 seeds were plated on glufosinate selection plates with ½MS medium. Seeds were sown on ½×MS salts, 1% Phytagel, 10 ug/ml BASTA. Plants were grown on vertical plates at a temperature of 22° C. at day, 20° C. at night and under low light (approximately 30 uE/m^2/s, far/red ratio (655/665/725/735) ~0.35 using PLAQ lights with GAM color filter #680). Twenty-three days after seedlings were sown, measurements were recorded including seedling status, number of rosette leaves, status of flower bud, petiole leaf angle, petiole length, and pooled fresh weights. A digital image of the whole plate was taken on the measurement day. Seedling weight and petiole length were analyzed as quantitative responses according to example 1M. The number of rosette leaves, flowering bud formation and leaf angel were analyzed as qualitative responses according to example 1L.

[0167] A list of recombinant DNA constructs that improve shade tolerance in plants illustrated in Table 10.

TABLE 10

				Leaf angle at day 23		Seedling weight at day 23		Petiole length at day 23	
PEP SEQ ID	Construct ID	Nomination ID	Orientation	RS mean	P-value	Delta mean	P-value	Delta mean	P-value
251	70755	CGPG4473	SENSE	NA	NA	−0.751	0.017	−0.307	0.059
244	70995	CGPG4154	SENSE	NA	NA	0.251	0.070	0.008	0.944
275	72709	CGPG5568	SENSE	NA	NA	−0.903	0.070	−0.608	0.019
210	72724	CGPG2292	SENSE	NA	NA	−0.707	0.098	−0.638	0.020
272	72774	CGPG5518	SENSE	NA	NA	−0.268	0.110	−0.195	0.087
258	72813	CGPG4977	SENSE	NA	NA	−0.469	0.092	−0.186	0.054
294	73020	CGPG5791	SENSE	NA	NA	−1.443	0.010	−1.265	0.010
288	73133	CGPG5714	SENSE	NA	NA	−0.852	0.009	−0.896	0.012
260	73628	CGPG5025	SENSE	NA	NA	0.311	0.011	0.317	0.146
271	73766	CGPG5432	SENSE	NA	NA	−0.988	0.048	−0.671	0.088
314	74435	CGPG6737	SENSE	NA	NA	−0.735	0.042	−0.755	0.049
331	74858	CGPG7371	SENSE	NA	NA	−0.667	0.010	−0.808	0.008
330	74863	CGPG7316	SENSE	NA	NA	0.176	0.060	0.168	0.515
332	74933	CGPG7457	SENSE	NA	NA	−0.100	0.801	−0.533	0.094
340	75657	CGPG7828	SENSE	NA	NA	0.193	0.059	0.244	0.085
337	75685	CGPG7767	SENSE	NA	NA	−0.917	0.075	−0.974	0.049
267	75822	CGPG5210	SENSE	NA	NA	−0.267	0.194	−0.297	0.090
324	76171	CGPG7206	SENSE	NA	NA	−0.350	0.065	−0.570	0.049
254	76202	CGPG4788	SENSE	NA	NA	−1.153	0.009	−1.713	0.019
326	76467	CGPG7267	SENSE	NA	NA	−0.484	0.177	−0.743	0.088
359	76961	CGPG9080	SENSE	NA	NA	−0.425	0.098	−0.265	0.051
360	76973	CGPG9081	SENSE	NA	NA	0.333	0.052	0.248	0.003
363	77103	CGPG9134	SENSE	NA	NA	0.363	0.093	0.198	0.072
374	77157	CGPG9186	SENSE	NA	NA	0.287	0.044	0.107	0.086
369	77165	CGPG9155	SENSE	NA	NA	−0.081	0.413	−0.572	0.012
368	77176	CGPG9148	SENSE	NA	NA	−0.577	0.025	−0.651	0.085
365	77187	CGPG9141	SENSE	NA	NA	0.335	0.002	0.263	0.046
385	77209	CGPG9278	SENSE	NA	NA	0.671	0.027	0.451	0.011
383	77220	CGPG9271	SENSE	NA	NA	0.463	0.008	0.231	0.228
225	77334	CGPG3638	SENSE	NA	NA	0.531	0.067	0.336	0.031
349	77349	CGPG8083	SENSE	NA	NA	0.133	0.001	0.035	0.781
319	77517	CGPG6952	SENSE	NA	NA	−0.843	0.142	−1.458	0.062
320	77518	CGPG6953	SENSE	NA	NA	0.354	0.007	0.380	0.010
307	77609	CGPG6326	SENSE	NA	NA	0.252	0.087	0.211	0.145

[0168] For "seeding weight" and "leaf angle", if $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait improvement as compared to the reference. If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait improvement as compared to the reference with $p<0.2$.

[0169] For "petiole length", if $p<0.05$ and delta <0, the transgenic plants showed statistically significant trait improvement as compared to the reference. If $p<0.2$ and delta <0, the transgenic plants showed a trend of trait improvement as compared to the reference.

[0170] Transgenic plants comprising recombinant DNA expressing a protein as set forth in SEQ ID NO: 246, 295, 303, 325, or 375 showed enhanced shade tolerance by the second criteria as illustrated in Example 1L and 1M.

I. Early Plant Growth and Development Screen

[0171] This example sets forth a plate based phenotypic analysis platform for the rapid detection of phenotypes that are evident during the first two weeks of growth. In this screen, we were looking for genes that confer advantages in the processes of germination, seedling vigor, root growth and root morphology under non-stressed growth conditions to plants. The transgenic plants with advantages in seedling growth and development were determined by the seedling weight and root length at day 14 after seed planting.

[0172] T2 seeds were plated on glufosinate selection plates and grown under standard conditions (~100 uE/m^2/s, 16 h photoperiod, 22° C. at day, 20° C. at night). Seeds were stratified for 3 days at 4° C. Seedlings were grown vertically (at a temperature of 22° C. at day 20° C. at night). Observations were taken on day 10 and day 14. Both seedling weight and root length at day 14 were analyzed as quantitative responses according to example 1M.

[0173] A list recombinant DNA constructs that improve early plant growth and development illustrated in Table 11.

TABLE 11

				Root length at day 10		Root length at day 14		Seedling weight at day 14	
PEP SEQ ID	Construct ID	Nomination ID	Orientation	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
227	19774	CGPG3920	SENSE	0.488	0.097	0.307	0.100	0.550	0.163
229	19956	CGPG3972	SENSE	0.248	0.062	0.154	0.214	0.284	0.001
232	19973	CGPG4026	SENSE	0.326	0.047	0.066	0.577	0.444	0.012
302	70812	CGPG607	SENSE	0.704	0.037	0.546	0.031	0.740	0.033
236	70915	CGPG4058	SENSE	0.292	0.005	0.278	0.008	0.331	0.114
230	70948	CGPG3990	SENSE	0.255	0.269	0.093	0.229	0.375	0.026
234	70950	CGPG4052	SENSE	0.106	0.577	0.124	0.374	0.239	0.041
235	70962	CGPG4057	SENSE	0.171	0.075	0.144	0.226	0.283	0.015
241	70963	CGPG4121	SENSE	0.149	0.057	0.112	0.074	0.062	0.513
242	70994	CGPG4122	SENSE	0.198	0.063	0.121	0.114	0.240	0.124
244	70995	CGPG4154	SENSE	0.132	0.052	0.101	0.006	0.198	0.045
249	71328	CGPG4454	SENSE	0.209	0.136	0.251	0.122	0.445	0.093
268	72001	CGPG5221	SENSE	0.183	0.060	0.142	0.042	0.195	0.149
274	72753	CGPG5540	SENSE	0.113	0.045	0.053	0.348	0.081	0.730
282	73105	CGPG5656	SENSE	0.046	0.577	0.138	0.057	0.298	0.142
292	73136	CGPG5764	SENSE	0.212	0.077	0.133	0.027	0.330	0.037
265	73256	CGPG5194	SENSE	0.123	0.503	0.371	0.135	0.623	0.069
313	74420	CGPG6712	SENSE	0.249	0.085	0.093	0.358	0.363	0.042
316	74566	CGPG6796	SENSE	0.169	0.003	0.147	0.114	0.173	0.171
304	74662	CGPG6185	SENSE	−0.205	0.337	0.009	0.878	−0.009	0.958
312	74688	CGPG6653	SENSE	0.221	0.083	0.059	0.358	0.295	0.163
329	74862	CGPG7308	SENSE	0.201	0.122	0.044	0.515	0.383	0.006
325	76178	CGPG7225	SENSE	0.217	0.018	0.093	0.364	0.240	0.234
322	77069	CGPG7163	SENSE	/	/	/	/	0.641	0.074
376	77124	CGPG9207	SENSE	0.337	0.121	0.256	0.045	0.762	0.034
371	77155	CGPG9170	SENSE	0.181	0.262	0.265	0.035	0.419	0.000
367	77164	CGPG9147	SENSE	0.589	0.068	0.369	0.066	0.899	0.051
370	77166	CGPG9163	SENSE	0.383	0.025	0.391	0.006	0.787	0.019
372	77180	CGPG9180	SENSE	0.442	0.058	0.267	0.031	0.402	0.339
362	77186	CGPG9133	SENSE	0.448	0.022	0.383	0.079	0.654	0.057
365	77187	CGPG9141	SENSE	0.453	0.043	0.227	0.127	0.660	0.013
375	77195	CGPG9205	SENSE	0.221	0.114	0.188	0.160	0.259	0.064
385	77209	CGPG9278	SENSE	0.360	0.092	0.181	0.203	0.594	0.047
382	77266	CGPG9259	SENSE	/	/	/	/	0.470	0.020
384	77268	CGPG9275	SENSE	0.353	0.111	0.170	0.244	0.386	0.041
378	77273	CGPG9220	SENSE	0.255	0.070	0.023	0.586	0.510	0.141
297	77312	CGPG5927	SENSE	/	/	/	/	1.006	0.065
393	77409	CGPG9345	SENSE	0.410	0.027	0.396	0.011	0.461	0.040
389	77430	CGPG9322	SENSE	0.209	0.183	0.211	0.247	0.399	0.092
390	77432	CGPG9335	SENSE	0.342	0.113	0.285	0.122	0.425	0.055
391	77433	CGPG9341	SENSE	0.204	0.120	0.222	0.041	0.382	0.085
392	77444	CGPG9344	SENSE	0.185	0.068	0.227	0.003	0.276	0.002
387	77451	CGPG9309	SENSE	0.266	0.097	0.208	0.042	0.014	0.981
388	77452	CGPG9311	SENSE	0.286	0.021	0.182	0.123	0.284	0.201
327	77536	CGPG7272	SENSE	0.121	0.389	0.147	0.026	0.384	0.027
342	77549	CGPG7933	SENSE	0.349	0.006	0.207	0.032	0.383	0.022
344	77568	CGPG8012	SENSE	0.312	0.020	0.157	0.015	0.359	0.071
351	77587	CGPG8107	SENSE	0.151	0.128	0.223	0.014	0.370	0.030
318	77618	CGPG6810	SENSE	0.179	0.018	0.104	0.276	0.154	0.388
334	77816	CGPG7529	SENSE	0.145	0.400	0.171	0.142	0.312	0.181
336	77821	CGPG7737	SENSE	0.114	0.406	0.126	0.208	0.311	0.079
343	77917	CGPG7986	SENSE	0.136	0.083	0.162	0.011	−0.242	0.458

[0174] If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait improvement as compared to the reference. If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait improvement as compared to the reference.

[0175] Transgenic plants comprising recombinant DNA expressing a protein as set forth in SEQ ID NO: 252, 309, or 310 showed improved early plant growth and development evidenced by the second criteria as illustrated in Example 1L and 1M.

J. Late Plant Growth and Development Screen

[0176] This example sets forth a soil based phenotypic platform to identify genes that confer advantages in the processes of leaf development, flowering production and seed maturity to plants.

[0177] *Arabidopsis* plants were grown on a commercial potting mixture (Metro Mix 360, Scotts Co., Marysville, Ohio) consisting of 30-40% medium grade horticultural vermiculite, 35-55% sphagnum peat moss, 10-20% processed bark ash, 1-15% pine bark and a starter nutrient charge. Soil was supplemented with Osmocote time-release fertilizer at a rate of 30 mg/ft^3. T2 seeds were imbibed in 1% agarose solution for 3 days at 4° C. and then sown at a density of ~5 per 2½" pot. Thirty-two pots were ordered in a 4 by 8 grid in standard greenhouse flat. Plants were grown in environmentally controlled rooms under a 16 h day length with an average light intensity of ~200 μmoles/m^2/s. Day and night temperature set points were 22° C. and 20° C., respectively. Humidity

was maintained at 65%. Plants were watered by sub-irrigation every two days on average until mid-flowering, at which point the plants were watered daily until flowering was complete.

[0178] Application of the herbicide glufosinate was performed to select T2 individuals containing the target transgene. A single application of glufosinate was applied when the first true leaves were visible. Each pot was thinned to leave a single glufosinate-resistant seedling ~3 days after the selection was applied.

[0179] The rosette radius was measured at day 25. The silique length was measured at day 40. The plant parts were harvested at day 49 for dry weight measurements if flowering production was stopped. Otherwise, the dry weights of rosette and silique were carried out at day 53. The seeds were harvested at day 58. All measurements were analyzed as quantitative responses according to example 1M.

[0180] A list of recombinant DNA constructs that improve late plant growth and development illustrated in Table 12.

TABLE 12

		Rosette dry weight at day 53		Rosette radius at day 25		Seed net dry weight at day 62		Silique dry weight at day 53		Silique length at day 40	
PEP SEQ ID	Construct ID	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value	Delta mean	P-value
394	12313	−0.075	0.489			0.654	0.000	0.157	0.174	−0.024	0.275
221	18258	−0.494	0.017	−0.183	0.083	0.533	0.006	−0.269	0.234	0.056	0.009
246	70657	0.373	0.040	0.187	0.037	0.355	0.081	−0.187	0.222	−0.003	0.972
247	70660	−0.010	0.936	−0.072	0.431	0.445	0.026	0.116	0.369	0.145	0.045
216	71538	−0.167	0.168	0.017	0.686	0.521	0.005	−0.196	0.113	0.023	0.557
269	72056	0.563	0.008	NA	NA	−0.251	0.159	−0.289	0.314	−0.046	0.314
279	73057	−0.266	0.035	0.167	0.114	0.396	0.034	−0.304	0.085	0.023	0.543
311	73568	−0.140	0.115	−0.085	0.340	0.553	0.019	0.344	0.010	0.040	0.458
222	19193	−0.296	0.110	0.081	0.385	1.076	0.011	NA	NA	0.073	0.001
262	73242	0.159	0.132	0.133	0.050	1.074	0.009	0.652	0.002	0.045	0.048
309	73433	0.477	0.026	0.113	0.120	1.140	0.006	0.552	0.016	−0.009	0.872
316	74566	−0.387	0.023	0.104	0.047	1.213	0.003	−0.169	0.130	0.012	0.598
338	75654	0.604	0.012	−0.006	0.899	−1.193	0.004	−0.258	0.057	−0.004	0.962
361	77150	0.611	0.003	−0.098	0.115	−0.363	0.011	−0.398	0.203	0.001	0.990
327	77536	0.043	0.692	0.089	0.040	0.725	0.015	0.419	0.016	0.075	0.105
334	77816	−0.324	0.021	0.005	0.954	1.207	0.000	−0.038	0.679	0.039	0.378

[0181] If $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait improvement as compared to the reference. If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait improvement as compared to the reference.

K. Low Nitrogen Tolerance Screen

[0182] Under low nitrogen conditions, *Arabidopsis* seedlings become chlorotic and have less biomass. This example sets forth the limited nitrogen tolerance screen to identify *Arabidopsis* plants transformed with the gene of interest that are altered in their ability to accumulate biomass and/or retain chlorophyll under low nitrogen condition.

[0183] T2 seeds were plated on glufosinate selection plates containing 0.5×N-Free Hoagland's T 0.1 mM NH_4NO_3 T 0.1% sucrose T 1% phytagel media and grown under standard light and temperature conditions. At 12 days of growth, plants were scored for seedling status (i.e., viable or non-viable) and root length. After 21 days of growth, plants were scored for BASTA resistance, visual color, seedling weight, number of green leaves, number of rosette leaves, root length and formation of flowering buds. A photograph of each plant was also taken at this time point.

[0184] The seedling weight and root length were analyzed as quantitative responses according to example 1M. The number green leaves, the number of rosette leaves and the flowerbud formation were analyzed as qualitative responses according to example 1L. The leaf color raw data were collected on each plant as the percentages of five color elements (Green, DarkGreen, LightGreen, RedPurple, YellowChlorotic) using a computer imaging system. A statistical logistic regression model was developed to predict an overall value based on five colors for each plant.

[0185] A list of recombinant DNA constructs that improve low nitrogen availability tolerance in plants illustrated in Table 13.

TABLE 13

				Root length		Leaf color		Rosette weight	
PEP SEQ ID	Construct ID	Nomination ID	Orientation	Delta mean	P-value	Risk score mean	P-value	Delta mean	P-value
200	10422	CGPG117	ANTI-SENSE	−0.435	0.008	1.311	0.021	0.050	0.396
206	12602	CGPG170	SENSE	−0.004	0.941	−0.052	0.895	0.115	0.048
202	13235	CGPG1288	SENSE	−0.047	0.267	−0.085	0.864	0.128	0.068
203	13411	CGPG1301	SENSE	0.323	0.202	−3.233	0.126	0.174	0.044

TABLE 13-continued

				Root length		Leaf color		Rosette weight	
PEP SEQ ID	Construct ID	Nomination ID	Orientation	Delta mean	P-value	Risk score mean	P-value	Delta mean	P-value
201	13485	CGPG1226	ANTI-SENSE	0.311	0.096	1.162	0.038	0.241	0.019
205	13846	CGPG1542	ANTI-SENSE	−0.267	0.190	1.506	0.004	0.176	0.281
212	16610	CGPG2499	SENSE	−0.037	0.677	1.325	0.004	−0.004	0.918
211	17805	CGPG2457	ANTI-SENSE	−0.348	0.016	3.523	0.067	−0.105	0.116
218	18231	CGPG3274	SENSE	−0.207	0.117	0.925	0.062	−0.093	0.094
224	18354	CGPG3534	SENSE	0.104	0.070	−0.407	0.124	0.189	0.048
252	70684	CGPG4588	SENSE	0.379	0.001	−3.676	0.003	0.328	0.030
223	71301	CGPG3528	SENSE	−0.394	0.027	1.269	0.042	−0.128	0.026
250	71329	CGPG4456	SENSE	−0.169	0.230	0.475	0.074	−0.365	0.337
258	72813	CGPG4977	SENSE	−0.361	0.193	0.521	0.076	0.013	0.120
309	73433	CGPG6429	SENSE	0.129	0.201	−0.091	0.794	0.186	0.002
300	74349	CGPG5967	SENSE	−0.139	0.019	0.592	0.080	0.045	0.080
313	74420	CGPG6712	SENSE	0.612	0.043	−3.086	0.063	0.173	0.002
298	75237	CGPG5941	SENSE	−0.097	0.237	0.948	0.031	0.074	0.136
333	75379	CGPG7520	SENSE	0.000	0.998	0.529	0.048	−0.017	0.755
335	75434	CGPG7636	SENSE	−0.336	0.039	1.208	0.076	−0.109	0.107
341	75622	CGPG7833	SENSE	−0.503	0.001	1.776	0.007	0.096	0.497
339	75692	CGPG7823	SENSE	−0.055	0.165	−0.377	0.328	0.132	0.083
301	76422	CGPG6040	SENSE	0.197	0.178	−0.263	0.734	0.162	0.094
359	76961	CGPG9080	SENSE	−0.361	0.136	1.472	0.013	−0.190	0.066
369	77165	CGPG9155	SENSE	0.366	0.041	−1.982	0.143	0.253	0.099
303	77322	CGPG6178	SENSE	/	/	1.691	0.060	−0.185	0.052
207	16322	CGPG1828	SENSE	/	/	−0.021	0.982	0.116	0.043
356	77832	CGPG8976	SENSE	/	/	2.472	0.011	−0.028	0.445

[0186] For leaf color and rosette weight, if $p<0.05$ and delta or risk score mean >0, the transgenic plants showed statistically significant trait improvement as compared to the reference. If $p<0.2$ and delta or risk score mean >0, the transgenic plants showed a trend of trait improvement as compared to the reference with $p<0.2$. For root length, if $p<0.05$, the transgenic plants showed statistically significant trait improvement as compared to the reference. If $p<0.2$, the transgenic plants showed a trend of trait improvement as compared to the reference.

[0187] Transgenic plants comprising recombinant DNA expressing a protein as set forth in SEQ ID NO: 198 or 327 showed improved tolerance to low nitrogen condition evidenced by the second criteria as illustrated in Example 1L and 1M.

L. Statistic Analysis for Qualitative Responses

[0188] A list of responses that were analyzed as qualitative responses illustrated in Table 14.

TABLE 14

response	screen	categories (success vs. failure)
Wilting response Risk Score	Soil drought tolerance screen	non-wilted vs. wilted
growth stage at day 14	heat stress tolerance screen	50% of plants reach stage1.03 vs. not
growth stage at day 14	salt stress tolerance screen	50% of plants reach stage1.03 vs. not
growth stage at day 14	PEG induced osmotic stress tolerance screen	50% of plants reach stage1.03 vs. not
growth stage at day 7	cold germination tolerance screen	50% of plants reach stage 0.5 vs. not
number of rosette leaves at day 23	Shade tolerance screen	5 leaves appeared vs. not
Flower bud formation at day 23	Shade tolerance screen	flower buds appear vs. not
leaf angle at day 23	Shade tolerance screen	>60 degree vs. <60 degree
number of green leaves at day 21	limited nitrogen tolerance screen	6 or 7 leaves appeared vs. not
number of rosette leaves at day 21	limited nitrogen tolerance screen	6 or 7 leaves appeared vs. not
Flower bud formation at day 21	limited nitrogen tolerance screen	flower buds appear vs. not

Plants were grouped into transgenic and reference groups and were scored as success or failure according to Table 14. First, the risk (R) was calculated, which is the proportion of plants that were scored as of failure plants within the group. Then the relative risk (RR) was calculated as the ratio of R (transgenic)

to R (reference). Risk score (RS) was calculated as $-\log_2^{RR}$. Two criteria were used to determine a transgenic with enhanced trait(s). Transgenic plants comprising recombinant DNA disclosed herein showed trait enhancement according to either or both of the two criteria.

[0189] For the first criteria, the risk scores from multiple events of the transgene of interest were evaluated for statistical significance by t-test using SAS statistical software (SAS 9, SAS/STAT User's Guide, SAS Institute Inc, Cary, N.C., USA). RS with a value greater than 0 indicates that the transgenic plants perform better than the reference. RS with a value less than 0 indicates that the transgenic plants perform worse than the reference. The RS with a value equal to 0 indicates that the performance of the transgenic plants and the reference don't show any difference. If $p<0.05$ and risk score mean >0, the transgenic plants showed statistically significant trait enhancement as compared to the reference. If $p<0.2$ and risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference.

[0190] For the second criteria, the RS from each event was evaluated for statistical significance by t-test using SAS statistical software (SAS 9, SAS/STAT User's Guide, SAS Institute Inc, Cary, N.C., USA). The RS with a value greater than 0 indicates that the transgenic plants from this events perform better than the reference. The RS with a value less than 0 indicates that the transgenic plants from this event perform worse than the reference. The RS with a value equal to 0 indicates that the performance of the transgenic plants from this event and the reference don't show any difference. If $p<0.05$ and risk score mean >0, the transgenic plants from this event showed statistically significant trait enhancement as compared to the reference. If $p<0.2$ and risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference. If two or more events of the transgene of interest showed improvement in the same response, the transgene was deemed to show trait enhancement.

M. Statistic Analysis for Quantitative Responses

[0191] A list of responses that were analyzed as quantitative responses illustrated in Table 15.

TABLE 15

response	screen
seed yield	Soil drought stress tolerance screen
seedling weight at day 14	heat stress tolerance screen
root length at day 14	heat stress tolerance screen
seedling weight at day 14	salt stress tolerance screen
root length at day 14	salt stress tolerance screen
root length at day 11	salt stress tolerance screen
seedling weight at day 14	PEG induced osmotic stress tolerance screen
root length at day 11	PEG induced osmotic stress tolerance screen
root length at day 14	PEG induced osmotic stress tolerance screen
rosette area at day 8	cold shock tolerance screen
rosette area at day28	cold shock tolerance screen
difference in rosette area from day 8 to day 28	cold shock tolerance screen
root length at day 28	cold germination tolerance screen
seedling weight at day 23	Shade tolerance screen
petiole length at day 23	Shade tolerance screen
root length at day 14	Early plant growth and development screen
Seedling weight at day14	Early plant growth and development screen
Rosette dry weight at day 53	Late plant growth and development screen
rosette radius at day 25	Late plant growth and development screen
seed dry weight at day 58	Late plant growth and development screen

TABLE 15-continued

response	screen
silique dry weight at day 53	Late plant growth and development screen
silique length at day 40	Late plant growth and development screen
Seedling weight at day 21	Limited nitrogen tolerance screen
Root length at day 21	Limited nitrogen tolerance screen

[0192] The measurements (M) of each plant were transformed by $\log_2$ calculation. The Delta was calculated as $\log_2$M(transgenic)−$\log_2$M(reference). Two criteria were used to determine trait enhancement. A transgene of interest could show trait enhancement according to either or both of the two criteria. The measurements (M) of each plant were transformed by $\log_2$ calculation. The Delta was calculated as $\log_2$M(transgenic)−$\log_2$M(reference). If the measured response was Petiole Length for the Low Light assay, Delta was subsequently multiplied by −1, to account for the fact that a shorter petiole length is considered an indication of trait enhancement.

[0193] For the first criteria, the Deltas from multiple events of the transgene of interest were evaluated for statistical significance by t-test using SAS statistical software (SAS 9, SAS/STAT User's Guide, SAS Institute Inc, Cary, N.C., USA). Delta with a value greater than 0 indicates that the transgenic plants perform better than the reference. Delta with a value less than 0 indicates that the transgenic plants perform worse than the reference. The Delta with a value equal to 0 indicates that the performance of the transgenic plants and the reference don't show any difference. If $p<0.05$ and risk score mean >0, the transgenic plants showed statistically significant trait enhancement as compared to the reference. If $p<0.2$ and risk score mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference.

[0194] For the second criteria, the delta from each event was evaluated for statistical significance by t-test using SAS statistical software (SAS 9, SAS/STAT User's Guide, SAS Institute Inc, Cary, N.C., USA). The Delta with a value greater than 0 indicates that the transgenic plants from this event performs better than the reference. The Delta with a value less than 0 indicates that the transgenic plants from this event perform worse than the reference. The Delta with a value equal to 0 indicates that the performance of the transgenic plants from this event and the reference don't show any difference. If $p<0.05$ and delta mean >0, the transgenic plants from this event showed statistically significant trait improvement as compared to the reference. If $p<0.2$ and delta mean >0, the transgenic plants showed a trend of trait enhancement as compared to the reference. If two or more events of the transgene of interest showed enhancement in the same response, the transgene was deemed to show trait improvement.

Example 2

Identification of Homologs

[0195] A BLAST searchable "All Protein Database" is constructed of known protein sequences using a proprietary sequence database and the National Center for Biotechnology Information (NCBI) non-redundant amino acid database (nr. aa). For each organism from which a DNA sequence provided herein was obtained, an "Organism Protein Database" is constructed of known protein sequences of the organism; the

Organism Protein Database is a subset of the All Protein Database based on the NCBI taxonomy ID for the organism.

[0196] The All Protein Database is queried using amino acid sequence of cognate protein for gene DNA used in trait-improving recombinant DNA, i.e., sequences of SEQ ID NO: 198 through SEQ ID NO: 394 using "blastp" with E-value cutoff of 1e−8. Up to 1000 top hits were kept, and separated by organism names. For each organism other than that of the query sequence, a list is kept for hits from the query organism itself with a more significant E-value than the best hit of the organism. The list contains likely duplicated genes, and is referred to as the Core List. Another list was kept for all the hits from each organism, sorted by E-value, and referred to as the Hit List.

[0197] The Organism Protein Database is queried using amino acid sequences of SEQ ID NO: 198 through SEQ ID NO: 394 using "blastp" with E-value cutoff of 1e−4. Up to 1000 top hits are kept. A BLAST searchable database is constructed based on these hits, and is referred to as "SubDB". SubDB was queried with each sequence in the Hit List using "blastp" with E-value cutoff of 1e−8. The hit with the best E-value is compared with the Core List from the corresponding organism. The hit is deemed a likely ortholog if it belongs to the Core List, otherwise it is deemed not a likely ortholog and there is no further search of sequences in the Hit List for the same organism. Likely orthologs from a large number of distinct organisms were identified and are reported by amino acid sequences of SEQ ID NO: 395 to SEQ ID NO: 19938. These orthologs are reported in Tables 2 as homologs to the proteins cognate to genes used in trait-improving recombinant DNA.

TABLE 2

SEQ ID NO:	homolog SEQ ID NOs											
198:	3331	2914	8408	6836	10845	14799	13562	8848	2509	13003	875	10945
	4176	7318	4820	19156	19137	14942	17166	13809	3506	3410	1343	8019
	7882	6490	3550	4999	3130	12635	8774	10864	17857	18089	16263	7295
	10882	18252	3728	14833	11485	15463	18826	2924	18723	1446	2812	7847
	3395	4209	15768	10679	18379	14040	3974	1087	11574	6329	5482	5609
	6441	5537	17042	4716	4516	12643	11384	12736	8137	1344	19473	8452
	4094	2460	18071	16891	5620	2364	7018	5200	11131	18133	12170	2731
	1687	5014	18511	9343	19283	6682	8123	8124	10597	10622	10608	10600
	16221	4280	11494	4867	9035	9507	7969	19159	19425	5248	17367	8135
	8773	1287	2671	9365	18729	13828	8754	7170	14529	16604	8341	1135
	6224	9739	11212	12962	4331	13555	14356	14357	14783	7509	2032	4692
	5243											
199:	15320											
200:	7710	14519	16336	7019	7872	7719	18299	10453	4650	15008	10089	699
	15645	10533	11751	12924	10526	5313	17532	8825	6941	7743	4155	14541
	9797	16905	8304	12080	19803	3087	1397	7534	5547	2423		
201:	11777	6444	1416	4353	15071	3413	14526					
202:	19073	6651	15740	7399	15791	2977	7789	9248	14697	15923	12131	5470
	965	11100	11069	12624	12892	3580	5270	18663	2916	1684	8107	4240
	19240	18582	19054	15775	7301	17416	10566	16351	13846	16386	18431	4439
	4056	8159	8292	12484	7316	3763	4783	18427	15501	16164	7762	4015
	4556	18955	12061	8636	9665	9713	10212	17555	5330	12850	16436	19045
	16034	16692	2571	11676	12666	11853	5348	8771	12218	3157	10749	
203:	5608	2382	17993	16598	7505	6976						
204:	11369	13527	10897	6893	6962	11592	837	5116	19669	1655	7244	2623
	2591	16504	17797	4636	15133	4141	7112	7939	6898	15965	16706	16979
	11784	16115	9620	15750	14652	3008	7838	14787	4563	1873	15811	7271
	4317	16603	1715	14288	11341	6188	1546	5683	5225	3033	6069	11268
	15981	15490	4181	8633	6058	7993	6763	9671	14892	17296	990	8184
	2935	8536	11232	12598	12638	5112	10787	1107	13858	5864	16398	16380
	17071	16520	1973	5455	13852	19228	1695	17402	2865	17120	2507	5601
	14952	1462	6616	6973	3092	1382	7755	3870	9765	5711	1257	6119
	15310	3792	15970	16032	14584	7282	15140	7273	3013	15249	13253	13241
	2265	17700	18976	4009	17354	2223	17559	3151	6320	17010	8939	11258
	734	573	15015	3050	16344	3931	11238	7691	11499	1112	4825	8344
	13519	11669	5640	13588	5473	15108	7210	17617	5994	5980	16627	17906
	5876	6079	18894	6956	12887	14694	10968	1061	2778	6096	10570	680
	974	3120	16300	5885	7626	13881	4244	4233	15039	4486	3103	3115
	7654	11890	12359	10800	9409	12657	8977	9182	17818	2942	9780	9899
	18496	4118	18188	10437	13907	17312	15730	13906	2603	12770	4837	12953
	16663	9237	9546	16293	18238	6022	13908	10266	9180	5538	15536	10370
	15958	5217	8154	13095	15972	14841	15262	12702	10766	15960	18726	19395
	10345	5964	13064	3946	17225	17262	17220	17266	17224	17252	5465	5495
	12800	12814	12758	3021	12400	12492	16461	13638	5616	17449	8397	17258
	5669	5675	6852	9796	176011	7569	9775	17664				
205:	14023	6117	12539	6696	18601	1463	19893	6621	9577	9166	17890	17889
	528	5413	18313	2784	8102	3988	890	19106	571	6791	2402	912
206:	17912	8799	6566	12137	4356	5803	5253	6078	9123	17523	12392	17806
	6917	19039	7350	17767	11311	17082	15535	19392	11233	470	8318	14963
	16736	8867	14135	5246	4674	2124	9901	13302	15459	18997	2954	1026
	667	7561	16841	8092	9084	4065	1836	13713	13697	17640	7422	19580
	4565	15193	526	13108	7065	11703	11362	3633	19430	6221	17433	15616
	10082	10189	3089	15238	6633	8106	16180	15317	16364			

TABLE 2-continued

SEQ ID NO:	homolog SEQ ID NOs											
207:	14575	8831	11211	14985	17619	18829	2521	5219	15413	15835	1204	6569
	4661	4457	6066	14578	932	13694	7541	4813	15707	19563	1326	16107
	5009	7518	14825	13777	6175	15925	13617	5765	14838	9091	10776	15679
	5909	19373	756									
208:	19581	18655	16310	7497	6382	8261	936	7358	8883	4866	2146	8601
	2932	1626	10354	15192	11509	9909	13503	488	17477	14483	16941	2824
	1072	4989	14179	4883	13751							
209:	3493	16588	7031	5155	11150	17294	5241	10621	5786	5591	16509	2021
	1324	12454	15061	1670	15143	16506	17002	8741	18091	4013	5959	19370
	4239	12885	12174	3709	3431	9596	3378	1018	5963	13212	3150	2952
	1619	19861	19114	15446	19582	12663	19603					
210:	17777	843	11020	1337	18495	1493	6396	15336	14087	2568	4517	1157
	10741	4553	14999	425	4258	17388	5327	748	11691	10174	17805	16628
	10117	7980	8902									
211:	9637	17261	13232	7387	10506	19067	12021	872	11620	13603	841	1450
	2848	16911										
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	9466	18102	610	9042	2431	18349	16650	14418	2251	4235	6826	1244
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	17223	16048	16071	2120	19847	10420	11239	18968	2995	7551	15854	12345
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	19618	18012	17233	10057	18222	15021	9371	5985	14888	14001	1279	7826
	14232	18172	7425	11502	15565	17431	8317	10294	17742	5564	5531	18144
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	3933	14263	11860	1907	4672	15599	13737	4944	2252	15415	11543	3433
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TABLE 2-continued

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	18049	15274	19470									
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222:	14820	18626	11591	649	3005	3037	5453	5430	14248	2371	4626	11661
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	5805	12934	12755	7504	1091	17904	17909	17926	17902	17938	17907	17929
	10598	17935	17933	5298	17980	10601	5383	14050	6585	11379	16583	17978
	17814	4838	17812	2633	3257	3189	774	12008	9988	14268	18392	12567
	14920	12980	11959	7682	7685	13235	4127	3740	3766	3770	3769	3795
	14966	457	8521	19464	4847	13386	5024	13387	13401	5957	6571	7932
	8369	10496	10492	10490	10495	10517	7943	4958	4956	4923	4986	4961
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	4988	18200	18196	7176	4739	5479	8351	7177	12886	9521	6464	17681
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	16762	9027	9568	9029	16788	9009	16780	14410	16781	16782	16802	3330
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	2417	11311	17082	17741	11253	11254	7473	13718	6269	3242	7085	5224
	8787	16268	19692	10769	8867	1434	16082	19530	14789	13615	18997	2954
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229:	7539	3499	12437	19471	14158	11575	6399	15966	17187	13512	7688	2131
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TABLE 2-continued

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	14459	5315	9268	16190	19143	15124	418	3076	16204	17414	18692	13164
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245:	11361	5661	8686	17264	8328	8330	7550	10232	18956	315	8720	1696
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	18584	3108	12724	15546	15764	15754	18354	18416	4890	19678	19130	15532
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	11586	14490	18301	18792	15378	7699	18803	19816	16104	14468	17612	11556
	1765	5525	2247	5751	11815	17200	10136	6205	16567	10487	18141	6202
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	4226	984	19513	8932	12905	4112	18873					
246:	13549	2112	6794	8833	12086	2984	5421	7868	9325	19092	9699	19026
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	10637	5281	17394	4637	9663	1828	12569	1215	14407	13300	6644	11688
	17465	631	16880	3874	16141	975	8011	16154	18389	13579	15094	8944
	3735	8021	2288	15334	16083	15801	12760	10618	13208	19889	18999	4870
	13710	12132	15259	9267	11470	13144	17588	628	17272	14844	14000	19900
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247:	14941	2202	18124	13094	7945	3968	8551	2458	18176	15639	12789	5427
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	10101	16816	4765	16287	5377	18675	7230	7964	876	9597	19802	11403
	4833	17530	18265	13417	12779	8885	11923	18564	3790	19147	1406	7066
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	9113	3248	6378	1799	14779	3630	4294	7608	13707	16321	15368	12743
	11299	2413	1584	11214	4012	2710	4268	19546	17625	6940	1273	5755
	413	5952	3098	15675	11098	3286	8068	2690	1222	13381	15257	4756
	4725	9351	7586	5770	10868	3420	12012	775	7742	8422	6103	15004
	16010	12445	13845	17033	16212	3842	19401	4100	8417	13255	1233	5307
	7664	11820	4960	4282	2333	17315	12161	4217	10485	8151	16203	1002
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	12930	14231	15548	11694	8266	16248	1579	4806	2747	11349	6186	8303
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	2563	3177	16370	10946	6177	11856	17835	15766	9377	14858	9666	2881
	4713	18553	10081	3260	6030	16206	11892	10319	18672	3859	2663	15443
	5089	10992	2411	12439	17434	6053	18213	1552	16896	16303	2170	4062
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	4172	3616	467	2220	2765	10994	7181	9294	9019	14302	16474	5797
	4407	12612	9186	18928	4415	11982	14037	3959	1335	507	14948	9483
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	11045	12403	2390	19573	11726	9949	5099	9853	16159	15920	13256	615
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	3341	11873	10613	7321	18101	12158	14798	8096	5837	1986	13521	5384
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	14339	12485	7233	18749	12207	7057	408	14300	5215	19033	14163	1226
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TABLE 2-continued

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	9181	2520	4618	7286	7290	7135	6455	7288	9787	11002	551	2679
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	15909	19108	8061	16885	8964	5642	15311	18841	8881	9067	2902	10703
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	13701	18247	5067	8858	2375	10780	12562	6618	1888	368	13569	16443
	14088	17735	6201	1162	9317	18221	17786	9563	9562	2386	3903	5156
	18001	547	12480	13049	2495	8339	18977	12208	19466	10488	15681	11974
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	4841	9829	9828	17831	4690	2646	9830	13874	14131	9842	9827	9849
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	7448	17662	1677	19490	2475	6216	13658	5135	4005	982	15959	17990
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254:	9072	16169	1130	12933	1592	17856	19381	14964	19031	3682		
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	17513	15910	6705	15441	15200	3272	16975	18974	12341	5796		
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	18891	11410	1475	11170	7067	17441	12196					
257:	1879	1595	12797	7459	8363	12502	12756	5854	465	1425	1893	12362
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258:	3828	1761	11325	17218	18307	14003	12997	4456	6236	19270	8499	7402
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	19077	1485	5898	5916	8835	2570	9910	10297	3025	18486	8908	14474
	11654	2349	10867	14488	9940	13901	7336	11511	19746	14836	1906	13400
	19527	5568	4351	18319	6689	10519	15977	15760	7605	16652	14204	14665
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	3667	10338	4125	14782	18479	18004	19084	12471	16645	866	1895	10049
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	7492	3451	18373	17125	5972	9777	16039	12350	4073	8962	17221	1961
	1958	11156	12899	18769	11606	3225	3930	12985	3908	7429	18285	10977
	15040	16234	17004	17293	13355	15499	2062	11463	11416	11708	6710	4422
	5817	13502	14378	14379	13504	1451	19815	12842	4405	10999	9565	11330
	5263	7189	6160	2372	3858	1248	6567	14455	1766	14550	2516	1656
	14989	16864	9312	19300	19408	13516	2556	2969	1952	2541	11207	10625
	19674	9198	10334	18065	3495	8519	12201	3921	13249	18592	857	17545
	11757	15455	2164	789	4350	3117	14133	12220	7087	11452	6125	4977
261:	6807	480	6337	12236	4678	12917	9439	9382	11513	11500	16670	16646
	16691	16660	11516	11515	11496	11498	16668	16683	16686	16664	11519	16659
	16643	14322	2737	1932	12955	12317	19334	12435	12976	5809	18730	11183
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TABLE 2-continued

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	15203	12952	14467	6645	6698	12807	6113	4709	8824	6274	8311	3411
	18810	17940	19805	17162	665	12693	1309	15412	18084	5235	8314	13722
	15858	15969	18135	2305	13611	4030	14864	5363	4470	8271	5178	12458
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	15215	10149	13783	1372	1370	13027	13294	4287	12578	1419	15077	2147
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	7286	551	9787	11002	1701	8942	8928	8930	1097	17269	12778	13750
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	1548	5257	1728	7766	17357	5647	10631	15019	1888	18777	18221	17786
	9562	9563	5156	2386	3903	18001	547	12480	13049	8197	2495	8339
	19466	12208	18977	11974	4385	19014	8302	19012	17408	8291	16077	5878
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	9844	7012	4019	15785	10234	7448	17896	1513	13878	7287		
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	13068	5215	5515	14163	8781	5775	1228	5424	1226	8505	8674	18275
	18314	10203	11707	15070	2693	15215	13884	10149	13783	13027	13294	15807
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	15267	13750	18947	15439	17593	9816	11871	13684	1453	19108	8061	5642
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	15183	1888	11394	1145	18221	17786	9563	9562	18001	3903	2495	17171
	19146	18977	12208	8339	19466	10488	15681	4385	17408	19012	8291	5878
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	8405	9865	8404	6995	7012	4019	7448	538	4587	4576	14863	2709
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266:	12371	1790	10658	8747	10474	4583						
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	547	12480	18001	13049	8197	2495	8339	12208	19466	18977	10488	11974
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	16016	4841	4690	2646	17831	9830	9842	9828	9829	13874	14131	9849
	7012	9847	9827	8403	9851	9865	8405	9844	8406	4019	10234	7448
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	12927	17662	982	4005	17990	6216	13658					
269:	14096	14101	3422	9935	9907	11404	3149	1688	10616	10023	13889	4400
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	3958	14094	14091	14074	7042	19574	7859	17118	9165	9458	1459	14832
	13165	14520	10512	17335	15352	14170	13097	5335	9461	13601	12995	8362
	2662	13567	14785	3435	11646	11805	18390	4017	8969	6711	4962	8794
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270:	16324	10027	16399	19626	19600	18167	7908	9950	15476	16909	13757	17032
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	16187	1329	14353	14351	14349	10819	8846	9429	16618	17714	16634	13050
	10112	19589	3140	14486	3444	16943	12766	19496	9070			
271:	2051	2869	19263	12625	10041	11778	3745	15945	19372	16735	5498	12285
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TABLE 2-continued

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273:	12662	15327	19093	953	5512	10971	2513	18064	17932	1221	19584	4462
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274:	4873	8617	18355	6309	6356	19579	11946	18342	7376	17347	13047	4927
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	15950	5128										
275:	3391	5673	17748	12970	2049	2756	10716	780	5570	15625	17600	2057
	17079	14041	6494	10663	7787	10440	10550	12319	2852	13899	6288	6170
	14404	7408	2857	4218	2808	18604	6362	17551	11818	511	5580	16146
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	1779	5989	19035	7368	11731	19702	17630	783	15741	15774	15442	17674
	2205	5474	2153	18915	13290	9728	17044	8267	18171	1334	15222	15195
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	17275	13703	15244	18936	16496	17942	12986	13118	16224	18419	10277	4864
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TABLE 2-continued

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TABLE 2-continued

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TABLE 2-continued

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TABLE 2-continued

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	7627	18249	9111	10610	1083	6509	17564	5851	15935	14750	1415	7919
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	17493	7527	18633	2515	3708	13536	7991	3379	16897			
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	3206	17127	17830	17527	19410	19413	12404	13866	13360	13864	13860	1092
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TABLE 2-continued

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	4216	12478	8586	7030	8614							
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294:	19341	4724	19896	3258	5111	599	6431	13589	6942	6192	6252	13509
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TABLE 2-continued

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TABLE 2-continued

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TABLE 2-continued

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TABLE 2-continued

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TABLE 2-continued

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	1686	10876	13040	17491	11393	2077	3299	874	13487	11838	9664	10552
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	15976	16374	10771	4277	14521	12901	18215	11495	3853	4255	1629	12007
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	5156	3903	547	18001	12480	13049	8197	2495	17171	18977	12208	19466
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	10026	16740	6793	1954	9499	1886	18780	8529	17665	18483	19399	13823
	10599	10014	11713	13942	16536	6829	13457	12144	4468	15992	10473	13518
	2219	10524	420	421	14605	14570	6724	1269	15608	11671	5125	6124
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	15861	9886	16290	1777	16807	13147	5390	5656	16417	11861	16848	8738
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	5408	17546	18797	5903	6042	1218	4848	19643	4899	6748	1341	2965
	13343	10436	3965	12507	16052	10080	14622	15172	1156	15431	19244	5027
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	4393	19491	1312	1238	437	18920	2620	5133	8260	9619	13014	8506
	10965	2373	14342	18448	19165	17471	5405	6607	1741	14959	15075	16265
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	6886	13963	12295	8982	13436	16066	11980	4664	9057	9034	16666	15687
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	10280	19593	3339	9629	3902	1154	10253	8577	7055	2366	3283	13877
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	16407	18284	16813	16160	19921	18470	14030	12523	13879	8162	18330	4380
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	9824	19506	10715	19649	3163	9998	2058	6584	7848	14615	15185	2020
	15445	16636	11375	18820	10331	1794	6619	8395	15426	6787	6658	7293
	10195	2815	19672	5744	14420	15534	15370	14303	15177	12323	14958	14797
	11491	452	5665	6655	9310	16947	3284	15338	17037	6312	3537	1320
	3839	8693	1070	13922	11570	9105	5536	5454	15484	14763	14487	9068
	12682	9682	10905	17502	4201	4406	8085	8086	7056	8194	4289	2788
	19086	10609	17621	1276	11826	13369	15331	5251	8761	8829	15454	5769
	6808	15129	1725	10525	13488	7737	8203	2464	17537	3566	8056	4191
	16861	7136	8740	1328	6582	7383	9441	7191	15884	17130	5403	5900
	19080	10011	3547	16174	11235	17910	5888	18291	17740	7117	12383	15552
	8043	8613	9367	10541	17801	13465	8616	10220	1388	8599	4600	15321
	13524	873	3602	1369	11422	7039	16732	1166	9497	14498	11817	691
	12683	11133	10036	10168	9240	7540	16302	2752	10828	18058	9911	15729
	17807	1719	19117	1924	3905	6227	4868	10358	11763	18113	5209	8329
	10740	6938	14512	17399	18121	12733	13966	5279	1953	15567	3818	2744
	18925	13352	15418	7193	635	9142	8342	1452	16526	8583	14626	10595
	15517	3675	15449	18995	1550	12913	1574	10748	15207	689	10793	12087
	9495	12369	16764	13313	16678	1034	9702	12049	15046	9046	15685	1505
	4817	6591	10004	17280	18300	1057	2209	13541	16242	6770	17146	11621
	11066	2735	11091	11096	19348	10928	13114	5818	18353	3156	18093	15157
	11263	11949	914	4681	7472	8852	624	7004	5368	718	17732	12259
	3028	1569	5910	8948	4159	5738	8737	15646	4723	4789	12067	16888
	18857	373	6948	802	5226	6977	6646	17557	2557			
377:	8393	9015	13413	2587	10796	17631	11121	634	433	4963	9556	575
	5319	15391	10530	431	9031	4635	9004	9073	3306	11645	3981	19141
	19101	19812	10554	16183	13822	14492	17246	1376	15351	19391	12231	4365
	5194	2111	5408	17546	18797	3789	5903	1218	4848	19643	6748	4899
	1341	2965	13343	10436	3965	12507	16052	10080	14622	1156	15431	5027
	7279	4985	13179	3070	3071	18612	2494	9230	6746	8566	5265	5208
	3815	11698	12148	18164	13048	16879	8300	4441	9892	11252	16442	505
	453	12406	1723	6094	17550	19037	5884	16347	17111	14923	4421	18481
	6530	12498	17991	3134	8890	3350	7985	7864	10001	10340	991	5289
	19317	10465	7319	2659	5841	13312	1585	8483	2167	16410	18310	17967
	11530	8907	847	867	8377	12935	12438	1630	8528	11657	18567	17817
	16778	524	942	2110	13396	13561	12813	15308	14883	14448	5321	8706
	4558	4612	4061	16274	14724	2777	607	3112	6814	11242	4393	19491
	1312	1238	437	18920	2620	5133	9619	8260	13014	8506	10965	3168
	2373	14342	18448	19165	17471	5405	6607	1741	14959	15075	16265	13994
	1258	14304	8744	10343	19837	12926	7213	3174	10993	14602	10617	7779
	10187	9485	15515	19398	18257	19349	1202	15472	7901	12094	13651	1646
	14731	1180	12154	16047	18288	7639	2248	8051	7996	7995	3855	1551
	14194	18409	5592	11704	8432	13409	18199	12052	7391	8999	15302	4964
	15580	16350	15735	14708	15312	6145	15699	6159	15221	18322	10493	501
	6886	13963	12295	8982	13436	16066	11980	4664	9057	9034	16666	15687
	2427	11094	13668	3320	14079	9090	11181	8003	4257	11638	6544	6957
	3999	12296	10381	2653	4772	4810	8751	10568	10162	5600	5649	15893
	14376	16307	17697	9785	10884	16276	6169	6176	1037	9196	8367	7783
	14533	9056	15139	19917	12676	3038	10673	5503	7023	15682	10198	898
	1297	5858	14777	6955	17092	945	3032	16741	4106	11060	10054	18270
	12505	13314	1821	7784	11537	6572	3603	13635	5021	9052	7601	6284
	8815	10431	18883	18773	17616	11724	3501	16356	11013	14805	14557	7384
	17109	7703	14347	18849	5364	8936	3979	19281	10693	13957	3977	7380
	13486	3384										
378:	13086	19930	5574	17164	15382	2809	1565	9389	817	831	5123	14538
	9536	1834	1833	13082	18812	19542	12765	13660	1610	1609	15422	15421
	1627	13773	5445	16272	10838	19127	19142	9628	10532	7251	8084	9179
	10060	3233	3234	10382	15456	12062	12060	8373	598	11569	18041	16210
	3876	5308	5310	4105	19053	17469	5866	18520	18518	17299	16592	13763
	1649	2826	1088	5244	17633	8002	6325	8510	8509	17342	10265	8523
	11182	2722	2708	14181	17828	10012	8552	6241	10590	5676	10274	8661
	3295	6576	8917	12079	16538	11322	11319	15823	16815	16795	13353	14432
	2003	1985	7807	7667	1870	12245	15011	15010	7081	7327	7326	3951
	11419	11420	5668	5402	2091	2088	10840	16194	9002	9003	8127	8141
	1440	6106	6104	17126	17005	4082	9591	9590	1915	6725	10684	7300
	3317	3316	9330	19487	19488	14152	14153	2122	1914	1911	10665	14295
	14309	2813	2489	17345	11755	18173	14628	16281	4570	426	12610	17201
	17057	16060	16058	9609	987	9610	15673	921	1086	18306	11336	2498
	17087	17085	12034	12035	14678	14675	1138	544	16271	12318	12812	4308
	19378	14598	14599	7369	18594	7648	17481	19008	14345	5166	7493	13726
	13725	8384	3400	16200	7902	8410	8409	13137	16958	16957	15723	12257

TABLE 2-continued

SEQ ID NO:	homolog SEQ ID NOs											
	12253	15978	12973	4460	4459	13017	1570	1078	2531	15107	15091	8965
	13199	13198	19203	19218	2645	523	5806	17244	17241	9229	13301	12697
	16182	14543	17648	7956	541	7604	12160	14921	4194	19094	17637	18276
	18272	14246	14245	6265	11350	6263	11351	1447	9984	5779	16703	16701
	8272	8270	15033	637	11702	3382	13215	6987	17734	17485	17484	8448
	11578	16065	14275	12748	19807	2279	9116	2296	2779	13325	13222	5611
	2538	12956	15346	10824	1158	4300	18255	6983	15168	4680	19799	12284
	6950	16092	3445	2799	10239	3660	12422	2797	18788	11987	9273	10359
	2829	13626	19734	592	14588	3599	6112	6093	6110	572	5844	11779
	4108	3093	11517	11539	455	10947	11127	13214	3927	11199	12891	15461
	15460	7465	5719	5718	3367	13458	13456	1149	14244	6969	12138	9126
	1661	15396	5031	16825	1467	3689	6716	6528	6526	8496	18877	
379:	16324	10027	16399	19626	19600	476	10737	6503	2637	5207	7908	18645
	13757	8204	17032	1213	10125	9070	5372	15085	10478	7338	18023	9641
	11812	14642	18106	9561	2651	1666	5437	14594	5439	12210	6002	12290
	5485	6003	14353	14349	14351	10819	8846	9429	2453	10112	16543	3140
	1146	1124	1121	15438	2354							
380:	15042	683	16630	18404	5663	2482	10670	11782	18811	18709	11700	19144
	6755	9799	13818	6126	2455	8789						
381:	17923	18890	5500	4771	6745	5378	3236	1210	11603	19433	19342	15300
	17953	11454	9261	12841	11591	5415	5453	5430	8278	14564	6761	17927
	18569	14781	10539	6214	3620	3528	17899	8748	12221	5504	5502	9489
	6425	8958										
382:	19132	10614	8139	10836	16040	11545	7879	2100	1703	14547		
383:	1189	16611	3586	4641	19633	17705	17150	8849	3552	7294	2029	6153
	18596											
384:	741	1633	5923	8765	16673	14609	3698	6449	2951	2093	11563	614
	14593	14762	6397	7731	14290	17038	4311	14640				
385:	11357	13113	2101	9359	2343	5986	9703	12857	8854	17190	4889	13808
	12572	3386	7845	17983	4794							
386:	1016	16046	10106	6272	16847	10542	15062	5576	4893	5448	15407	7831
	16578	18278	2702	7215	9961	6250	3252	18599	16433	3226	17007	
387:	7223	8111	7867	1322	9479	3291	18674	5132	12538	3515	18852	16518
	14682	5419	9781									
388:	13217	19387	1319	13219	1333	2384	4322	7600	13280	5924	13688	2181
	16877	16122	5091	927	6100	3686						
389:	11269	4678	13073	1755	1754	8654	3662	17371	3891	3973	2187	15246
	18462	4802	3390	619	643	13183	4014	1542	10000	19057	6229	1262
	14305	14256	17590	5708	4877	3775	8462					
390:	17182	3673	6158	5731	8195	15335	7264	7267	5346	10728	11675	2337
	19110	7961	8491	12046	10224	6729	18918	18228	3153	8723	3309	3313
	6222	15956	4632	12325	6835	6387	2622	4496	9897	10860	8044	10003
	13262	13236	6403	5331	4640	1303	4602	1304	18435	16053	18480	17646
	17644	17675	16363	4781	3269	8610	10852	3582	5717	9242	9340	9346
	13271	1345	3780	11086	14006	2264	5062	5146	16786	891	1282	11639
	2472	9621	19732	15665	10462	16384	18138	9510	19888	19119	4931	18991
	13945	18937	13580	18401	13863	1936	4639	10245	760	13679	14995	17389
	5259	10385	9763	15381	10901	10886	10888	12415	15437	8840	7871	4684
	12209	17107	11203	16435	8624	13410	8530	10422	11650	15110	13639	12675
	13689	19825	4662	13277	5625	9279	3369	5976	1377	2144	4086	18044
	16889	6767	18418	11859	8188	6500	16529	16528	13234	14259	18077	11012
	10071	11825	16181	6479	3800	9154	19377	924	923	7361	4574	14380
	13895	17168	14901	17969	13735	17599	10270	4099	18973	3523	14337	8378
	4490	18286	5203	2114	13850	9109	9096	7060	4161	6561	1211	9640
	13790	19180	14796	5771	15355	14027	6282	12681	16502	4842	4262	4930
	15500	16490	14450	18361	15929	1171	7624	13836	15083	19541	1490	8022
	9426	19755	13700	10435	8346	13719	8681	19368	10906	19116	1509	3865
	12853	3125	5889	8316	18315	9077	436	1977	8354	5002	5025	16553
	5171	17152	9352	17908	9960	9963	4907	2079	14164	3744	3102	18375
	4128	4129	14794									
391:	5830	10547	4780	6670	1560	15309	12977	11581	15243	10500	7299	19550
	4614	11584	18988	17503	13880	18201	7124	6036	17359	15414	19074	13696
	4180	810	12806	13939	1259	2434	12029	5666	8718	751	18491	15717
	1795	4475	1738	627	5732	18253	8660	11107	16309	12868	4299	14698
	14679	14502	8248	11990	9758	16167	9385	10043	10430	16906	12099	5791
	16810	13759	8562	2921	8889	10315	14077	2682	18457	14406	12241	10194
	5832	13548	15304	4676								
392:	18452	9432	5303	14233	9970	7637	14980	15265	7581	3016	10412	19809
393:	19384	19382	682	6463	1021	6039	6041	6057	7898	7896	13532	13533
	8037	9356	16887	16866	7150	7148	11880	11903	7084	7083	3381	13816
	13817	12463	4530	2311	2312	10624	10623	15054	2256	2257	14016	14018
	8801	6140	6142	8800	6138	8357	8375	8360	3666	3668	11044	11022
	9473	9494	5001	5000	4831	4836	18327	19232	5812	5815	9999	7941

TABLE 2-continued

SEQ ID NO:	homolog SEQ ID NOs											
	7942	749	3079	7426	7451	8001	7999	8005	19635	4051	15885	12205
	2860	786	784	15576	15575	12310	12307	2306	3461	7640	10242	
394:	12840	13577	8132	1535	5905	3211	3797	12558	6843	17949	15017	9231
	1310	17041	6367	18764	8461	15888	6866	6864	7983	8980	10079	15489
	11102	9933	7325	1749	8441	7720	17727					

Example 3

Consensus Sequence Build

[0198] ClustalW program is selected for multiple sequence alignments of an amino acid sequence of SEQ ID NO: 198 and its homologs, through SEQ ID NO: 394 and its homologs. Three major factors affecting the sequence alignments dramatically are (1) protein weight matrices; (2) gap open penalty; (3) gap extension penalty. Protein weight matrices available for ClustalW program include Blosum, Pam and Gonnet series. Those parameters with gap open penalty and gap extension penalty were extensively tested. On the basis of the test results, Blosum weight matrix, gap open penalty of 10 and gap extension penalty of 1 were chosen for multiple sequence alignment. The consensus sequence of SEQ ID NO: 227 and its 25 homologs were derived according to the procedure described above and is displayed in FIG. **1**.

Example 4

Identification of Amino Acid Domain by Pfam Analysis

[0199] This example illustrates the identification of amino acid domain by Pfam analysis.

[0200] The amino acid sequence of the expressed proteins that were shown to be associated with an enhanced trait were analyzed for Pfam protein family against the current Pfam collection of multiple sequence alignments and hidden Markov models using the HMMER software in the appended computer listing. The Pfam protein families for the proteins of SEQ ID NO: 198 through 394 are shown in Table 16. The Hidden Markov model databases for the identified patent families are also in the appended computer listing allowing identification of other homologous proteins and their cognate encoding DNA to enable the full breadth of the invention for a person of ordinary skill in the art. Certain proteins are identified by a single Pfam domain and others by multiple Pfam domains. For instance, the protein with amino acids of SEQ ID NO: 207 is characterized by two Pfam domains, i.e. "TFIIS_M" and "TFIIS_C". See also the protein with amino acids of SEQ ID NO: 213 which is characterized by three copies of the Pfam domain "WD40". In Table 16 "score" is the gathering score for the Hidden Markov Model of the domain which exceeds the gathering cutoff reported in Table 17.

TABLE 16

PEP SEQ ID NO	GENE ID	Pfam domain name	begin	stop	score	E-value
198	CGPG106	CMAS	69	306	−149.8	5.00E−05
198	CGPG106	Methyltransf_11	131	229	109.1	1.20E−29
198	CGPG106	Methyltransf_12	131	227	54.6	3.10E−13
200	CGPG117	SNF5	14	252	66.9	5.90E−17
202	CGPG1288	Cupin_3	57	131	130.8	3.40E−36
204	CGPG1458	Phosphorylase	180	958	1454.7	0
205	CGPG1542	LMBR1	11	488	715.1	4.40E−212
206	CGPG170	Metallophos	54	249	140.4	4.50E−39
207	CGPG1828	TFIIS_M	206	327	203.5	4.50E−58
207	CGPG1828	TFIIS_C	338	376	83.3	7.00E−22
209	CGPG2217	ORMDL	14	156	356.8	3.20E−104
210	CGPG2292	Tim17	52	186	16.1	4.20E−05
210	CGPG2292	SAM_1	192	253	13.8	0.019
212	CGPG2499	Glycolytic	4	339	588.8	4.50E−174
213	CGPG2653	WD40	135	172	40.3	6.20E−09
213	CGPG2653	WD40	235	271	40.7	4.60E−09
213	CGPG2653	WD40	276	313	38	3.00E−08
214	CGPG2813	HLH	204	251	34.1	4.60E−07
215	CGPG3002	eIF-4B	5	451	−50.3	1.90E−10
216	CGPG3154	C2	14	102	101.8	1.80E−27
216	CGPG3154	C2	198	272	57.8	3.20E−14
217	CGPG3235	B_lectin	66	176	156.8	5.30E−44
217	CGPG3235	S_locus_glycop	189	315	227	3.90E−65
217	CGPG3235	PAN_2	332	402	103.9	4.20E−28
217	CGPG3235	Pkinase_Tyr	488	757	75.6	2.10E−20
217	CGPG3235	Pkinase	488	757	109	1.30E−29
218	CGPG3274	Allene_ox_cyc	74	253	401.6	1.10E−117
219	CGPG3275	Auxin_inducible	50	155	135.6	1.30E−37
220	CGPG3363	zf-AN1	21	58	10.5	0.0033
220	CGPG3363	zf-AN1	103	148	12.4	0.0019

TABLE 16-continued

PEP SEQ ID NO	GENE ID	Pfam domain name	begin	stop	score	E-value
221	CGPG3367	TFIIA	9	375	556	3.40E−164
222	CGPG3375	Tryp_alpha_amyl	33	111	55.2	1.90E−13
224	CGPG3534	Ank	42	74	13.6	0.31
224	CGPG3534	Ank	75	107	36.8	6.90E−08
224	CGPG3534	Ank	108	140	1.6	17
224	CGPG3534	Pkinase_Tyr	160	413	202.4	9.90E−58
224	CGPG3534	Pkinase	160	413	198.5	1.40E−56
225	CGPG3638	Ribonuclease_T2	30	219	367.3	2.20E−107
226	CGPG3918	Metallophos	60	255	159.1	1.10E−44
229	CGPG3972	14-3-3	8	243	501.1	1.20E−147
230	CGPG3990	zf-C3HC4	259	299	47.3	4.60E−11
231	CGPG3994	Pkinase	554	802	207	4.10E−59
231	CGPG3994	Pkinase_Tyr	554	802	233	5.90E−67
232	CGPG4026	CMAS	59	320	−174.5	0.003
232	CGPG4026	Methyltransf_11	122	220	96.3	8.10E−26
232	CGPG4026	Methyltransf_12	122	218	37	5.90E−08
232	CGPG4026	Sterol_MT_C	229	358	301.1	1.80E−87
233	CGPG4048	Pkinase	21	275	342.1	8.80E−100
233	CGPG4048	Pkinase_Tyr	21	275	65.1	1.20E−19
233	CGPG4048	NAF	304	364	104.5	2.80E−28
234	CGPG4052	DUF298	127	242	222.4	9.20E−64
236	CGPG4058	Asp	99	437	−128.4	4.60E−06
237	CGPG4069	adh_short	31	218	−16.7	4.80E−05
239	CGPG4088	SWIB	324	399	96.4	7.80E−26
241	CGPG4121	Cyclin_N	58	190	133.7	4.80E−37
241	CGPG4121	Cyclin_C	192	314	44.3	3.70E−10
242	CGPG4122	zf-C3HC4	100	141	27.6	4.10E−05
243	CGPG4140	p450	48	484	140.8	3.30E−39
244	CGPG4154	zf-CCCH	90	115	22.6	0.0012
245	CGPG4311	FBPase	70	395	347.9	1.50E−101
247	CGPG4369	BoIA	10	79	92.1	1.60E−24
248	CGPG442	2-Hacid_dh	85	394	140.9	3.20E−39
248	CGPG442	2-Hacid_dh_C	187	362	293	5.20E−85
248	CGPG442	ACT	551	621	39.9	8.10E−09
249	CGPG4454	p450	45	447	−35.5	2.10E−09
250	CGPG4456	p450	75	502	103.6	5.30E−28
252	CGPG4588	Auxin_inducible	1	102	151.5	2.00E−42
253	CGPG4765	DUF868	28	304	175.5	1.20E−49
255	CGPG4912	WD40	243	281	31	3.80E−06
256	CGPG4926	WD40	42	79	22.8	0.0012
256	CGPG4926	WD40	126	163	25.8	0.00014
257	CGPG4967	Asp	71	424	−94.7	4.70E−08
258	CGPG4977	Usp	3	157	85.3	1.80E−22
259	CGPG5001	adh_short	5	181	6.4	1.40E−06
260	CGPG5025	adh_short	30	212	5.7	1.50E−06
261	CGPG5041	DUF26	77	132	84.3	3.40E−22
261	CGPG5041	DUF26	188	242	100.7	4.00E−27
261	CGPG5041	Pkinase	333	558	60.3	5.70E−15
262	CGPG5116	ArfGap	15	137	174.1	3.20E−49
262	CGPG5116	C2	182	261	101.4	2.40E−27
263	CGPG5144	p450	61	535	157.9	2.40E−44
264	CGPG5171	p450	35	496	137	4.60E−38
265	CGPG5194	DUF1191	25	308	616.2	2.60E−182
268	CGPG5221	p450	30	499	135.4	1.40E−37
269	CGPG5269	PCI	297	401	108.9	1.30E−29
270	CGPG5404	Peptidase_S10	68	480	683.3	1.70E−202
271	CGPG5432	MtN3_slv	12	99	145.4	1.40E−40
271	CGPG5432	MtN3_slv	133	219	140.4	4.40E−39
272	CGPG5518	Ribosomal_S8e	1	238	325.9	6.30E−95
273	CGPG5535	WD40	335	371	28.8	1.80E−05
273	CGPG5535	WD40	434	471	37.1	5.50E−08
273	CGPG5535	WD40	476	513	47.2	5.20E−11
273	CGPG5535	WD40	518	555	35.6	1.60E−07
273	CGPG5535	WD40	567	604	36.1	1.10E−07
273	CGPG5535	WD40	621	658	34.9	2.50E−07
273	CGPG5535	WD40	663	706	35.5	1.60E−07
274	CGPG5540	ESCRT-III	21	207	265.7	8.40E−77
275	CGPG5568	AA_permease	69	521	−67.1	0.00013
276	CGPG5577	SMC_N	21	1049	−2.8	1.50E−11
277	CGPG5587	Thioredoxin	78	199	0.1	0.00015
278	CGPG5594	Histone	27	100	99.6	8.80E−27
279	CGPG5633	PGAM	91	277	153.2	6.30E−43
280	CGPG5640	Aminotran_1_2	30	385	362.1	8.00E−106

TABLE 16-continued

PEP SEQ ID NO	GENE ID	Pfam domain name	begin	stop	score	E-value
281	CGPG5646	iPGM_N	2	363	876.8	9.10E−261
281	CGPG5646	Metalloenzyme	373	488	173.3	5.40E−49
282	CGPG5656	Gln-synt_N	17	99	85.7	1.30E−22
282	CGPG5656	Gln-synt_C	105	358	528.1	8.50E−156
283	CGPG5659	Aminotran_3	35	361	321.7	1.20E−93
284	CGPG5661	PK	1	345	702	3.80E−208
284	CGPG5661	PK_C	355	469	115.4	1.50E−31
285	CGPG5684	Glycolytic	4	339	578.6	5.60E−171
286	CGPG5694	TIM	4	246	465.9	4.50E−137
287	CGPG5704	NDK	2	136	329	7.30E−96
288	CGPG5714	NDK	4	138	266.4	5.20E−77
289	CGPG5721	Rib_5-P_isom_A	47	215	354.4	1.70E−103
290	CGPG5728	zf-CCCH	80	106	39.3	1.20E−08
291	CGPG5757	Sad1_UNC	203	330	195.6	1.00E−55
292	CGPG5764	Actin	11	140	36.4	6.60E−08
293	CGPG5783	TPT	272	442	71.5	2.40E−18
294	CGPG5791	AA_permease	114	588	704.9	5.40E−209
295	CGPG5799	Aa_trans	206	601	453	3.60E−133
296	CGPG5856	Pkinase	79	353	159.5	8.00E−45
296	CGPG5856	Pkinase_Tyr	79	353	149.4	9.00E−42
297	CGPG5927	AAA	58	248	252.4	8.70E−73
297	CGPG5927	AAA	322	510	290.8	2.40E−84
298	CGPG5941	PfkB	42	336	86.2	9.00E−23
299	CGPG5957	CBM_20	86	178	23	5.70E−07
300	CGPG5967	DUF822	2	147	307.1	2.90E−89
301	CGPG6040	LEA_3	1	88	178.7	1.30E−50
302	CGPG607	PurA	28	275	44.4	5.80E−12
303	CGPG6178	DUF1336	53	267	427.9	1.30E−125
304	CGPG6185	UQ_con	7	148	197.9	2.10E−56
305	CGPG6306	APC8	1	161	401.5	1.10E−117
305	CGPG6306	TPR_1	339	372	34.7	2.90E−07
305	CGPG6306	TPR_2	339	372	23.8	0.00058
305	CGPG6306	TPR_2	373	406	23.7	0.00062
305	CGPG6306	TPR_1	373	406	34.1	4.40E−07
305	CGPG6306	TPR_2	407	440	22	0.0019
305	CGPG6306	TPR_1	407	440	24.3	0.00039
306	CGPG6318	MFS_1	31	496	35.3	1.90E−07
306	CGPG6318	PTR2	92	484	208.6	1.30E−59
307	CGPG6326	Kelch_1	34	79	45	2.40E−10
307	CGPG6326	Kelch_2	34	79	43.5	6.80E−10
307	CGPG6326	Kelch_1	152	198	26.7	7.70E−05
307	CGPG6326	Kelch_2	152	198	32.1	1.80E−06
307	CGPG6326	Kelch_2	203	249	20.2	0.0067
307	CGPG6326	Kelch_1	204	248	7.9	0.45
308	CGPG6370	Gp_dh_N	3	151	326	5.80E−95
308	CGPG6370	Gp_dh_C	156	313	362	8.80E−106
309	CGPG6429	ADH_N	25	135	159.4	8.40E−45
309	CGPG6429	ADH_zinc_N	166	305	105.1	1.90E−28
310	CGPG6440	PK	1	345	789.4	1.90E−234
310	CGPG6440	PK_C	357	471	167.5	3.10E−47
310	CGPG6440	PEP-utilizers	486	575	134	3.60E−37
311	CGPG6516	Aldedh	19	478	778.3	4.10E−231
312	CGPG6653	LRRNT_2	23	66	49.3	1.20E−11
312	CGPG6653	LRR_1	71	93	12.1	1.4
312	CGPG6653	LRR_1	95	117	10.5	2.8
312	CGPG6653	LRR_1	119	142	13	0.93
312	CGPG6653	LRR_1	144	166	19.5	0.011
312	CGPG6653	LRR_1	168	190	10.6	2.7
312	CGPG6653	LRR_1	192	214	8.8	5.7
312	CGPG6653	LRR_1	289	311	17.4	0.046
312	CGPG6653	LRR_1	313	335	10.8	2.4
312	CGPG6653	LRR_1	337	359	10.7	2.5
312	CGPG6653	LRR_1	361	384	12	1.5
312	CGPG6653	LRR_1	409	431	10.4	2.9
312	CGPG6653	LRR_1	457	479	11.9	1.5
312	CGPG6653	LRR_1	481	503	10.4	3
312	CGPG6653	LRR_1	505	527	10.5	2.8
312	CGPG6653	LRR_1	529	551	11.1	2.2
312	CGPG6653	LRR_1	553	575	9.3	4.7
312	CGPG6653	LRR_1	577	598	11.1	2.1
312	CGPG6653	Pkinase	695	966	134.8	2.20E−37
312	CGPG6653	Pkinase_Tyr	695	966	134.5	2.60E−37
313	CGPG6712	PGAM	91	277	154.6	2.30E−43

TABLE 16-continued

PEP SEQ ID NO	GENE ID	Pfam domain name	begin	stop	score	E-value
314	CGPG6737	PGAM	92	253	173	6.80E−49
315	CGPG6747	FBPase	106	429	448.6	7.20E−132
316	CGPG6796	Alpha-amylase	14	452	199.5	7.00E−57
318	CGPG6810	GH3	12	561	1261.5	0
320	CGPG6953	Ank	121	153	50.4	5.60E−12
321	CGPG7121	L51_S25_CI-B8	20	93	108.9	1.40E−29
322	CGPG7163	Prenylcys_lyase	149	500	788	5.20E−234
324	CGPG7206	Aldo_ket_red	14	298	389.4	4.80E−114
325	CGPG7225	Subtilisin_N	48	125	84.3	3.30E−22
326	CGPG7267	DUF588	34	164	154.6	2.40E−43
327	CGPG7272	DUF1005	50	254	524.8	8.50E−155
328	CGPG7281	FA_hydroxylase	86	229	361.9	9.30E−106
329	CGPG7308	CoA_binding	1	100	−10.8	0.04
329	CGPG7308	NAD_Gly3P_dh_N	4	147	−0.6	2.00E−06
329	CGPG7308	F420_oxidored	5	251	282.5	7.50E−82
330	CGPG7316	Anti-silence	1	155	419.9	3.20E−123
331	CGPG7371	Response_reg	29	157	94.8	2.30E−25
332	CGPG7457	PfkB	114	408	146.6	6.00E−41
335	CGPG7636	LSM	13	81	78.2	2.40E−20
338	CGPG7804	FAR1	62	279	364.9	1.20E−106
338	CGPG7804	SWIM	556	589	37.3	4.90E−08
339	CGPG7823	Rotamase	104	188	91.8	1.90E−24
339	CGPG7823	Rhodanese	203	298	44.1	4.40E−10
340	CGPG7828	DnaJ	12	81	66.1	1.00E−16
340	CGPG7828	zf-CSL	96	174	25.2	0.00021
343	CGPG7986	F-box	48	96	31.2	3.40E−06
343	CGPG7986	LRR_1	189	216	9	5.4
343	CGPG7986	LRR_1	428	451	8.2	7.7
343	CGPG7986	LRR_1	561	584	8.4	6.9
345	CGPG8015	zf-CCHC	18	35	24.2	7.90E−05
349	CGPG8083	Tryp_alpha_amyl	28	105	37.6	3.90E−08
350	CGPG8106	BURP	56	280	380	3.20E−111
353	CGPG8152	PAP_fibrillin	9	124	45.9	1.20E−10
354	CGPG8166	PBD	118	166	49.9	7.80E−12
355	CGPG8377	Oleosin	30	109	55	2.20E−13
356	CGPG8976	Ceramidase_alk	50	795	1545.5	0
357	CGPG8987	FH2	439	839	552.9	3.10E−163
358	CGPG9013	NAD_binding_1	234	350	138.6	1.50E−38
359	CGPG9080	EGF_CA	315	357	42.2	1.60E−09
359	CGPG9080	Pkinase	433	716	120.3	4.90E−33
359	CGPG9080	Pkinase_Tyr	433	704	113.1	7.40E−31
360	CGPG9081	DUF676	30	247	319	7.50E−93
361	CGPG9130	MMR_HSR1	266	369	71.9	1.80E−18
362	CGPG9133	PPR	125	159	13.2	0.19
362	CGPG9133	PPR	161	195	2.8	3.2
362	CGPG9133	PPR	196	230	22.7	0.0012
362	CGPG9133	PPR	232	266	42.1	1.70E−09
362	CGPG9133	PPR	267	301	29.4	1.20E−05
362	CGPG9133	PPR	302	336	49.4	1.10E−11
362	CGPG9133	PPR	337	371	32.9	1.00E−06
362	CGPG9133	PPR	372	407	7.9	0.8
362	CGPG9133	PPR	408	442	49.7	8.80E−12
362	CGPG9133	PPR	443	477	22.6	0.0013
362	CGPG9133	PPR	478	512	37.8	3.40E−08
362	CGPG9133	PPR	513	547	42.9	1.00E−09
362	CGPG9133	PPR	548	582	30.2	6.70E−06
362	CGPG9133	PPR	583	617	38.4	2.20E−08
363	CGPG9134	HD	91	232	46.2	1.00E−10
364	CGPG9137	RrnaAD	65	337	122.2	1.30E−33
365	CGPG9141	Pantoate_transf	40	306	402.9	4.40E−118
366	CGPG9145	Lung_7-TM_R	168	423	385.2	8.80E−113
367	CGPG9147	DNA_pol_E_B	178	389	249.9	5.00E−72
368	CGPG9148	p450	36	502	128.8	1.40E−35
369	CGPG9155	Pkinase	86	347	56.9	6.10E−14
369	CGPG9155	Pkinase_Tyr	86	351	73.7	2.90E−20
370	CGPG9163	Na_H_Exchanger	12	378	280.1	3.80E−81
370	CGPG9163	TrkA_N	416	531	118.8	1.50E−32
371	CGPG9170	Complex1_30 kDa	90	158	103.8	4.70E−28
371	CGPG9170	Complex1_49 kDa	298	537	2.8	6.10E−13
373	CGPG9183	HTH_11	1	56	72.4	1.30E−18
373	CGPG9183	BPL_LipA_LipB	84	182	94.5	2.90E−25
373	CGPG9183	BPL_C	275	322	43.3	7.80E−10
374	CGPG9186	DHBP_synthase	8	203	370.6	2.20E−108

TABLE 16-continued

PEP SEQ ID NO	GENE ID	Pfam domain name	begin	stop	score	E-value
374	CGPG9186	GTP_cyclohydro2	208	366	−2.3	3.80E−10
375	CGPG9205	NTP_transferase	4	288	421	1.50E−123
375	CGPG9205	MannoseP_isomer	299	465	350.8	2.00E−102
375	CGPG9205	Cupin_2	380	450	55.3	1.80E−13
376	CGPG9207	HTH_11	6	59	50.9	3.90E−12
376	CGPG9207	BPL_LipA_LipB	83	180	104.5	2.80E−28
376	CGPG9207	BPL_C	271	317	46.5	8.50E−11
377	CGPG9219	Complex1_30 kDa	107	175	99.8	7.60E−27
377	CGPG9219	Complex1_49 kDa	311	537	−11.6	5.90E−12
378	CGPG9220	GDC-P	3	443	700.9	8.30E−208
379	CGPG9230	Peptidase_S10	88	488	657.2	1.20E−194
381	CGPG9238	Tryp_alpha_amyl	36	114	56	1.20E−13
382	CGPG9259	Mit_rib_S27	14	93	135.3	1.50E−37
383	CGPG9271	NPH3	215	418	189.9	5.60E−54
384	CGPG9275	ETC_C1_NDUFA5	35	91	112.8	9.00E−31
386	CGPG9283	DUF1195	6	161	180.3	4.30E−51
387	CGPG9309	MAP65_ASE1	38	575	52.8	1.10E−12
389	CGPG9322	Pkinase	103	383	170	5.40E−48
389	CGPG9322	Pkinase_Tyr	103	383	158.7	1.30E−44
390	CGPG9335	Sugar_tr	7	726	210.6	3.30E−60
390	CGPG9335	MFS_1	11	685	107.7	3.00E−29
391	CGPG9341	RMMBL	531	573	35.9	1.20E−07
392	CGPG9344	TPR_2	531	564	23.9	0.00051
393	CGPG9345	UPF0261	5	432	483.7	2.00E−142
394	CGPG976	Glyco_transf_8	216	533	401.3	1.30E−117

TABLE 17

Pfam domain name	accession number	gathering cutoff	domain description
14-3-3	PF00244.9	25	14-3-3 protein
2-Hacid_dh	PF00389.19	11.2	D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
2-Hacid_dh_C	PF02826.7	−82.2	D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain
AAA	PF00004.18	12.3	ATPase family associated with various cellular activities (AAA)
AA_permease	PF00324.10	−120.8	Amino acid permease
ACT	PF01842.13	0	ACT domain
ADH_N	PF08240.2	−14.5	Alcohol dehydrogenase GroES-like domain
ADH_zinc_N	PF00107.16	23.8	Zinc-binding dehydrogenase
APC8	PF04049.3	−19.8	Anaphase promoting complex subunit 8/ Cdc23
Aa_trans	PF01490.7	−128.4	Transmembrane amino acid transporter protein
Actin	PF00022.8	−30	Actin
Aldedh	PF00171.11	−209.3	Aldehde dehydrogenase family
Aldo_ket_red	PF00248.10	−97	Aldo/keto reductase family
Allene_ox_cyc	PF06351.2	25	Allene oxide cyclase
Alpha-amylase	PF00128.12	−93	Alpha amylase, catalytic domain
Aminotran_1_2	PF00155.10	−57.5	Aminotransferase class I and II
Aminotran_3	PF00202.10	−207.6	Aminotransferase class-III
Ank	PF00023.18	0	Ankyrin repeat
Anti-silence	PF04729.4	25	Anti-silencing protein, ASF1-like
ArfGap	PF01412.8	−17	Putative GTPase activating protein for Arf
Asp	PF00026.13	−186.1	Eukaryotic aspartyl protease
Auxin_inducible	PF02519.4	−15	Auxin responsive protein
BPL_C	PF02237.6	16	Biotin protein ligase C terminal domain
BPL_LipA_LipB	PF03099.8	−0.2	Biotin/lipoate A/B protein ligase family
BURP	PF03181.5	−52	BURP domain
B_lectin	PF01453.14	28.2	D-mannose binding lectin
BolA	PF01722.7	23	BolA-like protein
C2	PF00168.18	3.7	C2 domain
CBM_20	PF00686.9	−3	Starch binding domain
CMAS	PF02353.10	−177.9	Cyclopropane-fatty-acyl-phospholipid synthase
Ceramidase_alk	PF04734.3	25	Neutral/alkaline non-lysosomal ceramidase
CoA_binding	PF02629.8	−12.8	CoA binding domain

TABLE 17-continued

Pfam domain name	accession number	gathering cutoff	domain description
Complex1_30kDa	PF00329.8	−3	Respiratory-chain NADH dehydrogenase, 30 Kd subunit
Complex1_49kDa	PF00346.8	−108	Respiratory-chain NADH dehydrogenase, 49 Kd subunit
Cupin_2	PF07883.1	16.6	Cupin domain
Cupin_3	PF05899.2	4.4	Protein of unknown function (DUF861)
Cyclin_C	PF02984.8	−13	Cyclin, C-terminal domain
Cyclin_N	PF00134.13	−14.7	Cyclin, N-terminal domain
DHBP_synthase	PF00926.10	−116	3,4-dihydroxy-2-butanone 4-phosphate synthase
DNA_pol_E_B	PF04042.5	−47.5	DNA polymerase alpha/epsilon subunit B
DUF1005	PF06219.2	25	Protein of unknown function (DUF1005)
DUF1191	PF06697.2	25	Protein of unknown function (DUF1191)
DUF1195	PF06708.1	25	Protein of unknown function (DUF1195)
DUF1336	PF07059.2	−78.2	Protein of unknown function (DUF1336)
DUF26	PF01657.7	0	Domain of unknown function DUF26
DUF298	PF03556.6	25	Domain of unknown function (DUF298)
DUF588	PF04535.2	25	Domain of unknown function (DUF588)
DUF676	PF05057.4	−60.7	Putative serine esterase (DUF676)
DUF822	PF05687.3	25	Plant protein of unknown function (DUF822)
DUF868	PF05910.2	25	Plant protein of unknown function (DUF868)
DnaJ	PF00226.19	−8	DnaJ domain
EGF_CA	PF07645.4	24.5	Calcium binding EGF domain
ESCRT-III	PF03357.10	−35.4	ESCRT-III complex subunit
ETC_C1_NDUFA5	PF04716.3	25	ETC complex I subunit conserved region
F-box	PF00646.21	13.6	F-box domain
F420_oxidored	PF03807.6	−34.5	NADP oxidoreductase coenzyme F420-dependent
FAR1	PF03101.4	0	FAR1 family
FA_hydroxylase	PF04116.2	−64.1	Fatty acid hydroxylase
FBPase	PF00316.10	−170.3	Fructose-1-6-bisphosphatase
FH2	PF02181.13	−98.3	Formin Homology 2 Domain
GDC-P	PF02347.5	−306.2	Glycine cleavage system P-protein
GH3	PF03321.3	−336	GH3 auxin-responsive promoter
GTP_cyclohydro2	PF00925.11	−49	GTP cyclohydrolase II
Gln-synt_C	PF00120.14	−124	Glutamine synthetase, catalytic domain
Gln-synt_N	PF03951.9	9	Glutamine synthetase, beta-Grasp domain
Glyco_transf_8	PF01501.9	−43.2	Glycosyl transferase family 8
Glycolytic	PF00274.9	−174.5	Fructose-bisphosphate aldolase class-I
Gp_dh_C	PF02800.9	−64.1	Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain
Gp_dh_N	PF00044.12	−74.2	Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain
HD	PF01966.11	18	HD domain
HLH	PF00010.15	8.2	Helix-loop-helix DNA-binding domain
HTH_11	PF08279.1	11.3	HTH domain
Histone	PF00125.13	17.4	Core histone H2A/H2B/H3/H4
Kelch_1	PF01344.14	7.8	Kelch motif
Kelch_2	PF07646.4	14	Kelch motif
L51_S25_CI-B8	PF05047.5	25	Mitochondrial ribosomal protein L51/S25/CI-B8 domain
LEA_3	PF03242.3	25	Late embryogenesis abundant protein
LMBR1	PF04791.5	−116.3	LMBR1-like membrane protein
LRRNT_2	PF08263.2	18.6	Leucine rich repeat N-terminal domain
LRR_1	PF00560.21	7.7	Leucine Rich Repeat
LSM	PF01423.12	13.7	LSM domain
Lung_7-TM_R	PF06814.3	25	Lung seven transmembrane receptor
MAP65_ASE1	PF03999.2	−134.8	Microtubule associated protein (MAP65/ASE1 family)
MFS_1	PF07690.5	23.5	Major Facilitator Superfamily
MMR_HSR1	PF01926.11	31.2	GTPase of unknown function
MannoseP_isomer	PF01050.8	−70	Mannose-6-phosphate isomerase
Metalloenzyme	PF01676.7	−14.4	Metalloenzyme superfamily
Metallophos	PF00149.17	22	Calcineurin-like phosphoesterase
Methyltransf_11	PF08241.1	17.1	Methyltransferase domain
Methyltransf_12	PF08242.1	21.4	Methyltransferase domain
Mit_rib_S27	PF08293.1	25	Mitochondrial ribosomal subunit S27
MtN3_slv	PF03083.5	−0.8	MtN3/saliva family
NAD_Gly3P_dh_N	PF01210.12	−44	NAD-dependent glycerol-3-phosphate dehydrogenase N-terminus
NAD_binding_1	PF00175.10	−3.9	Oxidoreductase NAD-binding domain
NAF	PF03822.4	4.5	NAF domain
NDK	PF00334.9	−59.9	Nucleoside diphosphate kinase

TABLE 17-continued

Pfam domain name	accession number	gathering cutoff	domain description
NPH3	PF03000.4	25	NPH3 family
NTP_transferase	PF00483.12	−90.5	Nucleotidyl transferase
Na_H_Exchanger	PF00999.10	−67.9	Sodium/hydrogen exchanger family
ORMDL	PF04061.4	25	ORMDL family
Oleosin	PF01277.7	−27	Oleosin
PAN_2	PF08276.2	−4.9	PAN-like domain
PAP_fibrillin	PF04755.2	25	PAP_fibrillin
PBD	PF00786.17	12.2	P21-Rho-binding domain
PCI	PF01399.15	25	PCI domain
PEP-utilizers	PF00391.12	10	PEP-utilising enzyme, mobile domain
PGAM	PF00300.12	−3	Phosphoglycerate mutase family
PK	PF00224.10	−244	Pyruvate kinase, barrel domain
PK_C	PF02887.5	−44	Pyruvate kinase, alpha/beta domain
PPR	PF01535.11	0	PPR repeat
PTR2	PF00854.12	−50	POT family
Pantoate_transf	PF02548.5	−93	Ketopantoate hydroxymethyltransferase
Peptidase_S10	PF00450.11	−198	Serine carboxypeptidase
PfkB	PF00294.13	−67.8	pfkB family carbohydrate kinase
Phosphorylase	PF00343.9	−601.1	Carbohydrate phosphorylase
Pkinase	PF00069.14	−70.8	Protein kinase domain
Pkinase_Tyr	PF07714.5	65	Protein tyrosine kinase
Prenylcys_lyase	PF07156.3	−164.1	Prenylcysteine lyase
PurA	PF04845.3	25	PurA ssDNA and RNA-binding protein
RMMBL	PF07521.1	18.5	RNA-metabolising metallo-beta-lactamase
Response_reg	PF00072.12	4	Response regulator receiver domain
Rhodanese	PF00581.9	25	Rhodanese-like domain
Rib_5-P_isom_A	PF06026.4	25	Ribose 5-phosphate isomerase A (phosphoriboisomerase A)
Ribonuclease_T2	PF00445.8	−53	Ribonuclease T2 family
Ribosomal_S8e	PF01201.11	25	Ribosomal protein S8e
Rotamase	PF00639.10	4	PPIC-type PPIASE domain
RrnaAD	PF00398.9	−73.3	Ribosomal RNA adenine dimethylase
SAM_1	PF00536.18	11.3	SAM domain (Sterile alpha motif)
SMC_N	PF02463.8	−95.8	RecF/RecN/SMC N terminal domain
SNF5	PF04855.3	25	SNF5/SMARCB1/INI1
SWIB	PF02201.9	−7	SWIB/MDM2 domain
SWIM	PF04434.7	10	SWIM zinc finger
S_locus_glycop	PF00954.11	−12.7	S-locus glycoprotein family
Sad1_UNC	PF07738.2	−20.4	Sad1/UNC-like C-terminal
Sterol_MT_C	PF08498.1	30.5	Sterol methyltransferase C-terminal
Subtilisin_N	PF05922.6	26.1	Subtilisin N-terminal Region
Sugar_tr	PF00083.13	−85	Sugar (and other) transporter
TFIIA	PF03153.4	25	Transcription factor IIA, alpha/beta subunit
TFIIS_C	PF01096.9	15	Transcription factor S-II (TFIIS)
TFIIS_M	PF07500.3	7.4	Transcription factor S-II (TFIIS), central domain
TIM	PF00121.8	−97	Triosephosphate isomerase
TPR_1	PF00515.16	7.7	Tetratricopeptide repeat
TPR_2	PF07719.5	20.1	Tetratricopeptide repeat
TPT	PF03151.7	−15.3	Triose-phosphate Transporter family
Thioredoxin	PF00085.9	−25.7	Thioredoxin
Tim17	PF02466.8	2.7	Tim17/Tim22/Tim23 family
TrkA_N	PF02254.7	4.7	TrkA-N domain
Tryp_alpha_amyl	PF00234.10	−4	Protease inhibitor/seed storage/LTP family
UPF0261	PF06792.1	25	Uncharacterised protein family (UPF0261)
UQ_con	PF00179.16	−30	Ubiquitin-conjugating enzyme
Usp	PF00582.16	36.1	Universal stress protein family
WD40	PF00400.20	21.5	WD domain, G-beta repeat
adh_short	PF00106.14	−17	short chain dehydrogenase
elF-4B	PF06273.1	−205.7	Plant specific eukaryotic initiation factor 4B
iPGM_N	PF06415.3	−263.4	BPG-independent PGAM N-terminus (iPGM_N)
p450	PF00067.11	−105	Cytochrome P450
zf-AN1	PF01428.6	0	AN1-like Zinc finger
zf-C3HC4	PF00097.13	16.9	Zinc finger, C3HC4 type (RING finger)
zf-CCCH	PF00642.14	0	Zinc finger C-x8-C-x5-C-x3-H type (and similar)
zf-CCHC	PF00098.12	17.9	Zinc knuckle
zf-CSL	PF05207.3	2.9	CSL zinc finger

Example 5

Plasmid Contraction for Transferring Recombinant DNA

[0201] This example illustrates the construction of plasmids for transferring recombinant DNA into the nucleus of a plant cell which can be regenerated into a transgenic crop plant of this invention. Primers for PCR amplification of protein coding nucleotides of recombinant DNA are designed at or near the start and stop codons of the coding sequence, in order to eliminate most of the 5' and 3' untranslated regions. DNA of interest, i.e. each DNA identified in Table 1 and the DNA for the identified homologous genes, are cloned and amplified by PCR prior to insertion into the insertion site the base vector.

[0202] A. Corn Transformation Vector

[0203] Elements of an exemplary common expression vector, pMON93093 are illustrated in Table 18. The exemplary base vector which is especially useful for corn transformation is illustrated in FIG. **2** and assembled using technology known in the art. The DNA of interest are inserted in a expression vector at the insertion site between the intron1 of rice act 1 gene and the termination sequence of PinII gene.

TABLE 18

pMON93093

function	name	annotation	Coordinates of SEQ ID NO: 19940
Agro transforamtion	B-AGRtu.right border	Agro right border sequence, essential for transfer of T-DNA.	11364-11720
Gene of interest expression cassette	E-Os.Act1	upstream promoter region of the rice actin 1 gene	19-775
	E-CaMV.35S.2xA1-B3	duplicated35S A1-B3 domain without TATA box	788-1120
	P-Os.Act1	promoter region of the rice actin 1 gene	1125-1204
	L-Ta.Lhcb1	5' untranslated leader of wheat major chlorophyll a/b binding protein	1210-1270
	I-Os.Act1	first intron and flanking UTR exon sequences from the rice actin 1 gene	1287-1766
	T-St.Pis4	3' non-translated region of the potato proteinase inhibitor II gene which functions to direct polyadenylation of the mRNA	1838-2780
Plant selectable marker expression cassette	P-Os.Act1	Promoter from the rice actin 1 gene	2830-3670
	L-Os.Act1	first exon of the rice actin 1 gene	3671-3750
	I-Os.Act1	first intron and flanking UTR exon sequences from the rice actin 1 gene	3751-4228
	TS-At.ShkG-CTP2	Transit peptide region of Arabidopsis EPSPS	4238-4465
	CR-AGRtu.aroA-CP4.nat	Synthetic CP4 coding region with dicot preferred codon usage.	4466-5833
	T-AGRtu.nos	A 3' non-translated region of the nopaline synthase gene of Agrobacterium tumefaciens Ti plasmid which functions to direct polyadenylation of the mRNA.	5849-6101
Agro transformation	B-AGRtu.left border	Agro left border sequence, essential for transfer of T-DNA.	6168-6609
Maintenance in *E. coli*	OR-Ec.oriV-RK2	The vegetative origin of replication from plasmid RK2.	6696-7092

TABLE 18-continued

pMON93093			
function	name	annotation	Coordinates of SEQ ID NO: 19940
	CR-Ec.rop	Coding region for repressor of primer from the ColE1 plasmid. Expression of this gene product interferes with primer binding at the origin of replication, keeping plasmid copy number low.	8601-8792
	OR-Ec.ori-ColE1	The minimal origin of replication from the *E. coli* plasmid ColE1.	9220-9808
	P-Ec.aadA-SPC/STR	romoter for Tn7 adenylyltransferase (AAD(3"))	10339-10380
	CR-Ec.aadA-SPC/STR	Coding region for Tn7 adenylyltransferase (AAD(3")) conferring spectinomycin and streptomycin resistance.	10381-11169
	T-Ec.aadA-SPC/STR	3' UTR from the Tn7 adenylyltransferase (AAD(3")) gene of *E. coli*.	11170-11227

[0204] B. Soybean Transformation Vector

[0205] Plasmids for use in transformation of soybean are also prepared. Elements of an exemplary common expression vector plasmid pMON82053 are shown in Table 19 below. This exemplary soybean or canola transformation base vector illustrated in FIG. **3** is assembled using the technology known in the art. Recombinant DNA of interest, i.e. each DNA identified in Table 1 and the DNA for the identified homologous genes, is cloned and amplified by PCR prior to insertion into the insertion site the base vector at the insertion site between the enhanced 35S CaMV promoter and the termination sequence of cotton E6 gene.

TABLE 19

pMON82053			
function	name	annotation	Coordinates of SEQ ID NO: 19941
Agro transforamtion	B-AGRtu.left border	Agro left border sequence, essential for transfer of T-DNA.	6144-6585
Plant selectable marker expression cassette	P-At.Act7	Promoter from the *arabidopsis* actin 7 gene	6624-7861
	L-At.Act7	5'UTR of *Arabidopsis* Act7 gene	
	I-At.Act7	Intron from the *Arabidopsis* actin7 gene	
	TS-At.ShkG-CTP2	Transit peptide region of *Arabidopsis* EPSPS	7864-8091
	CR-AGRtu.aroA-CP4.nno_At	Synthetic CP4 coding region with dicot preferred codon usage.	8092-9459
	T-AGRtu.nos	A 3' non-translated region of the nopaline synthase gene of *Agrobacterium tumefaciens* Ti plasmid which functions to direct polyadenylation of the mRNA.	9466-9718
Gene of interest expression cassette	P-CaMV.35S-enh	Promoter for 35S RNA from CaMV containing a duplication of the −90 to −350 region.	1-613
	T-Gb.E6-3b	3' untranslated region from the fiber protein E6 gene of sea-island cotton;	688-1002
Agro transformation	B-AGRtu.right border	Agro right border sequence, essential for transfer of T-DNA.	1033-1389
Maintenance in *E. coli*	OR-Ec.oriV-RK2	The vegetative origin of replication from plasmid RK2.	5661-6057

TABLE 19-continued

pMON82053			
function	name	annotation	Coordinates of SEQ ID NO: 19941
	CR-Ec.rop	Coding region for repressor of primer from the ColE1 plasmid. Expression of this gene product interferes with primer binding at the origin of replication, keeping plasmid copy number low.	3961-4152
	OR-Ec.ori-ColE1	The minimal origin of replication from the *E. coli* plasmid ColE1.	2945-3533
	P-Ec.aadA-SPC/STR	romoter for Tn7 adenylyltransferase (AAD(3"))	2373-2414
	CR-Ec.aadA-SPC/STR	Coding region for Tn7 adenylyltransferase (AAD(3")) conferring spectinomycin and streptomycin resistance.	1584-2372
	T-Ec.aadA-SPC/STR	3' UTR from the Tn7 adenylyltransferase (AAD(3")) gene of *E. coli*.	1526-1583

[0206] C. Cotton Transformation Vector

[0207] Plasmids for use in transformation of cotton are also prepared. Elements of an exemplary common expression vector plasmid pMON99053 are shown in Table 20 below and FIG. **4**. Primers for PCR amplification of protein coding nucleotides of recombinant DNA are designed at or near the start and stop codons of the coding sequence, in order to eliminate most of the 5' and 3' untranslated regions. Each recombinant DNA coding for a protein identified in Table 1 is amplified by PCR prior to insertion into the insertion site within the gene of interest expression cassette of one of the base.

TABLE 20

function	name	annotation	Coordinates of SEQ ID NO: 19942
Agro transforamtion	B-AGRtu.right border	Agro right border sequence, essential for transfer of T-DNA.	11364-11720
Gene of interest expression cassette	Exp-CaMV.35S-enh + ph.DnaK	Enhanced version of the 35S RNA promoter from CaMV plus the petunia hsp70 5' untranslated region	7794-8497
	T-Ps.RbcS2-E9	The 3' non-translated region of the pea RbcS2 gene which functions to direct polyadenylation of the mRNA.	67-699
Plant selectable marker expression cassette	Exp-CaMV.35S	Promoter and 5' untranslated region of the 35S RNA from CaMV	730-1053
	CR-Ec.nptII-Tn5	Neomycin Phosphotransferase II gene that confers resistance to neomycin and kanamycin	1087-1881
	T-AGRtu.nos	A 3' non-translated region of the nopaline synthase gene of *Agrobacterium tumefaciens* Ti plasmid which functions to direct polyadenylation of the mRNA.	1913-2165
Agro transformation	B-AGRtu.left border	Agro left border sequence, essential for transfer of T-DNA.	2211-2652
Maintenance in *E. coli*	OR-Ec.oriV-RK2	The vegetative origin of replication from plasmid RK2.	2739-3135
	CR-Ec.rop	Coding region for repressor of primer from the ColE1 plasmid. Expression of this	4644-4835

TABLE 20-continued

function	name	annotation	Coordinates of SEQ ID NO: 19942
		gene product interferes with primer binding at the origin of replication, keeping plasmid copy number low.	
	OR-Ec.ori-ColE1	The minimal origin of replication from the *E. coli* plasmid ColE1.	5263-5851
	P-Ec.aadA-SPC/STR	romoter for Tn7 adenylyltransferase (AAD(3"))	6382-6423
	CR-Ec.aadA-SPC/STR	Coding region for Tn7 adenylyltransferase (AAD(3")) conferring spectinomycin and streptomycin resistance.	6424-7212
	T-Ec.aadA-SPC/STR	3' UTR from the Tn7 adenylyltransferase (AAD(3")) gene of *E. coli*.	7213-7270

Example 6

Corn Plant Transformation

[0208] This example illustrates the production and identification of transgenic corn cells in seed of transgenic corn plants having an enhanced agronomic trait, i.e. enhanced nitrogen use efficiency, increased yield, enhanced water use efficiency, enhanced tolerance to cold and/or improved seed compositions as compared to control plants. Transgenic corn cells are prepared with recombinant DNA expressing each of the protein encoding DNAs listed in Table 1 by *Agrobacterium*-mediated transformation using the corn transformation vectors pMON93093 as disclosed in Example 6. Corn transformation is effected using methods disclosed in U.S. Patent Application Publication 2004/0344075 A1 where corn embryos are inoculated and co-cultured with the *Agrobacterium tumefaciens* strain ABI and the corn transformation vector. To regenerate transgenic corn plants the transgenic callus resulting from transformation is placed on media to initiate shoot development in plantlets which are transferred to potting soil for initial growth in a growth chamber followed by a mist bench before transplanting to pots where plants are grown to maturity. The plants are self fertilized and seed is harvested for screening as seed, seedlings or progeny R2 plants or hybrids, e.g., for yield trials in the screens indicated above.

[0209] Many transgenic events which survive to fertile transgenic plants that produce seeds and progeny plants do not exhibit an enhanced agronomic trait. The transgenic plants and seeds having the transgenic cells of this invention which have recombinant DNA imparting the enhanced agronomic traits are identified by screening for nitrogen use efficiency, yield, water use efficiency, cold tolerance and improved seed composition.

Example 7

Soybean Plant Transformation

[0210] This example illustrates the production and identification of transgenic soybean cells in seed of transgenic soybean plants having an enhanced agronomic trait, i.e. enhanced nitrogen use efficiency, increased yield, enhanced water use efficiency, enhanced tolerance to cold and/or improved seed compositions as compared to control plants. Transgenic soybean cells are prepared with recombinant DNA expressing each of the protein encoding DNAs listed in Table 1 by *Agrobacterium*-mediated transformation using the soybean transformation vectors pMON82053 disclosed in Example 7. Soybean transformation is effected using methods disclosed in U.S. Pat. No. 6,384,301 where soybean meristem explants are wounded then inoculated and co-cultured with the soybean transformation vector, then transferred to selection media for 6-8 weeks to allow selection and growth of transgenic shoots.

[0211] The transformation is repeated for each of the protein encoding DNAs identified in Table 1.

[0212] Transgenic shoots producing roots are transferred to the greenhouse and potted in soil. Many transgenic events which survive to fertile transgenic plants that produce seeds and progeny plants do not exhibit an enhanced agronomic trait. The transgenic plants and seeds having the transgenic cells of this invention which have recombinant DNA imparting the enhanced agronomic traits are identified by screening for nitrogen use efficiency, yield, water use efficiency, cold tolerance and improved seed composition.

Example 8

Canola Transformation

[0213] This example illustrates plant transformation useful in producing the transgenic canola plants of this invention and the production and identification of transgenic seed for transgenic canola having enhanced water use efficiency, enhanced cold tolerance, increased yield, enhanced nitrogen use efficiency, enhanced seed protein and enhanced seed oil.

[0214] Tissues from in vitro grown canola seedlings are prepared and inoculated with overnight-grown *Agrobacterium* cells containing plasmid DNA with the gene of interest cassette and a plant selectable marker cassette. Following co-cultivation with *Agrobacterium*, the infected tissues are allowed to grow on selection to promote growth of transgenic shoots, followed by growth of roots from the transgenic shoots. The selected plantlets are then transferred to the greenhouse and potted in soil. Molecular characterization are

performed to confirm the presence of the gene of interest, and its expression in transgenic plants and progenies. Progeny transgenic plants are selected from a population of transgenic canola events under specified growing conditions and are compared with control canola plants. Control canola plants are substantially the same canola genotype but without the recombinant DNA, for example, either a parental canola plant of the same genotype that is not transformed with the identical recombinant DNA or a negative isoline of the transformed plant

[0215] Transgenic canola plant cells are transformed with recombinant DNA from each of the genes identified in Table 1. Transgenic progeny plants and seed of the transformed plant cells are screened for enhanced water use efficiency, enhanced cold tolerance, increased yield, enhanced nitrogen use efficiency, enhanced seed protein and enhanced seed oil as reported in Example 9.

Example 9

Selection of Transgenic Plants with Enhanced Agronomic Trait(s)

[0216] This example illustrates identification of nuclei of the invention by screening derived plants and seeds for an enhanced trait identified below.

[0217] Many transgenic events which survive to fertile transgenic plants that produce seeds and progeny plants will not exhibit an enhanced agronomic trait. Populations of transgenic seed and plants prepared in Examples 6 and 7 are screened to identify those transgenic events providing transgenic plant cells with a nucleus having recombinant DNA imparting an enhanced trait. Each population is screened for enhanced nitrogen use efficiency, increased yield, enhanced water use efficiency, enhanced tolerance to cold and heat, increased level of oil and protein in seed using assays described below. Plant cell nuclei having recombinant DNA with each of the genes identified in Table 1 and the identified homologs are identified in plants and seeds with at least one of the enhanced traits.

A. Selection for Enhanced Nitrogen Use Efficiency

[0218] Transgenic corn plants with nuclei of the invention are planted in fields with three levels of nitrogen (N) fertilizer being applied, i.e. low level (0 pounds per acre N), medium level (80 pounds per acre N) and high level (180 pounds per acre N). Liquid 28% or 32% UAN (Urea, Ammonium Nitrogen) are used as the N source and apply by broadcast boom and incorporate with a field cultivator with rear rolling basket in the same direction as intended crop rows. Although there is no N applied in the low level treatment, the soil should still be disturbed in the same fashion as the treated area. Transgenic plants and control plants can be grouped by genotype and construct with controls arranged randomly within genotype blocks. For improved statistical analysis each type of transgenic plant can be tested by 3 replications and across 4 locations. Nitrogen levels in the fields are analyzed before planting by collecting sample soil cores from 0-24" and 24 to 48" soil layer. Soil samples are analyzed for nitrate-nitrogen, phosphorus (P), potassium (K), organic matter and pH to provide baseline values. P, K and micronutrients are applied based upon soil test recommendations.

[0219] Transgenic corn plants prepared in Example 6 and which exhibit a 2 to 5% yield increase as compared to control plants when grown in the high nitrogen field are selected as having nuclei of the invention. Transgenic corn plants which have at least the same or higher yield as compared to control plants when grown in the medium nitrogen field are selected as having nuclei of the invention. Transgenic corn plants having a nucleus with DNA identified in Table 3 as imparting nitrogen use efficiency (LN) and homologous DNA are selected from a nitrogen use efficiency screen as having a nucleus of this invention.

B. Selection for Increased Yield

[0220] Many transgenic plants of this invention exhibit improved yield as compared to a control plant. Improved yield can result from enhanced seed sink potential, i.e. the number and size of endosperm cells or kernels and/or enhanced sink strength, i.e. the rate of starch biosynthesis. Sink potential can be established very early during kernel development, as endosperm cell number and size are determined within the first few days after pollination.

[0221] Much of the increase in corn yield of the past several decades has resulted from an increase in planting density. During that period, corn yield has been increasing at a rate of 2.1 bushels/acre/year, but the planting density has increased at a rate of 250 plants/acre/year. A characteristic of modern hybrid corn is the ability of these varieties to be planted at high density. Many studies have shown that a higher than current planting density should result in more biomass production, but current germplasm does not perform. well at these higher densities. One approach to increasing yield is to increase harvest index (HI), the proportion of biomass that is allocated to the kernel compared to total biomass, in high density plantings.

[0222] Effective yield selection of enhanced yielding transgenic corn events uses hybrid progeny of the transgenic event over multiple locations with plants grown under optimal production management practices, and maximum pest control. A useful target for improved yield is a 5% to 10% increase in yield as compared to yield produced by plants grown from seed for a control plant. Selection methods may be applied in multiple and diverse geographic locations, for example up to 16 or more locations, over one or more planting seasons, for example at least two planting seasons to statistically distinguish yield improvement from natural environmental effects. It is to plant multiple transgenic plants, positive and negative control plants, and pollinator plants in standard plots, for example 2 row plots, 20 feet long by 5 feet wide with 30 inches distance between rows and a 3 foot alley between ranges. Transgenic events can be grouped by recombinant DNA constructs with groups randomly placed in the field. A pollinator plot of a high quality corn line is planted for every two plots to allow open pollination when using male sterile transgenic events. A useful planting density is about 30,000 plants/acre. High planting density is greater than 30,000 plants/acre, preferably about 40,000 plants/acre, more preferably about 42,000 plants/acre, most preferably about 45,000 plants/acre. Each of the transgenic corn plants and soybean plants with a nucleus of the invention prepared in Examples 6 and 7 are screened for yield enhancement. At least one event from each of the corn and soybean plants is selected as having at least between 3 and 5% increase in yield as compared to a control plant as having a nucleus of this invention.

C. Selection for Enhanced Water Use Efficiency (WUE)

[0223] The following is a high-throughput method for screening for water use efficiency in a greenhouse to identify

the transgenic corn plants with a nucleus of this invention. This selection process imposes 3 drought/re-water cycles on plants over a total period of 15 days after an initial stress free growth period of 11 days. Each cycle consists of 5 days, with no water being applied for the first four days and a water quenching on the 5th day of the cycle. The primary phenotypes analyzed by the selection method are the changes in plant growth rate as determined by height and biomass during a vegetative drought treatment. The hydration status of the shoot tissues following the drought is also measured. The plant height are measured at three time points. The first is taken just prior to the onset drought when the plant is 11 days old, which is the shoot initial height (SIH). The plant height is also measured halfway throughout the drought/re-water regimen, on day 18 after planting, to give rise to the shoot mid-drought height (SMH). Upon the completion of the final drought cycle on day 26 after planting, the shoot portion of the plant is harvested and measured for a final height, which is the shoot wilt height (SWH) and also measured for shoot wilted biomass (SWM). The shoot is placed in water at 40 degree Celsius in the dark. Three days later, the shoot is weighted to give rise to the shoot turgid weight (STM). After drying in an oven for four days, the shoots are weighted for shoot dry biomass (SDM). The shoot average height (SAH) is the mean plant height across the 3 height measurements. The procedure described above may be adjusted for +/− ~one day for each step given the situation.

[0224] To correct for slight differences between plants, a size corrected growth value is derived from SIH and SWH. This is the Relative Growth Rate (RGR). Relative Growth Rate (RGR) is calculated for each shoot using the formula [RGR %=(SWH−SIH)/((SWH+SIH)/2)×100]. Relative water content (RWC) is a measurement of how much (%) of the plant was water at harvest. Water Content (RWC) is calculated for each shoot using the formula [RWC %=(SWM−SDM)/(STM−SDM)×100]. Fully watered corn plants of this age run around 98% RWC.

[0225] Transgenic corn plants and soybean plants prepared in Examples 6 and 7 are screened for water use efficiency. Transgenic plants having at least a 1% increase in RGR and RWC as compared to control plants are identified as having enhanced water used efficiency and are selected as having a nucleus of this invention. Transgenic corn and soybean plants having in their nucleus DNA identified in Table 3 as imparting drought tolerance improvement (DS) and homologous DNA are identified as showing increased water use efficiency as compared to control plants and are selected as having a nucleus of this invention.

D. Selection for Growth Under Cold Stress

[0226] Cold germination assay—Three sets of seeds are used for the assay. The first set consists of positive transgenic events (F1 hybrid) where the genes of the present invention are expressed in the seed. The second seed set is nontransgenic, wild-type negative control made from the same genotype as the transgenic events. The third set consisted of two cold tolerant and one cold sensitive commercial check lines of corn. All seeds are treated with a fungicide "Captan" (MAESTRO® 80DF Fungicide, Arvesta Corporation, San Francisco, Calif., USA). 0.43 mL Captan is applied per 45 g of corn seeds by mixing it well and drying the fungicide prior to the experiment.

[0227] Corn kernels are placed embryo side down on blotter paper within an individual cell (8.9×8.9 cm) of a germination tray (54×36 cm). Ten seeds from an event are placed into one cell of the germination tray. Each tray can hold 21 transgenic events and 3 replicates of wildtype (LH244SDms+LH59), which is randomized in a complete block design. For every event there are five replications (five trays). The trays are placed at 9.7 C for 24 days (no light) in a Convrion® growth chamber (Conviron Model PGV36, Controlled Environments, Winnipeg, Canada). Two hundred and fifty milliliters of deionized water are added to each germination tray. Germination counts are taken 10th, 11th, 12th, 13th, 14th, 17th, 19th, 21st, and 24th day after start date of the experiment. Seeds are considered germinated if the emerged radicle size is 1 cm. From the germination counts germination index is calculated.

[0228] The germination index is calculated as per:

$$\text{Germination index}=(\Sigma([T+1-n_i]*[P_i-P_{i-1}]))/T$$

where T is the total number of days for which the germination assay is performed. The number of days after planting is defined by n. "i" indicated the number of times the germination had been counted, including the current day. P is the percentage of seeds germinated during any given rating. Statistical differences are calculated between transgenic events and wild type control. After statistical analysis, the events that show a statistical significance at the p level of less than 0.1 relative to wild-type controls will advance to a secondary cold selection. The secondary cold screen is conducted in the same manner of the primary selection only increasing the number of repetitions to ten. Statistical analysis of the data from the secondary selection is conducted to identify the events that show a statistical significance at the p level of less than 0.05 relative to wild-type controls.

[0229] Transgenic corn plants and soybean plants prepared in Examples 6 and 7 are screened for water use efficiency. Transgenic plants having at least a 5% increase in germination index as compared to control plants are identified as having enhanced cold stress tolerance and are selected as having a nucleus of this invention. Transgenic corn and soybean plants having in their nucleus DNA identified in Table 3 as imparting cold tolerance improvement (CK or CS) and homologous DNA are identified as showing increased cold stress tolerance as compared to control plants and are selected as having a nucleus of this invention.

E. Screens for Transgenic Plant Seeds with Increased Protein and/or Oil Levels

[0230] The following is a high-throughput selection method for identifying plant seeds with improvement in seed composition using the Infratec® 1200 series Grain Analyzer, which is a near-infrared transmittance spectrometer used to determine the composition of a bulk seed sample. Near infrared analysis is a non-destructive, high-throughput method that can analyze multiple traits in a single sample scan. An NIR calibration for the analytes of interest is used to predict the values of an unknown sample. The NIR spectrum is obtained for the sample and compared to the calibration using a complex chemometric software package that provides a predicted values as well as information on how well the sample fits in the calibration.

[0231] Infratec® Model 1221, 1225, or 1227 analyzer with transport module by Foss North America is used with cuvette, item #1000-4033, Foss North America or for small samples with small cell cuvette, Foss standard cuvette modified by Leon Girard Co. Corn and soy check samples of varying composition maintained in check cell cuvettes are supplied

by Leon Girard Co. NIT collection software is provided by Maximum Consulting Inc. Calculations are performed automatically by the software. Seed samples are received in packets or containers with barcode labels from the customer. The seed is poured into the cuvettes and analyzed as received.

TABLE 21

Typical sample(s):	Whole grain corn and soybean seeds
Analytical time to run method:	Less than 0.75 min per sample
Total elapsed time per run:	1.5 minute per sample
Typical and minimum sample size:	Corn typical: 50 cc; minimum 30 cc Soybean typical: 50 cc; minimum 5 cc
Typical analytical range:	Determined in part by the specific calibration. Corn - moisture 5-15%, oil 5-20%, protein 5-30%, starch 50-75%, and density 1.0-1.3%. Soybean - moisture 5-15%, oil 15-25%, and protein 35-50%.

Transgenic corn plants and soybean plants prepared in Examples 6 and 7 are screened for increased protein and oil in seed. Transgenic inbred corn and soybean plants having an increase of at least 1 percentage point in the total percent seed protein or at least 0.3 percentage point in total seed oil and transgenic hybrid corn plants having an increase of at least 0.4 percentage point in the total percent seed protein as compared to control plants are identified as having enhanced seed protein or enhanced seed oil and are selected as having a nucleus of this invention.

Example 10

Cotton Transgenic Plants with Enhanced Agronomic Traits

[0232] Cotton transformation is performed as generally described in WO0036911 and in U.S. Pat. No. 5,846,797. Transgenic cotton plants containing each of the recombinant DNA having a sequence of SEQ ID NO: 1 through SEQ ID NO: 197 are obtained by transforming with recombinant DNA from each of the genes identified in Table 1. Progeny transgenic plants are selected from a population of transgenic cotton events under specified growing conditions and are compared with control cotton plants. Control cotton plants are substantially the same cotton genotype but without the recombinant DNA, for example, either a parental cotton plant of the same genotype that was not transformed with the identical recombinant DNA or a negative isoline of the transformed plant. Additionally, a commercial cotton cultivar adapted to the geographical region and cultivation conditions, i.e. cotton variety ST474, cotton variety FM 958, and cotton variety Siokra L-23, are used to compare the relative performance of the transgenic cotton plants containing the recombinant DNA. The specified culture conditions are growing a first set of transgenic and control plants under "wet" conditions, i.e. irrigated in the range of 85 to 100 percent of evapotranspiration to provide leaf water potential of −14 to −18 bars, and growing a second set of transgenic and control plants under "dry" conditions, i.e. irrigated in the range of 40 to 60 percent of evapotranspiration to provide a leaf water potential of −21 to −25 bars. Pest control, such as weed and insect control is applied equally to both wet and dry treatments as needed. Data gathered during the trial includes weather records throughout the growing season including detailed records of rainfall; soil characterization information; any herbicide or insecticide applications; any gross agronomic differences observed such as leaf morphology, branching habit, leaf color, time to flowering, and fruiting pattern; plant height at various points during the trial; stand density; node and fruit number including node above white flower and node above crack boll measurements; and visual wilt scoring. Cotton boll samples are taken and analyzed for lint fraction and fiber quality. The cotton is harvested at the normal harvest timeframe for the trial area. Enhanced water use efficiency is indicated by increased yield, improved relative water content, enhanced leaf water potential, increased biomass, enhanced leaf extension rates, and improved fiber parameters.

[0233] The transgenic cotton plants of this invention are identified from among the transgenic cotton plants by agronomic trait screening as having increased yield and enhanced water use efficiency.

Example 11

Monocot and Dicot Plant Transformation for the Suppression of Endogeneous Protein

[0234] This example illustrates monocot and dicot plant transformation to produce nuclei of this invention in cells of a transgenic plant by transformation where the recombinant DNA suppresses the expression of an endogenous protein identified by Pfam, SNF5, LMBR1, TFIIS_M, TFIIS_C, or Glyco_transf__8. Corn callus and soybean tissue are transformed as describe in Examples 6 and 7 using recombinant DNA in the nucleus with DNA that transcribes to RNA that forms double-stranded RNA targeted to an endogenous gene with DNA encoding the protein. The genes for which the double-stranded RNAs are targeted are the native gene in corn and soybean that are homolog of the genes encoding the protein with an amino acid sequence of SEQ ID NO:200, 201, 205, 207, 211, and 394.

[0235] Populations of transgenic corn plants and soybean plants prepared in Examples 6 and 7 with DNA for suppressing a gene identified in Table 3 as providing an enhanced trait by gene suppression are screened to identify an event from those plants with a nucleus of the invention by selecting the trait identified in this specification.

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20080295196A1). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

We claim:

1. A plant cell nucleus with stably integrated, recombinant DNA comprising a promoter that is functional in plant cells and that is operably linked to DNA from a plant, bacteria or yeast that encodes a protein having at least one domain of amino acids in a sequence that exceeds the Pfam gathering cutoff for amino acid sequence alignment with a protein domain family identified by a Pfam name selected from the group of Pfam names consisting of L51_S25_CI-B8, iPGM_N, WD40, BPL_LipA_LipB, DUF676, AAA, S_locus_glycop, ArfGap, Rotamase, Metallophos, CMAS, Sugar_tr, LMBR1, RmaAD, NAF, BolA, Pkinase, C2, FA_hydroxylase, p450, Complex1__30 kDa, Histone, DUF822, PEP-utilizers, PCI, ETC_C1_NDUFA5,2-Hacid_dh, Tryp_alpha_amyl, PK_C, MAP65_ASE1, FBPase, SWIB, Ank, Ribosomal_S8e, 2-Hacid_dh_C, SMC_N, GTP_cyclohydro2, PfkB, ORMDL, ADH_zinc_N, SWIM, TrkA_N, HLH, GH3, SNF5, Ceramidase_alk, Ribonuclease_T2, Complex1__49 kDa, Gp_dh_C, Aldo_ket_red, zf-AN1, TFIIS_C, MFS__1, Thioredoxin, DUF1005, LEA__3, Sterol_MT_C, Gp_dh_N, TFIIS_M, PAN__2, BPL_C, DUF26, Aa_trans, ACT, ADH_N, NAD_binding__1, Auxin_inducible, B_lectin, Anti-silence, Response_reg, 14-3-3, LRRNT__2, GDC-P, zf-CCHC, NPH3, TPR__1, TFIIA, DHBP_synthase, UQ_con, TPR__2, TPT, F-box, adh_short, Cyclin_C, Na_H_Exchanger, AA_permease, MtN3_slv, TIM, NDK, Pantoate_transf, Allene_ox_cyc, Cyclin_N, Methyltransf__1, CBM__20, Methyltransf__12, Rhodanese, Glycolytic, Actin, Usp, eIF-4B, Glyco_transf__8, BURP, Alpha-amylase, F420_oxidored, EGF_CA, Kelch__1, PGAM, Aminotran__1__2, Kelch__2, UPF0261, CoA_binding, DUF868, Peptidase_S10, Lung__7-TM_R, Oleosin, Sad1_UNC, Gln-synt_C, LSM, NTP_transferase, Metalloenzyme, Prenylcys_lyase, Subtilisin_N, SAM__1, DUF298, ESCRT-III, DNA_pol_E_B, Aminotran__3, NAD_Gly3P_dh_N, Gln-synt_N, MMR_HSR1, DUF588, zf-CCCH, DnaJ, Pkinase_Tyr, Cupin__2, LRR__1, Cupin__3, zf-CSL, FAR1, HD, FH2, APC8, PTR_2, MannoseP_isomer, Rib__5-P_isom_A, DUF1336, Phosphorylase, DUF1191, Asp, Mit_rib_S27, PAP_fibrillin, DUF1195, Aldedh, zf-C3HC4, PPR, PK, PurA, RMMBL, HTH__11, Tim17, and PBD wherein said Pfam gathering cutoff for said protein domain families are stated in Table 17; wherein said plant cell nucleus is selected by screening a population of transgenic plants that have said recombinant DNA and express said protein for an enhanced trait as compared to control plants that do not have said recombinant DNA in their nuclei; and wherein said enhanced trait is selected from group of enhanced traits consisting of enhanced water use efficiency, enhanced cold tolerance, enhanced heat tolerance, enhanced resistance to salt exposure, enhanced shade tolerance, increased yield, enhanced nitrogen use efficiency, enhanced seed protein and enhanced seed oil.

2. The plant cell nucleus of claim **1** wherein said protein has an amino acid sequence with at least 90% identity to a consensus amino acid sequence in the group of consensus amino acid sequences consisting of the consensus amino acid sequence constructed for SEQ ID NO: 198 and homologs thereof listed in Table 2 through the consensus amino acid sequence constructed for SEQ ID NO: 394 and homologs thereof listed in Table 2.

3. The plant cell nucleus of claim **1** wherein said protein is selected from the group of proteins identified in Table 1.

4. A plant cell nucleus with stably integrated, recombinant DNA to suppress the level of an endogenous protein having at least one domain of amino acids in a sequence that exceeds the Pfam gathering cutoff for amino acid sequence alignment with a protein domain family identified by Pfam name in the group of Pfam names consisting of SNF5, LMBR1, TFIIS_M, TFIIS_C, and Glyco_transf__8, wherein the Pfam gathering cutoff for said protein domain families is stated in Table 17 wherein said plant cell nucleus is selected by screening a population of transgenic plants with said recombinant DNA and have the level of said endogenous protein suppressed for an enhanced trait as compared to control plants that do not have said recombinant DNA; and wherein said enhanced trait is selected from the group of enhanced traits consisting of enhanced water use efficiency, enhanced cold tolerance, enhanced heat tolerance, enhanced resistance to salt exposure, enhanced shade tolerance, increased yield, enhanced nitrogen use efficiency, enhanced seed protein and enhanced seed oil.

5. The plant cell nucleus of claim **1** or **4** further comprising DNA expressing a protein that provides tolerance from exposure to an herbicide applied at levels that are lethal to a wild type of said plant cell.

6. The plant cell nucleus of claim **5** wherein the agent of said herbicide is a glyphosate, dicamba, or glufosinate compound.

7. A transgenic plant cell or plant comprising a plurality of plant cells with a plant cell nucleus of claim **1** or **4**.

8. The transgenic plant cell or plant of claim **7** which is homozygous for said recombinant DNA.

9. A transgenic seed comprising a plurality of plant cells with a plant cell nucleus of claim **1** or **4**.

10. The transgenic seed of claim **9** from a corn, soybean, cotton, canola, alfalfa, wheat or rice plant.

11. The transgenic corn seed of claim **10** wherein said seed can produce corn plants that are resistant to disease from the Mal de Rio Cuarto virus or the *Puccina sorghi* fungus or both.

12. A transgenic pollen grain comprising a haploid derivative of a plant cell nucleus of claim **1** or **4**.

13. A method for manufacturing non-natural, transgenic seed that can be used to produce a crop of transgenic plants with an enhanced trait resulting from expression of stably-integrated recombinant DNA in a nucleus of claim **1** or **4**, wherein said method for manufacturing said transgenic seed comprising:

(a) screening a population of plants for said enhanced trait and said recombinant DNA, wherein individual plants in said population can exhibit said trait at a level less than, essentially the same as or greater than the level that said trait is exhibited in control plants which do not express the recombinant DNA,

(b) selecting from said population one or more plants that exhibit said trait at a level greater than the level that said trait is exhibited in control plants,

(c) verifying that said recombinant DNA is stably integrated in said selected plants,

(d) analyzing tissue of said selected plant to determine the production or suppression of a protein having the function of a protein encoded by nucleotides having a sequence selected from the group consisting of one of SEQ ID NO:198-394; and

(e) collecting seed from said selected plant.

14. The method of claim **14** wherein plants in said population further comprise DNA expressing a protein that provides tolerance to exposure to an herbicide applied at levels

that are lethal to wild type plant cells, and wherein said selecting is effected by treating said population with said herbicide.

15. The method of claim **14** wherein said herbicide comprises a glyphosate, dicamba, or glufosinate compound.

16. The method of claim **15** wherein said selecting is effected by identifying plants with said enhanced trait.

17. The method of claim **16** wherein said seed is corn, soybean, cotton, alfalfa, wheat or rice seed.

18. A method of producing hybrid corn seed comprising:

(a) acquiring hybrid corn seed from a herbicide tolerant corn plant which also has stably-integrated, recombinant DNA in a nucleus of claim **1** or **4**;

(b) producing corn plants from said hybrid corn seed, wherein a fraction of the plants produced from said hybrid corn seed is homozygous for said recombinant DNA, a fraction of the plants produced from said hybrid corn seed is hemizygous for said recombinant DNA, and a fraction of the plants produced from said hybrid corn seed has none of said recombinant DNA;

(c) selecting corn plants which are homozygous and hemizygous for said recombinant DNA by treating with an herbicide;

(d) collecting seed from herbicide-treated-surviving corn plants and planting said seed to produce further progeny corn plants;

(e) repeating steps (c) and (d) at least once to produce an inbred corn line;

(f) crossing said inbred corn line with a second corn line to produce hybrid seed.

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