

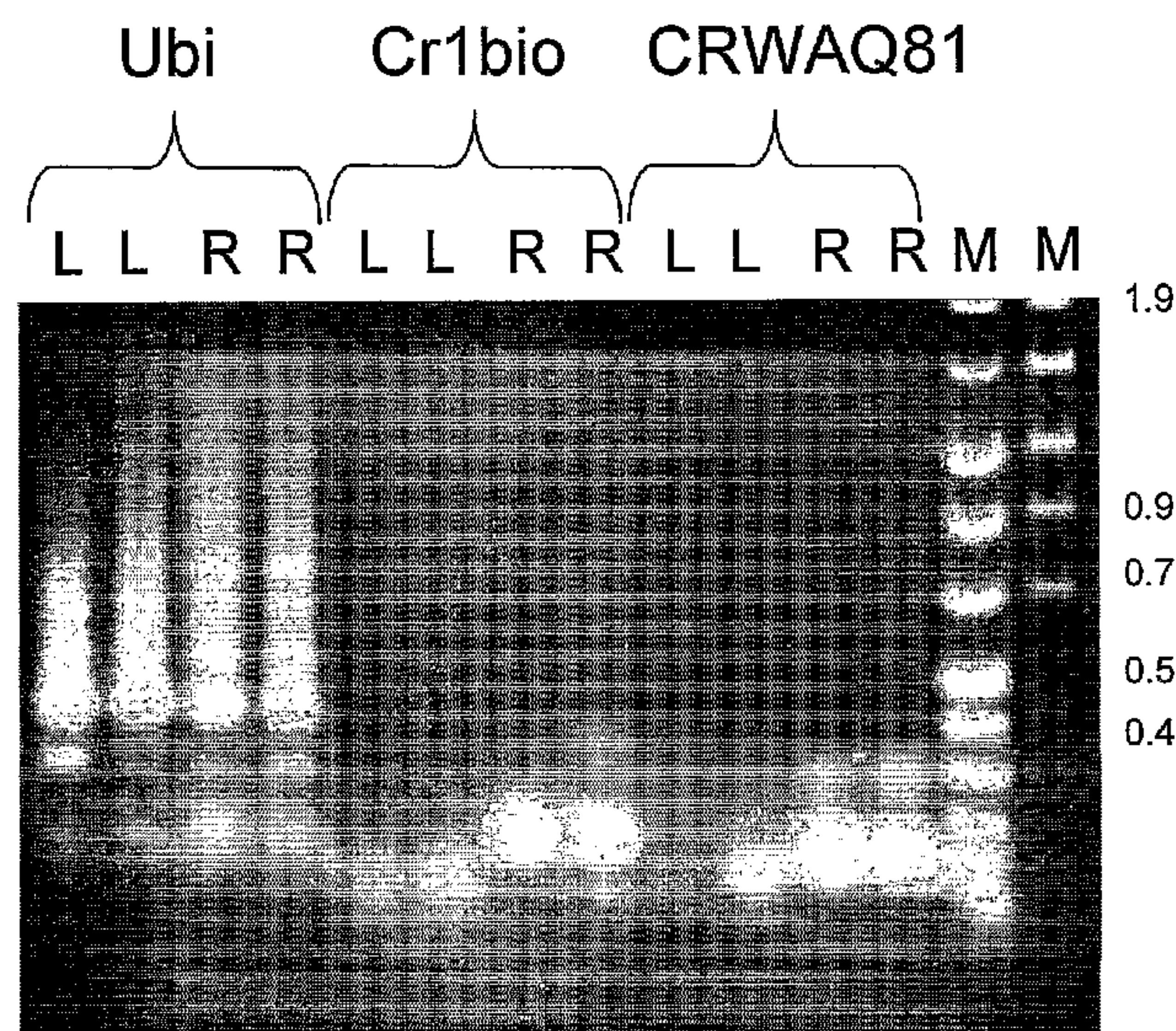


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(54) Titre : PROMOTEUR DU GENE DE MAIS CR1BIO ET UTILISATION DANS L'EXPRESSION TRANSGENIQUE DES
PLANTES A LA RACINE
(54) Title: MAIZE CR1BIO GENE PROMOTER AND ITS USE TO DIRECT ROOT-PREFERRED TRANSGENE
EXPRESSION IN PLANTS

Gel Showing Root Preferred Expression of Cr1bio



Controls: Ubiquitin for leaf and root
CRWAQ81 for root preferred

(57) Abrégé/Abstract:

The present invention provides compositions and methods for regulating expression of heterologous nucleotide sequences in a plant. Compositions include a novel nucleotide sequence for a root-preferred promoter for the gene encoding Cr1Bio. A method for expressing a heterologous nucleotide sequence in a plant using the promoter sequences disclosed herein is provided. The method comprises stabling incorporating into the genome of a plant cell a nucleotide sequence operably linked to the root-preferred promoter of the present invention and regenerating a stably transformed plant that expresses the nucleotide sequence.

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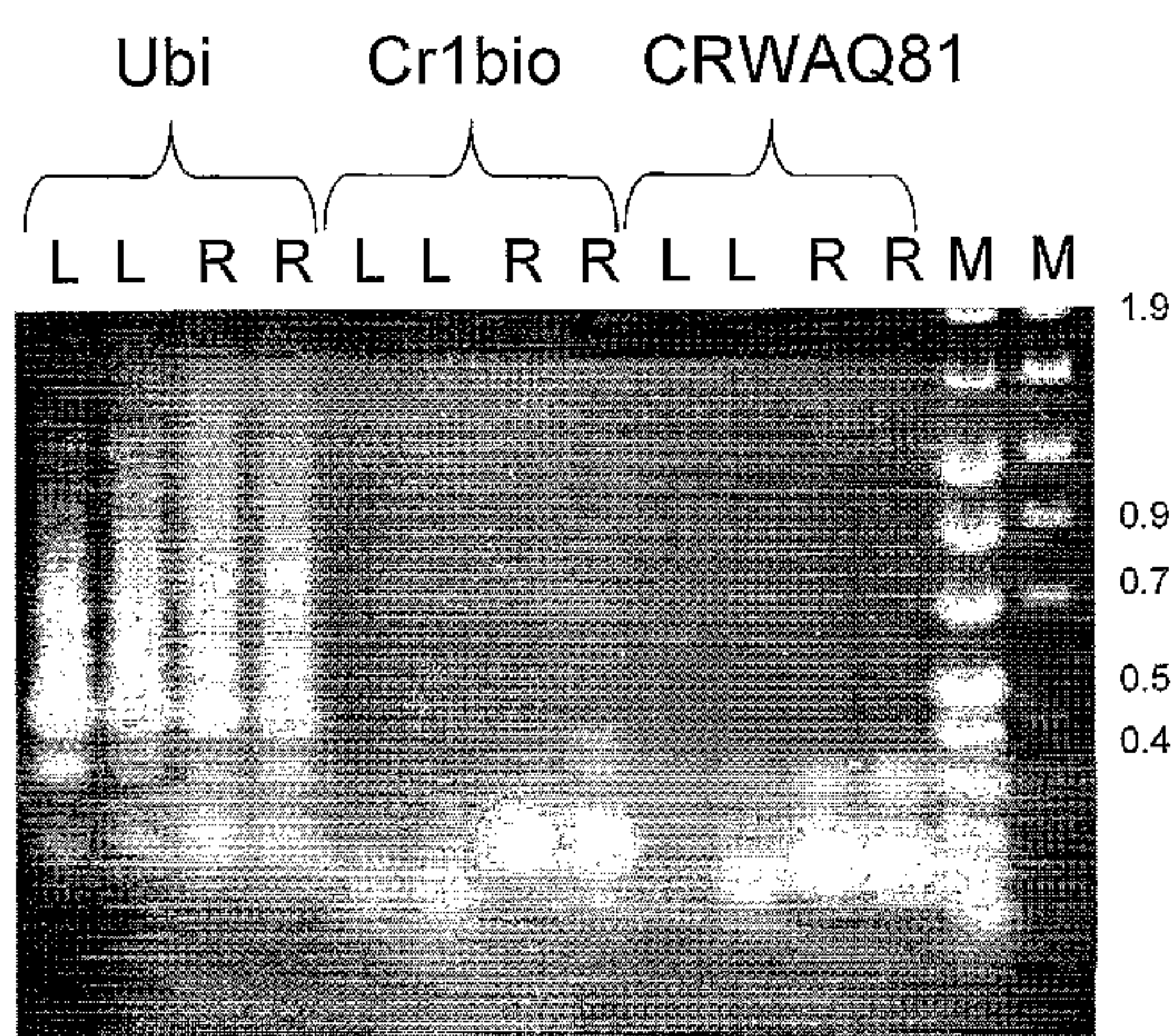
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MAIZE CR1BIO GENE PROMOTER AND ITS USE TO DIRECT ROOT-PREFERRED TRANSGENE EXPRESSION IN PLANTS

FIELD OF THE INVENTION

The present invention relates to the field of plant molecular biology, more
5 particularly to regulation of gene expression in plants.

BACKGROUND OF THE INVENTION

Recent advances in plant genetic engineering have enabled the engineering
of plants having improved characteristics or traits, such as disease resistance,
10 insect resistance, herbicide resistance, enhanced stability or shelf-life of the ultimate
consumer product obtained from the plants and improvement of the nutritional
quality of the edible portions of the plant. Thus, one or more desired genes from a
source different than the plant, but engineered to impart different or improved
characteristics or qualities, can be incorporated into the plant's genome. New
15 gene(s) can then be expressed in the plant cell to exhibit the desired phenotype
such as a new trait or characteristic.

The proper regulatory signals must be present and be in the proper location
with respect to the gene in order to obtain expression of the newly inserted gene in
the plant cell. These regulatory signals may include a promoter region, a 5' non-
20 translated leader sequence and a 3' transcription termination/polyadenylation
sequence.

A promoter is a DNA sequence that directs cellular machinery of a plant to
produce RNA from the contiguous coding sequence downstream (3') of the
promoter. The promoter region influences the rate, developmental stage, and cell
25 type in which the RNA transcript of the gene is made. The RNA transcript is
processed to produce messenger RNA (mRNA) which serves as a template for
translation of the RNA sequence into the amino acid sequence of the encoded
polypeptide. The 5' non-translated leader sequence is a region of the mRNA
upstream of the protein coding region that may play a role in initiation and
30 translation of the mRNA. The 3' transcription termination/polyadenylation signal is a

non-translated region downstream of the protein coding region that functions in the plant cells to cause termination of the RNA transcript and the addition of polyadenylate nucleotides to the 3' end of the RNA.

Expression of heterologous DNA sequences in a plant host is dependent upon the presence of an operably linked promoter that is functional within the plant host. The type of promoter sequence chosen is based on when and where within the organism expression of the heterologous DNA is desired. Where expression in specific tissues or organs is desired, tissue-preferred promoters may be used. Where gene expression in response to a stimulus is desired, inducible promoters are the regulatory element of choice. In contrast, where continuous expression is desired throughout the cells of a plant, constitutive promoters are utilized.

An inducible promoter is a promoter that is capable of directly or indirectly activating transcription of one or more DNA sequences or genes in response to an inducer. In the absence of an inducer, the DNA sequences or genes will not be transcribed or will be transcribed at a level lower than in an induced state. The inducer can be a chemical agent, such as a metabolite, growth regulator, herbicide or phenolic compound, or a physiological stress directly imposed upon the plant such as cold, heat, salt, drought, or toxins. In the case of fighting plant pests, it is also desirable to have a promoter which is induced by plant pathogens, including plant insect pests, nematodes or disease agents such as a bacterium, virus or fungus. Contact with the pathogen will induce activation of transcription, such that a pathogen-fighting protein will be produced at a time when it will be effective in defending the plant. A pathogen-induced promoter may also be used to detect contact with a pathogen, for example by expression of a detectable marker, so that the need for application of pesticides can be assessed. A plant cell containing an inducible promoter may be exposed to an inducer by externally applying the inducer to the cell or plant such as by spraying, watering, heating, or by exposure to the operative pathogen.

A constitutive promoter is a promoter that directs expression of a gene throughout the various parts of a plant and continuously throughout plant development. Examples of some constitutive promoters that are widely used for inducing the expression of heterologous genes in transgenic plants include the nopaline synthase (NOS) gene promoter, from *Agrobacterium tumefaciens*, (U.S.

Patent No. 5,034,322), the cauliflower mosaic virus (CaMv) 35S and 19S promoters (U.S. Patent No. 5,352,605), those derived from any of the several actin genes, which are known to be expressed in most cells types (U.S. Patent No. 6,002,068), and the ubiquitin promoter, which is a gene product known to accumulate in many
5 cell types.

Additional regulatory sequences upstream and/or downstream from the core promoter sequence may be included in expression constructs of transformation vectors to bring about varying levels of expression of heterologous nucleotide sequences in a transgenic plant. Genetically altering plants through the use of
10 genetic engineering techniques to produce plants with useful traits thus requires the availability of a variety of promoters.

In order to maximize the commercial application of transgenic plant technology, it is important to direct the expression of the introduced DNA in a site-specific manner. For example, it is desirable to produce toxic defensive compounds
15 in tissues subject to pathogen attack, but not in tissues that are to be harvested and eaten by consumers. By site-directing the synthesis or storage of desirable proteins or compounds, plants can be manipulated as factories, or production systems, for a tremendous variety of compounds with commercial utility. Cell-specific promoters provide the ability to direct the synthesis of compounds, spatially and temporally, to
20 highly specialized tissues or organs, such as roots, leaves, vascular tissues, embryos, seeds, or flowers.

Alternatively, it might be desirable to inhibit expression of a native DNA sequence within a plant's tissues to achieve a desired phenotype. Such inhibition might be accomplished with transformation of the plant to comprise a tissue-
25 preferred promoter operably linked to an antisense nucleotide sequence, such that expression of the antisense sequence produces an RNA transcript that interferes with translation of the mRNA of the native DNA sequence.

To date, the regulation of gene expression in plant roots has not been adequately studied despite the root's importance to plant development. To some
30 degree this is attributable to a lack of readily available, root-specific biochemical functions whose genes may be cloned, studied, and manipulated. Several genes that are preferentially expressed in plant root tissues have been identified. See, for example, Takahashi *et al.* (1991) *Plant J.* 1:327-332; Takahashi *et al.* (1990) *Proc.*

Natl. Acad. Sci. USA 87:8013-8016; Hertig *et al.* (1991) *Plant Mol Biol.* 16:171-174; Xu *et al.* (1995) *Plant Mol. Biol.* 27:237-248; Capone *et al.* (1994) *Plant Mol. Biol.* 25:681-691; Masuda *et al.* (1999) *Plant Cell Physiol.* 40(11):1177-81; Luschnig *et al.* (1998) *Genes Dev.* 12(14):2175-87; Goddemeier *et al.* (1998) *Plant Mol. Biol.* 36(5):799-802; and Yamamoto *et al.* (1991) *Plant Cell* 3(4):371-82. Though root-specific promoters have been characterized in several types of plants, no root specific promoters from maize have been described in the literature.

Constitutive expression of some heterologous proteins, such as insecticides, leads to undesirable phenotypic and agronomic effects. Limiting expression of insecticidal proteins, for example, to the target tissues of insect feeding (root, in this case), allows the plant to devote more energy to normal growth rather than toward expression of the protein throughout the plant. Using root-preferred promoters, one can also limit expression of the protein in non-desirable portions of the plant. However, many of the root-preferred promoters that have been isolated do not direct the expression of sufficient amounts of transgene for efficacy in plants. Thus, the isolation and characterization of tissue-preferred, particularly root-preferred, promoters that can direct transcription of a sufficiently high level of a desired heterologous nucleotide sequence is needed.

Since the patterns of expression of a chimeric gene (or genes) introduced into a plant are controlled using promoters, there is an ongoing interest in the isolation and identification of novel promoters which are capable of controlling expression of a chimeric gene or (genes).

SUMMARY OF THE INVENTION

Compositions and methods for regulating gene expression in a plant are provided. Compositions comprise novel nucleotide sequences for an inducible promoter that initiates transcription in a root-preferred manner. More particularly, a transcriptional initiation region isolated from maize is provided. Further embodiments of the invention comprise the nucleotide sequence set forth in SEQ ID NO:1 and a fragment of SEQ ID NO: 1, which is set forth in SEQ ID NO:2. These plant promoter sequences were deposited with the American Type Culture Collection (ATCC) on November 3, 2004 in bacterial hosts as Patent Deposit No. PTA-6275. The compositions of the embodiments further comprise nucleotide

sequences having at least 95% sequence identity to the sequences set forth in SEQ ID NOs:1 and 2, and which drive root-preferred expression of an operably linked nucleotide sequence. Also included are functional fragments of the sequence set forth as SEQ ID NOs:1 and 2 which drive root-preferred expression of an operably linked nucleotide sequence.

Compositions of the present invention also include DNA constructs comprising a promoter of the embodiments operably linked to a heterologous nucleotide sequence of interest wherein said promoter is capable of driving expression of said nucleotide sequence in a plant cell and said promoter comprises the nucleotide sequences of the present invention. The embodiments further provide expression vectors, and plants or plant cells having stably incorporated into their genomes a DNA construct mentioned above. Additionally, compositions include transgenic seed of such plants.

Methods of the embodiments comprise a means for selectively expressing a nucleotide sequence in a plant root, comprising transforming a plant cell with a DNA construct, and regenerating a transformed plant from said plant cell, said DNA construct comprising a promoter and a heterologous nucleotide sequence operably linked to said promoter, wherein said promoter initiates root-preferred transcription of said nucleotide sequence in a plant cell. In this manner, the promoter sequences are useful for controlling the expression of operably linked coding sequences in a root-preferred manner.

Downstream from and under the transcriptional initiation regulation of the promoter will be a sequence of interest that will provide for modification of the phenotype of the plant. Such modification includes modulating the production of an endogenous product, as to amount, relative distribution, or the like, or production of an exogenous expression product to provide for a novel function or product in the plant. For example, a heterologous nucleotide sequence that encodes a gene product that confers herbicide, salt, cold, drought, pathogen or insect resistance is encompassed.

In a further aspect, methods of the embodiments relate to a method for modulating expression of a gene in the root of a stably transformed plant comprising the steps of (a) transforming a plant cell with a DNA construct comprising the promoter of the present invention operably linked to at least one

nucleotide sequence; (b) growing the plant cell under plant growing conditions and (c) regenerating a stably transformed plant from the plant cell wherein expression of the nucleotide sequence alters the phenotype of the plant.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the sequence of the Cr1Bio promoter sequence. The positions of the TATA box, the transcriptional start site (TSS) mapped by 5' RACE, the location of the truncated promoter relative to the full sequence, and other motifs of interest.

Figure 2 is a picture of PCR products generated as part of the 5' RACE protocol, showing the root-preferred expression pattern of the Cr1Bio promoter. Controls include the ubiquitin promoter for expression in leaf and root tissues, and the CRWAQ81 promoter (See U.S. Patent Application Serial No. 10/961,629) for root-preferred expression.

DETAILED DESCRIPTION OF THE INVENTION

The compositions of the present invention comprise novel nucleotide sequences for plant promoters, particularly a root-preferred promoter for a maize Cr1Bio gene, more particularly, the Cr1Bio gene promoter. In particular, the present invention provides for isolated nucleic acid molecules comprising the nucleotide sequence set forth in SEQ ID NOs:1 and 2, and the plant promoter sequence deposited in bacterial hosts as Patent Deposit No. PTA-6275, on November 3, 2004, and fragments, variants, and complements thereof.

Plasmids containing the plant promoter nucleotide sequences of the embodiments were deposited on November 3, 2004 with the Patent Depository of the American Type Culture Collection (ATCC), at 10801 University Blvd., Manassas, VA 20110-2209, and assigned Patent Deposit No. PTA-6275. This deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. This deposit was made merely as a convenience for those of skill in the art and is not an admission that a deposit is required under 35 U.S.C. §112. The deposit will irrevocably and without restriction or condition be available

to the public upon issuance of a patent. However, it should be understood that the availability of a deposit does not constitute a license to practice the subject invention in derogation of patent rights granted by government action.

The promoter sequences of the embodiments are useful for expressing operably linked nucleotide sequences in a tissue-preferred, particularly a root-preferred manner. The sequences of the embodiments also find use in the construction of expression vectors for subsequent transformation into plants of interest, as probes for the isolation of other Cr1Bio gene promoters, as molecular markers, and the like.

The Cr1Bio promoter of the embodiments was isolated from maize genomic DNA. The specific method used to obtain the Cr1Bio promoter of the present invention is described in detail in Examples 3 and 4 in the experimental section of this application.

The embodiments encompass isolated or substantially purified nucleic acid compositions. An "isolated" or "purified" nucleic acid molecule, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. Generally, an "isolated" nucleic acid is free of sequences (for example, protein encoding sequences) that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived.

The Cr1Bio gene encodes a gene product that is a homologue of CRWAQ81 (See U.S. Patent Application Serial No. 10/961,629), a root specific maize gene with unknown function. The identity to CRWAQ81 at the amino acid level is 86%. The maize Cr1Bio gene is preferentially expressed in maize root tissue as demonstrated by gene tissue profile comparisons derived from Lynx Massively Parallel Signature Sequencing (MPSS), as further discussed in Example 1.

The Cr1Bio promoter sequences of the present invention direct expression of operably linked nucleotide sequences in a root-preferred manner. Therefore, the

Cr1Bio promoter sequences find use in the root-preferred expression of an operably linked nucleotide sequence of interest.

The compositions of the embodiments include isolated nucleic acid molecules comprising the promoter nucleotide sequence set forth in SEQ ID NOs: 1 and 2. The term "promoter" is intended to mean a regulatory region of DNA usually comprising a TATA box capable of directing RNA polymerase II to initiate RNA synthesis at the appropriate transcription initiation site for a particular coding sequence. A promoter may additionally comprise other recognition sequences generally positioned upstream or 5' to the TATA box, referred to as upstream promoter elements, which influence the transcription initiation rate. It is recognized that having identified the nucleotide sequences for the promoter regions disclosed herein, it is within the state of the art to isolate and identify further regulatory elements in the 5' untranslated region upstream from the particular promoter regions identified herein. Thus, for example, the promoter regions disclosed herein may further comprise upstream regulatory elements such as those responsible for tissue and temporal expression of the coding sequence, enhancers, and the like. See particularly Australian Patent No. AU-A-77751/94 and U.S. Patent Nos. 5,466,785 and 5,635,618. In the same manner, the promoter elements that enable expression in the desired tissue such as the root, can be identified, isolated, and used with other core promoters to confer root-preferred expression. In this aspect of the embodiments, a "core promoter" is intended to mean a promoter without promoter elements.

In the context of this disclosure, the term "regulatory element" also refers to a sequence of DNA, usually, but not always, upstream (5') to the coding sequence of a structural gene, which includes sequences which control the expression of the coding region by providing the recognition for RNA polymerase and/or other factors required for transcription to start at a particular site. An example of a regulatory element that provides for the recognition for RNA polymerase or other transcriptional factors to ensure initiation at a particular site is a promoter element. A promoter element comprises a core promoter element, responsible for the initiation of transcription, as well as other regulatory elements (as discussed elsewhere in this application) that modify gene expression. It is to be understood that nucleotide sequences, located within introns, or 3' of the coding region

sequence may also contribute to the regulation of expression of a coding region of interest. Examples of suitable introns include, but are not limited to, the maize IVS6 intron, or the maize actin intron. A regulatory element may also include those elements located downstream (3') to the site of transcription initiation, or within
5 transcribed regions, or both. In the context of the present invention a post-transcriptional regulatory element may include elements that are active following transcription initiation, for example translational and transcriptional enhancers, translational and transcriptional repressors, and mRNA stability determinants.

The regulatory elements, or fragments thereof, of the present invention may
10 be operatively associated with heterologous regulatory elements or promoters in order to modulate the activity of the heterologous regulatory element. Such modulation includes enhancing or repressing transcriptional activity of the heterologous regulatory element, modulating post-transcriptional events, or both enhancing or repressing transcriptional activity of the heterologous regulatory
15 element and modulating post-transcriptional events. For example, one or more regulatory elements, or fragments thereof, of the present invention may be operatively associated with constitutive, inducible, or tissue specific promoters or fragment thereof, to modulate the activity of such promoters within desired tissues within plant cells.

20 The maize Cr1Bio root-preferred promoter sequence of the present invention, when assembled within a DNA construct such that the promoter is operably linked to a nucleotide sequence of interest, enables expression of the nucleotide sequence in the cells of a plant stably transformed with this DNA construct. The term "operably linked" is intended to mean that the transcription or
25 translation of the heterologous nucleotide sequence is under the influence of the promoter sequence. "Operably linked" is also intended to mean the joining of two nucleotide sequences such that the coding sequence of each DNA fragment remain in the proper reading frame. In this manner, the nucleotide sequences for the promoters of the embodiments are provided in DNA constructs along with the
30 nucleotide sequence of interest, typically a heterologous nucleotide sequence, for expression in the plant of interest. The term "heterologous nucleotide sequence" is intended to mean a sequence that is not naturally operably linked with the promoter sequence. While this nucleotide sequence is heterologous to the promoter

sequence, it may be homologous, or native; or heterologous, or foreign, to the plant host.

The regulatory sequences of the present invention, when operably linked to a heterologous nucleotide sequence of interest and stably incorporated into the plant genome drive "root-preferred" expression of the heterologous nucleotide sequence. The term, "root-preferred" is intended to mean that expression of the heterologous nucleotide sequence is most abundant in the root. The term "root" is intended to mean any part of the root structure, including but not limited to, the root cap, apical meristem, protoderm, ground meristem, procambium, endodermis, cortex, vascular cortex, epidermis, and the like. While some level of expression of the heterologous nucleotide sequence may occur in other plant tissue types, expression occurs most abundantly in the root; which may include, but is not limited to primary, lateral, and adventitious roots.

It is recognized that the promoters of the embodiments thereof may be used with their native coding sequences to increase or decrease expression, thereby resulting in a change in phenotype of the transformed plant.

Modifications of the isolated promoter sequences of the present invention can provide for a range of expression of the heterologous nucleotide sequence. Thus, they may be modified to be weak promoters or strong promoters. Generally, a "weak promoter" is intended to mean a promoter that drives expression of a coding sequence at a low level. A "low level" of expression is intended to mean expression at levels of about 1/10,000 transcripts to about 1/100,000 transcripts to about 1/500,000 transcripts. Conversely, a strong promoter drives expression of a coding sequence at a high level, or at about 1/10 transcripts to about 1/100 transcripts to about 1/1,000 transcripts.

Fragments and variants of the disclosed promoter sequences are also encompassed by the present invention. A "fragment" is intended to mean a portion of the promoter sequence. Fragments of a promoter sequence may retain biological activity and hence encompass fragments capable of driving root-preferred expression of an operably linked nucleotide sequence. Thus, for example, less than the entire promoter sequence disclosed herein may be utilized to drive expression of an operably linked nucleotide sequence of interest, such as a nucleotide sequence encoding a heterologous protein. It is within skill in the art to

determine whether such fragments decrease expression levels or alter the nature of expression, i.e., constitutive or inducible expression. Alternatively, fragments of a promoter nucleotide sequence that are useful as hybridization probes, such as described below, generally do not retain this regulatory activity. Thus, fragments of
5 a nucleotide sequence may range from at least about 20 nucleotides, about 50 nucleotides, about 100 nucleotides, and up to the full-length nucleotide sequence of the embodiments.

Thus, a fragment of a Cr1Bio promoter nucleotide sequence may encode a biologically active portion of the Cr1Bio promoter or it may be a fragment that can
10 be used as a hybridization probe or PCR primer using methods disclosed below. A biologically active portion of a Cr1Bio promoter can be prepared by isolating a portion of the Cr1Bio promoter nucleotide sequence of the embodiments and assessing the activity of that portion of the Cr1Bio promoter. Nucleic acid molecules that are fragments of a promoter nucleotide sequence comprise at least
15 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 325, 350, 375, 400, 425, 450, 500, 550, 600, 650, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, or up to the number of nucleotides present in the full-length promoter nucleotide sequence disclosed herein, e.g. 1623 nucleotides for SEQ ID NO:1.

The nucleotides of such fragments will usually comprise the TATA
20 recognition sequence of the particular promoter sequence. Such fragments may be obtained by use of restriction enzymes to cleave the naturally occurring promoter nucleotide sequence disclosed herein; by synthesizing a nucleotide sequence from the naturally occurring sequence of the promoter DNA sequence; or may be obtained through the use of PCR technology. See particularly, Mullis *et al.* (1987)
25 *Methods Enzymol.* 155:335-350, and Erlich, ed. (1989) *PCR Technology* (Stockton Press, New York). Variants of these promoter fragments, such as those resulting from site-directed mutagenesis and a procedure such as DNA "shuffling", are also encompassed by the compositions of the present invention.

An "analogue" of the regulatory elements of the present invention includes
30 any substitution, deletion, or addition to the sequence of a regulatory element provided that said analogue maintains at least one regulatory property associated with the activity of the regulatory element of the present invention. Such properties

include directing organ specificity, tissue specificity, or a combination thereof, or temporal activity, or developmental activity, or a combination thereof.

The term "variants" is intended to mean sequences having substantial similarity with a promoter sequence disclosed herein. For nucleotide sequences, naturally occurring variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques as outlined below. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those generated, for example, by using site-directed mutagenesis. Generally, variants of a particular nucleotide sequence of the embodiments will have at least 40%, 50%, 60%, 65%, 70%, generally at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, to 95%, 96%, 97%, 98%, 99% or more sequence identity to that particular nucleotide sequence as determined by sequence alignment programs described elsewhere herein using default parameters. Biologically active variants are also encompassed by the present invention. Biologically active variants include, for example, the native promoter sequence of the embodiments having one or more nucleotide substitutions, deletions, or insertions. Promoter activity may be measured by using techniques such as Northern blot analysis, reporter activity measurements taken from transcriptional fusions, and the like. See, for example, Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York), hereinafter "Sambrook," herein incorporated by reference. Alternatively, levels of a reporter gene such as green fluorescent protein (GFP) or the like produced under the control of a promoter fragment or variant can be measured. See, for example, U.S. Patent No. 6,072,050, herein incorporated by reference.

Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel (1985) *Proc. Natl. Acad. Sci. USA* 82:488-492; Kunkel *et al.* (1987) *Methods in Enzymol.* 154:367-382; U.S. Patent No. 4,873,192; Walker and Gaastra, eds. (1983) *Techniques in Molecular Biology* (MacMillan Publishing Company, New York) and the references cited therein.

Variant promoter nucleotide sequences also encompass sequences derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different promoter sequences can be manipulated to

create a new promoter possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined in vitro or in vivo.

5 Strategies for such DNA shuffling are known in the art. See, for example, Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751; Stemmer (1994) *Nature* 370:389-391; Cramer *et al.* (1997) *Nature Biotech.* 15:436-438; Moore *et al.* (1997) *J. Mol. Biol.* 272:336-347; Zhang *et al.* (1997) *Proc. Natl. Acad. Sci. USA* 94:4504-4509; Cramer *et al.* (1998) *Nature* 391:288-291; and U.S. Patent Nos. 5,605,793
10 and 5,837,458.

The nucleotide sequences of the embodiments can be used to isolate corresponding sequences from other organisms, particularly other plants, for example, other monocots. In this manner, methods such as PCR, hybridization, and the like can be used to identify such sequences based on their sequence
15 homology to the sequence set forth herein. Sequences isolated based on their sequence identity to the entire Cr1Bio promoter sequence set forth herein or to fragments thereof are encompassed by the present invention. The promoter regions of the embodiments may be isolated from any plant, including, but not limited to corn (*Zea mays*), *Brassica* (*Brassica napus*, *Brassica rapa ssp.*), alfalfa
20 (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), sunflower (*Helianthus annuus*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea spp.*),
25 coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus spp.*), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa spp.*), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), oats, safflower, barley, vegetables, ornamentals, and conifers.

30 In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any plant of interest. Methods for designing PCR primers and PCR cloning are generally known in the art and are disclosed in Sambrook, *supra*. See

also Innis *et al.*, eds. (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, New York); Innis and Gelfand, eds. (1995) *PCR Strategies* (Academic Press, New York); and Innis and Gelfand, eds. (1999) *PCR Methods Manual* (Academic Press, New York). Known methods of PCR include, but are not
5 limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially-mismatched primers, and the like.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide
10 sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P , or any other detectable marker. Thus, for example, probes for
15 hybridization can be made by labeling synthetic oligonucleotides based on the Cr1Bio promoter sequence of the embodiments. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook, *supra*.

For example, the entire Cr1Bio promoter sequence disclosed herein, or one
20 or more portions thereof, may be used as a probe capable of specifically hybridizing to corresponding Cr1Bio promoter sequences. To achieve specific hybridization under a variety of conditions, such probes include sequences that are unique among Cr1Bio promoter sequences and are at least about 10 nucleotides in length, and generally at least about 20 nucleotides in length. Such probes may be used to
25 amplify corresponding Cr1Bio promoter sequences from a chosen plant by PCR. This technique may be used to isolate additional coding sequences from a desired plant or as a diagnostic assay to determine the presence of coding sequences in a plant. Hybridization techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, for example, Sambrook *supra*).

30 Hybridization of such sequences may be carried out under stringent conditions. By "stringent conditions" or "stringent hybridization conditions" is intended conditions under which a probe will hybridize to its target sequence to a detectably greater degree than to other sequences (e.g., at least 2-fold over

background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences that are 100% complementary to the probe can be identified (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, often less than 500 nucleotides in length.

Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C for at least 30 minutes. Duration of hybridization is generally less than about 24 hours, usually about 4 to about 12 hours.

Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the thermal melting point (T_m) can be approximated from the equation of Meinkoth and Wahl (1984) *Anal. Biochem.* 138:267-284: $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to

hybridize to sequences of the desired identity. For example, if sequences with $\geq 90\%$ identity are sought, the T_m can be decreased 10°C . Generally, stringent conditions are selected to be about 5°C lower than the T_m for the specific sequence and its complement at a defined ionic strength and pH. However, severely
5 stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the T_m ; moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the T_m ; low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the T_m . Using the equation, hybridization and wash compositions, and desired T_m , those of
10 ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen
15 (1993) *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 (Elsevier, New York); and Ausubel *et al.*, eds. (1995) *Current Protocols in Molecular Biology*, Chapter 2 (Greene Publishing and Wiley-Interscience, New York), hereinafter “Ausubel”. See also Sambrook *supra*.

20 Thus, isolated sequences that have root-preferred promoter activity and which hybridize under stringent conditions to the Cr1Bio promoter sequences disclosed herein, or to fragments thereof, are encompassed by the present invention.

In general, sequences that have promoter activity and hybridize to the
25 promoter sequences disclosed herein will be at least 40% to 50% homologous, about 60% to 70% homologous, and even about 80%, 85%, 90%, 95% to 98% homologous or more with the disclosed sequences. That is, the sequence similarity of sequences may range, sharing at least about 40% to 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to 98% sequence similarity.

30 The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) “reference sequence”, (b) “comparison window”, (c) “sequence identity”, (d) “percentage of sequence identity”, and (e) “substantial identity”.

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

5 (b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences.

10 Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

15 Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent sequence identity between any two sequences can be accomplished using a mathematical algorithm. Preferred, non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller (1988) *CABIOS* 4:11-17; the local homology algorithm of Smith *et al.* (1981) *Adv. Appl. Math.* 2:482; the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443-453; the search-for-similarity-method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci.* 85:2444-2448; the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877.

25 Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0); the ALIGN PLUS program (Version 3.0, copyright 1997); and GAP, 30 BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package of Genetics Computer Group, Version 10 (available from Accelrys, 9685 Scranton Road, San Diego, CA, 92121, USA). The scoring matrix used in Version

10 of the Wisconsin Genetics Software Package is BLOSUM62 (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).

Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins *et al.* (1988) *Gene* 5 73:237-244 (1988); Higgins *et al.* (1989) *CABIOS* 5:151-153; Corpet *et al.* (1988) *Nucleic Acids Res.* 16:10881-90; Huang *et al.* (1992) *CABIOS* 8:155-65; and Pearson *et al.* (1994) *Meth. Mol. Biol.* 24:307-331. The ALIGN and the ALIGN PLUS programs are based on the algorithm of Myers and Miller (1988) *supra*. A PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 10 can be used with the ALIGN program when comparing amino acid sequences. The BLAST programs of Altschul *et al.* (1990) *J. Mol. Biol.* 215:403 are based on the algorithm of Karlin and Altschul (1990) *supra*. BLAST nucleotide searches can be performed with the BLASTN program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleotide sequence encoding a protein of 15 the embodiments. BLAST protein searches can be performed with the BLASTX program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to a protein or polypeptide of the embodiments. To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389. Alternatively, PSI-BLAST (in 20 BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul *et al.* (1997) *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g., BLASTN for nucleotide sequences, BLASTX for proteins) can be used. See the web site for the National Center for Biotechnology Information on the 25 world wide web. Alignment may also be performed manually by inspection.

Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using the GAP program with default parameters, or any equivalent program. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an 30 alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by GAP.

The GAP program uses the algorithm of Needleman and Wunsch (1970) *supra*, to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. GAP considers all possible alignments and gap positions and creates the alignment with the largest number of
5 matched bases and the fewest gaps. It allows for the provision of a gap creation penalty and a gap extension penalty in units of matched bases. GAP must make a profit of gap creation penalty number of matches for each gap it inserts. If a gap extension penalty greater than zero is chosen, GAP must, in addition, make a profit for each gap inserted of the length of the gap times the gap extension penalty.

10 Default gap creation penalty values and gap extension penalty values in Version 10 of the Wisconsin Genetics Software Package for protein sequences are 8 and 2, respectively. For nucleotide sequences the default gap creation penalty is 50 while the default gap extension penalty is 3. The gap creation and gap extension penalties can be expressed as an integer selected from the group of integers
15 consisting of from 0 to 200. Thus, for example, the gap creation and gap extension penalties can be 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65 or greater.

(c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences makes reference to the residues in the two
20 sequences that are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g.,
25 charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity". Means for making this adjustment
30 are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of

zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

(d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70% sequence identity, at least 80%, at least 90%, and at least 95%, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 60%, 70%, 80%, 90%, or 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. Generally, stringent conditions are selected to be about 5°C lower than the T_m for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C lower than the T_m , depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum

codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

5 The Cr1Bio promoter sequence disclosed herein, as well as variants and fragments thereof, are useful for genetic engineering of plants, e.g. for the production of a transformed or transgenic plant, to express a phenotype of interest. As used herein, the terms "transformed plant" and "transgenic plant" refer to a plant that comprises within its genome a heterologous polynucleotide. Generally, the
10 heterologous polynucleotide is stably integrated within the genome of a transgenic or transformed plant such that the polynucleotide is passed on to successive generations. The heterologous polynucleotide may be integrated into the genome alone or as part of a recombinant DNA construct or expression cassette. It is to be understood that as used herein the term "transgenic" includes any cell, cell line,
15 callus, tissue, plant part, or plant the genotype of which has been altered by the presence of heterologous nucleic acid including those transgenics initially so altered as well as those created by sexual crosses or asexual propagation from the initial transgenic. The term "transgenic" as used herein does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional
20 plant breeding methods or by naturally occurring events such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition, or spontaneous mutation.

 A transgenic "event" is produced by transformation of plant cells with a heterologous DNA construct, including a nucleic acid expression cassette that
25 comprises a transgene of interest, the regeneration of a population of plants resulting from the insertion of the transgene into the genome of the plant, and selection of a particular plant characterized by insertion into a particular genome location. An event is characterized phenotypically by the expression of the transgene. At the genetic level, an event is part of the genetic makeup of a plant.
30 The term "event" also refers to progeny produced by a sexual outcross between the transformant and another variety that include the heterologous DNA.

 As used herein, the term "plant" includes reference to whole plants, plant organs (e.g., leaves, stems, roots, etc.), seeds, plant cells, and progeny of same.

Parts of transgenic plants are to be understood within the scope of the embodiments to comprise, for example, plant cells, protoplasts, tissues, callus, embryos as well as flowers, stems, fruits, ovules, leaves, or roots originating in transgenic plants or their progeny previously transformed with a DNA molecule of the embodiments, and therefore consisting at least in part of transgenic cells, are also an object of the present invention.

As used herein, the term "plant cell" includes, without limitation, seeds suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores. The class of plants that can be used in the methods of the embodiments is generally as broad as the class of higher plants amenable to transformation techniques, including both monocotyledonous and dicotyledonous plants.

The promoter sequences and methods disclosed herein are useful in regulating expression of any heterologous nucleotide sequence in a host plant.

Thus, the heterologous nucleotide sequence operably linked to the promoters disclosed herein may be a structural gene encoding a protein of interest. Genes of interest are reflective of the commercial markets and interests of those involved in the development of the crop. Crops and markets of interest change, and as developing nations open up world markets, new crops and technologies will emerge also. In addition, as our understanding of agronomic traits and characteristics such as yield and heterosis increase, the choice of genes for transformation will change accordingly. General categories of genes of interest for the present invention include, for example, those genes involved in information, such as zinc fingers, those involved in communication, such as kinases, and those involved in housekeeping, such as heat shock proteins. More specific categories of transgenes, for example, include genes encoding proteins conferring resistance to abiotic stress, such as drought, temperature, salinity, and toxins such as pesticides and herbicides, or to biotic stress, such as attacks by fungi, viruses, bacteria, insects, and nematodes, and development of diseases associated with these organisms. Various changes in phenotype are of interest including modifying expression of a gene in a plant root, altering a plant's pathogen or insect defense mechanism, increasing the plant's tolerance to herbicides, altering root development to respond to environmental stress, and the like. The results can be

achieved by providing expression of heterologous or increased expression of endogenous products in plants. Alternatively, the results can be achieved by providing for a reduction of expression of one or more endogenous products, particularly enzymes, transporters, or cofactors, or affecting nutrients uptake in the plant. These changes result in a change in phenotype of the transformed plant.

It is recognized that any gene of interest can be operably linked to the promoter sequences of the embodiments and expressed in a plant root.

A DNA construct comprising one of these genes of interest can be used with transformation techniques, such as those described below, to create disease or insect resistance in susceptible plant phenotypes or to enhance disease or insect resistance in resistant plant phenotypes. Accordingly, the embodiments encompass methods that are directed to protecting plants against fungal pathogens, bacteria, viruses, nematodes, insects, and the like. By "disease resistance" or "insect resistance" is intended that the plants avoid the harmful symptoms that are the outcome of the plant-pathogen interactions.

Disease resistance and insect resistance genes such as lysozymes, cecropins, maganins, or thionins for antibacterial protection, or the pathogenesis-related (PR) proteins such as glucanases and chitinases for anti-fungal protection, or *Bacillus thuringiensis* endotoxins, protease inhibitors, collagenases, lectins, and glycosidases for controlling nematodes or insects are all examples of useful gene products.

Pathogens of the embodiments include, but are not limited to, viruses or viroids, bacteria, insects, nematodes, fungi, and the like. Viruses include tobacco or cucumber mosaic virus, ringspot virus, necrosis virus, maize dwarf mosaic virus, etc. Nematodes include parasitic nematodes such as root knot, cyst, and lesion nematodes, etc.

Insect resistance genes may encode resistance to pests that have great yield drag such as rootworm, cutworm, European Corn Borer, and the like. Such genes include, for example, *Bacillus thuringiensis* toxic protein genes (U.S. Pat. Nos. 5,366,892; 5,747,450; 5,737,514; 5,723,756; 5,593,881; and Geiser *et al.* (1986) *Gene* 48:109); lectins (Van Damme *et al.* (1994) *Plant Mol. Biol.* 24:825); and the like.

Genes encoding disease resistance traits include detoxification genes, such as against fumonisin (U.S. Patent No. 5,792,931) avirulence (avr) and disease resistance (R) genes (Jones *et al.* (1994) *Science* 266:789; Martin *et al.* (1993) *Science* 262:1432; Mindrinos *et al.* (1994) *Cell* 78:1089); and the like.

5 Herbicide resistance traits may be introduced into plants by genes coding for resistance to herbicides that act to inhibit the action of acetolactate synthase (ALS), in particular the sulfonylurea-type herbicides (e.g., the acetolactate synthase (ALS) gene containing mutations leading to such resistance, in particular the S4 and/or Hra mutations), genes coding for resistance to herbicides that act to inhibit action of
10 glutamine synthase, such as phosphinothricin or basta (e.g., the *bar* gene), or other such genes known in the art. The *bar* gene encodes resistance to the herbicide basta, the *nptII* gene encodes resistance to the antibiotics kanamycin and geneticin, and the ALS gene encodes resistance to the herbicide chlorsulfuron.

 Glyphosate resistance is imparted by mutant 5-enol pyruvylshikimate-3-
15 phosphate synthase (EPSPS) and *aroA* genes. See, for example, U.S. Patent No. 4,940,835 to Shah *et al.*, which discloses the nucleotide sequence of a form of EPSPS which can confer glyphosate resistance. U.S. Patent No. 5,627,061 to Barry *et al.* also describes genes encoding EPSPS enzymes. See also U.S. Patent Nos. 6,248,876; 6,040,497; 5,804,425; 5,633,435; 5,145,783; 4,971,908;
20 5,312,910; 5,188,642; 4,940,835; 5,866,775; 6,225,114; 6,130,366; 5,310,667; 4,535,060; 4,769,061; 5,633,448; 5,510,471; RE 36,449; RE 37,287; and 5,491,288; and international publications WO 97/04103; WO 97/04114; WO 00/66746; WO 01/66704; WO 00/66747 and WO 00/66748, which are incorporated herein by reference for this purpose. Glyphosate resistance is also imparted to
25 plants that express a gene that encodes a glyphosate oxido-reductase enzyme as described more fully in U.S. Patent Nos. 5,776,760 and 5,463,175, which are incorporated herein by reference for this purpose. In addition glyphosate resistance can be imparted to plants by the over-expression of genes encoding glyphosate N-acetyltransferase. See, for example, U.S. Patent Application Serial
30 Nos. 10/004,357; 10/427,692, and 10/835,615.

 Sterility genes can also be encoded in an expression cassette and provide an alternative to physical detasseling. Examples of genes used in such ways include male tissue-preferred genes and genes with male sterility phenotypes such

as QM, described in U.S. Patent No. 5,583,210. Other genes include kinases and those encoding compounds toxic to either male or female gametophytic development.

Commercial traits can also be encoded on a gene or genes that could
5 increase for example, starch for ethanol production, or provide expression of proteins. Another important commercial use of transformed plants is the production of polymers and bioplastics such as described in U.S. Patent No. 5,602,321. Genes such as β -Ketothiolase, PHBase (polyhydroxybutyrate synthase), and acetoacetyl-CoA reductase (see Schubert *et al.* (1988) *J. Bacteriol.* 170:5837-5847) facilitate
10 expression of polyhydroxyalkanoates (PHAs).

Agronomically important traits that affect quality of grain, such as levels and types of oils, saturated and unsaturated, quality and quantity of essential amino acids, levels of cellulose, starch, and protein content can be genetically altered using the methods of the present invention. Modifications include increasing
15 content of oleic acid, saturated and unsaturated oils, increasing levels of lysine and sulfur, providing essential amino acids, and modifying starch. Hordothionin protein modifications in corn are described in U.S. Patent Nos. 5,990,389; 5,885,801; 5,885,802 and 5,703,049; herein incorporated by reference. Another example is lysine and/or sulfur rich seed protein encoded by the soybean 2S albumin
20 described in U.S. Patent No. 5,850,016, filed March 20, 1996, and the chymotrypsin inhibitor from barley, Williamson *et al.* (1987) *Eur. J. Biochem.* 165:99-106, the disclosures of which are herein incorporated by reference.

Exogenous products include plant enzymes and products as well as those from other sources including prokaryotes and other eukaryotes. Such products
25 include enzymes, cofactors, hormones, and the like.

Examples of other applicable genes and their associated phenotype include the gene that encodes viral coat protein and/or RNA, or other viral or plant genes that confer viral resistance; genes that confer fungal resistance; genes that confer insect resistance; genes that promote yield improvement; and genes that provide
30 for resistance to stress, such as dehydration resulting from heat and salinity, toxic metal or trace elements, or the like.

In other embodiments of the present invention, the Cr1Bio promoter sequences are operably linked to genes of interest that improve plant growth or

increase crop yields under high plant density conditions. For example, the Cr1Bio promoter may be operably linked to nucleotide sequences expressing agronomically important genes that result in improved primary or lateral root systems. Such genes include, but are not limited to, nutrient/water transporters and growth inducers. Examples of such genes, include but are not limited to, maize plasma membrane H⁺-ATPase (MHA2) (Frias *et al.* (1996) *Plant Cell* 8:1533-44); AKT1, a component of the potassium uptake apparatus in *Arabidopsis* (Spalding *et al.* (1999) *J. Gen. Physiol.* 113:909-18); RML genes, which activate cell division cycle in the root apical cells (Cheng *et al.* (1995) *Plant Physiol.* 108:881); maize glutamine synthetase genes (Sukanya *et al.* (1994) *Plant Mol. Biol.* 26:1935-46); and hemoglobin (Duff *et al.* (1997) *J. Biol. Chem.* 27:16749-16752; Arredondo-Peter *et al.* (1997) *Plant Physiol.* 115:1259-1266; Arredondo-Peter *et al.* (1997) *Plant Physiol.* 114:493-500 and references cited therein). The Cr1Bio promoter may also be useful in expressing antisense nucleotide sequences of genes that negatively affect root development under high-planting density conditions.

"RNAi" refers to a series of related techniques to reduce the expression of genes (See for example U.S. Patent No. 6,506,559). Older techniques referred to by other names are now thought to rely on the same mechanism, but are given different names in the literature. These include "antisense inhibition," the production of antisense RNA transcripts capable of suppressing the expression of the target protein, and "co-suppression" or "sense-suppression," which refer to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar foreign or endogenous genes (U.S. Patent No. 5,231,020, incorporated herein by reference). Such techniques rely on the use of constructs resulting in the accumulation of double stranded RNA with one strand complementary to the target gene to be silenced. The Cr1Bio promoter sequence of the embodiments, and its related biologically active fragments or variants disclosed herein, may be used to drive expression of constructs that will result in RNA interference including microRNAs and siRNAs.

The heterologous nucleotide sequence operably linked to the Cr1Bio promoter and its related biologically active fragments or variants disclosed herein may be an antisense sequence for a targeted gene. The terminology "antisense DNA nucleotide sequence" is intended to mean a sequence that is in inverse

orientation to the 5'-to-3' normal orientation of that nucleotide sequence. When delivered into a plant cell, expression of the antisense DNA sequence prevents normal expression of the DNA nucleotide sequence for the targeted gene. The antisense nucleotide sequence encodes an RNA transcript that is complementary to and capable of hybridizing to the endogenous messenger RNA (mRNA) produced by transcription of the DNA nucleotide sequence for the targeted gene. In this case, production of the native protein encoded by the targeted gene is inhibited to achieve a desired phenotypic response. Modifications of the antisense sequences may be made as long as the sequences hybridize to and interfere with expression of the corresponding mRNA. In this manner, antisense constructions having, for example, 70%, 80%, or 85% sequence identity to the corresponding antisense sequences may be used. Furthermore, portions of the antisense nucleotides may be used to disrupt the expression of the target gene. Generally, sequences of at least 50 nucleotides, 100 nucleotides, 200 nucleotides, or greater may be used. Thus, the promoter sequences disclosed herein may be operably linked to antisense DNA sequences to reduce or inhibit expression of a native protein in the plant.

In one embodiment, DNA constructs will comprise a transcriptional initiation region comprising one of the promoter nucleotide sequences disclosed herein, or variants or fragments thereof, operably linked to a heterologous nucleotide sequence whose expression is to be controlled by the inducible promoter of the embodiments. Such a DNA construct is provided with a plurality of restriction sites for insertion of the nucleotide sequence to be under the transcriptional regulation of the regulatory regions. The DNA construct may additionally contain selectable marker genes.

The DNA construct will include in the 5'-3' direction of transcription, a transcriptional initiation region (i.e., a root-preferred promoter of the embodiments), translational initiation region, a heterologous nucleotide sequence of interest, a translational termination region and, optionally, a transcriptional termination region functional in the host organism. The regulatory regions (i.e., promoters, transcriptional regulatory regions, and translational termination regions) and/or the polynucleotide of the embodiments may be native/analogous to the host cell or to each other. Alternatively, the regulatory regions and/or the polynucleotide of the

embodiments may be heterologous to the host cell or to each other. As used herein, "heterologous" in reference to a sequence is a sequence that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human
5 intervention. For example, a promoter operably linked to a heterologous polynucleotide is from a species different from the species from which the polynucleotide was derived, or, if from the same/analogous species, one or both are substantially modified from their original form and/or genomic locus, or the promoter is not the native promoter for the operably linked polynucleotide.

10 The optionally included termination region may be native with the transcriptional initiation region, may be native with the operably linked polynucleotide of interest, may be native with the plant host, or may be derived from another source (i.e., foreign or heterologous) to the promoter, the polynucleotide of interest, the host, or any combination thereof. Convenient termination regions are
15 available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also Guerineau *et al.* (1991) *Mol. Gen. Genet.* 262:141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon *et al.* (1991) *Genes Dev.* 5:141-149; Mogen *et al.* (1990) *Plant Cell* 2:1261-1272; Munroe *et al.* (1990) *Gene* 91:151-158; Ballas *et al.* (1989) *Nucleic Acids Res.* 17:7891-7903;
20 and Joshi *et al.* (1987) *Nucleic Acids Res.* 15:9627-9639. In particular embodiments, the potato protease inhibitor II gene (PinII) terminator is used. See, for example, Keil *et al.* (1986) *Nucl. Acids Res.* 14:5641-5650; and An *et al.* (1989) *Plant Cell* 1:115-122, herein incorporated by reference in their entirety.

The DNA construct comprising a promoter sequence of the present invention
25 operably linked to a heterologous nucleotide sequence may also contain at least one additional nucleotide sequence for a gene to be cotransformed into the organism. Alternatively, the additional sequence(s) can be provided on another DNA construct.

Where appropriate, the heterologous nucleotide sequence whose
30 expression is to be under the control of the inducible promoter sequence of the present invention and any additional nucleotide sequence(s) may be optimized for increased expression in the transformed plant. That is, these nucleotide sequences can be synthesized using plant preferred codons for improved expression. Methods

are available in the art for synthesizing plant-preferred nucleotide sequences. See, for example, U.S. Pat. Nos. 5,380,831 and 5,436,391, and Murray *et al.* (1989) *Nucleic Acids Res.* 17:477-498, herein incorporated by reference.

Additional sequence modifications are known to enhance gene expression in
5 a cellular host. These include elimination of sequences encoding spurious
polyadenylation signals, exon-intron splice site signals, transposon-like repeats,
and other such well-characterized sequences that may be deleterious to gene
expression. The G-C content of the heterologous nucleotide sequence may be
adjusted to levels average for a given cellular host, as calculated by reference to
10 known genes expressed in the host cell. When possible, the sequence is modified
to avoid predicted hairpin secondary mRNA structures.

The DNA constructs may additionally contain 5' leader sequences. Such
leader sequences can act to enhance translation. Translation leaders are known in
the art and include: picornavirus leaders, for example, EMCV leader
15 (Encephalomyocarditis 5' noncoding region) (Elroy-Stein *et al.* (1989) *Proc. Nat.
Acad. Sci. USA* 86:6126-6130); potyvirus leaders, for example, TEV leader
(Tobacco Etch Virus) (Allison *et al.* (1986) *Virology* 154:9-20); MDMV leader (Maize
Dwarf Mosaic Virus); human immunoglobulin heavy-chain binding protein (BiP)
(Macejak *et al.* (1991) *Nature* 353:90-94); untranslated leader from the coat protein
20 mRNA of alfalfa mosaic virus (AMV RNA 4) (Jobling *et al.* (1987) *Nature* 325:622-
625); tobacco mosaic virus leader (TMV) (Gallie *et al.* (1989) *Molecular Biology of
RNA*, pages 237-256); and maize chlorotic mottle virus leader (MCMV) (Lommel *et
al.* (1991) *Virology* 81:382-385). See also Della-Cioppa *et al.* (1987) *Plant
Physiology* 84:965-968. Other methods known to enhance translation and/or
25 mRNA stability can also be utilized, for example, introns, such as the maize
Ubiquitin intron (Christensen and Quail (1996) *Transgenic Res.* 5:213-218;
Christensen *et al.* (1992) *Plant Molecular Biology* 18:675-689) or the maize Adhl
intron (Kyoizuka *et al.* (1991) *Mol. Gen. Genet.* 228:40-48; Kyoizuka *et al.* (1990)
Maydica 35:353-357), and the like.

30 The DNA constructs of the present invention can also include further
enhancers, either translation or transcription enhancers, as may be required. These
enhancer regions are well known to persons skilled in the art, and can include the
ATG initiation codon and adjacent sequences. The initiation codon must be in

phase with the reading frame of the coding sequence to ensure translation of the entire sequence. The translation control signals and initiation codons can be from a variety of origins, both natural and synthetic. Translational initiation regions may be provided from the source of the transcriptional initiation region, or from the structural gene. The sequence can also be derived from the regulatory element selected to express the gene, and can be specifically modified so as to increase translation of the mRNA. It is recognized that to increase transcription levels enhancers may be utilized in combination with the promoter regions of the embodiments. Enhancers are known in the art and include the SV40 enhancer region, the 35S enhancer element, and the like.

In preparing the DNA construct, the various DNA fragments may be manipulated, so as to provide for the DNA sequences in the proper orientation and, as appropriate, in the proper reading frame. Toward this end, adapters or linkers may be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites. Restriction sites may be added or removed, superfluous DNA may be removed, or other modifications of the like may be made to the sequences of the embodiments. For this purpose, *in vitro* mutagenesis, primer repair, restriction, annealing, re-substitutions, for example, transitions and transversions, may be involved.

Reporter genes or selectable marker genes may be included in the DNA constructs. Examples of suitable reporter genes known in the art can be found in, for example, Jefferson *et al.* (1991) in *Plant Molecular Biology Manual*, ed. Gelvin *et al.* (Kluwer Academic Publishers), pp. 1-33; DeWet *et al.* (1987) *Mol. Cell. Biol.* 7:725-737; Goff *et al.* (1990) *EMBO J.* 9:2517-2522; Kain *et al.* (1995) *BioTechniques* 19:650-655; and Chiu *et al.* (1996) *Current Biology* 6:325-330.

Selectable marker genes for selection of transformed cells or tissues can include genes that confer antibiotic resistance or resistance to herbicides. Examples of suitable selectable marker genes include, but are not limited to, genes encoding resistance to chloramphenicol (Herrera Estrella *et al.* (1983) *EMBO J.* 2:987-992); methotrexate (Herrera Estrella *et al.* (1983) *Nature* 303:209-213; Meijer *et al.* (1991) *Plant Mol. Biol.* 16:807-820); hygromycin (Waldron *et al.* (1985) *Plant Mol. Biol.* 5:103-108; Zhijian *et al.* (1995) *Plant Science* 108:219-227); streptomycin (Jones *et al.* (1987) *Mol. Gen. Genet.* 210:86-91); spectinomycin (Bretagne-

Sagnard *et al.* (1996) *Transgenic Res.* 5:131-137); bleomycin (Hille *et al.* (1990) *Plant Mol. Biol.* 7:171-176); sulfonamide (Guerineau *et al.* (1990) *Plant Mol. Biol.* 15:127-136); bromoxynil (Stalker *et al.* (1988) *Science* 242:419-423); glyphosate (Shaw *et al.* (1986) *Science* 233:478-481); phosphinothricin (DeBlock *et al.* (1987) *EMBO J.* 6:2513-2518).

Other genes that could serve utility in the recovery of transgenic events but might not be required in the final product would include, but are not limited to, examples such as GUS (b-glucuronidase; Jefferson (1987) *Plant Mol. Biol. Rep.* 5:387), GFP (green florescence protein; Chalfie *et al.* (1994) *Science* 263:802), luciferase (Riggs *et al.* (1987) *Nucleic Acids Res.* 15(19):8115 and Luehrsen *et al.* (1992) *Methods Enzymol.* 216:397-414), and the maize genes encoding for anthocyanin production (Ludwig *et al.* (1990) *Science* 247:449).

The nucleic acid molecules of the present invention are useful in methods directed to expressing a nucleotide sequence in a plant. This may be accomplished by transforming a plant cell of interest with a DNA construct comprising a promoter identified herein, operably linked to a heterologous nucleotide sequence, and regenerating a stably transformed plant from said plant cell. The methods of the embodiments are also directed to inducibly expressing a nucleotide sequence in a plant. Those methods comprise transforming a plant cell with a DNA construct comprising a promoter identified herein that initiates transcription in a plant cell in an inducible manner, operably linked to a heterologous nucleotide sequence, regenerating a transformed plant from said plant cell, and subjecting the plant to the required stimulus to induce expression.

The DNA construct comprising the particular promoter sequence of the present invention operably linked to a nucleotide sequence of interest can be used to transform any plant. In this manner, genetically modified, i.e. transgenic or transformed, plants, plant cells, plant tissue, seed, root, and the like can be obtained.

Plant species suitable for the embodiments include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail

millet (*Setaria italica*), finger millet (*Eleusine coracana*), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers.

Vegetables include tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum.

Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*); Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). For example, plants of the present invention may be crop plants (for example, corn, alfalfa, sunflower, *Brassica*, soybean, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.). This invention is, for example, suitable for any member of the monocot plant family including, but not limited to, maize, rice, barley, oats, wheat, sorghum, rye, sugarcane, pineapple, yams, onion, banana, coconut, and dates.

As used herein, "vector" refers to a DNA molecule such as a plasmid, cosmid, or bacterial phage for introducing a nucleotide construct, for example, a DNA construct, into a host cell. Cloning vectors typically contain one or a small number of restriction endonuclease recognition sites at which foreign DNA sequences can be inserted in a determinable fashion without loss of essential biological function of the vector, as well as a marker gene that is suitable for use in the identification and selection of cells transformed with the cloning vector. Marker genes typically include genes that provide tetracycline resistance, hygromycin resistance, or ampicillin resistance.

The methods of the embodiments involve introducing a nucleotide construct into a plant. By "introducing" is intended presenting to the plant the nucleotide construct in such a manner that the construct gains access to the interior of a cell of the plant. The methods of the embodiments do not depend on a particular method for introducing a nucleotide construct to a plant, only that the nucleotide construct gains access to the interior of at least one cell of the plant. Methods for introducing nucleotide constructs into plants are known in the art including, but not limited to, stable transformation methods, transient transformation methods, and virus-mediated methods.

By "stable transformation" is intended that the nucleotide construct introduced into a plant integrates into the genome of the plant and is capable of being inherited by progeny thereof. By "transient transformation" is intended that a nucleotide construct introduced into a plant does not integrate into the genome of the plant.

The nucleotide constructs of the embodiments may be introduced into plants by contacting plants with a virus or viral nucleic acids. Generally, such methods involve incorporating a nucleotide construct of the embodiments within a viral DNA or RNA molecule. Methods for introducing nucleotide constructs into plants and expressing a protein encoded therein, involving viral DNA or RNA molecules, are known in the art. See, for example, U.S. Patent Nos. 5,889,191, 5,889,190, 5,866,785, 5,589,367, and 5,316,931; herein incorporated by reference.

Transformation protocols as well as protocols for introducing nucleotide sequences into plants may vary depending on the type of plant or plant cell, i.e., monocot or dicot, targeted for transformation. Suitable methods of introducing

nucleotide sequences into plant cells and subsequent insertion into the plant genome include microinjection (Crossway *et al.* (1986) *Biotechniques* 4:320-334), electroporation (Riggs *et al.* (1986) *Proc. Natl. Acad. Sci. USA* 83:5602-5606, *Agrobacterium*-mediated transformation (U.S. Patent Nos. 5,981,840 and 5,563,055), direct gene transfer (Paszkowski *et al.* (1984) *EMBO J.* 3:2717-2722), and ballistic particle acceleration (see, for example, U.S. Patent Nos. 4,945,050; 5,879,918; 5,886,244; 5,932,782; Tomes *et al.* (1995) in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg and Phillips (Springer-Verlag, Berlin); and McCabe *et al.* (1988) *Biotechnology* 6:923-926). Also see Weissinger *et al.* (1988) *Ann. Rev. Genet.* 22:421-477; Sanford *et al.* (1987) *Particulate Science and Technology* 5:27-37 (onion); Christou *et al.* (1988) *Plant Physiol.* 87:671-674 (soybean); McCabe *et al.* (1988) *Bio/Technology* 6:923-926 (soybean); Finer and McMullen (1991) *In Vitro Cell Dev. Biol.* 27P:175-182 (soybean); Singh *et al.* (1998) *Theor. Appl. Genet.* 96:319-324 (soybean); Datta *et al.* (1990) *Biotechnology* 8:736-740 (rice); Klein *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:4305-4309 (maize); Klein *et al.* (1988) *Biotechnology* 6:559-563 (maize); U.S. Patent Nos. 5,240,855; 5,322,783 and 5,324,646; Klein *et al.* (1988) *Plant Physiol.* 91:440-444 (maize); Fromm *et al.* (1990) *Biotechnology* 8:833-839 (maize); Hooykaas-Van Slogteren *et al.* (1984) *Nature (London)* 311:763-764; U.S. Patent No. 5,736,369 (cereals); Bytebier *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:5345-5349 (Liliaceae); De Wet *et al.* (1985) in *The Experimental Manipulation of Ovule Tissues*, ed. Chapman *et al.* (Longman, New York), pp. 197-209 (pollen); Kaeppler *et al.* (1990) *Plant Cell Reports* 9:415-418 and Kaeppler *et al.* (1992) *Theor. Appl. Genet.* 84:560-566 (whisker-mediated transformation); D'Halluin *et al.* (1992) *Plant Cell* 4:1495-1505 (electroporation); Li *et al.* (1993) *Plant Cell Reports* 12:250-255 and Christou and Ford (1995) *Annals of Botany* 75:407-413 (rice); Osjoda *et al.* (1996) *Nature Biotechnology* 14:745-750 (maize via *Agrobacterium tumefaciens*); all of which are herein incorporated by reference.

The cells that have been transformed may be grown into plants in accordance with conventional ways. See, for example, McCormick *et al.* (1986) *Plant Cell Reports* 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having inducible expression of the desired phenotypic characteristic identified. Two or

more generations may be grown to ensure that inducible expression of the desired phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure inducible expression of the desired phenotypic characteristic has been achieved. Thus as used herein, "transformed seeds" refers to seeds that
5 contain the nucleotide construct stably integrated into the plant genome.

There are a variety of methods for the regeneration of plants from plant tissue. The particular method of regeneration will depend on the starting plant tissue and the particular plant species to be regenerated. The regeneration, development and cultivation of plants from single plant protoplast transformants or
10 from various transformed explants is well known in the art (Weissbach and Weissbach, (1988) In.: Methods for Plant Molecular Biology, (Eds.), Academic Press, Inc., San Diego, CA). This regeneration and growth process typically includes the steps of selection of transformed cells, culturing those individualized cells through the usual stages of embryonic development through the rooted
15 plantlet stage. Transgenic embryos and seeds are similarly regenerated. The resulting transgenic rooted shoots are thereafter planted in an appropriate plant growth medium such as soil. Preferably, the regenerated plants are self-pollinated to provide homozygous transgenic plants. Otherwise, pollen obtained from the regenerated plants is crossed to seed-grown plants of agronomically important
20 lines. Conversely, pollen from plants of these important lines is used to pollinate regenerated plants. A transgenic plant of the present invention containing a desired polypeptide is cultivated using methods well known to one skilled in the art.

The embodiments provide compositions for screening compounds that modulate expression within plants. The vectors, cells, and plants can be used for
25 screening candidate molecules for agonists and antagonists of the Cr1Bio promoter. For example, a reporter gene can be operably linked to a Cr1Bio promoter and expressed as a transgene in a plant. Compounds to be tested are added and reporter gene expression is measured to determine the effect on promoter activity.

30 The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

The present invention is further defined in the following Examples, in which parts and percentages are by weight and degrees are Celsius, unless otherwise stated. Techniques in molecular biology were typically performed as described in Ausubel or Sambrook, *supra*. It should be understood that these Examples, while indicating certain 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 embodiments to adapt it to various usages and conditions. Thus, various modifications of the embodiments in addition to those shown and described herein will be apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims.

The disclosure of each reference set forth herein is incorporated herein by reference in its entirety.

Example 1: Expression Pattern of the Cr1Bio Gene

Evidence that Cr1Bio is a root-preferred gene was obtained using Lynx Massively Parallel Signature Sequencing technology (MPSS) (see Brenner S, *et al.* (2000) *Nature Biotechnology* 18:630-634, Brenner S *et al.* (2000) *Proc Natl Acad Sci USA* 97:1665-1670). This technology involves the generation of 17 base signature tags from mRNA samples that have been reverse transcribed. The tags are simultaneously sequenced and assigned to genes or ESTs. The abundance of these tags is given a number value that is normalized to parts per million (PPM) which then allows the tag expression, or tag abundance, to be compared across different tissues. Thus, the MPSS platform can be used to determine the expression pattern of a particular gene and its expression level in different tissues.

The sequence of the Cr1Bio EST (expressed sequence tag) was entered into the MPSS database and the signature tag was identified. The data associated with the tag indicated that the gene was expressed in a highly root-preferred manner, expressed at moderately high levels, and expressed during a time and stage (V2-V6) corresponding to when corn rootworm would typically be feeding on

plants. The combination of these three quantitative, spatial and temporal characteristics suggested that the Cr1Bio gene promoter is a suitable candidate to drive transgene expression specifically in the roots of plants, such as maize, during a time corresponding to when the plant will be attacked by corn rootworm. Such transgenes will include insecticidal genes but may also include other biotic and abiotic stress-resistance genes (drought, salt, cold, etc), and agronomic trait genes. The promoter sequence will also be useful to identify plant cis-acting regulatory elements that are responsible for root expression.

Example 2: 5' RACE Protocol and Analysis of Cr1Bio Expression

5' RACE was performed in order to determine the transcriptional start site according to the protocol provided with the 5' RACE System for the Rapid Amplification of cDNA Ends (Invitrogen, Carlsbad, CA) using RNA isolated from roots of maize inbred B73 plants. Gene-specific primers (GSP) were designed to the 3' UTR (using the EST sequence).

Omniscript Reverse Transcriptase (Qiagen, Valencia, CA) was used for first strand synthesis using GSP1 (SEQ ID NO:3) and the general system protocol was followed for the subsequent steps of RNase treatment, reaction clean-up and dC-tailing of the cDNA. HotStarTaq (Qiagen) was used for the PCR reactions using GSP2 (SEQ ID NO:4) and the Abridged Anchor Primer (supplied in the kit), followed by a nested reaction using GSP3 (SEQ ID NO:5) and AUAP (supplied in the kit) primers. The resulting PCR products were subcloned into TA vector (Invitrogen) and candidate clones were sequenced.

Sequence analysis indicated that the transcription start site (TSS) is located 30 base pairs upstream of the translational start site.

During the course of mapping the Cr1bio transcript by 5' RACE, both leaf and root derived RNA was used in PCR reactions that were integral to the 5' RACE procedures. A RACE product corresponding to Cr1bio was observed only in the root RNA sample, while in a control using Ubiquitin 1, RACE products were observed in both leaf and root RNA. See Figure 2 for a gel picture demonstrating these results. Another root preferred gene, CRWAQ81, was used as a second control, and also showed a 5' RACE product only in the root RNA samples. Given

the sensitivity of PCR, these results strongly support the MPSS results that Cr1Bio is a root preferred gene.

Example 3. Isolation of the Promoter for the Cr1bio Gene:

BAC clone sequencing

BAC bacc.pk093.f02 DNA, containing the cr1bio gene, was isolated from an overnight 250mL 2xYT+cloramphenicol culture by a modified alkaline lysis method. Cells were harvested by centrifugation 15 minutes at 4000 xg, resuspended in 20 mL 10mM EDTA and lysed by gently adding 40 mL 0.2N NaOH/1% SDS at room temperature. The lysate was neutralized by gently adding 30 mL cold 3M potassium acetate (pH 4.8). Cell debris was removed by centrifugation at 4 °C for 15 minutes at 15000 xg, followed by filtration through MiraclothTM (Calbiochem Corp. La Jolla, CA). DNA was precipitated by adding 0.7 volumes of isopropanol, followed by centrifugation at 4000 xg for 15 minutes at 4 °C. The resulting pellet was resuspended in 9 mL 50 mM Tris/50mM EDTA, mixed with 4.5 mL 7.5M potassium acetate and placed 30 minutes at -70 °C. The thawed mixture was centrifuged 20 minutes at 3500 xg, the supernatant transferred to a new polypropylene tube with 27 mL ethanol and centrifuged again 20 minutes at 3500 xg. The new pellet was resuspended in 0.7 mL 50 mM Tris/50mM EDTA and DNase-free RNase A was added to a final concentration of 150 µg/mL. The solution was incubated 1 hour at 37 °C and extracted once with phenol:chloroform:isoamyl alcohol 25:24:1, followed by ethanol precipitation at -20 °C overnight. The sample was centrifuged at 4 °C for 1 hour at 12K rpm and washed once in 80% ethanol. Final DNA was resuspended in a total of 400 µL sterile nuclease-free water.

BAC DNA was mechanically sheared using a nebulizer (Invitrogen) according to the manufacturer's recommendations, except that the nebulizer cup contained 1 mL TGM buffer (50% glycerol, 50 mM Tris-HCl, 15 mM magnesium chloride) and 200 µL DNA solution. Nebulized DNA was repaired using the End Repair Kit (Epicentre technologies) and 1.4 to 3 kb fragments were size-selected by Agarose-gel fractionation using the Qiaquick gel extraction system (Qiagen), according to the manufacturers' protocols. Approximately 100 ng size-selected DNA was ligated to 10 ng of EcoRV-digested, dephosphorylated pBuescript SK+ II

in a 10 μ L T4 ligase reaction (NEB) according to the manufacturer's recommendations. Ligation products were electroporated into DH10B cells and a total of 1,536 white colonies were picked and arrayed for sequencing.

The BAC clones were sequenced using the double-stranded random
5 shotgun approach (Bodenteich *et al.*, (1994) *Shotgun cloning or the strategy of choice to generate template for high-throughput dideoxynucleotide sequencing*, in: M.D. Adams, C. Fields, J.C. Venter (Eds.), *Automated DNA Sequencing and Analysis*, Academic Press, San Diego, 1994, pp. 42–50). The arrayed clones first were recovered from archived glycerol cultures grown/frozen in 384-well freezing
10 media plates, and inoculated with an automatic Q-Pix colony picker (Genetix) in 96-well deep-well plates containing LB + 100 μ g/mL ampicillin. After growing 20 hours at 37 °C, cells were pelleted by centrifugation and stored at –20 °C. Plasmids then were isolated on an Eppendorf 5Prime robot, using a modified 96-well format alkaline lysis miniprep method (Eppendorf PerfectPrep). Briefly, that modified
15 method uses a filter and vacuum manifold to facilitate removal of cellular debris after acetate precipitation, and the plasmid DNA then is bound on a second filter plate directly from the filtrate, washed, dried and eluted. Plasmids were end-sequenced in 384-well plates, using vector-primed M13 oligonucleotides and the ABI PRISM Big Dye terminator sequencing kit (Perkin Elmer - Applied Biosystems
20 Inc., Boston, MA). After ethanol-based cleanup, cycle sequencing reaction products were resolved and detected on Perkin-Elmer ABI 3700 automated sequencers, and individual sequences were assembled with the public domain Phred/Phrap/Consed package. While Phred reads DNA sequencing trace files, calls bases, assigns a quality value to each called base and writes the base calls
25 and quality values to output files, Phrap uses Phred-based sequencing files for assembling shotgun DNA sequence data (see the following website, which can be accessed by inputting the following website address into any web browser, when preceded by the “www.” prefix: phrap.org/phredphrapconsed.html). Consed is a tool for viewing, editing and finishing sequence assemblies generated with Phred and Phrap (Gordon *et al.*, (1998) *Genome Res.* 8 (1998) 195–202). Contig order
30 was viewed and confirmed with Exgap (A. Hua, University of Oklahoma, personal communication). Exgap is a local graphic tool that uses pair read informations to

order contigs generated by Phred, Phrap and Consed, and confirm the accuracy of the Phrap-based assembly.

Example 4: Isolation of the Promoter for the Cr1bio Gene:

Genome walking and genome survey sequence database searches

The Cr1Bio promoter and 5'UTR was isolated using multiple strategies involving a combination of genome walking, BAC clone sequencing (see Example 3), and searches of the Genome Survey Sequence (GSS) database. Using these combined approaches 1623 bp of the Cr1bio promoter and 5'UTR were obtained (SEQ ID NO: 1).

Genome walking upstream of the cr1bio EST sequence was performed using the Universal Genome Walker Kit (BD Biosciences Clontech, Palo Alto, CA). Genomic libraries were constructed from maize B73 genomic DNA according to the kit protocol. The gene-specific primers (SEQ ID NOs: 3, 4, and 5) used were identical to those used for 5' RACE (see Example 2). PCR reactions were performed as directed for optimization for the GC-Melt concentration using the Advantage Genomic PCR Kit (BD BioSciences Clontech). Oligonucleotides used for "Round 1" and "Round 2" reactions were GSP2 (SEQ ID NO:4) and AP1 (provided in kit) and GSP3 (SEQ ID NO:5) and AP2 (provided in kit), respectively. PCR products were subcloned into TA vector (Invitrogen) and candidate clones were sequenced. Using this method an additional 690 base pairs of sequence upstream of the ATG was obtained from this first round of Genome Walking (GW) reactions. Another set of nested oligos (GSP4 (SEQ ID NO:6) and GSP5 (SEQ ID NO:7)) designed near the 5' end of the 690 bp of sequence failed to produce additional upstream sequence after further GW reactions.

In order to obtain additional cr1bio upstream promoter sequence BAC clone sequencing (see Example 3) was initiated on clones previously identified to contain the cr1bio gene. Concurrently, GSS database searching using BLASTN identified additional upstream overlapping sequence to the 690 bp fragment obtained by genome walking. The genomic sequence revealed a 70 bp AT-repeat region immediately upstream of the sequence derived from Genome Walking. Based on the contig assembly of the GSS sequence and the 690 bp GW sequence PCR primers, OligoNotI (SEQ ID NO:9) and OligoBamHI (SEQ ID NO:10) were designed

in order to isolate a fragment representing the sequence available for the cr1bio promoter and 5'UTR from the BAC DNA used for BAC clone sequencing. NotI and BamHI restriction enzyme sites were added to the 5' ends to facilitate subsequent cloning.

5 Sequence confirmation of the resulting cloned PCR products indicated that deletions within the AT-rich region had occurred. An alternative strategy was used to assemble the cr1bio promoter consisting of PCR amplification of the sequences between OligoNotI (SEQ ID NO: 9) and GSP5 (SEQ ID NO:7) and between OligoBamHI (SEQ ID NO:10) and GSP6 (SEQ ID NO:8). The PCR products were
10 cloned into pBlueScriptSK+ along with a 660 bp ClaI-SphI fragment containing the AT-rich repeats from the BAC clone resulting in the reconstruction of the cr1bio promoter. The fragment order is: PCR product from Oligo NotI (SEQ ID NO:9) and GSP5 (SEQ ID NO:7) digested with NotI and ClaI; BAC clone ClaI and SphI; PCR product from Oligo BamHI (SEQ ID NO:10) and GSP6 (SEQ ID NO:8) digested with
15 BamHI and SphI; pBlueScriptSK+ Naol/BamHI.

Example 5: Cr1Bio Promoter Sequence Analysis

Analysis of the Cr1Bio promoter sequence indicated the presence of some motifs of interest.

20 The TATA box was identified and is indicated in Figure 1. It is located at positions 1570 through 1576 of SEQ ID NO: 1.

The "ATATT" motif, previously identified as being present in other promoters with root specific expression (Elmayan & Tepfer (1995) *Transgenic Research* 4, 388-396), was identified. Its location in the promoter can be seen in Figure 1.

25 An A-box motif (AATAAAYAAA (SEQ ID NO: 11)) was identified in the promoter and runs from position 69 to 78 of SEQ ID NO: 1. This motif is known to be associated with scaffold attachment regions. (Gasser *et al.* (1989) *Intnatl Rev Cyto* 119:57-96)

30 The transcriptional start site (TSS) was mapped by 5' RACE (see Example 2) and is at position 1601, also indicated on Figure 1.

A deletion fragment of the promoter (SEQ ID NO: 2) was generated to compare the temporal, spatial and quantitative expression to that of the full-length

promoter. The fragment spans from nucleotide 908 to 1600 or is about 40% of the original promoter.

Example 6: Promoter Activity of Cr1Bio

5 To demonstrate that the DNA isolated as the Cr1Bio promoter does function as a promoter, transient particle bombardment assays were performed. These assays provided a rapid assessment of whether a DNA fragment is able to direct gene expression.

10 The isolated DNA was PCR amplified from genomic DNA and cloned into an expression vector behind the B-glucuronidase (GUS) gene, with and without the *ADH1* intron 1, to test whether the fragment would direct expression. Biolistic bombardment of 3-day-old maize seedlings with this expression cassette resulted in numerous GUS staining foci on the coleoptile (>30 foci/coleoptile). The level of staining was comparable but slightly less than observed to a control, which
15 consisted of the strong, constitutive promoter, *Ubi-1*, directing GUS expression. These results indicated the 1623 bp Cr1Bio promoter fragment is able to direct expression at high levels.

Materials and Methods Utilized for the Biolistic Transient Root Expression Assay

20 B73 seeds were placed along one edge of a piece of germination paper that had been soaked in a solution of 7% sucrose. An additional piece of germination paper, identical in size to the first, was also soaked in 7% sucrose and was used to overlay the kernels. The germination paper – kernel – germination paper sandwich was subsequently rolled and placed into a beaker of 7% sucrose solution, such that
25 the solution would wick up the paper to the kernels at the top of the roll. This allowed for straight root growth. Kernels were permitted to germinate and develop for 2-3 days in the dark at 27-28 °C prior to bombardment: The sheath covering the coleoptile was removed and the seedlings were placed in a sterile petri dish (60 mm) on a layer filter paper moistened with distilled water. Two seedlings per plate
30 were arranged in opposite orientations and anchored to the filter paper with a 0.5% agarose solution.

DNA/gold particle mixtures were prepared for bombardment in the following method: 60 mg of 0.6 – 1.0 micron gold particles were pre-washed with ethanol,

rinsed with sterile distilled H₂O, and resuspended in a total of 1 mL of sterile H₂O. DNA was precipitated onto the surface of the gold particles by combining, in the following order, 50 µL of pre-washed 0.6 µM gold particles, 5-10 µg of test DNA, 50 µL 2.5 M CaCl₂ and 25 µL of 0.1 M spermidine. The solution was immediately
5 vortexed for 3 minutes and centrifuged briefly to pellet the DNA/gold particles. The DNA/gold was washed once with 500 µL of 100% ethanol and suspended in a final volume of 50 µL of 100% ethanol. The DNA/gold solution was incubated at -20 °C for at least 60 minutes prior to applying 6 µL of the DNA/gold mixture onto each mylar macrocarrier.

10 Seedlings prepared as indicated above were bombarded twice using the PDS-1000/He gun at 1100 psi under 27-28 inches of Hg vacuum. The distance between macrocarrier and stopping screen was between 6-8 cm. Plates were incubated in sealed containers for 18-24 h in the dark at 27-28 °C following bombardment.

15 The bombarded seedlings were assayed for transient GUS expression by immersing the seedlings in 10 -15 mL of GUS assay buffer containing 100 mM NaH₂PO₄-H₂O (pH 7.0), 10 mM EDTA, 0.5 mM K₄Fe(CN)₆-3H₂O, 0.1% Triton X-100 and 2 mM 5-bromo-4-chloro-3-indoyl glucuronide. The tissues were incubated in the dark for 24 h at 37 °C. Replacing the GUS staining solution with 100%
20 ethanol stopped the assay. GUS expression/staining was visualized under a microscope.

Example 7: Expression Pattern of Cr1Bio

Stable transformed plants were created using *Agrobacterium* protocols
25 (detailed in Example 8) to allow for a more detailed characterization of promoter activity, including expression pattern, expression level, and temporal regulation of the promoter. The Cr1Bio promoter (SEQ ID NO:1) was operably connected to the GUS gene (abbreviated as Cr1Bio:GUS) or operably linked to the *Adh1* intron and GUS gene (abbreviated as Cr1Bio(*Adh1* intron1):GUS) which allowed for Cr1Bio
30 promoter activity to be detected by histochemically staining tissue for GUS activity or through quantitative GUS fluorometric assays. The *Adh1* intron was included for the purpose of increased expression as it has been shown that in cereal cells the expression of foreign genes is enhanced by the presence of an intron in gene

constructs (See Callis *et al.* (1987) *Genes and Development* 1: 1183-1200; Kyoizuka *et al.* (1990) *Maydica* 35:353-357). A truncated version of the Cr1Bio promoter fragment (SEQ ID NO: 2) was also generated and tested in plants, with or without the Adh1 intron to observe the effect of the truncation on the quantitative, spatial and temporal properties of the promoter.

For each of the 4 plasmids, 17 plants growing on nutrient agar were examined in detail. Leaf and root tissue were sampled from each plant and histochemically assayed for GUS activity. Results showed that GUS was expressed in the roots of each plant. The intensity of GUS staining tended to be strongest in mature regions of the root with little or no staining in the root tips, including the root cap, meristem, and region of elongation. This staining pattern was similar for the truncated version of the promoter and whether or not the ADH intron was present. Staining was detected in the leaves of many of the plants. Depending on the plasmid, anywhere from 12 to 16 plants showed some type of leaf expression. The staining intensity in the leaves appeared to be at or below the intensity of the roots.

The plants were forwarded to the greenhouse for further evaluation at V5-V6 and R1-R2 developmental stages. V5-V6 stage plants have 5-6 collared leaves and R1-R2 plants are characterized by silking and pollen shed. Leaf and root tissue were sampled when the plants were at V5-V6 stage in development. Once again, staining was observed in both leaf and root tissue. In the root, the staining pattern was similar to that observed when the plants were growing on nutrient agarose. Most of the staining was detected in the mature areas of the root, with little or no staining in the root cap, meristem, and region of elongation. However, staining in the leaves was different than observed previously, such that the GUS staining was less intense compared to the roots. This observation was supported with quantitative fluorometric assays that showed the highest levels of GUS activity were in the mature region of the root and that the lowest levels of GUS activity were in the leaves (Table 1). These data provided evidence that the isolated Cr1Bio promoter does have a root preference and that this preference may be more distinguishable when the plants are older or not growing in a tissue culture format.

Interestingly, the expression level of the truncated (Cr1Bio-t) Cr1Bio promoter (SEQ ID NO: 2) was similar to that observed with the full-length Cr1Bio

promoter (SEQ ID NO: 1). The expression pattern was also similar between the two promoters (Table 2). This indicates that the elements required for root-preferred expression are found within the first 716 bp of the promoter.

5 **Table 1: Plant Expression Results for the Cr1bio Promoter**

	V5-V6		R1-R2		
	Leaf	Root	Tassel	Silk	Pollen
Cr1bio (SEQ ID NO: 1)	++	++++	++	+	-
Cr1bio-t (SEQ ID NO: 2)	++	++++	++	+	-
Cr1bio:ADH (SEQ ID NO: 1)	++	++++	+++	++	-
Cr1bio-t:ADH (SEQ ID NO: 2)	++	++++	+++	++	-
untransformed (negative control)	-	-	-	-	-

When the plants reached the R1 and R2 developmental stages, silk, pollen, and tassels were assayed for Cr1bio promoter activity via histochemical GUS staining. Once again, a similarity in expression pattern between the full-length and truncated versions of the Cr1Bio promoter was observed (Table 2). For silks, only 2 plants for the full-length and the truncated promoter had any type of silk expression. The expression that was observed was minimal and found in only a very few strands, $\leq 5\%$ of those in the sample. In pollen, expression was absent. This was true for both versions of the promoters and whether or not the ADH intron was present. Tassels had the most GUS staining of the 3 tissues sampled at this stage. But while the staining intensity was less than that observed in V5-V6 roots, the expression pattern in tassels was the most variable of all the tissues examined (Table 3). Despite the variability, there were still significant similarities in expression between the full-length and truncated versions of the Cr1Bio promoter and even between the ADH intron versions.

Table 2: MUG Assay Results for the Cr1bio Promoter

	Leaf	Root Tip	Mature Region
Cr1bio (SEQ ID NO: 1)	4	70	467
Cr1bio-t (SEQ ID NO: 2)	15	110	468
Cr1bio:ADH (SEQ ID NO: 1)	16	67	301
Cr1bio-t:ADH (SEQ ID NO: 2)	12	53	354
untransformed (negative control)	0	0	0

Values given are median values, as nmole MU/mg total protein/hr

MU= 4-methyl umbelliferone

MUG = 4-methyl umbelliferyl-B-D-glucuronide

5

Table 3: Tassel Expression Results for the Cr1bio Promoter

	A	B	C	D	E	F
Cr1bio (SEQ ID NO: 1)	6	5	3	-	-	-
Cr1bio-t (SEQ ID NO: 2)	3	5	5	-	-	-
Cr1bio:ADH (SEQ ID NO: 1)	-	9	3	1	1	-
Cr1bio-t:ADH (SEQ ID NO: 2)	1	9	1	3	-	1

Data expressed as number of events.

A: negative

B: glumes, rachis, lodicule region

10 C: glumes, lodicule region

D: lodicule region

E: glumes

F: rachis, lodicule region

15 Differences in expression between the full-length and truncated promoters begin to appear in the kernels. In 13 of the 16 plants assayed, the full-length Cr1Bio promoter directed expression primarily in the coleoptile and plumule of the embryo with some leaching of GUS activity into the scutellum (Table 4).

Expression was also observed in the brown abscission layer, but this was
 20 secondary to the expression in the observed in the coleoptile and plumule. None of the kernels assayed had observable expression in the endosperm.

Table 4: Kernel Expression Results for the Cr1bio Promoter

	A	B	C
Cr1bio (SEQ ID NO: 1)	++	+	-
Cr1bio-t (SEQ ID NO: 2)	+	++	-
Cr1bio:ADH (SEQ ID NO: 1)	++	+	++
Cr1bio-t:ADH (SEQ ID NO: 2)	+	++	+

A: coleoptile/plumule

B: brown abscission layer

C: 1st internode/primary root

5

In contrast, the truncated promoter directed kernel expression in only half of the events assayed (7 out of 14). Expression was weaker than observed with the full-length promoter, and where there was expression, it was strongest and most prevalent in the brown abscission layer. Expression in the coleoptile and plumule was now secondary. Additionally, 3 events had GUS expression in the endosperm.

10

The presence of the ADH intron had an effect on expression in the kernel. For the full-length promoter, expression was still predominately in the coleoptile and plumule, with leaching of GUS activity into the scutellum. Expression in the brown abscission layer was still observed. However, the addition of the ADH intron resulted in expression other tissues, namely the 1st internode and primary root of the embryo. Thirteen of the 16 plants assayed now had expression there. This was a striking difference compared to the promoter without the ADH intron, in which only 1 plant was observed to have kernels with expression in the primary root. There was still no expression in the endosperm.

15

20

The truncated Cr1Bio promoter was influenced similarly in that 9 out of 13 plants assayed had kernels with GUS expression in the 1st internode and primary root. This compares to no kernels having expression in these tissues when the intron was absent. Eight of these 9 events also had expression in the coleoptile and the plumule. But like the intron-less version of this promoter, expression was still strongest in the brown abscission layer and weaker in the coleoptile, plumule, 1st internode, and primary root. No expression was observed in the endosperm.

25

Histochemical Staining Of Calli and Plant Tissues For GUS Activity

Detection of GUS activity was accomplished by placing tissue from transformed plants into 48-well, 12-well or 6-well plates containing 0.5 to 5 mL GUS assay buffer (assay buffer recipe described in Example 4). Plates were placed under house vacuum for 10 min, then incubated overnight at 37 °C. Tissue was cleared of pigmentation with 1 to 3 successive 12 hour incubations in 100% ethanol at room temperature. The tissues were stored in 70% ethanol at 4 °C.

Example 8: *Agrobacterium*-Mediated Transformation of Maize and Regeneration of Transgenic Plants

For *Agrobacterium*-mediated transformation of maize with a promoter sequence of the embodiments, the method of Zhao was employed (See: U.S. Patent No. 5,981,840, (hereinafter the '840 patent) and PCT patent publication WO98/32326, the contents of both of which are hereby incorporated by reference).

Agrobacterium were grown on a master plate of 800 medium and cultured at 28 °C in the dark for 3 days, and thereafter stored at 4 °C for up to one month. Working plates of *Agrobacterium* were grown on 810 medium plates and incubated in the dark at 28 °C for one to two days.

Briefly, embryos were dissected from fresh, sterilized corn ears and kept in 561Q medium until all required embryos were collected. Embryos were then contacted with an *Agrobacterium* suspension prepared from the working plate, in which the *Agrobacterium* contained a plasmid comprising the promoter sequence of the embodiments. The embryos were co-cultivated with the *Agrobacterium* on 562P plates, with the embryos placed axis down on the plates, as per the '840 patent protocol.

After one week on 562P medium, the embryos were transferred to 563O medium. The embryos were subcultured on fresh 563O medium at 2 week intervals and incubation was continued under the same conditions. Callus events began to appear after 6 to 8 weeks on selection.

After the calli had reached the appropriate size, the calli were cultured on regeneration (288W) medium and kept in the dark for 2-3 weeks to initiate plant regeneration. Following somatic embryo maturation, well-developed somatic

embryos were transferred to medium for germination (272V) and moved to a lighted culture room. Approximately 7-10 days later, developing plantlets were transferred to 272V hormone-free medium in tubes for 7-10 days until plantlets were well established. Plants were then transferred to inserts in flats (equivalent to 2.5" pot) containing potting soil and grown for 1 week in a growth chamber, subsequently grown an additional 1-2 weeks in the greenhouse, then transferred to classic 600 pots (1.6 gallon) and grown to maturity.

Media used in *Agrobacterium*-mediated transformation and regeneration of transgenic maize plants:

561Q medium comprises 4.0 g/L N6 basal salts (SIGMA C-1416), 1.0 mL/L Eriksson's Vitamin Mix (1000x SIGMA-1511), 0.5 mg/L thiamine HCl, 68.5 g/L sucrose, 36.0 g/L glucose, 1.5 mg/L 2,4-D, and 0.69 g/L L-proline (brought to volume with dl H₂O following adjustment to pH 5.2 with KOH); 2.0 g/L Gelrite™ (added after bringing to volume with dl H₂O); and 8.5 mg/L silver nitrate (added after sterilizing the medium and cooling to room temperature).

800 medium comprises 50.0 mL/L stock solution A and 850 mL dl H₂O, and brought to volume minus 100 mL/L with dl H₂O, after which is added 9.0 g of phytagar. After sterilizing and cooling, 50.0 mL/L stock solution B is added, along with 5.0 g of glucose and 2.0 mL of a 50 mg/mL stock solution of spectinomycin. Stock solution A comprises 60.0 g of dibasic K₂HPO₄ and 20.0 g of monobasic sodium phosphate, dissolved in 950 mL of water, adjusted to pH 7.0 with KOH, and brought to 1.0 L volume with dl H₂O. Stock solution B comprises 20.0 g NH₄Cl, 6.0 g MgSO₄•7H₂O, 3.0 g potassium chloride, 0.2 g CaCl₂, and 0.05 g of FeSO₄•7H₂O, all brought to volume with dl H₂O, sterilized, and cooled.

810 medium comprises 5.0 g yeast extract (Difco), 10.0 g peptone (Difco), 5.0 g NaCl, dissolved in dl H₂O, and brought to volume after adjusting pH to 6.8. 15.0 g of bacto-agar is then added, the solution is sterilized and cooled, and 1.0 mL of a 50 mg/mL stock solution of spectinomycin is added.

562P medium comprises 4.0 g/L N6 basal salts (SIGMA C-1416), 1.0 mL/L Eriksson's Vitamin Mix (1000x SIGMA-1511), 0.5 mg/L thiamine HCl, 30.0 g/L sucrose, and 2.0 mg/L 2,4-D (brought to volume with dl H₂O following adjustment to pH 5.8 with KOH); 3.0 g/L Gelrite™ (added after bringing to volume with dl H₂O);

and 0.85 mg/L silver nitrate and 1.0 mL of a 100mM stock of acetosyringone (both added after sterilizing the medium and cooling to room temperature).

563O medium comprises 4.0 g/L N6 basal salts (SIGMA C-1416), 1.0 mL/L Eriksson's Vitamin Mix (1000x SIGMA-1511), 0.5 mg/L thiamine HCl, 30.0 g/L sucrose, 1.5 mg/L 2,4-D, 0.69 g L-proline, and 0.5 g MES buffer (brought to volume with dl H₂O following adjustment to pH 5.8 with KOH). Then, 6.0 g/L Ultrapure™ agar-agar (EM Science) is added and the medium is sterilized and cooled. Subsequently, 0.85 mg/L silver nitrate, 3.0 mL of a 1 mg/mL stock of Bialaphos, and 2.0 mL of a 50 mg/mL stock of carbenicillin are added.

288 W comprises 4.3 g/L MS salts (GIBCO 11117-074), 5.0 mL/L MS vitamins stock solution (0.100 g nicotinic acid, 0.02 g/L thiamine HCl, 0.10 g/L pyridoxine HCl, and 0.40 g/L Glycine brought to volume with polished D-I H₂O) (Murashige and Skoog (1962) *Physiol. Plant.* 15:473), 100 mg/L myo-inositol, 0.5 mg/L zeatin, and 60 g/L sucrose, which is then brought to volume with polished D-I H₂O after adjusting to pH 5.6. Following, 6.0 g/L of Ultrapure™ agar-agar (EM Science) is added and the medium is sterilized and cooled. Subsequently, 1.0 mL/L of 0.1 mM abscisic acid; 1.0 mg/L indoleacetic acid and 3.0 mg/L Bialaphos are added, along with 2.0 mL of a 50 mg/mL stock of carbenicillin.

Hormone-free medium (272V) comprises 4.3 g/L MS salts (GIBCO 11117-074), 5.0 mL/L MS vitamins stock solution (0.100 g/L nicotinic acid, 0.02 g/L thiamine HCl, 0.10 g/L pyridoxine HCl, and 0.40 g/L Glycine brought to volume with polished dl H₂O), 0.1 g/L myo-inositol, and 40.0 g/L sucrose (brought to volume with polished dl H₂O after adjusting pH to 5.6); and 6 g/L Bacto-agar (added after bringing to volume with polished dl H₂O), sterilized and cooled to 60 °C.

All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious

that certain changes and modifications may be practiced within the scope of the appended claims.

SEQUENCE LISTING

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E. I. du Pont de Nemours & Co.

<120> MAIZE CR1BIO GENE PROMOTER AND ITS USE
TO DIRECT ROOT-PREFERRED TRANSGENE EXPRESSION IN PLANTS

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<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer OligoNotI

<400> 9
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<400> 10
ccacccttca tgaggatcca tgctctc 27

<210> 11
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> A-Box Motif

<400> 11
aataaayaaa 10

THAT WHICH IS CLAIMED:

1. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

5 a) a nucleotide sequence comprising the sequence set forth in SEQ ID NOs:1 or 2, or a complement thereof;

b) a nucleotide sequence comprising the plant promoter sequences of the plasmids deposited as Patent Deposit No. PTA-6275 or a complement thereof;

10 c) a nucleotide sequence comprising at least 200 contiguous nucleotides of the sequence set forth in SEQ ID NOs:1 or 2, wherein said sequence initiates transcription in a plant cell; and

d) a nucleotide sequence comprising a sequence having at least 95% sequence identity to the sequence set forth in SEQ ID NO:1 or 2, wherein said
15 sequence initiates transcription in the plant cell.

2. A DNA construct comprising a nucleotide sequence of claim 1 operably linked to a heterologous nucleotide sequence of interest.

3. A vector comprising the DNA construct of claim 2.

20 4. A plant cell having stably incorporated into its genome the DNA construct of claim 2.

5. The plant cell of claim 4, wherein said plant cell is from a monocot.

6. The plant cell of claim 5, wherein said monocot is maize.

7. The plant cell of claim 4, wherein said plant cell is from a dicot.

25 8. A plant having stably incorporated into its genome the DNA construct of claim 2.

9. The plant of claim 8, wherein said plant is a monocot.

10. The plant of claim 9, wherein said monocot is maize.

11. The plant of claim 8, wherein said plant is a dicot.

12. A transgenic seed of the plant of claim 8, wherein said seed comprises the DNA construct.

13. The plant of claim 8, wherein the heterologous nucleotide sequence
5 of interest encodes a gene product that confers herbicide, salt, cold, drought, pathogen, or insect resistance.

14. A method for expressing a nucleotide sequence in a plant, said method comprising introducing into a plant a DNA construct, said DNA construct comprising a promoter and operably linked to said promoter a heterologous
10 nucleotide sequence of interest, wherein said promoter comprises a nucleotide sequence selected from the group consisting of:

a) a nucleotide sequence comprising the sequence set forth in SEQ ID NOs: 1 or 2;

b) a nucleotide sequence comprising the plant promoter
15 sequences of the plasmids designated as Patent Deposit No. PTA-6275;

c) a nucleotide sequence comprising at least 20 contiguous nucleotides of the sequence set forth in SEQ ID NOs: 1 or 2, wherein said nucleotide sequence initiates transcription in said plant; and

d) a nucleotide sequence comprising a sequence having at least
20 95% sequence identity to the sequence set forth in SEQ ID NOs: 1 or 2, wherein said nucleotide sequence initiates transcription in a plant cell.

15. The method of claim 14, wherein said plant is a dicot.

16. The method of claim 14, wherein said plant is a monocot.

17. The method of claim 16, wherein said monocot is maize.

18. The method of claim 14, wherein the heterologous nucleotide
25 sequence encodes a gene product that confers herbicide, salt, cold, drought, pathogen, or insect resistance.

19. The method of claim 14, wherein said heterologous nucleotide sequence of interest is selectively expressed in the root.

20. A method for expressing a nucleotide sequence in a plant cell, said method comprising introducing into a plant cell a DNA construct comprising a promoter operably linked to a heterologous nucleotide sequence of interest, wherein said promoter comprises a nucleotide sequence selected from the group consisting of:

a) a nucleotide sequence comprising the sequence set forth in SEQ ID NOs: 1 or 2;

b) a nucleotide sequence comprising the plant promoter sequences of the plasmids designated as Patent Deposit No. PTA-6275;

c) a nucleotide sequence comprising at least 20 contiguous nucleotides of the sequence set forth in SEQ ID NOs: 1 or 2, wherein said nucleotide sequence initiates transcription in said plant cell; and

d) a nucleotide sequence comprising a sequence having at least 95% sequence identity to the sequence set forth in SEQ ID NOs: 1 or 2, wherein said nucleotide sequence initiates transcription in a plant cell.

21. The method of claim 20, wherein said plant cell is from a monocot.

22. The method of claim 21, wherein said monocot is maize.

23. The method of claim 20, wherein said plant cell is from a dicot.

24. The method of claim 20, wherein the heterologous nucleotide sequence encodes a gene product that confers herbicide, salt, cold, drought, pathogen, or insect resistance.

25. A method for selectively expressing a nucleotide sequence in a plant root, said method comprising introducing into a plant cell a DNA construct, and regenerating a transformed plant from said plant cell, said DNA construct comprising a promoter and a heterologous nucleotide sequence operably linked to said promoter, wherein said promoter comprises a nucleotide sequence selected from the group consisting of:

a) a nucleotide sequence comprising the sequence set forth in SEQ ID NOs: 1 or 2;

b) a nucleotide sequence comprising the plant promoter sequences of the plasmids deposited as Patent Deposit No. PTA-6275;

c) a nucleotide sequence comprising at least 20 contiguous nucleotides of the sequence set forth in SEQ ID NOs: 1 or 2, wherein said

5 sequence initiates transcription in a plant root cell; and

d) a nucleotide sequence comprising a sequence having at least 95% sequence identity to the sequence set forth in SEQ ID NOs: 1 or 2, wherein said sequence initiates transcription in a plant root cell.

10 26. The method of claim 25, wherein expression of said heterologous nucleotide sequence alters the phenotype of said plant.

27. The method of claim 25, wherein the plant is a monocot.

28. The method of claim 27, wherein the monocot is maize.

29. The method of claim 25, wherein the plant is a dicot.

15 30. The method of claim 25, wherein the heterologous nucleotide sequence encodes a gene product that confers herbicide, salt, pathogen, or insect resistance.

Figure 1:**Cr1Bio Promoter and 5'UTR (SEQ ID NO: 1)**

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TATAGTAGAT GTAGATCACA ACTTTTTTATT TATTTTAAGC TGCATGAGGT TCAAGTTGTA 60
GTATAGTAAA TAAATAAATA TGCGATCCAA TCATCTCTGC TATCCGATCG GCCGGTCTCA 120
TAAAGGCAGC CCATACCTGT TGGTCGTTGT GTCGTCTGTA TTAAAATTCA GGCCGCGTAT 180
CGGTTTTTCC TTCCCACCAA CAAATTTACT ATCCGGATTT TTTTGGTGC ATGCTCGGTA 240
GGGCATTCCC AACGAAAGTT TCGTACTCTC AACAAAAATT TCATACTCAT TATATACGAT 300
GATACACCAT CATACATAGT GACATGACAT ACAATTAAAA GCAGAGATAT AGAAAGAGCT 360
TATGGGAGAT GGTAGAGTTT CATAGAGATA AAATTCTATA TATACAATTA CCTAGTTTAA 420
ATATGGTGTG ACAACATGGA AAACATTGTA CCGAAGCTCA CCGCTGAAAA TGGCCTTACA 480
AAACTGAAAA GAAGATGTCA CTTGTTGTGA AGCTCACCGA TGAAACTGGC CTAACAAAAC 540
TGAAACAAAA AGATCTCATC TCACTTGTTT TGAAGCTCAC CACTAAGAAT GACCTTACAA 600
AACTGAAACA AAAAGATGTC ACTTGTTCTA AAGCTCACCA CTGAGAAAGG CCTTACAAAA 660
CTAAACAAAA AAAAATATGT CACATGTTCT GAAGCTCACC ACTGAGAATG GCCTTACAAA 720
ACTGAAACAA AAATATGTCA TTTGTTTAGC TTGTCACCTCT ACTTTAGGAA AACAAAAATC 780
ATCGATATGT TTTTCTTGAT GCCTGCTCGA TATGGTTGTT ATATATATAT ATATATATAT 840
ATATATATAT ATATATATAT ATATATATAT ATATATATAT ATATATATAT ACCGTTTATA 900
AATATATGAC ATCGCTGACT TTTTAAAAAA CTTTAATCAC TTGTCTTATT TAAAAAATAA 960
TGAGTTGTCA TTTATTTTTT GTGTGGTTTG TTTTATCACT TAAGGTAGTT TGTGCTTAAT 1020
TAAAATTTTA TACTTTTGAA TAAGATAAAT GGTCAAAGTT TTTTAAAAAA ATCAACATGT 1080
CATATATCTG TGAACGGAGG TTGTATTACA GAATGTGCGA CGTACACGCT ACCCAATAAA 1140
ATACAACAAA CATTTGGTAC TGGAATTTTG CTCTTTGCGC ATAGAATCCA ATACATAAAA 1200
TAAGTATAGG CAGCGAACCA AACACGTCCC AAGTTTTATA ATTTGTAAAG AAAATGACAG 1260
CATTTAAATA TGATAACACA ATAATTAACC AGCGGGTAAG GGTAGTTTTT GTTGAGCACT 1320
GTTGCGGTTT AGAATCGCTG GACCTGCGTG TTTATGAGAC ACAGCGGGTA GCAGTTGGAA 1380
GAGATGATTG GGCTAGCTAG CTTGAGCGAT TCAGTCATCA ACCCCAATAT TGTTCCATTG 1440
CTGCATGCAC ATTTATCTAT ACCACGACGA CACAACGTGA ACCTCGTGCA GCTTTTTTAA 1500
ATACAGCCAG TTGTGATCCA TCTACCTGTC TGTCAGACGT GCTACAGCCT ACAGTTTAGT 1560
GACTGCTGCC TATAAAATGG CTGGCTGCTG GAGCAAAGCC AAACCAATCA GATAGAGAGC 1620
ATG 1623

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AATAAAYAAA (SEQ ID NO: 11) – This motif is shown in bold and underlined text.

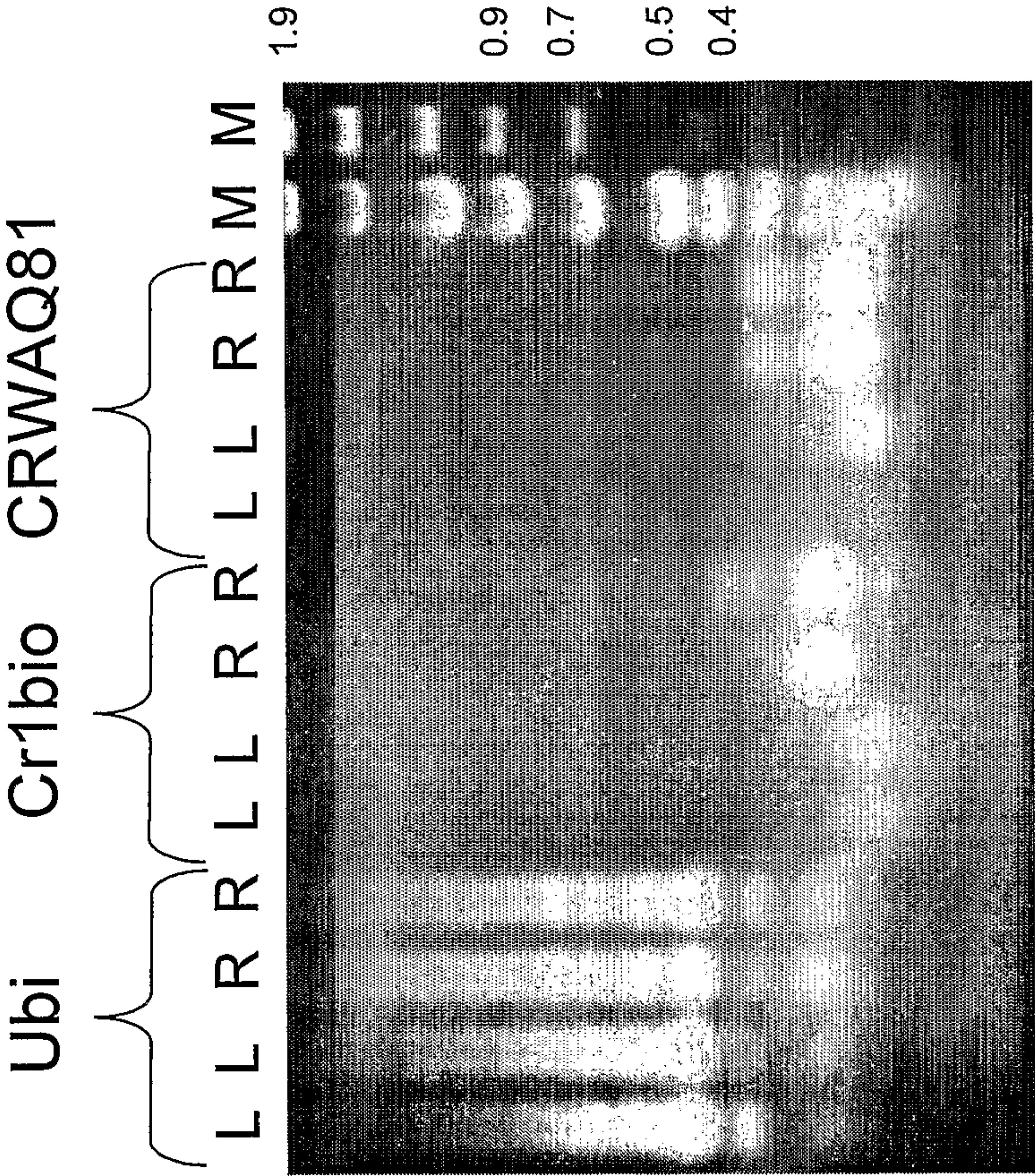
ATATT – This motif is shown in double-underlined text.

The **TATA box** is shown in bold text.

The transcriptional start site (TSS) mapped by 5' RACE is indicated at position 1601 by an "A" in a box.

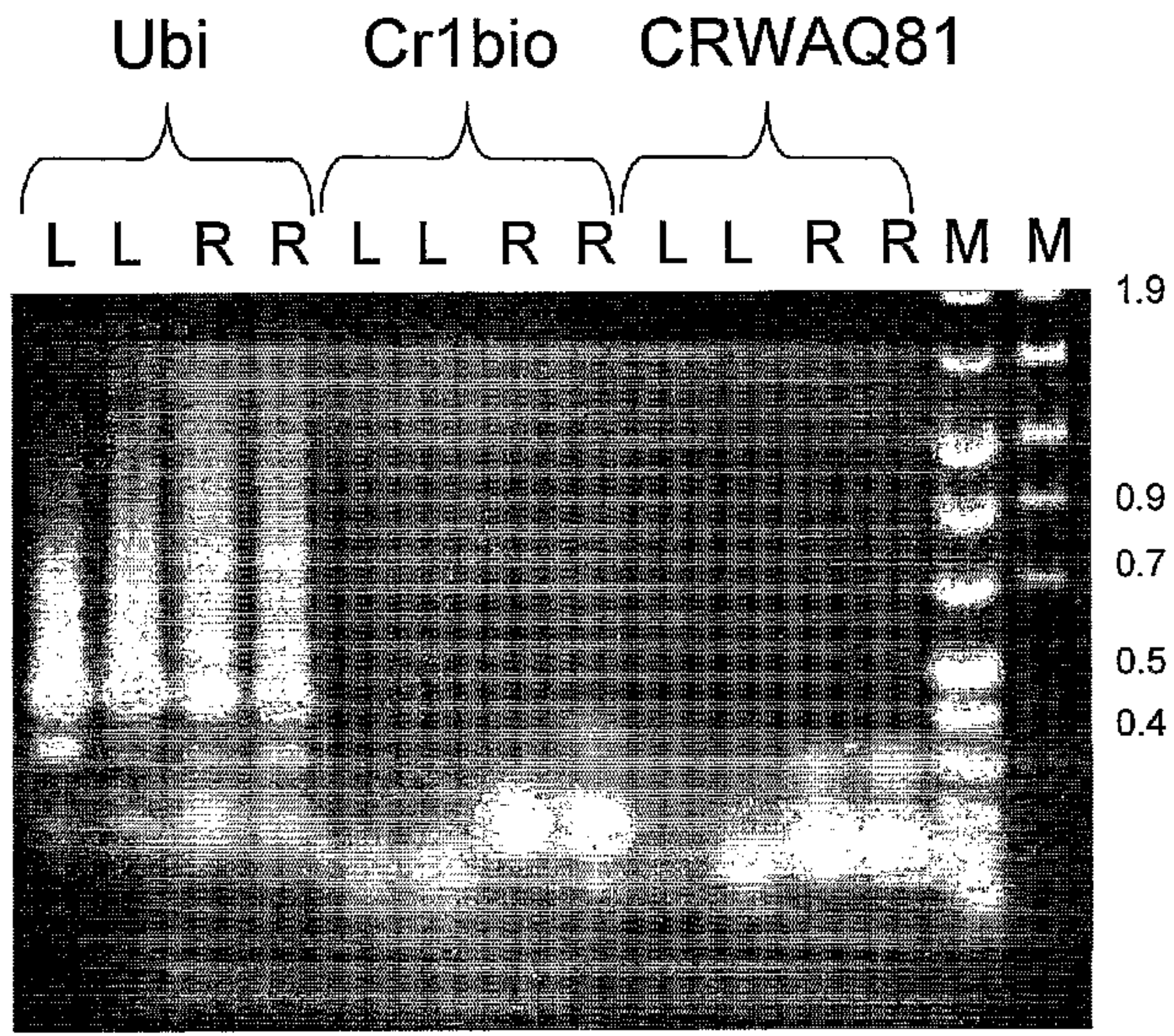
A deletion fragment of the promoter (SEQ ID NO: 2), spans from nucleotide 908 to 1623 of this figure.

Figure 2
Gel Showing Root Preferred Expression of Cr1bio



Controls: Ubiquitin for leaf and root
CRWAQ81 for root preferred

Gel Showing Root Preferred Expression of Cr1bio



Controls: Ubiquitin for leaf and root
CRWAQ81 for root preferred