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(21) International Application Number: PCT/US99/16479 (22) International Filing Date: 21 July 1999 (21.07.99) (30) Priority Data: 60/093,687 22 July 1998 (22.07.98) US (71) Applicant (for all designated States except US): E.I. DU PONT DE NEMOURS AND COMPANY [US/US]; 1007 Market Street, Wilmington, DE 19898 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): CAHOON, Rebecca, E. [US/US]; 2331 West 18th Street, Wilmington, DE 19806 (US). CAIMI, Perry, G. [US/US]; 7 Holly Drive, Kennett Square, PA 19348 (US). ODELL, Joan, T. [US/US]; P.O. Box 826, Unionville, PA 19375 (US). SAKAI, Hajime [DE/US]; 105 Banbury Drive, Wilmington, DE 19803 (US). ZHU, Qun [CN/US]; Apartment B, 2221 Prior Road, Wilmington, DE 19809 (US). (74) Agent: MAJARIAN, William, R.; E.I. du Pont de Nemours and Company, Legal Patent Records Center, 1007 Market Street, Wilmington, DE 19898 (US).		(81) Designated States: AE, AL, AU, BA, BB, BG, BR, CA, CN, CU, CZ, EE, GD, GE, HR, HU, ID, IL, IN, IS, JP, KP, KR, LC, LK, LR, LT, LV, MG, MK, MN, MX, NO, NZ, PL, RO, SG, SI, SK, SL, TR, TT, UA, US, UZ, VN, YU, ZA, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: PC4 TRANSCRIPTIONAL COACTIVATORS (57) Abstract This invention relates to an isolated nucleic acid fragment encoding a PC4 transcription coactivator. The invention also relates to the construction of a chimeric gene encoding all or a portion of the PC4 transcription coactivator, in sense or antisense orientation, wherein expression of the chimeric gene results in production of altered levels of the PC4 transcription coactivator in a transformed host cell.		

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TITLE

PC4 TRANSCRIPTIONAL COACTIVATORS

This application claims the benefit of U.S. Provisional Application No. 60/093,687, filed July 22, 1998.

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FIELD OF THE INVENTION

This invention is in the field of plant molecular biology. More specifically, this invention pertains to nucleic acid fragments encoding PC4 transcription coactivators in plants and seeds.

BACKGROUND OF THE INVENTION

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Activation of transcription in eukaryotes depends upon the interplay between sequence specific transcriptional activators and general transcription factors. While direct contacts between activators and general factors have been demonstrated *in vitro*, an additional class of proteins, termed coactivators, appear to be required for transcriptional activation of some genes. For example, transcription of class II genes depends upon the assembly of basal transcription machinery containing RNA polymerase II and the general transcription factors (GTFs): TFIIA, TFIIB, TFIID, TFIIE, TFIIIF, and TFIIH. Class II genes contain core-promoter elements recognized by the general transcription factors and gene-specific sequences recognized by the activators. Coactivators mediate the interaction between the transcriptional activators the GTFs. Transcription activation is the output of the interaction between the sequence-specific activator and basal transcription machinery, which increases the efficiency and/or stability of the entire transcription machinery complex.

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The positive cofactor 4 (PC4) functions as both an activator-dependent, and a general transcription factor-dependent coactivator. It interacts with activation domains such as VP16 and the general transcription factors such as TFIIA, TFIIB, TFIIH and TAFs in TFIID. PC4 is a bridge or signal mediator between a set of specific activators and general transcription factors in transcription initiation complex (Wu et al. (1998) *EMBO J.* 17:4478-4490; and Zhu et al. (1995) *Plant Cell* 7:1681-1689.) Positive Cofactor 4 has been purified from the Upstream Stimulatory Fraction of HeLa cells and found to mediate activator dependent transcriptional activation. PC4 has been demonstrated to be a promiscuous and potent coactivator interacting with several activators, including Gal4/VP16. PC4 itself is a non-specific DNA binding protein that binds to both ssDNA and dsDNA, but has a higher affinity for ssDNA (Ge et al. (1994) *Cell* 78:513-523; Henry et al. (1996) *J. Biol. Chem.* 271:21842-21847; Kaiser et al. (1995) *EMBO J.* 14:3520-3527; Kretzschmar et al. (1994) *Cell* 78:525-534; and Werten et al. (1998) *EMBO J.* 5:5103-5111. PC4 has also been shown to interact with members of the basal transcriptional machinery. Specifically, the TFIIA-DNA and TFIIA-TFIIB-DNA complexes. Phosphorylation of PC4 by TFIIH or TATA associated factors abolish PC4 DNA-binding activity. Additionally, PC4 and Gal4/VP16 have been shown to be required during TFIID-TFIIA-DNA complex formation

(D-A complex) in order to stimulate transcription. This ability to affect D-A complex formation is linked to PC4's dsDNA-binding characteristic.

SUMMARY OF THE INVENTION

The instant invention relates to isolated nucleic acid fragments encoding PC4 transcription coactivators. Specifically, this invention concerns an isolated nucleic acid fragment encoding a PC4(P15) type 1 or PC4(P15) type 2 protein and an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding a PC4(P15) type 1 or PC4(P15) type 2 protein. In addition, this invention relates to a nucleic acid fragment that is complementary to the nucleic acid fragment encoding PC4(P15) type 1 or PC4(P15) type 2 protein.

An additional embodiment of the instant invention pertains to a polypeptide encoding all or a substantial portion of a PC4 transcription coactivator selected from the group consisting of PC4(P15) type 1 or PC4(P15) type 2 protein.

In another embodiment, the instant invention relates to a chimeric gene encoding a PC4(P15) type 1 or PC4(P15) type 2 protein, or to a chimeric gene that comprises a nucleic acid fragment that is complementary to a nucleic acid fragment encoding a PC4(P15) type 1 or PC4(P15) type 2 protein, operably linked to suitable regulatory sequences, wherein expression of the chimeric gene results in production of levels of the encoded protein in a transformed host cell that is altered (i.e., increased or decreased) from the level produced in an untransformed host cell.

In a further embodiment, the instant invention concerns a transformed host cell comprising in its genome a chimeric gene encoding a PC4(P15) type 1 or PC4(P15) type 2 protein, operably linked to suitable regulatory sequences. Expression of the chimeric gene results in production of altered levels of the encoded protein in the transformed host cell. The transformed host cell can be of eukaryotic or prokaryotic origin, and include cells derived from higher plants and microorganisms. The invention also includes transformed plants that arise from transformed host cells of higher plants, and seeds derived from such transformed plants.

An additional embodiment of the instant invention concerns a method of altering the level of expression of a PC4(P15) type 1 or PC4(P15) type 2 protein in a transformed host cell comprising: a) transforming a host cell with a chimeric gene comprising a nucleic acid fragment encoding a PC4(P15) type 1 or PC4(P15) type 2 protein; and b) growing the transformed host cell under conditions that are suitable for expression of the chimeric gene wherein expression of the chimeric gene results in production of altered levels of PC4(P15) type 1 or PC4(P15) type 2 protein in the transformed host cell.

An addition embodiment of the instant invention concerns a method for obtaining a nucleic acid fragment encoding all or a substantial portion of an amino acid sequence encoding a PC4(P15) type 1 or PC4(P15) type 2 protein.

BRIEF DESCRIPTION OF THE
DRAWINGS AND SEQUENCE DESCRIPTIONS

The invention can be more fully understood from the following detailed description and the accompanying Sequence Listing which form a part of this application.

5 Figure 1 shows organization of PC4 in the rice genome.

Table 1 lists the polypeptides that are described herein, the designation of the cDNA clones that comprise the nucleic acid fragments encoding polypeptides representing all or a substantial portion of these polypeptides, and the corresponding identifier (SEQ ID NO:) as used in the attached Sequence Listing. The sequence descriptions and Sequence Listing
10 attached hereto comply with the rules governing nucleotide and/or amino acid sequence disclosures in patent applications as set forth in 37 C.F.R. §1.821-1.825.

TABLE 1
PC4 Transcription Coactivators

Protein	Clone Designation	SEQ ID NO:	
		(Nucleotide)	(Amino Acid)
PC4(P15) Transcription Adaptor Type 1	cca.pk0020.d2	1	2
PC4(P15) Transcription Adaptor Type 1	rr1.pk0003.a12	3	4
PC4(P15) Transcription Adaptor Type 1	sfl1.pk0008.a4	5	6
PC4(P15) Transcription Adaptor Type 1	wdk2c.pk015.g20	7	8
PC4(P15) Transcription Adaptor Type 1	ecs1c.pk008.m20	9	10
PC4(P15) Transcription Adaptor Type 1	vs1n.pk013.f21	11	12
PC4(P15) Transcription Adaptor Type 2	Contig composed of: p0014.ctuth59r ceb5.pk0070.e3 cpi1c.pk017.j22	13	14
PC4(P15) Transcription Adaptor Type 2	Contig composed of: p0118.chsbi09r cpd1c.pk006.i3 cbn10.pk0063.h8	15	16
PC4(P15) Transcription Adaptor Type 2	ses4d.pk0016.g2	17	18

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The Sequence Listing contains the one letter code for nucleotide sequence characters and the three letter codes for amino acids as defined in conformity with the IUPAC-IUBMB standards described in *Nucleic Acids Research* 13:3021-3030 (1985) and in the *Biochemical Journal* 219 (No. 2):345-373 (1984) which are herein incorporated by reference. The

symbols and format used for nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. §1.822.

DETAILED DESCRIPTION OF THE INVENTION

The instant invention concerns the identification and isolation of PC4s in plants and the discovery that recombinant PC4 molecules can potentially interact with Gal4/VP16 and Gal4/ALF. In other systems, PC4-mediated enhancement by Gal4/VP16 occurs via increased template commitment where it accelerates the assembly efficiency of transcription initiation complex. By manipulating the expression level of PC4, it may be possible to control and/ or modulate the functional properties of specific transcriptional activators. Furthermore, it may be possible to use different domains of PC4, to generate chimeric transcription factors that stimulate transcription initiation at a very high rate. Interestingly, casein kinase II can phosphorylate PC4 inactivating its DNA-binding activity. By replacing the casein kinase II site, it may be possible to generate constantly active PC4 molecules or by domain swapping or deletion, constantly inactive PC4 molecules could also be produced. Thus the PC4 coactivator can be used to modulate gene expression in plants.

Accordingly, the availability of nucleic acid sequences encoding all or a portion of a plant PC4 transcription cofactor protein would facilitate studies to better understand the mechanisms that control transcription in plants. The PC4 promoter may itself be useful in the expression of genes under induced conditions in transgenic plants.

In the context of this disclosure, a number of terms shall be utilized. As used herein, a “nucleic acid fragment” is a polymer of RNA or DNA that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. A nucleic acid fragment in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

As used herein, “contig” refers to a nucleotide sequence that is assembled from two or more constituent nucleotide sequences that share common or overlapping regions of sequence homology. For example, the nucleotide sequences of two or more nucleic acid fragments can be compared and aligned in order to identify common or overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acid fragments, the sequences (and thus their corresponding nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

As used herein, “substantially similar” refers to nucleic acid fragments wherein changes in one or more nucleotide bases results in substitution of one or more amino acids, but do not affect the functional properties of the polypeptide encoded by the nucleotide sequence. “Substantially similar” also refers to nucleic acid fragments wherein changes in one or more nucleotide bases does not affect the ability of the nucleic acid fragment to mediate alteration of gene expression by gene silencing through for example antisense or co-suppression technology. “Substantially similar” also refers to modifications of the nucleic

acid fragments of the instant invention such as deletion or insertion of one or more nucleotides that do not substantially affect the functional properties of the resulting transcript vis-à-vis the ability to mediate gene silencing or alteration of the functional properties of the resulting protein molecule. It is therefore understood that the invention encompasses more than the specific exemplary nucleotide or amino acid sequences and includes functional equivalents thereof.

For example, it is well known in the art that antisense suppression and co-suppression of gene expression may be accomplished using nucleic acid fragments representing less than the entire coding region of a gene, and by nucleic acid fragments that do not share 100% sequence identity with the gene to be suppressed. Moreover, alterations in a nucleic acid fragment which result in the production of a chemically equivalent amino acid at a given site, but do not effect the functional properties of the encoded polypeptide, are well known in the art. Thus, a codon for the amino acid alanine, a hydrophobic amino acid, may be substituted by a codon encoding another less hydrophobic residue, such as glycine, or a more hydrophobic residue, such as valine, leucine, or isoleucine. Similarly, changes which result in substitution of one negatively charged residue for another, such as aspartic acid for glutamic acid, or one positively charged residue for another, such as lysine for arginine, can also be expected to produce a functionally equivalent product. Nucleotide changes which result in alteration of the N-terminal and C-terminal portions of the polypeptide molecule would also not be expected to alter the activity of the polypeptide. Each of the proposed modifications is well within the routine skill in the art, as is determination of retention of biological activity of the encoded products.

Moreover, substantially similar nucleic acid fragments may also be characterized by their ability to hybridize. Estimates of such homology are provided by either DNA-DNA or DNA-RNA hybridization under conditions of stringency as is well understood by those skilled in the art (Hames and Higgins, Eds. (1985) *Nucleic Acid Hybridisation*, IRL Press, Oxford, U.K.). Stringency conditions can be adjusted to screen for moderately similar fragments, such as homologous sequences from distantly related organisms, to highly similar fragments, such as genes that duplicate functional enzymes from closely related organisms. Post-hybridization washes determine stringency conditions. One set of preferred conditions uses a series of washes starting with 6X SSC, 0.5% SDS at room temperature for 15 min, then repeated with 2X SSC, 0.5% SDS at 45°C for 30 min, and then repeated twice with 0.2X SSC, 0.5% SDS at 50°C for 30 min. A more preferred set of stringent conditions uses higher temperatures in which the washes are identical to those above except for the temperature of the final two 30 min washes in 0.2X SSC, 0.5% SDS was increased to 60°C. Another preferred set of highly stringent conditions uses two final washes in 0.1X SSC, 0.1% SDS at 65°C.

Substantially similar nucleic acid fragments of the instant invention may also be characterized by the percent identity of the amino acid sequences that they encode to the amino acid sequences disclosed herein, as determined by algorithms commonly employed by those skilled in this art. Preferred are those nucleic acid fragments whose nucleotide sequences encode amino acid sequences that are 80% identical to the amino acid sequences reported herein. More preferred nucleic acid fragments encode amino acid sequences that are 90% identical to the amino acid sequences reported herein. Most preferred are nucleic acid fragments that encode amino acid sequences that are 95% identical to the amino acid sequences reported herein. Sequence alignments and percent identity calculations were performed using the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Multiple alignment of the sequences was performed using the Clustal method of alignment (Higgins and Sharp (1989) *CABIOS*. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Default parameters for pairwise alignments using the Clustal method were KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5.

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410; see also www.ncbi.nlm.nih.gov/BLAST/). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

“Codon degeneracy” refers to divergence in the genetic code permitting variation of the nucleotide sequence without effecting the amino acid sequence of an encoded polypeptide. Accordingly, the instant invention relates to any nucleic acid fragment comprising a nucleotide sequence that encodes all or a substantial portion of the amino acid sequences set forth herein. The skilled artisan is well aware of the “codon-bias” exhibited by a specific host cell in usage of nucleotide codons to specify a given amino acid. Therefore, when synthesizing a nucleic acid fragment for improved expression in a host cell, it is desirable to design the nucleic acid fragment such that its frequency of codon usage approaches the frequency of preferred codon usage of the host cell.

“Synthetic nucleic acid fragments” can be assembled from oligonucleotide building blocks that are chemically synthesized using procedures known to those skilled in the art. These building blocks are ligated and annealed to form larger nucleic acid fragments which may then be enzymatically assembled to construct the entire desired nucleic acid fragment. “Chemically synthesized”, as related to nucleic acid fragment, means that the component nucleotides were assembled *in vitro*. Manual chemical synthesis of nucleic acid fragments may be accomplished using well established procedures, or automated chemical synthesis can be performed using one of a number of commercially available machines. Accordingly, the nucleic acid fragments can be tailored for optimal gene expression based on optimization of nucleotide sequence to reflect the codon bias of the host cell. The skilled artisan appreciates the likelihood of successful gene expression if codon usage is biased towards those codons favored by the host. Determination of preferred codons can be based on a survey of genes derived from the host cell where sequence information is available.

“Gene” refers to a nucleic acid fragment that expresses a specific protein, including regulatory sequences preceding (5' non-coding sequences) and following (3' non-coding sequences) the coding sequence. “Native gene” refers to a gene as found in nature with its own regulatory sequences. “Chimeric gene” refers any gene that is not a native gene, comprising regulatory and coding sequences that are not found together in nature. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are derived from different sources, or regulatory sequences and coding sequences derived from the same source, but arranged in a manner different than that found in nature. “Endogenous gene” refers to a native gene in its natural location in the genome of an organism. A “foreign” gene refers to a gene not normally found in the host organism, but that is introduced into the host organism by gene transfer. Foreign genes can comprise native genes inserted into a non-native organism, or chimeric genes. A “transgene” is a gene that has been introduced into the genome by a transformation procedure.

“Coding sequence” refers to a nucleotide sequence that codes for a specific amino acid sequence. “Regulatory sequences” refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence,

and which influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences may include promoters, translation leader sequences, introns, and polyadenylation recognition sequences.

“Promoter” refers to a nucleotide sequence capable of controlling the expression of a coding sequence or functional RNA. In general, a coding sequence is located 3' to a promoter sequence. The promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an “enhancer” is a nucleotide sequence which can stimulate promoter activity and may be an innate element of the promoter or a heterologous element inserted to enhance the level or tissue-specificity of a promoter. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even comprise synthetic nucleotide segments. It is understood by those skilled in the art that different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. Promoters which cause a nucleic acid fragment to be expressed in most cell types at most times are commonly referred to as “constitutive promoters”. New promoters of various types useful in plant cells are constantly being discovered; numerous examples may be found in the compilation by Okamuro and Goldberg (1989) *Biochemistry of Plants* 15:1-82. It is further recognized that since in most cases the exact boundaries of regulatory sequences have not been completely defined, nucleic acid fragments of different lengths may have identical promoter activity.

The “translation leader sequence” refers to a nucleotide sequence located between the promoter sequence of a gene and the coding sequence. The translation leader sequence is present in the fully processed mRNA upstream of the translation start sequence. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency. Examples of translation leader sequences have been described (Turner and Foster (1995) *Molecular Biotechnology* 3:225).

The “3' non-coding sequences” refer to nucleotide sequences located downstream of a coding sequence and include polyadenylation recognition sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by Ingelbrecht et al. (1989) *Plant Cell* 1:671-680.

“RNA transcript” refers to the product resulting from RNA polymerase-catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. “Messenger RNA (mRNA)” refers to the RNA that is

without introns and that can be translated into polypeptide by the cell. "cDNA" refers to a double-stranded DNA that is complementary to and derived from mRNA. "Sense" RNA refers to an RNA transcript that includes the mRNA and so can be translated into a polypeptide by the cell. "Antisense RNA" refers to an RNA transcript that is

5 complementary to all or part of a target primary transcript or mRNA and that blocks the expression of a target gene (see U.S. Patent No. 5,107,065, incorporated herein by reference). The complementarity of an antisense RNA may be with any part of the specific nucleotide sequence, i.e., at the 5' non-coding sequence, 3' non-coding sequence, introns, or the coding sequence. "Functional RNA" refers to sense RNA, antisense RNA, ribozyme
10 RNA, or other RNA that may not be translated but yet has an effect on cellular processes.

The term "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
15 the transcriptional control of the promoter). Coding sequences can be operably linked to regulatory sequences in sense or antisense orientation.

The term "expression", as used herein, refers to the transcription and stable accumulation of sense (mRNA) or antisense RNA derived from the nucleic acid fragment of the invention. Expression may also refer to translation of mRNA into a polypeptide.

20 "Antisense inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of the target protein. "Overexpression" refers to the production of a gene product in transgenic organisms that exceeds levels of production in normal or non-transformed organisms. "Co-suppression" refers to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar foreign
25 or endogenous genes (U.S. Patent No. 5,231,020, incorporated herein by reference).

"Altered levels" refers to the production of gene product(s) in transgenic organisms in amounts or proportions that differ from that of normal or non-transformed organisms.

"Mature" protein refers to a post-translationally processed polypeptide; i.e., one from which any pre- or propeptides present in the primary translation product have been removed.
30 "Precursor" protein refers to the primary product of translation of mRNA; i.e., with pre- and propeptides still present. Pre- and propeptides may be but are not limited to intracellular localization signals.

A "chloroplast transit peptide" is an amino acid sequence which is translated in conjunction with a protein and directs the protein to the chloroplast or other plastid types
35 present in the cell in which the protein is made. "Chloroplast transit sequence" refers to a nucleotide sequence that encodes a chloroplast transit peptide. A "signal peptide" is an amino acid sequence which is translated in conjunction with a protein and directs the protein to the secretory system (Chrispeels (1991) *Ann. Rev. Plant Phys. Plant Mol. Biol.* 42:21-53).

If the protein is to be directed to a vacuole, a vacuolar targeting signal (*supra*) can further be added, or if to the endoplasmic reticulum, an endoplasmic reticulum retention signal (*supra*) may be added. If the protein is to be directed to the nucleus, any signal peptide present should be removed and instead a nuclear localization signal included (Raikhel (1992) *Plant Phys.* 100:1627-1632).

“Transformation” refers to the transfer of a nucleic acid fragment into the genome of a host organism, resulting in genetically stable inheritance. Host organisms containing the transformed nucleic acid fragments are referred to as “transgenic” organisms. Examples of methods of plant transformation include *Agrobacterium*-mediated transformation (De Blaere et al. (1987) *Meth. Enzymol.* 143:277) and particle-accelerated or “gene gun” transformation technology (Klein et al. (1987) *Nature (London)* 327:70-73; U.S. Patent No. 4,945,050, incorporated herein by reference).

Standard recombinant DNA and molecular cloning techniques used herein are well known in the art and are described more fully in Sambrook et al. *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, 1989 (hereinafter “Maniatis”).

Nucleic acid fragments encoding at least a portion of several PC4 transcription coactivators have been isolated and identified by comparison of random plant cDNA sequences to public databases containing nucleotide and protein sequences using the BLAST algorithms well known to those skilled in the art. The nucleic acid fragments of the instant invention may be used to isolate cDNAs and genes encoding homologous proteins from the same or other plant species. Isolation of homologous genes using sequence-dependent protocols is well known in the art. Examples of sequence-dependent protocols include, but are not limited to, methods of nucleic acid hybridization, and methods of DNA and RNA amplification as exemplified by various uses of nucleic acid amplification technologies (e.g., polymerase chain reaction, ligase chain reaction).

For example, genes encoding other PC4(P15) type 1 or PC4(P15) type 2 proteins, either as cDNAs or genomic DNAs, could be isolated directly by using all or a portion of the instant nucleic acid fragments as DNA hybridization probes to screen libraries from any desired plant employing methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the instant nucleic acid sequences can be designed and synthesized by methods known in the art (Maniatis). Moreover, the entire sequences can be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primer DNA labeling, nick translation, or end-labeling techniques, or RNA probes using available *in vitro* transcription systems. In addition, specific primers can be designed and used to amplify a part or all of the instant sequences. The resulting amplification products can be labeled directly during amplification reactions or labeled after amplification

reactions, and used as probes to isolate full length cDNA or genomic fragments under conditions of appropriate stringency.

In addition, two short segments of the instant nucleic acid fragments may be used in polymerase chain reaction protocols to amplify longer nucleic acid fragments encoding homologous genes from DNA or RNA. The polymerase chain reaction may also be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the instant nucleic acid fragments, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, the skilled artisan can follow the RACE protocol (Frohman et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:8998) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Primers oriented in the 3' and 5' directions can be designed from the instant sequences. Using commercially available 3' RACE or 5' RACE systems (BRL), specific 3' or 5' cDNA fragments can be isolated (Ohara et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:5673; Loh et al. (1989) *Science* 243:217). Products generated by the 3' and 5' RACE procedures can be combined to generate full-length cDNAs (Frohman and Martin (1989) *Techniques* 1:165).

Availability of the instant nucleotide and deduced amino acid sequences facilitates immunological screening of cDNA expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides can be used to immunize animals to produce polyclonal or monoclonal antibodies with specificity for peptides or proteins comprising the amino acid sequences. These antibodies can be then be used to screen cDNA expression libraries to isolate full-length cDNA clones of interest (Lerner (1984) *Adv. Immunol.* 36:1; Maniatis).

The nucleic acid fragments of the instant invention may be used to create transgenic plants in which the disclosed polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of transcription of specific genes in those cells.

Overexpression of the proteins of the instant invention may be accomplished by first constructing a chimeric gene in which the coding region is operably linked to a promoter capable of directing expression of a gene in the desired tissues at the desired stage of development. For reasons of convenience, the chimeric gene may comprise promoter sequences and translation leader sequences derived from the same genes. 3' Non-coding sequences encoding transcription termination signals may also be provided. The instant chimeric gene may also comprise one or more introns in order to facilitate gene expression.

Plasmid vectors comprising the instant chimeric gene can then be constructed. The choice of plasmid vector is dependent upon the method that will be used to transform host

plants. The skilled artisan is well aware of the genetic elements that must be present on the plasmid vector in order to successfully transform, select and propagate host cells containing the chimeric gene. The skilled artisan will also recognize that different independent transformation events will result in different levels and patterns of expression (Jones et al. (1985) *EMBO J.* 4:2411-2418; De Almeida et al. (1989) *Mol. Gen. Genetics* 218:78-86), and thus that multiple events must be screened in order to obtain lines displaying the desired expression level and pattern. Such screening may be accomplished by Southern analysis of DNA, Northern analysis of mRNA expression, Western analysis of protein expression, or phenotypic analysis.

For some applications it may be useful to direct the instant polypeptides to different cellular compartments, or to facilitate its secretion from the cell. It is thus envisioned that the chimeric gene described above may be further supplemented by altering the coding sequence to encode the instant polypeptides with appropriate intracellular targeting sequences such as transit sequences (Keegstra (1989) *Cell* 56:247-253), signal sequences or sequences encoding endoplasmic reticulum localization (Chrispeels (1991) *Ann. Rev. Plant Phys. Plant Mol. Biol.* 42:21-53), or nuclear localization signals (Raikhel (1992) *Plant Phys.* 100:1627-1632) added and/or with targeting sequences that are already present removed. While the references cited give examples of each of these, the list is not exhaustive and more targeting signals of utility may be discovered in the future.

It may also be desirable to reduce or eliminate expression of genes encoding the instant polypeptides in plants for some applications. In order to accomplish this, a chimeric gene designed for co-suppression of the instant polypeptide can be constructed by linking a gene or gene fragment encoding that polypeptide to plant promoter sequences. Alternatively, a chimeric gene designed to express antisense RNA for all or part of the instant nucleic acid fragment can be constructed by linking the gene or gene fragment in reverse orientation to plant promoter sequences. Either the co-suppression or antisense chimeric genes could be introduced into plants via transformation wherein expression of the corresponding endogenous genes are reduced or eliminated.

Molecular genetic solutions to the generation of plants with altered gene expression have a decided advantage over more traditional plant breeding approaches. Changes in plant phenotypes can be produced by specifically inhibiting expression of one or more genes by antisense inhibition or cosuppression (U. S. Patent Nos. 5,190,931, 5,107,065 and 5,283,323). An antisense or cosuppression construct would act as a dominant negative regulator of gene activity. While conventional mutations can yield negative regulation of gene activity these effects are most likely recessive. The dominant negative regulation available with a transgenic approach may be advantageous from a breeding perspective. In addition, the ability to restrict the expression of specific phenotype to the reproductive tissues of the plant by the use of tissue specific promoters may confer agronomic

advantages relative to conventional mutations which may have an effect in all tissues in which a mutant gene is ordinarily expressed.

The person skilled in the art will know that special considerations are associated with the use of antisense or cosuppression technologies in order to reduce expression of particular genes. For example, the proper level of expression of sense or antisense genes may require the use of different chimeric genes utilizing different regulatory elements known to the skilled artisan. Once transgenic plants are obtained by one of the methods described above, it will be necessary to screen individual transgenics for those that most effectively display the desired phenotype. Accordingly, the skilled artisan will develop methods for screening large numbers of transformants. The nature of these screens will generally be chosen on practical grounds, and is not an inherent part of the invention. For example, one can screen by looking for changes in gene expression by using antibodies specific for the protein encoded by the gene being suppressed, or one could establish assays that specifically measure enzyme activity. A preferred method will be one which allows large numbers of samples to be processed rapidly, since it will be expected that a large number of transformants will be negative for the desired phenotype.

The instant polypeptides (or portions thereof) may be produced in heterologous host cells, particularly in the cells of microbial hosts, and can be used to prepare antibodies to these proteins by methods well known to those skilled in the art. The antibodies are useful for detecting the polypeptides of the instant invention *in situ* in cells or *in vitro* in cell extracts. Preferred heterologous host cells for production of the instant polypeptides are microbial hosts. Microbial expression systems and expression vectors containing regulatory sequences that direct high level expression of foreign proteins are well known to those skilled in the art. Any of these could be used to construct a chimeric gene for production of the instant polypeptides. This chimeric gene could then be introduced into appropriate microorganisms via transformation to provide high level expression of the encoded PC4 transcription coactivators. An example of a vector for high level expression of the instant polypeptides in a bacterial host is provided (Example 8).

All or a substantial portion of the nucleic acid fragments of the instant invention may also be used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. For example, the instant nucleic acid fragments may be used as restriction fragment length polymorphism (RFLP) markers. Southern blots (Maniatis) of restriction-digested plant genomic DNA may be probed with the nucleic acid fragments of the instant invention. The resulting banding patterns may then be subjected to genetic analyses using computer programs such as MapMaker (Lander et al. (1987) *Genomics* 1:174-181) in order to construct a genetic map. In addition, the nucleic acid fragments of the instant invention may be used to probe Southern blots containing

restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. Segregation of the DNA polymorphisms is noted and used to calculate the position of the instant nucleic acid sequence in the genetic map previously obtained using this population (Botstein et al. (1980) *Am. J. Hum. Genet.* 32:314-331).

5 The production and use of plant gene-derived probes for use in genetic mapping is described in Bernatzky and Tanksley (1986) *Plant Mol. Biol. Reporter* 4(1):37-41. Numerous publications describe genetic mapping of specific cDNA clones using the methodology outlined above or variations thereof. For example, F2 intercross populations, backcross populations, randomly mated populations, near isogenic lines, and other sets of
10 individuals may be used for mapping. Such methodologies are well known to those skilled in the art.

Nucleic acid probes derived from the instant nucleic acid sequences may also be used for physical mapping (i.e., placement of sequences on physical maps; see Hoheisel et al. In: *Nonmammalian Genomic Analysis: A Practical Guide*, Academic press 1996, pp. 319-346, and references cited therein).

In another embodiment, nucleic acid probes derived from the instant nucleic acid sequences may be used in direct fluorescence *in situ* hybridization (FISH) mapping (Trask (1991) *Trends Genet.* 7:149-154). Although current methods of FISH mapping favor use of large clones (several to several hundred KB; see Laan et al. (1995) *Genome Research* 5:13-20), improvements in sensitivity may allow performance of FISH mapping using shorter probes.

A variety of nucleic acid amplification-based methods of genetic and physical mapping may be carried out using the instant nucleic acid sequences. Examples include allele-specific amplification (Kazazian (1989) *J. Lab. Clin. Med.* 114(2):95-96), polymorphism of PCR-amplified fragments (CAPS; Sheffield et al. (1993) *Genomics* 16:325-332), allele-specific ligation (Landegren et al. (1988) *Science* 241:1077-1080), nucleotide extension reactions (Sokolov (1990) *Nucleic Acid Res.* 18:3671), Radiation Hybrid Mapping (Walter et al. (1997) *Nature Genetics* 7:22-28) and Happy Mapping (Dear and Cook (1989) *Nucleic Acid Res.* 17:6795-6807). For these methods, the sequence of a nucleic acid fragment is used to design and produce primer pairs for use in the amplification reaction or in primer extension reactions. The design of such primers is well known to those skilled in the art. In methods employing PCR-based genetic mapping, it may be necessary to identify DNA sequence differences between the parents of the mapping cross in the region corresponding to the instant nucleic acid sequence. This, however, is generally not
35 necessary for mapping methods.

Loss of function mutant phenotypes may be identified for the instant cDNA clones either by targeted gene disruption protocols or by identifying specific mutants for these

genes contained in a maize population carrying mutations in all possible genes (Ballinger and Benzer (1989) *Proc. Natl. Acad. Sci USA* 86:9402; Koes et al. (1995) *Proc. Natl. Acad. Sci USA* 92:8149; Bensen et al. (1995) *Plant Cell* 7:75). The latter approach may be accomplished in two ways. First, short segments of the instant nucleic acid fragments may be used in polymerase chain reaction protocols in conjunction with a mutation tag sequence primer on DNAs prepared from a population of plants in which Mutator transposons or some other mutation-causing DNA element has been introduced (see Bensen, *supra*). The amplification of a specific DNA fragment with these primers indicates the insertion of the mutation tag element in or near the plant gene encoding the instant polypeptides.

Alternatively, the instant nucleic acid fragment may be used as a hybridization probe against PCR amplification products generated from the mutation population using the mutation tag sequence primer in conjunction with an arbitrary genomic site primer, such as that for a restriction enzyme site-anchored synthetic adaptor. With either method, a plant containing a mutation in the endogenous gene encoding the instant polypeptides can be identified and obtained. This mutant plant can then be used to determine or confirm the natural function of the instant polypeptides disclosed herein.

EXAMPLES

The present invention is further defined in the following Examples, in which all parts and percentages are by weight and degrees are Celsius, unless otherwise stated. It should be understood that these Examples, while indicating preferred embodiments of the invention, are given by way of illustration only. From the above discussion and these Examples, one skilled in the art can ascertain the essential characteristics of this invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the invention to adapt it to various usages and conditions.

EXAMPLE 1

Composition of cDNA Libraries; Isolation and Sequencing of cDNA Clones

cDNA libraries representing mRNAs from various corn, marigold, rice, soybean, *Vernonia* and wheat tissues were prepared. The characteristics of the libraries are described below.

TABLE 2

cDNA Libraries from Corn, Marigold, Rice, Soybean, *Vernonia* and Wheat

Library	Tissue	Clone
cbn10	Corn developing kernel (embryo and endosperm); 10 days after pollination	cbn10.pk0063.h8
cca	Corn callus type II tissue, undifferentiated	cca.pk0020.d2
ceb5	Corn embryo 30 days after pollination	ceb5.pk0070.e3
cpd1c	Corn pooled BMS treated with chemicals related to protein kinases****	cpd1c.pk0006.i3
cpilc	Corn pooled BMS treated with chemicals related to biochemical compound synthesis***	cpilc.pk017.j22
ecs1c	Marigold (<i>Calendula officinalis</i>) developing seeds	ecs1c.pk008.m20
p0014	Leaf: plant 3 ft tall, leaf 7 and leaf 8	p0014.ctuth59r
p0118	Corn stem tissue pooled from the 4-5 internodes subtending the tassel at stages V8-V12*, **	p0118.chsbi09r
rr1	Rice root of two week old developing seedling	rr1.pk0003.a12
ses4d	Soybean mbryogenic suspension 4 days after subculture	ses4d.pk0016.g2
sfl1	Soybean immature flower	sfl1.pk0008.a4
vs1n	<i>Vernonia</i> seed	vs1n.pk013.f21
wdk2c	Wheat developing kernel, 7 days after anthesis	wdk2c.pk015.g20

*This library was normalized essentially as described in U.S. Patent No. 5,482,845, incorporated herein by reference.

5 **The descriptions can be found in "How a Corn Plant Develops" Special Report No.48, Iowa State University of Science and Technology Cooperative Extension Service Ames,Iowa, Reprinted February 1993.

***Chemicals used included sorbitol, egosterol, taxifolin, methotrexate, D-mannose, D-glactose, alpha-amino adipic acid, ancymidol

10 ****Chemicals used included 1,2-didecanoyl rac glycerol, straurosporine, K-252, A3, H-7, olomoucine, rapamycin

cDNA libraries may be prepared by any one of many methods available. For example, the cDNAs may be introduced into plasmid vectors by first preparing the cDNA
 15 libraries in Uni-ZAP* XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA). The Uni-ZAP* XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into precut Bluescript II SK(+) vectors (Stratagene) using T4 DNA
 20 ligase (New England Biolabs), followed by transfection into DH10B cells according to the manufacturer's protocol (GIBCO BRL Products). Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared from randomly picked bacterial colonies containing recombinant pBluescript plasmids, or the insert cDNA sequences are amplified via

polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Amplified insert DNAs or plasmid DNAs are sequenced in dye-primer sequencing reactions to generate partial cDNA sequences (expressed sequence tags or “ESTs”; see Adams et al., (1991) *Science* 252:1651). The resulting ESTs are analyzed using a Perkin Elmer Model 377 fluorescent sequencer.

EXAMPLE 2

Identification of cDNA Clones

cDNA clones encoding PC4 transcription coactivators were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410; see also www.ncbi.nlm.nih.gov/BLAST/) searches for similarity to sequences contained in the BLAST “nr” database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the “nr” database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the “nr” database using the BLASTX algorithm (Gish and States (1993) *Nature Genetics* 3:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as “pLog” values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST “hit” represent homologous proteins.

EXAMPLE 3

Characterization of cDNA Clones Encoding PC4(P15) Type 1 Homologs

The BLASTX search using the EST sequences from clones listed in Table 3 revealed similarity of the polypeptides encoded by the cDNAs to PC4(P15) from *Arabidopsis thaliana* (NCBI Identifier No. gi 2997684). Shown in Table 3 are the BLAST results for individual ESTs (“EST”), the sequences of the entire cDNA inserts comprising the indicated cDNA clones (“FIS”), or contigs assembled from two or more ESTs (“Contig”):

TABLE 3

BLAST Results for Sequences Encoding Polypeptides Homologous
to *Arabidopsis thaliana* PC4(P15)

Clone	Status	BLAST pLog Score to gi 2997684
cca.pk0020.d2	FIS	19.52
rr1.pk0003.a12	FIS	23.52
sfl1.pk0008.a4	FIS	31.52
wdk2c.pk015.g20	EST	24.00
ecs1c.pk008.m20	EST	13.22
vs1n.pk013.f21	EST	26.00

- 5 The data in Table 4 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:2, 4, 6, 8, 10 and 12 and the *Arabidopsis thaliana* sequence (SEQ ID NO:19).

TABLE 4

- 10 Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to *Arabidopsis thaliana* PC4(P15)

SEQ ID NO.	Percent Identity to gi 2997684
2	38%
4	45%
6	59%
8	45%
10	36%
12	41%

- 15 Sequence alignments and percent identity calculations were performed using the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Multiple alignment of the sequences was performed using the Clustal method of alignment (Higgins and Sharp (1989) *CABIOS*. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Default parameters for pairwise alignments using the Clustal method were KTUPLE 1, GAP PENALTY=3,
- 20 WINDOW=5 and DIAGONALS SAVED=5. Sequence alignments and BLAST scores and probabilities indicate that the nucleic acid fragments comprising the instant cDNA clones encode a substantial portion of a PC4(P15) protein. These sequences represent the first corn, maigold, rice, *Vernonia* and wheat sequences encoding PC4(P15).

EXAMPLE 4Characterization of cDNA Clones Encoding PC4(P15) Type 2 Homologs

The BLASTX search using the EST sequences from clones listed in Table 5 revealed similarity of the polypeptides encoded by the cDNAs to PC4(P15) from *Arabidopsis thaliana* (NCBI Identifier No. gi 2997686). Shown in Table 5 are the BLAST results for individual ESTs ("EST"), the sequences of the entire cDNA inserts comprising the indicated cDNA clones ("FIS"), or contigs assembled from two or more ESTs ("Contig"):

TABLE 5

BLAST Results for Sequences Encoding Polypeptides Homologous
to *Arabidopsis thaliana* PC4(P15) Type 2

Clone	Status	BLAST pLog Score to gi 2997686
Contig composed of: p0014.ctuth59r ceb5.pk0070.e3 cpilc.pk017.j22	Contig	40.52
Contig composed of: p0118.chsbi09r cpd1c.pk006.i3 cbn10.pk0063.h8	Contig	38.00
ses4d.pk0016.g2	FIS	47.70

The data in Table 6 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:14, 16 and 18 and the *Arabidopsis thaliana* sequence (SEQ ID NO:20).

TABLE 6

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences
of cDNA Clones Encoding Polypeptides Homologous
to *Arabidopsis thaliana* PC4(P15) Type 2

SEQ ID NO.	Percent Identity to gi 2997684
14	53%
16	50%
18	66%

Sequence alignments and percent identity calculations were performed using the Megalign program of the LASARGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). Multiple alignment of the sequences was performed using the Clustal method of alignment (Higgins and Sharp (1989) *CABIOS*. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Default parameters for

pairwise alignments using the Clustal method were KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5. Sequence alignments and BLAST scores and probabilities indicate that the nucleic acid fragments comprising the instant cDNA clones encode a substantial portion of a PC4(P15) type 2 protein. These sequences represent the first corn, and soybean sequences encoding PC4(P15) type 2.

EXAMPLE 5

Organization of PC4 Genes in the Rice Genome

To estimate the number of PC4 genes in the rice genome, Southern blots of genomic DNA from rice were hybridized with the full coding region of the PC4 gene.

10 Rice (*Oryza Sativa* L. cv. Yashiro-mochi, and Nipponbare) seeds were germinated on wet filteres in petri dishes. Leaves from two week old seedlings were used for DNA isolation. Rice genomic DNA, prepared according to the method of Ausubel et al. ((1987), *Current Protocols In Molecular Biology*, Wiley, New York). The genomic DNA was digested with various restriction enzymes, separated by electrophoresis on an 1% agarose
15 gel and blotted onto Hybond N+ membrane (Amersham Co., Piscataway, NJ) using alkaline (0.4 N NaOH) blotting procedure. Kilobase marker was used as molecular weight standard (GIBCO-BRL, Rockville, MD). The genomic DNA was hybridized with the coding region of the rice PC4 gene. The fragment was labeled with 32P-dCTP using RadPrime DNA Labeling system (GIBCO-BRL). Hybrization was carried out in 5x SSC, 5x denhardt, 1%
20 SDS, 100 µg/ml denatured sperm DNA and 50% formamide at 60°C for 24 hr (Ausubel et al., 1987).

As shown in Fig. 1, the PC4 gene probe hybridized to 2 to 3 restriction fragments of rice genomic DNA digested with BamH I, EcoR I, Hind III and Nco I. There are four EcoR V digested genomic DNA fragments hybridized with the PC4 gene, two of them are shorter
25 than 1 kb. There are two EcoR V sites which are 17 bp away from each other in the PC4 gene probe. This information suggests that there is a small gene family which is comprised of no more than 3 PC4 genes in the rice genome.

EXAMPLE 6

Expression of Chimeric Genes in Monocot Cells

30 A chimeric gene comprising a cDNA encoding the instant polypeptides in sense orientation with respect to the maize 27 kD zein promoter that is located 5' to the cDNA fragment, and the 10 kD zein 3' end that is located 3' to the cDNA fragment, can be constructed. The cDNA fragment of this gene may be generated by polymerase chain reaction (PCR) of the cDNA clone using appropriate oligonucleotide primers. Cloning sites
35 (NcoI or SmaI) can be incorporated into the oligonucleotides to provide proper orientation of the DNA fragment when inserted into the digested vector pML103 as described below. Amplification is then performed in a standard PCR. The amplified DNA is then digested with restriction enzymes NcoI and SmaI and fractionated on an agarose gel. The appropriate

band can be isolated from the gel and combined with a 4.9 kb NcoI-SmaI fragment of the plasmid pML103. Plasmid pML103 has been deposited under the terms of the Budapest Treaty at ATCC (American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209), and bears accession number ATCC 97366. The DNA segment from pML103 contains a 1.05 kb SalI-NcoI promoter fragment of the maize 27 kD zein gene and a 0.96 kb SmaI-SalI fragment from the 3' end of the maize 10 kD zein gene in the vector pGem9Zf(+) (Promega). Vector and insert DNA can be ligated at 15°C overnight, essentially as described (Maniatis). The ligated DNA may then be used to transform *E. coli* XL1-Blue (Epicurian Coli XL-1 Blue™; Stratagene). Bacterial transformants can be screened by restriction enzyme digestion of plasmid DNA and limited nucleotide sequence analysis using the dideoxy chain termination method (Sequenase™ DNA Sequencing Kit; U.S. Biochemical). The resulting plasmid construct would comprise a chimeric gene encoding, in the 5' to 3' direction, the maize 27 kD zein promoter, a cDNA fragment encoding the instant polypeptides, and the 10 kD zein 3' region.

The chimeric gene described above can then be introduced into corn cells by the following procedure. Immature corn embryos can be dissected from developing caryopses derived from crosses of the inbred corn lines H99 and LH132. The embryos are isolated 10 to 11 days after pollination when they are 1.0 to 1.5 mm long. The embryos are then placed with the axis-side facing down and in contact with agarose-solidified N6 medium (Chu et al. (1975) *Sci. Sin. Peking* 18:659-668). The embryos are kept in the dark at 27°C. Friable embryogenic callus consisting of undifferentiated masses of cells with somatic proembryoids and embryoids borne on suspensor structures proliferates from the scutellum of these immature embryos. The embryogenic callus isolated from the primary explant can be cultured on N6 medium and sub-cultured on this medium every 2 to 3 weeks.

The plasmid, p35S/Ac (obtained from Dr. Peter Eckes, Hoechst Ag, Frankfurt, Germany) may be used in transformation experiments in order to provide for a selectable marker. This plasmid contains the *Pat* gene (see European Patent Publication 0 242 236) which encodes phosphinothricin acetyl transferase (PAT). The enzyme PAT confers resistance to herbicidal glutamine synthetase inhibitors such as phosphinothricin. The *pat* gene in p35S/Ac is under the control of the 35S promoter from Cauliflower Mosaic Virus (Odell et al. (1985) *Nature* 313:810-812) and the 3' region of the nopaline synthase gene from the T-DNA of the Ti plasmid of *Agrobacterium tumefaciens*.

The particle bombardment method (Klein et al. (1987) *Nature* 327:70-73) may be used to transfer genes to the callus culture cells. According to this method, gold particles (1 µm in diameter) are coated with DNA using the following technique. Ten µg of plasmid DNAs are added to 50 µL of a suspension of gold particles (60 mg per mL). Calcium chloride (50 µL of a 2.5 M solution) and spermidine free base (20 µL of a 1.0 M solution) are added to the particles. The suspension is vortexed during the addition of these solutions. After

10 minutes, the tubes are briefly centrifuged (5 sec at 15,000 rpm) and the supernatant removed. The particles are resuspended in 200 μ L of absolute ethanol, centrifuged again and the supernatant removed. The ethanol rinse is performed again and the particles resuspended in a final volume of 30 μ L of ethanol. An aliquot (5 μ L) of the DNA-coated
5 gold particles can be placed in the center of a Kapton™ flying disc (Bio-Rad Labs). The particles are then accelerated into the corn tissue with a Biolistic™ PDS-1000/He (Bio-Rad Instruments, Hercules CA), using a helium pressure of 1000 psi, a gap distance of 0.5 cm and a flying distance of 1.0 cm.

For bombardment, the embryogenic tissue is placed on filter paper over agarose-
10 solidified N6 medium. The tissue is arranged as a thin lawn and covered a circular area of about 5 cm in diameter. The petri dish containing the tissue can be placed in the chamber of the PDS-1000/He approximately 8 cm from the stopping screen. The air in the chamber is then evacuated to a vacuum of 28 inches of Hg. The macrocarrier is accelerated with a helium shock wave using a rupture membrane that bursts when the He pressure in the shock
15 tube reaches 1000 psi.

Seven days after bombardment the tissue can be transferred to N6 medium that contains gluphosinate (2 mg per liter) and lacks casein or proline. The tissue continues to grow slowly on this medium. After an additional 2 weeks the tissue can be transferred to fresh N6 medium containing gluphosinate. After 6 weeks, areas of about 1 cm in diameter
20 of actively growing callus can be identified on some of the plates containing the glufosinate-supplemented medium. These calli may continue to grow when sub-cultured on the selective medium.

Plants can be regenerated from the transgenic callus by first transferring clusters of tissue to N6 medium supplemented with 0.2 mg per liter of 2,4-D. After two weeks the
25 tissue can be transferred to regeneration medium (Fromm et al. (1990) *Bio/Technology* 8:833-839).

EXAMPLE 7

Expression of Chimeric Genes in Dicot Cells

A seed-specific expression cassette composed of the promoter and transcription
30 terminator from the gene encoding the β subunit of the seed storage protein phaseolin from the bean *Phaseolus vulgaris* (Doyle et al. (1986) *J. Biol. Chem.* 261:9228-9238) can be used for expression of the instant polypeptides transformed soybean. The phaseolin cassette includes about 500 nucleotides upstream in (5') from the translation initiation codon and about 1650 nucleotides downstream (3') from the translation stop codon of phaseolin.
35 Between the 5' and 3' regions are the unique restriction endonuclease sites Nco I (which includes the ATG translation initiation codon), Sma I, Kpn I and Xba I. The entire cassette is flanked by Hind III sites.

The cDNA fragment of this gene may be generated by polymerase chain reaction (PCR) of the cDNA clone using appropriate oligonucleotide primers. Cloning sites can be incorporated into the oligonucleotides to provide proper orientation of the DNA fragment when inserted into the expression vector. Amplification is then performed as described above, and the isolated fragment is inserted into a pUC18 vector carrying the seed expression cassette.

Soybean embryos may then be transformed with the expression vector comprising sequences encoding the instant polypeptides. To induce somatic embryos, cotyledons, 3-5 mm in length dissected from surface sterilized, immature seeds of the soybean cultivar A2872, can be cultured in the light or dark at 26°C on an appropriate agar medium for 6-10 weeks. Somatic embryos which produce secondary embryos are then excised and placed into a suitable liquid medium. After repeated selection for clusters of somatic embryos which multiplied as early, globular staged embryos, the suspensions are maintained as described below.

Soybean embryogenic suspension cultures can be maintained in 35 mL liquid media on a rotary shaker, 150 rpm, at 26°C with florescent lights on a 16:8 hour day/night schedule. Cultures are subcultured every two weeks by inoculating approximately 35 mg of tissue into 35 mL of liquid medium.

Soybean embryogenic suspension cultures may then be transformed by the method of particle gun bombardment (Klein et al. (1987) *Nature* (London) 327:70, U.S. Patent No. 4,945,050). A DuPont Biolistic™ PDS1000/HE instrument (helium retrofit) can be used for these transformations.

A selectable marker gene which can be used to facilitate soybean transformation is a chimeric gene composed of the 35S promoter from Cauliflower Mosaic Virus (Odell et al. (1985) *Nature* 313:810-812), the hygromycin phosphotransferase gene from plasmid pJR225 (from *E. coli*; Gritz et al. (1983) *Gene* 25:179-188) and the 3' region of the nopaline synthase gene from the T-DNA of the Ti plasmid of *Agrobacterium tumefaciens*. The seed expression cassette comprising the phaseolin 5' region, the fragment encoding the instant polypeptides and the phaseolin 3' region can be isolated as a restriction fragment. This fragment can then be inserted into a unique restriction site of the vector carrying the marker gene.

To 50 µL of a 60 mg/mL 1 µm gold particle suspension is added (in order): 5 µL DNA (1 µg/µL), 20 µl spermidine (0.1 M), and 50 µL CaCl₂ (2.5 M). The particle preparation is then agitated for three minutes, spun in a microfuge for 10 seconds and the supernatant removed. The DNA-coated particles are then washed once in 400 µL 70% ethanol and resuspended in 40 µL of anhydrous ethanol. The DNA/particle suspension can be sonicated three times for one second each. Five µL of the DNA-coated gold particles are then loaded on each macro carrier disk.

Approximately 300-400 mg of a two-week-old suspension culture is placed in an empty 60x15 mm petri dish and the residual liquid removed from the tissue with a pipette. For each transformation experiment, approximately 5-10 plates of tissue are normally bombarded. Membrane rupture pressure is set at 1100 psi and the chamber is evacuated to a vacuum of 28 inches mercury. The tissue is placed approximately 3.5 inches away from the retaining screen and bombarded three times. Following bombardment, the tissue can be divided in half and placed back into liquid and cultured as described above.

Five to seven days post bombardment, the liquid media may be exchanged with fresh media, and eleven to twelve days post bombardment with fresh media containing 50 mg/mL hygromycin. This selective media can be refreshed weekly. Seven to eight weeks post bombardment, green, transformed tissue may be observed growing from untransformed, necrotic embryogenic clusters. Isolated green tissue is removed and inoculated into individual flasks to generate new, clonally propagated, transformed embryogenic suspension cultures. Each new line may be treated as an independent transformation event. These suspensions can then be subcultured and maintained as clusters of immature embryos or regenerated into whole plants by maturation and germination of individual somatic embryos.

EXAMPLE 8

Expression of Chimeric Genes in Microbial Cells

The rice PC4 gene of the instant invention was expressed in *E. coli* in the following manner. *Nco*I and *Xho*I sites were introduced into rice PC4 cDNA (clone rr1.pk0003.a12) around its translation initiation and stop codons respectively by *in vitro* mutagenesis according to the instructions of the *in vitro* mutagenesis kit manufacturer (Pharmacia Biotech). The *Nco*I and *Xho*I fragment of rice PC4 DNA was then inserted into the *Nco*I and *Xho*I sites of the pRet vector (Novagen) which is a modified version of pET29 (Novagen) to generate pRet/PC4. The pRet/PC4 construct contains a S-peptide tag at the N-terminus and a 6xHis-tag at the C-terminus of the expressed protein. This construct was transformed into *E. coli* BL21 (DE3) cells. rPC4 was bound in batch to Ni-NTA agarose resin (Qiagen) and eluted with an imidazole gradient. The purification was analyzed by SDS-PAGE and Coomassie Blue staining. Fractions having high level of rPC4 were subjected to secondary purification, which was carried out using an S-tag purification kit (Novagen, Madison WI). rPC4 was eluted from the S-protein agarose by thrombin digestion, leaving the S-tag domain on the resin. The purification was analyzed by SDS-PAGE and Coomassie Blue staining. The purified rPC4 was partially denatured with 2 M urea, and dialyzed in renaturation buffer (20 mM Hepes-KOH, 1 mM MgCl₂, 50 mM KCl, 1 mM DTT, 20% glycerol and 0.02% NP40) overnight, frozen in liquid N₂ and stored at -80°C.

The purified rPC4 was analyzed by gel electrophoresis in a 4-20% Tris-Glycine gel (Sigma-Aldrich) and rPC4 was the only protein detected by Coomassie Brilliant Blue

staining. The calculated molecular weight (MW) of S-tag-cleaved rPC4 (rPC4S-) is 12 kDa.

In yeast and human systems, PC4 has been shown to bind to both ssDNA and dsDNA, independent of DNA sequence, having a higher affinity for ssDNA (Ge et al. (1994) *Cell* 78:513-523; Henry et al. (1996) *J. Biol. Chem.* 271:21842-21847; Kaiser et al. (1995) *EMBO J.* 14:3520-3527; Kretzschmar et al. (1994) *Cell* 78:525-534; and Werten et al. (1998) *EMBO J.* 5:5103-5111). In order to study the function of the rice PC4 homolog, purified rPC4 was used to assess its DNA binding activities. These results of these experiments suggest that purified rPC4 can bind both ssDNA and dsDNA which is in agreement with what has been demonstrated with its homologues in yeast and mammalian systems.

CLAIMS

What is claimed is:

1. An isolated nucleic acid fragment encoding a PC4(P15) Type 1 transcriptional coactivator comprising a member selected from the group consisting of:
 - 5 (a) an isolated nucleic acid fragment encoding an amino acid sequence that is at least 90 amino acids in length and is at least 80% identical to the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:2, 6, 8, 10 and 12;
 - (b) an isolated nucleic acid fragment that is complementary to (a).
- 10 2. The isolated nucleic acid fragment of Claim 1 wherein nucleic acid fragment is a functional RNA.
3. The isolated nucleic acid fragment of Claim 1 wherein the nucleotide sequence of the fragment comprises the sequence set forth in a member selected from the group consisting of SEQ ID NO:1, 5, 7, 9 and 11.
- 15 4. A chimeric gene comprising the nucleic acid fragment of Claim 1 operably linked to suitable regulatory sequences.
5. A transformed host cell comprising the chimeric gene of Claim 4.
6. A PC4(P15) Type 1 transcriptional coactivator polypeptide comprising all or a substantial portion of the amino acid sequence set forth in a member selected from the group
20 consisting of SEQ ID NO:2, 6, 8, 10 and 12.
7. An isolated nucleic acid fragment encoding a functional PC4(P15) Type 1 transcriptional coactivator comprising a member selected from the group consisting of:
 - 25 (a) an isolated nucleic acid fragment encoding an amino acid sequence that is at least 90 amino acids in length and is at least 80% identical to the amino acid sequence set forth in SEQ ID NO:4;
 - (b) an isolated nucleic acid fragment that is complementary to (a).
8. The isolated nucleic acid fragment of Claim 7 wherein nucleic acid fragment is a functional RNA.
9. The isolated nucleic acid fragment of Claim 7 wherein the nucleotide sequence
30 of the fragment comprises the sequence set forth in SEQ ID NO:3.
10. A chimeric gene comprising the nucleic acid fragment of Claim 7 operably linked to suitable regulatory sequences.
11. A transformed host cell comprising the chimeric gene of Claim 10.
12. A PC4(P15) Type 1 transcriptional coactivator polypeptide comprising all or a
35 substantial portion of the amino acid sequence set forth in SEQ ID NO:4.
13. An isolated nucleic acid fragment encoding a PC4(P15) Type 2 transcriptional coactivator comprising a member selected from the group consisting of:

- (a) an isolated nucleic acid fragment encoding a amino acid sequence that is at least 100 amino acids in length and is at least 80% identical to the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:14, 16 and 18;
- 5 (b) an isolated nucleic acid fragment that is complementary to (a).
14. The isolated nucleic acid fragment of Claim 13 wherein nucleic acid fragment is a functional RNA.
15. The isolated nucleic acid fragment of Claim 13 wherein the nucleotide sequence of the fragment comprises the sequence set forth in a member selected from the
- 10 group consisting of SEQ ID NO:14, 16 and 18.
16. A chimeric gene comprising the nucleic acid fragment of Claim 13 operably linked to suitable regulatory sequences.
17. A transformed host cell comprising the chimeric gene of Claim 16.
18. A PC4(P15) Type 2 transcriptional coactivator polypeptide comprising all or a
- 15 substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:14, 16 and 18.
19. A method of altering the level of expression of a PC4 transcription coactivator in a host cell comprising:
- (a) transforming a host cell with the chimeric gene of any of Claims 4, 10
- 20 and 16; and
- (b) growing the transformed host cell produced in step (a) under conditions that are suitable for expression of the chimeric gene
- wherein expression of the chimeric gene results in production of altered levels of a PC4 transcription coactivator in the transformed host cell.
- 25 20. A method of obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence encoding a PC4 transcription coactivator comprising:
- (a) probing a cDNA or genomic library with the nucleic acid fragment of any of Claims 1, 7 and 13;
- (b) identifying a DNA clone that hybridizes with the nucleic acid fragment
- 30 of any of Claims 1, 7 and 13;
- (c) isolating the DNA clone identified in step (b); and
- (d) sequencing the cDNA or genomic fragment that comprises the clone isolated in step (c)
- wherein the sequenced nucleic acid fragment encodes all or a substantial portion of the
- 35 amino acid sequence encoding a PC4 transcription coactivator.
21. A method of obtaining a nucleic acid fragment encoding a substantial portion of an amino acid sequence encoding a PC4 transcription coactivator comprising:

- (a) synthesizing an oligonucleotide primer corresponding to a portion of the sequence set forth in any of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15 and 17; and
- 5 (b) amplifying a cDNA insert present in a cloning vector using the oligonucleotide primer of step (a) and a primer representing sequences of the cloning vector

wherein the amplified nucleic acid fragment encodes a substantial portion of an amino acid sequence encoding a PC4 transcription coactivator.

22. The product of the method of Claim 20.
- 10 23. The product of the method of Claim 21.

1/1

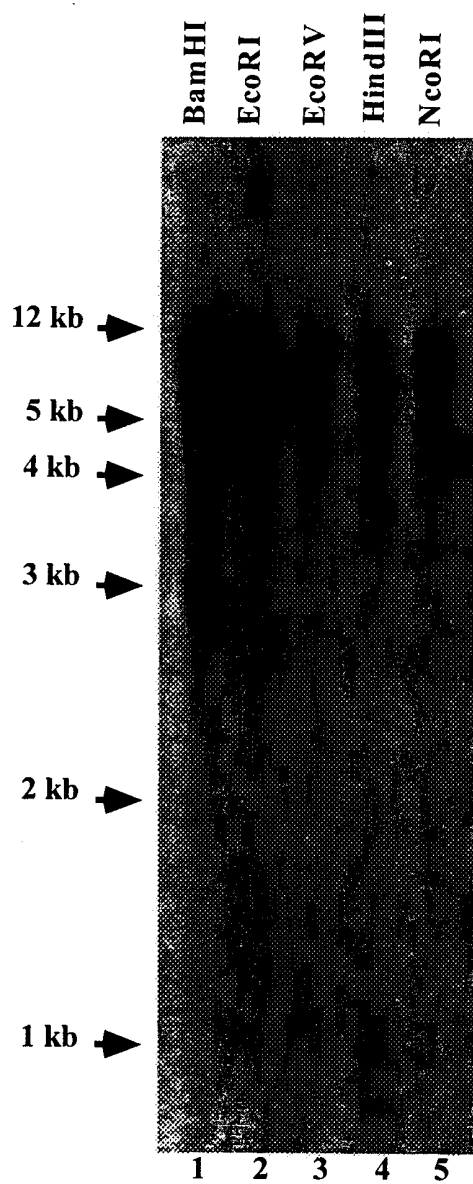


Figure 1

SEQUENCE LISTING

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 Gln Trp Glu Ala Phe Cys Asn Ala Val Pro Ala Ile Glu Asp Ala Ile
 165 170 175
 Lys Lys Leu Glu Asp Ser Asp
 180

<210> 15
 <211> 939
 <212> DNA
 <213> Zea mays

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 gcgaaggcgg cggaggaggg cgacgctggc agggagagca aggacaagga acggaaggaa 180
 gatgaggagg aggatgaagg taagggtggc gggaagagag agtacgacga ccaagggtgac 240
 cttatcctgt gccgcctttc gagcaagagg aggggtgactt tatcggagtt taagggcagg 300
 tcgttggtgt ccatccgcga gttctacgtg aaggacggca aggagatgcc ctccgccaaa 360
 ggtattagta tgactttgga gcagtgggaa gcattttgca atgctgtacc tgcaatagac 420
 gatgccatca aaaagcttga agattcagac tgaactggtt ttaagagcct cttcttatgc 480

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ccgtgtcaaa tgaaaaagcc tgggaagcat ttcgcaatgc tgtatctgca atagatgatg 540
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caaataaaaa agcctatttc tgacccttaa cgagggccat atatgtgtct tgcaagagct 660
aagttctgta aaagatttct acatgtacca tgtgtaggag ttaggataga gtgatagacg 720
tactgtgca tacagttcgg aatatttgct agtaacaagt aatctaccat taggtggcct 780
ggattcacat gctatgctat gtgatgatcg gggatgtgtc ctagcaatag caagtcatga 840
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<210> 16
 <211> 140
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 Ala Ala Glu Glu Gly Asp Ala Gly Arg Glu Ser Lys Asp Lys Glu Arg
 35 40 45
 Lys Glu Asp Glu Glu Glu Asp Glu Gly Lys Gly Gly Gly Lys Arg Glu
 50 55 60
 Tyr Asp Asp Gln Gly Asp Leu Ile Leu Cys Arg Leu Ser Ser Lys Arg
 65 70 75 80
 Arg Val Thr Leu Ser Glu Phe Lys Gly Arg Ser Leu Val Ser Ile Arg
 85 90 95
 Glu Phe Tyr Val Lys Asp Gly Lys Glu Met Pro Ser Ala Lys Gly Ile
 100 105 110
 Ser Met Thr Leu Glu Gln Trp Glu Ala Phe Cys Asn Ala Val Pro Ala
 115 120 125
 Ile Glu Asp Ala Ile Lys Lys Leu Glu Asp Ser Asp
 130 135 140

<210> 17
 <211> 740
 <212> DNA
 <213> Glycine max

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 gacctgtctc agccttattt caaagccttt gtcaaacagg tcgtgaaggc ttttctccaa 180
 gaagaagaac aacgacagaa acaacaacaa caagatgaag atgaagaaga agaactagga 240
 ggaggttcca agggcaagga gtacgatgat gaaggcgatc tcatcatctg caggctttca 300
 gataagagaa gggtagcat tcaggatttc agagggaaaa cattggtctc cattcgggag 360
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 cagtggtcag cctttaagaa aaatgtgcct gccatagaaa aagccattaa gaaaatggag 480
 tcaagttgac acatggcttt gcttgtttct ttttgttgaa tatatcctgc accgcacat 540
 ggtgcctctt tgatattgga ccattttgtt aaaggacttg gagtcaactgt ttaagtgtt 600
 tgcaacctga gtgcctaaag ccatttcagg aagactaaac tgaatgccag taactttaaa 660

aactcaatac atttaattct gttaaaaaaa aaaaaaaata cttgaggggg cgccggggcca 720
 ggtaaggga ggggggaccg 740

<210> 18
 <211> 141
 <212> PRT
 <213> Glycine max

<400> 18
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 Leu Gly Leu Asp Leu Ser Gln Pro Tyr Phe Lys Ala Phe Val Lys Gln
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 Val Val Lys Ala Phe Leu Gln Glu Glu Gln Arg Gln Lys Gln Gln
 35 40 45
 Gln Gln Asp Glu Asp Glu Glu Glu Glu Leu Gly Gly Gly Ser Lys Gly
 50 55 60
 Lys Glu Tyr Asp Asp Glu Gly Asp Leu Ile Ile Cys Arg Leu Ser Asp
 65 70 75 80
 Lys Arg Arg Val Thr Ile Gln Asp Phe Arg Gly Lys Thr Leu Val Ser
 85 90 95
 Ile Arg Glu Tyr Tyr Lys Lys Asp Gly Lys Glu Leu Pro Thr Ser Lys
 100 105 110
 Gly Ile Ser Leu Thr Glu Glu Gln Trp Ser Ala Phe Lys Lys Asn Val
 115 120 125
 Pro Ala Ile Glu Lys Ala Ile Lys Lys Met Glu Ser Ser
 130 135 140

<210> 19
 <211> 83
 <212> PRT
 <213> Arabidopsis thaliana

<400> 19
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 Ser Thr His Ala Ala Lys Lys Val Ala Lys Ala Asp Asp Ser Asp Ser
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 Asp Asp Val Val Cys Asn Ser Lys Asn Arg Arg Val Ser Val Arg Asn
 35 40 45
 Trp Asn Gly Lys Trp Asp Arg Tyr Val Lys Asp Gly Lys Thr Gly Lys
 50 55 60
 Lys Gly Ser Ser Val Asp Trp Asn Thr Arg Asn His Ala Asp Lys Ala
 65 70 75 80
 Ser Asp Ser

<210> 20
 <211> 165
 <212> PRT
 <213> Arabidopsis thaliana putative transcriptional coactivator

 <400> 20
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 1 5 10 15

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 20 25 30

 Leu Ala Ser Glu Lys Leu Ala Ile Asp Leu Ser Glu Lys Ser His Lys
 35 40 45

 Ala Phe Val Arg Ser Val Val Glu Lys Phe Leu Asp Glu Glu Arg Ala
 50 55 60

 Arg Glu Tyr Glu Asn Ser Gln Val Asn Lys Glu Glu Glu Asp Gly Asp
 65 70 75 80

 Lys Asp Cys Gly Lys Gly Asn Lys Glu Phe Asp Asp Asp Gly Asp Leu
 85 90 95

 Ile Ile Cys Arg Leu Ser Asp Lys Arg Arg Val Thr Ile Gln Glu Phe
 100 105 110

 Lys Gly Lys Ser Leu Val Ser Ile Arg Glu Tyr Tyr Lys Lys Asp Gly
 115 120 125

 Lys Glu Leu Pro Thr Ser Lys Gly Ile Ser Leu Thr Asp Glu Gln Trp
 130 135 140

 Ser Thr Phe Lys Lys Asn Met Pro Ala Ile Glu Asn Ala Val Lys Lys
 145 150 155 160

 Met Glu Ser Arg Val
 165