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(54) Title: CHIMERIC COMPOSITIONS AND METHODS FOR REGULATING PLANT GENE EXPRESSION

(57) Abstract: The invention provides a method for producing a chimeric promoter polynucleotide capable of controlling transcription of an operably linked polynucleotide in a plant cell or plant, wherein the method comprises combining: a) at least one sequence motif comprising a sequence with at least 70% identity to SEQ ID NO:1, 11 or 12, and b) another polynucleotide sequence. The invention also provides chimeric promoters polynucleotides comprising the sequences defined in a) and b). The invention also provides constructs, vectors, host cells, plant cells and plants comprising the chimeric promoter polynucleotides of the invention. The invention also provided methods for modifying gene expression and phenotype of plant cells and plants by transforming the plant cells and plants with the chimeric promoter polynucleotides of the invention.



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CHIMERIC COMPOSITIONS AND METHODS FOR REGULATING PLANT GENE EXPRESSION

TECHNICAL FIELD

The present invention relates to polynucleotides for regulating gene expression in plants, and uses thereof.

BACKGROUND ART

An important goal for agriculture is to produce plants with beneficial agronomic traits. Recent advances in genetic manipulation provide the tools to transform plants with polynucleotide sequences of interest and to express such sequences within the transformed plants. This has led to the development of plants capable of expressing pharmaceuticals and other chemicals, plants with increased pest resistance, increased stress tolerance and many other beneficial traits.

It is often desirable to control expression of a polynucleotide of interest, in a particular tissue, at a particular developmental stage, or under particular conditions, in which the polynucleotide is not normally expressed. The polynucleotide of interest may encode a protein or alternatively may be intended to effect silencing of a corresponding target gene.

Plant promoter sequences are useful in genetic manipulation for directing expression of polynucleotides in transgenic plants. To achieve this, a genetic construct is often introduced into a plant cell or plant. Typically such constructs include a plant promoter operably linked to the polynucleotide sequence of interest. Such a promoter need not normally be associated with the gene of interest. Once transformed, the promoter controls expression of the operably linked polynucleotide of interest thus leading to the desired transgene expression and resulting desired phenotypic characteristics in the plant.

Promoters used in genetic manipulation are typically derived from the 5' un-transcribed region of genes and contain regulatory elements that are necessary to control expression of the operably linked polynucleotide. Promoters useful for plant biotechnology can be classified depending on when and where they direct expression. For example promoters may be tissue specific or

constitutive (capable of transcribing sequences in multiple tissues). Other classes of promoters include inducible promoters that can be triggered by external stimuli such as environmental and chemical stimuli.

Often a relatively high level of expression of the transformed sequence of interest is desirable. This is often achieved through use of viral promoter sequences such as the Cauliflower Mosaic Virus 35S promoter. In some circumstances it may be more preferable to use a plant derived promoter rather than a promoter derived from a microorganism. It may also be preferable in some circumstances to use a promoter derived from, or produced from sequences derived from, the species to be transformed.

It would be beneficial to have a variety of promoters available in order to ensure that transgenes are transcribed at an appropriate level in the right tissues, and at an appropriate stage of growth or development.

The apple (*Malus* species) is a major fruit species grown in New Zealand and other temperate climates throughout the world. Valuable traits that may be improved by genetic manipulation of apple include: fruit flavour, fruit colour, content of health promoting components (such as anthocyanins and flavanoids) in fruit, stress tolerance/resistance, pest tolerance/resistance and disease tolerance/resistance.

Genetic manipulation of such traits in apple, and these and other traits in other species, is limited by the availability of promoters capable of appropriately controlling the expression of genes of interest.

It is therefore an object of the present invention to provide a promoter useful for controlling gene expression in apple and other plants and/or at least to provide a useful choice.

SUMMARY OF THE INVENTION

In the first aspect the invention provides a method for producing a chimeric promoter polynucleotide capable of controlling transcription of an operably linked polynucleotide in a plant cell or plant, wherein the method comprises combining:

- a) at least one sequence motif comprising a sequence with at least 70% identity to SEQ ID NO:1, 11 or 12, and
- b) another polynucleotide sequence.

In a preferred embodiment the method comprises combining:

- a) at least two sequence motifs, each comprising a sequence with at least 70% identity to any one of SEQ ID NO:1, 11 or 12, and
- b) another polynucleotide sequence.

The chimeric promoter polynucleotide more preferably produced by combining:

- a) at least three, more preferably at least four, more preferably at least five, more preferably at least six, and most preferably at least seven sequence motifs, each comprising a sequence with at least 70% identity to any one of SEQ ID NO: 1, 11 or 12, and
- b) another polynucleotide sequence.

Preferably at least one of the sequence motifs in a) comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 1.

Preferably at least one motif in a) comprises the sequence of SEQ ID NO: 41.

Preferably at least one motif in a) comprises the sequence of SEQ ID NO: 42.

In one embodiment at least one sequence motif in a) comprises the sequence of SEQ ID NO: 1.

In another embodiment at least one sequence motif in a) comprises the sequence of SEQ ID NO: 11.

In another embodiment at least one sequence motif in a) comprises the sequence of SEQ ID NO: 12.

The chimeric promoter may comprise several of the motifs in a) as defined above. The motifs within the promoter may all be the same, or may be a combination of different motifs as defined above.

In another embodiment at least one of the sequence motifs is interrupted by at least one of the other sequence motifs.

In a further embodiment the sequence motif in a) is part of a promoter polynucleotide sequence that naturally occurs in a plant.

In a further embodiment the polynucleotide in b) is a promoter polynucleotide sequence.

In a further embodiment the polynucleotide in b) is a promoter polynucleotide sequence that naturally occurs in a plant.

In a preferred embodiment both the sequence motif in a) and the polynucleotide, or promoter polynucleotide in b) naturally occur in plants

Preferably the sequence motif in a) and the polynucleotide in b) naturally occur in the same species, or interfertile species.

Preferably the sequence motif in a) and the polynucleotide in b) naturally occur in the same promoter.

In this embodiment a further copy, or copies, of a motif with at least 70% identity to SEQ ID NO:1, 11 or 12, that is present in a naturally occurring promoter polynucleotide, may be added to the naturally occurring promoter polynucleotide to produce the chimeric promoter polynucleotide.

In an alternative embodiment one or more motifs with at least 70% identity to SEQ ID NO:1, 11 or 12, that are naturally occurring in plant promoters, may be added to a different naturally occurring promoter.

The motif or motifs with at least 70% identity to SEQ ID NO:1, 11 or 12, may be naturally occurring in different species, or different promoters, and may be combined with a promoter from one of the the same species, or from a different species.

In one embodiment the naturally occurring promoter polynucleotide in b) comprises a sequence with at least 70% identity to SEQ ID NO:13.

In a further embodiment the naturally occurring promoter polynucleotide comprises the sequence of SEQ ID NO:13.

In one embodiment the chimeric promoter is produced by combining:

- a) the sequence of SEQ ID NO:14, and
- b) the sequence of SEQ ID NO:8.

In one embodiment the chimeric promoter is produced by combining:

- a) the sequence of SEQ ID NO:14, and
- b) the sequence of SEQ ID NO:13.

In one embodiment the chimeric promoter is produced by combining:

- a) the sequence of SEQ ID NO:14, and
- b) the sequence of SEQ ID NO:36.

In one embodiment the chimeric promoter is produced by combining:

- a) the sequence of SEQ ID NO:14, and
- b) the sequence of SEQ ID NO:38.

In a further embodiment the chimeric promoter polynucleotide comprises a sequence with at least 70% identity to SEQ ID NO:15.

In a further embodiment the chimeric promoter polynucleotide comprises the sequence of SEQ ID NO:15.

In a further embodiment the chimeric promoter polynucleotide comprises a sequence with at least 70% identity to SEQ ID NO:37.

In a further embodiment the chimeric promoter polynucleotide comprises the sequence of SEQ ID NO:37.

In a further embodiment the chimeric promoter polynucleotide comprises a sequence with at least 70% identity to SEQ ID NO:39.

In a further embodiment the chimeric promoter polynucleotide comprises the sequence of SEQ ID NO:39.

In a further embodiment the chimeric promoter polynucleotide comprises a sequence with at least 70% identity to SEQ ID NO:40.

In a further embodiment the chimeric promoter polynucleotide comprises the sequence of SEQ ID NO:40.

In a further aspect the invention provides a chimeric promoter produced by the method of the invention.

In a further aspect the invention provides a chimeric promoter polynucleotide capable of controlling transcription of an operably linked polynucleotide in a plant cell or plant, wherein the promoter polynucleotide comprises:

- a) at least one sequence motif comprising a sequence with at least 70% identity to SEQ ID NO:1, 11 or 12
- b) another polynucleotide sequence.

In a preferred embodiment the chimeric promoter polynucleotide comprises at least two sequence motifs comprising a sequence with at least 70% identity to SEQ ID NO:1, 11 or 12.

The chimeric promoter polynucleotide more preferably comprises at least three, more preferably at least four, more preferably at least five, more preferably at least six, and most preferably at least seven sequence motifs comprising a sequence with at least 70% identity to SEQ ID NO: 1, 11 or 12.

Preferably at least one of the sequence motifs comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 1.

Preferably at least one motif in a) comprises the sequence of SEQ ID NO: 41.

Preferably at least one motif in a) comprises the sequence of SEQ ID NO: 42.

In one embodiment at least one sequence motif comprises the sequence of SEQ ID NO: 1.

In another embodiment at least one sequence motif comprises the sequence of SEQ ID NO: 11.

In another embodiment at least one sequence motif comprises the sequence of SEQ ID NO: 12.

The chimeric promoter may comprise several of the motifs in a) as defined above. The motifs within the promoter may all be the same, or may be a combination of different motifs as defined above.

In another embodiment at least one of the sequence motifs is interrupted by at least one of the other sequence motifs.

In a further embodiment the sequence motif in a) is part of a promoter polynucleotide sequence that naturally occurs in a plant.

In a further embodiment the polynucleotide in b) is a promoter polynucleotide sequence.

In a further embodiment the polynucleotide in b) is a promoter polynucleotide sequence that naturally occurs in a plant.

In a preferred embodiment both the sequence motif in a) and the polynucleotide in b) naturally occur in plants

Preferably the sequence motif in a) and the polynucleotide in b) naturally occur in the same species, or interfertile species.

Preferably the sequence motif in a) and the polynucleotide in b) naturally occur in the same promoter.

In this embodiment the chimeric promoter may comprise the naturally occurring promoter with an additional inserted copy, or copies, of a motif with at least 70% identity to SEQ ID NO: 1, 12 or 13 that is present in the naturally occurring promoter polynucleotide.

In an alternative embodiment the chimeric promoter may comprise a naturally occurring promoter, with an additional inserted copy or copies of a motif with at least 70% identity to SEQ ID NO: 1, 12 or 13 that is not present in the naturally occurring promoter polynucleotide.

The motif or motifs comprising a sequence with at least 70% identity to SEQ ID NO:1, 11 or 12, may be naturally occurring in different species, or different promoters, and may have been combined with a promoter from one of the the same species, or from a different species.

In one embodiment the naturally occurring promoter polynucleotide comprises a sequence with at least 70% identity to SEQ ID NO:13.

In a further embodiment the naturally occurring promoter polynucleotide comprises the sequence of SEQ ID NO:13.

In one embodiment the chimeric promoter comprises:

- a) the sequence of SEQ ID NO:14, combined with
- b) the the sequence of SEQ ID NO:8.

In one embodiment the chimeric promoter comprises:

- a) the sequence of SEQ ID NO:14, combined with
- b) the the sequence of SEQ ID NO:13.

In one embodiment the chimeric promoter comprises:

- a) the sequence of SEQ ID NO:14, combined with
- b) the the sequence of SEQ ID NO:36.

In one embodiment the chimeric promoter comprises:

- a) the sequence of SEQ ID NO:14, combined with
- b) the the sequence of SEQ ID NO:38.

In a further embodiment the chimeric promoter polynucleotide comprises a sequence with at least 70% identity to SEQ ID NO:15.

In a further embodiment the chimeric promoter polynucleotide comprises the sequence of SEQ ID NO:15.

In a further embodiment the chimeric promoter polynucleotide comprises a sequence with at least 70% identity to SEQ ID NO:37.

In a further embodiment the chimeric promoter polynucleotide comprises the sequence of SEQ ID NO:37.

In a further embodiment the chimeric promoter polynucleotide comprises a sequence with at least 70% identity to SEQ ID NO:39.

In a further embodiment the chimeric promoter polynucleotide comprises the sequence of SEQ ID NO:39.

In a further embodiment the chimeric promoter polynucleotide comprises a sequence with at least 70% identity to SEQ ID NO:40.

In a further embodiment the chimeric promoter polynucleotide comprises the sequence of SEQ ID NO:40.

In a further embodiment the chimeric promoter polynucleotide is modulated by a MYB transcription factor.

In a further embodiment the chimeric promoter polynucleotide is positively modulated, or activated, or up-regulated by the MYB transcription factor.

Preferably the MYB transcription factor comprises an R2R3 DNA binding domain.

Preferably the MYB transcription factor comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 6.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 6.

Preferably the MYB transcription factor comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 17.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 17.

Preferably the MYB transcription factor comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 32.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 32.

Preferably the MYB transcription factor comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 34.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 34.

Preferably the chimeric promoter polynucleotide is up-regulated by the gene product of the gene with which at least one of the sequence motifs of the chimeric promoter polynucleotide is endogenously associated.

Preferably at least one of the sequence motifs of the chimeric promoter polynucleotide in its natural environment is endogenously associated with the MYB transcription factor. Preferably the chimeric promoter is positively regulated by the MYB transcription factor.

Preferably the chimeric promoter polynucleotide is capable of controlling transcription of an operably linked polynucleotide sequence constitutively in substantially all tissues of a plant.

More preferably the promoter polynucleotide is capable of controlling transcription of an operably linked polynucleotide sequence in any plant, plant cell, or plant tissue in which the MYB transcription factor is expressed.

The MYB transcription factor may be naturally expressed in the plant or may be expressed in the plant through genetic manipulation of the plant.

In a further aspect the invention provides a genetic construct comprising a chimeric promoter polynucleotide of the invention.

In one embodiment the chimeric promoter polynucleotide is operably linked to a polynucleotide sequence to be expressed.

In a further aspect the invention provides a vector comprising a genetic construct of the invention.

In a further aspect the invention provides a host cell transformed with the chimeric promoter polynucleotide of the invention.

In a further aspect the invention provides a plant cell or plant transformed with the chimeric promoter polynucleotide of the invention.

In a further aspect the invention provides a plant cell or plant transformed with a genetic construct of the invention.

In one embodiment the plant cell or plant is also transformed with a polynucleotide or genetic construct for expressing a MYB transcription factor that modulates expression of the chimeric promoter polynucleotide of the invention.

In a further embodiment the plant cell or plant naturally expresses the MYB transcription factor.

In a further embodiment the MYB transcription factor comprises an amino acid sequence with at least 70% identity to the sequence of any one of SEQ ID NO: 6, 17, 32 and 34.

Preferably the MYB transcription factor comprises the sequence of any one of SEQ ID NO: 6, 17, 32 and 34.

In a further embodiment the MYB transcription factor comprises an amino acid sequence with at least 70% identity to the sequence of SEQ ID NO: 6.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 6.

In a further embodiment the MYB transcription factor comprises an amino acid sequence with at least 70% identity to the sequence of SEQ ID NO: 17.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 17.

In a further embodiment the MYB transcription factor comprises an amino acid sequence with at least 70% identity to the sequence of SEQ ID NO: 32.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 32.

In a further embodiment the MYB transcription factor comprises an amino acid sequence with at least 70% identity to the sequence of SEQ ID NO: 34.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 34.

In a further aspect the invention provides a method for producing a plant cell or plant with modified expression of at least one polynucleotide, the method comprising transformation of the plant cell or plant with a chimeric promoter polynucleotide of the invention

In one embodiment the plant cell or plant is transformed with a genetic construct of the invention.

In a further embodiment the plant cell or plant is also transformed with a polynucleotide or genetic construct capable of expressing a MYB transcription factor that modulates expression of the chimeric promoter polynucleotide of the invention.

In a further embodiment the plant cell or plant naturally expresses the MYB transcription factor.

In a further embodiment the MYB transcription factor comprises an amino acid sequence with at least 70% identity to the sequence of any one of SEQ ID NO: 6, 17, 32 and 34.

Preferably the MYB transcription factor comprises the sequence of any one of SEQ ID NO: 6, 17, 32 and 34.

In a further embodiment the MYB transcription factor comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 6.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 6.

In a further embodiment the MYB transcription factor comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 17.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 17.

In a further embodiment the MYB transcription factor comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 32.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 32.

In a further embodiment the MYB transcription factor comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 34.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 34.

It will be appreciated by those skilled in the art that, the chimeric promoter polynucleotide of the invention may be transformed into the plant to control expression of a polynucleotide that is operably linked to the promoter prior to transformation.

Alternatively the promoter polynucleotide may be transformed into the genome of the plant without an operably linked polynucleotide, but the promoter may control expression of an endogenous polynucleotide, typically adjacent to the insert site, and typically, to the 3' end of the inserted promoter polynucleotide.

In a further aspect of the invention provides a method for producing a plant cell or plant with a modified phenotype, the method comprising the stable incorporation into the genome of the plant, of a chimeric promoter polynucleotide of the invention

In one embodiment the plant cell or plant is transformed within a genetic construct of the invention.

In a further embodiment the plant cell or plant is also transformed with a genetic construct for expressing a MYB transcription factor that modulates expression of the chimeric promoter polynucleotide of the invention.

In a further embodiment the plant cell or plant naturally expresses the MYB transcription factor.

In a further embodiment the MYB transcription factor comprises an amino acid sequence with at least 70% identity to the sequence of any one of SEQ ID NO: 6, 17, 32 and 34.

Preferably the MYB transcription factor comprises the sequence of any one of SEQ ID NO: 6, 17, 32 and 34.

In a further embodiment the MYB transcription factor comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 6.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 6.

In a further embodiment the MYB transcription factor comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 17.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 17.

In a further embodiment the MYB transcription factor comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 32.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 32.

In a further embodiment the MYB transcription factor comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 34.

Preferably the MYB transcription factor comprises the sequence of SEQ ID NO: 34.

In a further aspect the invention provides a plant cell or plant produced by a method of the invention.

In a further aspect the invention provides a seed, propagule, progeny, part, fruit or harvested material of a plant, of the invention.

Preferably the seed, propagule, progeny, part, fruit or harvested material of the plant comprises a chimeric promoter polynucleotide of the invention.

The naturally occurring sequences that may be used to produce the chimeric promoter polynucleotide of the invention may be derived from any species.

In one embodiment the naturally occurring sequence, is derived from a plant species.

In a further embodiment the naturally occurring sequence, is derived from a gymnosperm plant species.

In a further embodiment the naturally occurring sequence, is derived from an angiosperm plant species.

In a further embodiment the naturally occurring sequence, is derived from a from dicotyledonous plant species.

In a further embodiment the naturally occurring sequence, is derived from a monocotyledonous plant species.

The polypeptide encoded by the polynucleotide to be expressed in a construct of the invention, may be derived from any species and/or may be produced synthetically or recombinantly.

In one embodiment the polypeptide is derived from a plant species.

In a further embodiment the polypeptide is derived from a gymnosperm plant species.

In a further embodiment the polypeptide is derived from an angiosperm plant species.

In a further embodiment the polypeptide is derived from a from dicotyledonous plant species.

In a further embodiment the polypeptide is derived from a monocotyledonous plant species.

The MYB transcription factor that regulates the chimeric promoter polynucleotide of the invention may be derived from any species and/or may be produced synthetically or recombinantly.

In one embodiment the MYB transcription factor, is derived from a plant species.

In a further embodiment the MYB transcription factor, is derived from a gymnosperm plant species.

In a further embodiment the MYB transcription factor, is derived from an angiosperm plant species.

In a further embodiment the MYB transcription factor, is derived from a from dicotyledonous plant species.

In a further embodiment the MYB transcription factor, is derived from a monocotyledonous plant species.

The plant cells and plants, of the invention, or produced by the methods of the invention, may be derived from any species.

In one embodiment the plant cell or plant, is derived from a gymnosperm plant species.

In a further embodiment the plant cell or plant, is derived from an angiosperm plant species.

In a further embodiment the plant cell or plant, is derived from a from dicotyledonous plant species.

In a further embodiment the plant cell or plant, is derived from a monocotyledonous plant species.

Preferred plant species (from which the naturally occurring sequence and variants, polypeptides and variants, MYB transcription factor and variants, and plant cells and plants may be derived) include fruit plant species selected from a group comprising but not limited to the following genera: *Malus*, *Pyrus*, *Prunus*, *Rubus*, *Rosa*, *Fragaria*, *Actinidia*, *Cydonia*, *Citrus*, and *Vaccinium*.

Particularly preferred fruit plant species are: *Malus domestica*, *Pyrus communis*, *Actinidia deliciosa*, *A. chinensis*, *A. eriantha*, *A. arguta* and hybrids of the four *Actinidia* species, *Fragaria ananassa* and *Prunus persica*.

Preferred plants also include vegetable plant species selected from a group comprising but not limited to the following genera: *Brassica*, *Lycopersicon* and *Solanum*.

Particularly preferred vegetable plant species are: *Lycopersicon esculentum* and *Solanum tuberosum*.

Preferred plants also include crop plant species selected from a group comprising but not limited to the following genera: *Glycine*, *Zea*, *Hordeum* and *Oryza*.

Particularly preferred crop plant species include *Glycine max*, *Zea mays* and *Oryza sativa*.

Preferred plants also include those of the Rosaceae family.

Preferred Rosaceae genera include *Exochorda*, *Maddenia*, *Oemleria*, *Osmaronia*, *Prinsepia*, *Prunus*, *Maloideae*, *Amelanchier*, *Aria*, *Aronia*, *Chaenomeles*, *Chamaemespilus*, *Cormus*, *Cotoneaster*, *Crataegus*, *Osmaronia*, *Prinsepia*, *Prunus*, *Maloideae*, *Amelanchier*, *Aria*, *Aronia*, *Chaenomeles*, *Chamaemespilus*, *Cormus*, *Cotoneaster*, *Crataegus*, *Cydonia*, *Dichotomanthes*, *Docynia*, *Docyniopsis*, *Eriobotrya*, *Eriolobus*, *Heteromeles*, *Kageneckia*, *Lindleya*, *Malacomeles*, *Malus*, *Mespilus*, *Osteomeles*, *Peraphyllum*, *Photinia*, *Pseudocydonia*, *Pyracantha*, *Pyrus*, *Rhaphiolepis*, *Sorbus*, *Stranvaesia*, *Torminalis*, *Vauquelinia*, *Rosoideae*, *Acaena*, *Acomastylis*, *Agrimonia*, *Alchemilla*, *Aphanes*, *Aremonia*, *Bencomia*, *Chamaebatia*, *Cliffortia*, *Cohuria*, *Cowania*, *Dalibarda*, *Dendriopoterium*, *Dryas*, *Duchesnea*, *Erythrocoma*,

Fallugia, Filipendula, Fragaria, Geum, Hagenia, Horkelia, Ivesia, Kerria, Leucosidea, Marcetella, Margyricarpus, Novosieversia, Oncostylus, Polylepis, Potentilla, Rosa, Rubus, Sanguisorba, Sarcopoterium, Sibbaldia, Sieversia, Taihangia, Tetraglochin, Waldsteinia, Rosaceae incertae sedis, Adenostoma, Aruncus, Cercocarpus, Chamaebatiaria, Chamaerhodos, Gillenia, Holodiscus, Lyonothamnus, Neillia, Neviusia, Physocarpus, Purshia, Rhodotypos, Sorbaria, Spiraea and Stephanandra.

Preferred Rosaceae species include *Exochorda giraldii, Exochorda racemosa, Exochorda, Exochorda giraldii, Exochorda racemosa, Exochorda serratifolia, Maddenia hypoleuca, Oemleria cerasiformis, Osmaronia cerasiformis, Prinsepia sinensis, Prinsepia uniflora, Prunus alleghaniensis, Prunus americana, Prunus andersonii, Prunus angustifolia, Prunus apetalata, Prunus argentea, Prunus armeniaca, Prunus avium, Prunus bifrons, Prunus brigantina, Prunus bucharica, Prunus buergeriana, Prunus campanulata, Prunus caroliniana, Prunus cerasifera, Prunus cerasus, Prunus choreiana, Prunus cocomilia, Prunus cyclamina, Prunus davidiana, Prunus debilis, Prunus domestica, Prunus dulcis, Prunus emarginata, Prunus fasciculata, Prunus ferganensis, Prunus fordiana, Prunus fremontii, Prunus fruticosa, Prunus geniculata, Prunus glandulosa, Prunus gracilis, Prunus grayana, Prunus hortulana, Prunus ilicifolia, Prunus incisa, Prunus jacquemontii, Prunus japonica, Prunus kuramica, Prunus laurocerasus, Prunus leveilleana, Prunus lusitanica, Prunus maackii, Prunus mahaleb, Prunus mandshurica, Prunus maritima, Prunus maximowiczii, Prunus mexicana, Prunus microcarpa, Prunus mira, Prunus mume, Prunus munsoniana, Prunus nigra, Prunus nipponica, Prunus padus, Prunus pennsylvanica, Prunus persica, Prunus petunnikowii, Prunus prostrata, Prunus pseudocerasus, Prunus pumila, Prunus rivularis, Prunus salicina, Prunus sargentii, Prunus sellowii, Prunus serotina, Prunus serrulata, Prunus sibirica, Prunus simonii, Prunus spinosa, Prunus spinulosa, Prunus subcordata, Prunus subhirtella, Prunus takesimensis, Prunus tenella, Prunus texana, Prunus tomentosa, Prunus tschonoskii, Prunus umbellata, Prunus verecunda, Prunus virginiana, Prunus webbii, Prunus x yedoensis, Prunus zippeliana, Prunus sp. BSP-2004-1, Prunus sp. BSP-2004-2, Prunus sp. EB-2002, Amelanchier alnifolia, Amelanchier arborea, Amelanchier asiatica, Amelanchier bartramiana, Amelanchier canadensis, Amelanchier cusickii, Amelanchier fernaldii, Amelanchier florida, Amelanchier humilis, Amelanchier intermedia, Amelanchier laevis, Amelanchier lucida, Amelanchier nantucketensis, Amelanchier pumila, Amelanchier quinti-martii, Amelanchier sanguinea, Amelanchier stolonifera, Amelanchier utahensis, Amelanchier wiegandii, Amelanchier x neglecta, Amelanchier bartramiana x Amelanchier sp. 'dentata', Amelanchier sp. 'dentata', Amelanchier*

*sp. 'erecta', Amelanchier sp. 'erecta' x Amelanchier laevis, Amelanchier sp. 'serotina', Aria
 alnifolia, Aronia prunifolia, Chaenomeles cathayensis, Chaenomeles speciosa, Chamaemespilus
 alpina, Cormus domestica, Cotoneaster apiculatus, Cotoneaster lacteus, Cotoneaster pannosus,
 Crataegus azarolus, Crataegus columbiana, Crataegus crus-galli, Crataegus curvisepala,
 Crataegus laevigata, Crataegus mollis, Crataegus monogyna, Crataegus nigra, Crataegus
 rivularis, Crataegus sinaica, Cydonia oblonga, Dichotomanthes tristaticarpa, Docynia
 delavayi, Docyniopsis tschonoskii, Eriobotrya japonica, Eriobotrya prunoides, Eriolobus
 trilobatus, Heteromeles arbutifolia, Kagehenkia angustifolia, Kagehenkia oblonga, Lindleya
 mespiloides, Malacomeles denticulata, Malus angustifolia, Malus asiatica, Malus baccata,
 Malus coronaria, Malus doumeri, Malus florentina, Malus floribunda, Malus fusca, Malus
 halliana, Malus honanensis, Malus hupehensis, Malus ioensis, Malus kansuensis, Malus
 mandshurica, Malus micromalus, Malus niedzwetzkyana, Malus ombrophilia, Malus
 orientalis, Malus prattii, Malus prunifolia, Malus pumila, Malus sargentii, Malus sieboldii,
 Malus sieversii, Malus sylvestris, Malus toringoides, Malus transitoria, Malus trilobata, Malus
 tschonoskii, Malus x domestica, Malus x domestica x Malus sieversii, Malus x domestica x
 Pyrus communis, Malus xiaojinensis, Malus yunnanensis, Malus sp., Mespilus germanica,
 Osteomeles anthyllidifolia, Osteomeles schwerinae, Peraphyllum ramosissimum, Photinia
 fraseri, Photinia pyrifolia, Photinia serrulata, Photinia villosa, Pseudocydonia sinensis,
 Pyracantha coccinea, Pyracantha fortuneana, Pyrus calleryana, Pyrus caucasica, Pyrus
 communis, Pyrus elaeagnifolia, Pyrus hybrid cultivar, Pyrus pyrifolia, Pyrus salicifolia, Pyrus
 ussuriensis, Pyrus x bretschneideri, Rhamphiolepis indica, Sorbus americana, Sorbus aria,
 Sorbus aucuparia, Sorbus californica, Sorbus commixta, Sorbus hupehensis, Sorbus scopulina,
 Sorbus sibirica, Sorbus torminalis, Stranvaesia davidiana, Torminalis clusii, Vauquelinia
 californica, Vauquelinia corymbosa, Acaena anserinifolia, Acaena argentea, Acaena
 caesiiglaucula, Acaena cylindristachya, Acaena digitata, Acaena echinata, Acaena elongata,
 Acaena eupatoria, Acaena fissistipula, Acaena inermis, Acaena laevigata, Acaena latebrosa,
 Acaena lucida, Acaena macrocephala, Acaena magellanica, Acaena masafuerana, Acaena
 montana, Acaena multifida, Acaena novaezealandiae, Acaena ovalifolia, Acaena pinnatifida,
 Acaena splendens, Acaena subincisa, Acaena x anserovina, Acomastylis elata, Acomastylis
 rossii, Acomastylis sikkimensis, Agrimonia eupatoria, Agrimonia nipponica, Agrimonia
 parviflora, Agrimonia pilosa, Alchemilla alpina, Alchemilla erythropoda, Alchemilla japonica,
 Alchemilla mollis, Alchemilla vulgaris, Aphanes arvensis, Aremonia agrimonioides, Bencomia
 brachystachya, Bencomia caudata, Bencomia exstipulata, Bencomia sphaerocarpa,
 Chamaebatia foliolosa, Cliffortia burmeana, Cliffortia cuneata, Cliffortia dentata, Cliffortia*

graminea, *Cliffortia heterophylla*, *Cliffortia nitidula*, *Cliffortia odorata*, *Cliffortia ruscifolia*,
Cliffortia sericea, *Coluria elegans*, *Coluria geoides*, *Cowania stansburiana*, *Dalibarda repens*,
Dendriopoterium menendezii, *Dendriopoterium pulidoi*, *Dryas drummondii*, *Dryas octopetala*,
Duchesnea chrysantha, *Duchesnea indica*, *Erythrocoma triflora*, *Fallugia paradoxa*,
Filipendula multijuga, *Filipendula purpurea*, *Filipendula ulmaria*, *Filipendula*
vulgaris, *Fragaria chiloensis*, *Fragaria daltoniana*, *Fragaria gracilis*, *Fragaria grandiflora*,
Fragaria iinumae, *Fragaria moschata*, *Fragaria nilgerrensis*, *Fragaria nipponica*, *Fragaria*
nubicola, *Fragaria orientalis*, *Fragaria pentaphylla*, *Fragaria vesca*, *Fragaria virginiana*,
Fragaria viridis, *Fragaria x ananassa*, *Fragaria* sp. CFRA 538, *Fragaria* sp., *Geum andicola*,
Geum borisi, *Geum bulgaricum*, *Geum calthifolium*, *Geum chiloense*, *Geum geniculatum*,
Geum heterocarpum, *Geum macrophyllum*, *Geum montanum*, *Geum reptans*, *Geum rivale*,
Geum schofieldii, *Geum speciosum*, *Geum urbanum*, *Geum vernum*, *Geum* sp. 'Chase 2507
K', *Hagenia abyssinica*, *Horkelia cuneata*, *Horkelia fusca*, *Ivesia gordonii*, *Kerria*
japonica, *Leucosidea sericea*, *Marcetella maderensis*, *Marcetella moquiniana*, *Margyricarpus*
pinnatus, *Margyricarpus setosus*, *Novosieversia glacialis*, *Oncostylus cockaynei*, *Oncostylus*
leiospermus, *Polylepis australis*, *Polylepis besseri*, *Polylepis crista-galli*, *Polylepis hieronymi*,
Polylepis incana, *Polylepis lanuginosa*, *Polylepis multijuga*, *Polylepis neglecta*, *Polylepis*
pauta, *Polylepis pepeii*, *Polylepis quadrijuga*, *Polylepis racemosa*, *Polylepis reticulata*,
Polylepis rugulosa, *Polylepis sericea*, *Polylepis subsericans*, *Polylepis tarapacana*, *Polylepis*
tomentella, *Polylepis weberbaueri*, *Potentilla anserina*, *Potentilla arguta*, *Potentilla bifurca*,
Potentilla chinensis, *Potentilla dickinsii*, *Potentilla erecta*, *Potentilla fragarioides*, *Potentilla*
fruticosa, *Potentilla indica*, *Potentilla micrantha*, *Potentilla multifida*, *Potentilla nivea*,
Potentilla norvegica, *Potentilla palustris*, *Potentilla peduncularis*, *Potentilla reptans*,
Potentilla salesoviana, *Potentilla stenophylla*, *Potentilla tridentata*, *Rosa abietina*, *Rosa*
abyssinica, *Rosa acicularis*, *Rosa agrestis*, *Rosa alba*, *Rosa alba x Rosa corymbifera*, *Rosa*
altaica, *Rosa arkansana*, *Rosa arvensis*, *Rosa banksiae*, *Rosa beggeriana*, *Rosa blanda*, *Rosa*
bracteata, *Rosa brunonii*, *Rosa caesia*, *Rosa californica*, *Rosa canina*, *Rosa carolina*, *Rosa*
chinensis, *Rosa cinnamomea*, *Rosa columnifera*, *Rosa corymbifera*, *Rosa cymosa*, *Rosa davurica*,
Rosa dumalis, *Rosa ecae*, *Rosa eglandaria*, *Rosa elliptica*, *Rosa fedtschenkoana*, *Rosa foetida*,
Rosa foliolosa, *Rosa gallica*, *Rosa gallica x Rosa dumetorum*, *Rosa gigantea*, *Rosa glauca*,
Rosa helenae, *Rosa henryi*, *Rosa hugonis*, *Rosa hybrid cultivar*, *Rosa inodora*, *Rosa*
jundzillii, *Rosa laevigata*, *Rosa laxa*, *Rosa luciae*, *Rosa majalis*, *Rosa marretii*, *Rosa*
maximowicziana, *Rosa micrantha*, *Rosa mollis*, *Rosa montana*, *Rosa moschata*, *Rosa*
moyesii, *Rosa multibracteata*, *Rosa multiflora*, *Rosa nitida*, *Rosa odorata*, *Rosa palustris*,

Rosa pendulina, *Rosa persica*, *Rosa phoenicia*, *Rosa platyacantha*, *Rosa primula*, *Rosa pseudoscabriuscula*, *Rosa roxburghii*, *Rosa rubiginosa*, *Rosa rugosa*, *Rosa sambucina*, *Rosa sempervirens*, *Rosa sericea*, *Rosa sertata*, *Rosa setigera*, *Rosa sherardii*, *Rosa sicular*, *Rosa spinosissima*, *Rosa stellata*, *Rosa stylosa*, *Rosa subcanina*, *Rosa subcollina*, *Rosa suffulta*, *Rosa tomentella*, *Rosa tomentosa*, *Rosa tunquinensis*, *Rosa villosa*, *Rosa virginiana*, *Rosa wichurana*, *Rosa willmottiae*, *Rosa woodsii*; *Rosa x damascena*, *Rosa x fortuniana*, *Rosa x macrantha*, *Rosa xanthina*, *Rosa sp.*, *Rubus alceifolius*, *Rubus allegheniensis*, *Rubus alpinus*, *Rubus amphidasys*, *Rubus arcticus*, *Rubus argutus*, *Rubus assamensis*, *Rubus australis*, *Rubus bifrons*, *Rubus caesius*, *Rubus caesius x Rubus idaeus*, *Rubus canadensis*, *Rubus canescens*, *Rubus caucasicus*, *Rubus chamaemorus*, *Rubus corchorifolius*, *Rubus crataegifolius*, *Rubus cuneifolius*, *Rubus deliciosus*, *Rubus divaricatus*, *Rubus ellipticus*, *Rubus flagellaris*, *Rubus fruticosus*, *Rubus geoides*, *Rubus glabratus*, *Rubus glaucus*, *Rubus gunnianus*, *Rubus hawaiiensis*, *Rubus hawaiiensis x Rubus rosifolius*, *Rubus hispidus*, *Rubus hochstetterorum*, *Rubus humulifolius*, *Rubus idaeus*, *Rubus lambertianus*, *Rubus lasiococcus*, *Rubus leucodermis*, *Rubus lineatus*, *Rubus macraei*, *Rubus maximiformis*, *Rubus minusculus*, *Rubus moorei*, *Rubus multibracteatus*, *Rubus neomexicanus*, *Rubus nepalensis*, *Rubus nessensis*, *Rubus nivalis*, *Rubus niveus*, *Rubus nubigenus*, *Rubus occidentalis*, *Rubus odoratus*, *Rubus palmatus*, *Rubus parviflorus*, *Rubus parvifolius*, *Rubus parvus*, *Rubus pectinellus*, *Rubus pedatus*, *Rubus pedemontanus*, *Rubus pensilvanicus*, *Rubus phoenicolasius*, *Rubus picticaulis*, *Rubus pubescens*, *Rubus rigidus*, *Rubus robustus*, *Rubus roseus*, *Rubus rosifolius*, *Rubus sanctus*, *Rubus sapidus*, *Rubus saxatilis*, *Rubus setosus*, *Rubus spectabilis*, *Rubus sulcatus*, *Rubus tephrodes*, *Rubus trianthus*, *Rubus tricolor*, *Rubus trifidus*, *Rubus trilobus*, *Rubus trivialis*, *Rubus ulmifolius*, *Rubus ursinus*, *Rubus urticifolius*, *Rubus vigorosus*, *Rubus sp.*
JPM-2004, *Sanguisorba albiflora*, *Sanguisorba alpina*, *Sanguisorba ancistroides*, *Sanguisorba annua*, *Sanguisorba canadensis*, *Sanguisorba filiformis*, *Sanguisorba hakusanensis*, *Sanguisorba japonensis*, *Sanguisorba minor*, *Sanguisorba obtusa*, *Sanguisorba officinalis*, *Sanguisorba parviflora*, *Sanguisorba stipulata*, *Sanguisorba tenuifolia*, *Sarcopoterium spinosum*, *Sibbaldia procumbens*, *Sieversia pentapetala*, *Sieversia pusilla*, *Taihangia rupestris*, *Tetraglochin cristatum*, *Waldsteinia fragarioides*, *Waldsteinia geoides*, *Adenostoma fasciculatum*, *Adenostoma sparsifolium*, *Aruncus dioicus*, *Cercocarpus betuloides*, *Cercocarpus ledifolius*, *Chamaebatiaria millefolium*, *Chamaerhodos erecta*, *Gillenia stipulata*, *Gillenia trifoliata*, *Holodiscus discolor*, *Holodiscus microphyllus*, *Lyonothamnus floribundus*, *Neillia affinis*, *Neillia gracilis*, *Neillia sinensis*, *Neillia sparsiflora*, *Neillia thibetica*, *Neillia thyrsiflora*, *Neillia uekii*, *Neviusia alabamensis*, *Physocarpus alternans*, *Physocarpus*

amurensis, *Physocarpus capitatus*, *Physocarpus malvaceus*, *Physocarpus monogynus*, *Physocarpus opulifolius*, *Purshia tridentata*, *Rhodotypos scandens*, *Sorbaria arborea*, *Sorbaria sorbifolia*, *Spiraea betulifolia*, *Spiraea cantoniensis*, *Spiraea densiflora*, *Spiraea japonica*, *Spiraea nipponica*, *Spiraea x vanhouttei*, *Spiraea sp.*, *Stephanandra chinensis*, *Stephanandra incisa* and *Stephanandra tanakae*.

Particularly preferred Rosaceae genera include: *Malus*, *Pyrus*, *Cydonia*, *Prunus*, *Eriobotrya*, and *Mespilus*.

Particularly preferred Rosaceae species include: *Malus domestica*, *Malus sylvestris*, *Pyrus communis*, *Pyrus pyrifolia*, *Pyrus bretschneideri*, *Cydonia oblonga*, *Prunus salicina*, *Prunus cerasifera*, *Prunus persica*, *Eriobotrya japonica*, *Prunus dulcis*, *Prunus avium*, *Mespilus germanica* and *Prunus domestica*.

A particularly preferred Rosaceae genus is *Malus*.

A particularly preferred *Malus* species is *Malus domestica*.

Particularly preferred *Malus* species/cultivars include *Malus sieversii* 93.051 G01-048, *Malus aldenhamii*, *Malus pumila* Niedzwetzkyana, *Malus x domestica* cv. 'Prairiefire', *Malus x domestica* cv. 'Geneva', *Malus sieversii* 92.103 30-312.

A particularly preferred *Malus* cultivar is *Malus x domestica* niedzwetzkyana.

Another preferred Rosaceae genus is *Pyrus*.

Particularly preferred *Pyrus* species include *Pyrus calleryana*, *Pyrus caucasica*, *Pyrus communis*, *Pyrus elaeagnifolia*, *Pyrus hybrid cultivar*, *Pyrus pyrifolia*, *Pyrus salicifolia*, *Pyrus ussuriensis*, *Pyrus x bretschneideri*.

A particularly preferred *Pyrus* species is *Pyrus communis*.

Another preferred genus is *Fragaria*.

Preferred *Fragaria* species include *Fragaria daltoniana*, *Fragaria gracilis*, *Fragaria grandiflora*, *Fragaria iinumae*, *Fragaria moschata*, *Fragaria nilgerrensis*, *Fragaria nipponica*, *Fragaria nubicola*, *Fragaria orientalis*, *Fragaria pentaphylla*, *Fragaria vesca*, *Fragaria virginiana*, *Fragaria viridis*, *Fragaria x ananassa*, *Fragaria sp. CFRA 538*.

Particularly preferred *Fragaria* species are *Fragaria x ananassa*, *Fragaria chiloensis* and *Fragaria vesca*.

DETAILED DESCRIPTION

In this specification where reference has been made to patent specifications, other external documents, or other sources of information, this is generally for the purpose of providing a context for discussing the features of the invention. Unless specifically stated otherwise, reference to such external documents is not to be construed as an admission that such documents, or such sources of information, in any jurisdiction, are prior art, or form part of the common general knowledge in the art.

Definitions

The term “comprising” as used in this specification and claims means “consisting at least in part of”; that is to say when interpreting statements in this specification and claims which include “comprising”, the features prefaced by this term in each statement all need to be present but other features can also be present. Related terms such as “comprise” and “comprised” are to be interpreted in similar manner.

However, in preferred embodiments comprising can be replaced with consisting.

The term “chimeric” as used herein, with respect to the chimeric promoter polynucleotide of the invention, means comprised of sequences that are “recombined”. Preferably the sequences that are “recombined” are not found together in nature.

Typically the chimeric promoter is comprised of sequence elements that are present in naturally occurring promoters. For example, one or more of the sequence elements present in a naturally occurring promoter may be duplicated or multiplied, in the context of a naturally occurring promoter, to produce a chimeric promoter of the invention. The naturally occurring promoter may be the same promoter as the sequence elements, or may be from a different promoter.

Preferably the chimeric promoter polynucleotide sequence of the invention is not found in naturally occurring plants in its entirety. However the chimeric promoter may be constructed from naturally occurring sequences that are recombined.

The term “recombine” as used herein means refers to any method of joining polynucleotides. The term includes end to end joining, and insertion of one sequence into another. The term is intended to encompass includes physical joining techniques such as sticky-end ligation and blunt-end ligation. The chimeric promoter polynucleotide sequence, or elements thereof, may also be artificially, or recombinantly synthesised to contain the recombined sequences.

Typically the chimeric promoter is synthesised by methods well known to those skilled in the art. However the chimeric promoter will contain the sequences as herein defined or specified, that are not normally found together in nature.

When a chimeric promoter of the invention comprises a particular element or motif, this means that the element or motif may be found within the chimeric promoter sequence or at either end of the chimeric promoter sequence.

A “naturally occurring” sequence, promoter or promoter element, is one that is found in at least one species in nature.

The term “derived from” with respect to plants or a particular type of plant, means the same as a sequence naturally occurring in those plants or that plant.

The term “sequence motif” as used herein means a stretch of nucleotides. Preferably the stretch of nucleotides is contiguous.

The term “MYB transcription factor” is a term well understood by those skilled in the art to refer to a class of transcription factors characterised by a structurally conserved DNA binding domain consisting of single or multiple imperfect repeats.

The term “A MYB transcription with an R2R3 DNA binding domain” is a term well understood by those skilled in the art to refer to MYB transcription factors of the two-repeat class.

The term “modified” with respect to a plant with “modified expression” or a “modified phenotype” means modified relative to the same plant, or plant of the same type, in the non-transformed state.

Polynucleotides and fragments

The term “polynucleotide(s),” as used herein, means a single or double-stranded deoxyribonucleotide or ribonucleotide polymer of any length but preferably at least 15 nucleotides, and include as non-limiting examples, coding and non-coding sequences of a gene, sense and antisense sequences complements, exons, introns, genomic DNA, cDNA, pre-mRNA, mRNA, rRNA, siRNA, miRNA, tRNA, ribozymes, recombinant polypeptides, isolated and purified naturally occurring DNA or RNA sequences, synthetic RNA and DNA sequences, nucleic acid probes, primers and fragments.

A “fragment” of a polynucleotide sequence provided herein is a subsequence of contiguous nucleotides that is preferably at least 15 nucleotides in length. The fragments of the invention preferably comprises at least 20 nucleotides, more preferably at least 30 nucleotides, more preferably at least 40 nucleotides, more preferably at least 50 nucleotides and most preferably at least 60 contiguous nucleotides of a polynucleotide of the invention. A fragment of a polynucleotide sequence can be used in antisense, gene silencing, triple helix or ribozyme technology, or as a primer, a probe, included in a microarray, or used in polynucleotide-based selection methods.

The term “fragment” in relation to promoter polynucleotide sequences is intended to include sequences comprising cis-elements and regions of the chimeric promoter polynucleotide sequence capable of regulating expression of a polynucleotide sequence to which the fragment is operably linked.

Preferably fragments of promoter polynucleotide sequences of the invention comprise at least 46, more preferably at least 69, more preferably at least 92, more preferably at least 115, more preferably at least 138, more preferably at least 150, more preferably at least 200, more preferably at least 300, more preferably at least 400, more preferably at least 500, more preferably at least 600, more preferably at least 700, more preferably at least 800, more preferably at least 900, more preferably at least 1000, more preferably at least 1100, more preferably at least 1200, more preferably at least 1300, more preferably at least 1400, more preferably at least 1500, more preferably at least 1600 and most preferably at least 1700 contiguous nucleotides of the specified polynucleotide. Fragments of the chimeric promoter polynucleotide sequences can be used to control expression of an operably linked polynucleotide in a transgenic plant cells or plants.

The term “primer” refers to a short polynucleotide, usually having a free 3'OH group, that is hybridized to a template and used for priming polymerization of a polynucleotide complementary to the template. Such a primer is preferably at least 5, more preferably at least 6, more preferably at least 7, more preferably at least 9, more preferably at least 10, more preferably at least 11, more preferably at least 12, more preferably at least 13, more preferably at least 14, more preferably at least 15, more preferably at least 16, more preferably at least 17, more preferably at least 18, more preferably at least 19, more preferably at least 20 nucleotides in length.

The term “probe” refers to a short polynucleotide that is used to detect a polynucleotide sequence, that is complementary to the probe, in a hybridization-based assay. The probe may consist of a “fragment” of a polynucleotide as defined herein. Preferably such a probe is at least 5, more preferably at least 10, more preferably at least 20, more preferably at least 30, more preferably at least 40, more preferably at least 50, more preferably at least 100, more preferably at least 200, more preferably at least 300, more preferably at least 400 and most preferably at least 500 nucleotides in length.

Polypeptides and fragments

The term “polypeptide”, as used herein, encompasses amino acid chains of any length but preferably at least 5 amino acids, including full-length proteins, in which amino acid residues are

linked by covalent peptide bonds. The polypeptides may be purified natural products, or may be produced partially or wholly using recombinant or synthetic techniques. The term may refer to a polypeptide, an aggregate of a polypeptide such as a dimer or other multimer, a fusion polypeptide, a polypeptide fragment, a polypeptide variant, or derivative thereof.

A “fragment” of a polypeptide is a subsequence of the polypeptide that performs a function that is required for the biological activity and/or provides three dimensional structure of the polypeptide. The term may refer to a polypeptide, an aggregate of a polypeptide such as a dimer or other multimer, a fusion polypeptide, a polypeptide fragment, a polypeptide variant, or derivative thereof capable of performing the above enzymatic activity.

The term “isolated” as applied to the polynucleotide or polypeptide sequences disclosed herein is used to refer to sequences that are removed from their natural cellular environment. An isolated molecule may be obtained by any method or combination of methods including biochemical, recombinant, and synthetic techniques.

The term “derived from” with respect to a polynucleotide or polypeptide sequence being derived from a particular genera or species, means that the sequence has the same sequence as a polynucleotide or polypeptide sequence found naturally in that genera or species. The sequence, derived from a particular genera or species, may therefore be produced synthetically or recombinantly.

Variants

As used herein, the term “variant” refers to polynucleotide or polypeptide sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variants may be from the same or from other species and may encompass homologues, paralogues and orthologues. In certain embodiments, variants of the inventive polynucleotides and polypeptides possess biological activities that are the same or similar to those of the inventive polynucleotides or polypeptides. The term “variant” with reference to polynucleotides and polypeptides encompasses all forms of polynucleotides and polypeptides as defined herein.

Polynucleotide variants

Variant polynucleotide sequences preferably exhibit at least 50%, more preferably at least 51%, more preferably at least 52%, more preferably at least 53%, more preferably at least 54%, more preferably at least 55%, more preferably at least 56%, more preferably at least 57%, more preferably at least 58%, more preferably at least 59%, more preferably at least 60%, more preferably at least 61%, more preferably at least 62%, more preferably at least 63%, more preferably at least 64%, more preferably at least 65%, more preferably at least 66%, more preferably at least 67%, more preferably at least 68%, more preferably at least 69%, more preferably at least 70%, more preferably at least 71%, more preferably at least 72%, more preferably at least 73%, more preferably at least 74%, more preferably at least 75%, more preferably at least 76%, more preferably at least 77%, more preferably at least 78%, more preferably at least 79%, more preferably at least 80%, more preferably at least 81%, more preferably at least 82%, more preferably at least 83%, more preferably at least 84%, more preferably at least 85%, more preferably at least 86%, more preferably at least 87%, more preferably at least 88%, more preferably at least 89%, more preferably at least 90%, more preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98%, and most preferably at least 99% identity to a specified polynucleotide sequence. Identity is found over a comparison window of at least 20 nucleotide positions, more preferably at least 50 nucleotide positions, more preferably at least 100 nucleotide positions, more preferably at least 200 nucleotide positions, more preferably at least 300 nucleotide positions, more preferably at least 400 nucleotide positions, more preferably at least 500 nucleotide positions, more preferably at least 600 nucleotide positions, more preferably at least 700 nucleotide positions, more preferably at least 800 nucleotide positions, more preferably at least 900 nucleotide positions, more preferably at least 1000 nucleotide positions, more preferably at least 1100 nucleotide positions, more preferably at least 1200 nucleotide positions, more preferably at least 1300 nucleotide positions, more preferably at least 1400 nucleotide positions, more preferably at least 1500 nucleotide positions, more preferably at least 1600 nucleotide positions, more preferably at least 1700 nucleotide positions and most preferably over the entire length of the specified polynucleotide sequence. For the 23 bp motifs in the chimeric promoters of the invention, or used in the methods of the invention, identity is preferably found over the whole 23 nucleotide positions.

Polynucleotide sequence identity can be determined in the following manner. The subject polynucleotide sequence is compared to a candidate polynucleotide sequence using BLASTN (from the BLAST suite of programs, version 2.2.5 [Nov 2002]) in bl2seq (Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250), which is publicly available from NCBI (<ftp://ftp.ncbi.nih.gov/blast/>). The default parameters of bl2seq are utilized except that filtering of low complexity parts should be turned off.

The identity of polynucleotide sequences may be examined using the following unix command line parameters:

```
bl2seq -i nucleotideseq1 -j nucleotideseq2 -F F -p blastn
```

The parameter -F F turns off filtering of low complexity sections. The parameter -p selects the appropriate algorithm for the pair of sequences. The bl2seq program reports sequence identity as both the number and percentage of identical nucleotides in a line "Identities = ".

Polynucleotide sequence identity may also be calculated over the entire length of the overlap between a candidate and subject polynucleotide sequences using global sequence alignment programs (e.g. Needleman, S. B. and Wunsch, C. D. (1970) J. Mol. Biol. 48, 443-453). A full implementation of the Needleman-Wunsch global alignment algorithm is found in the needle program in the EMBOSS package (Rice, P. Longden, I. and Bleasby, A. EMBOSS: The European Molecular Biology Open Software Suite, Trends in Genetics June 2000, vol 16, No 6. pp.276-277) which can be obtained from <http://www.hgmp.mrc.ac.uk/Software/EMBOSS/>. The European Bioinformatics Institute server also provides the facility to perform EMBOSS-needle global alignments between two sequences on line at <http://www.ebi.ac.uk/emboss/align/>.

Alternatively the GAP program, which computes an optimal global alignment of two sequences without penalizing terminal gaps, may be used to calculate sequence identity. GAP is described in the following paper: Huang, X. (1994) On Global Sequence Alignment. Computer Applications in the Biosciences 10, 227-235.

Sequence identity may also be calculated by aligning sequences to be compared using Vector NTI version 9.0, which uses a Clustal W algorithm (Thompson et al., 1994, Nucleic Acids

Research 24, 4876-4882), then calculating the percentage sequence identity between the aligned sequences using Vector NTI version 9.0 (Sept 02, 2003 ©1994-2003 InforMax, licenced to Invitrogen).

Polynucleotide variants of the present invention also encompass those which exhibit a similarity to one or more of the specifically identified sequences that is likely to preserve the functional equivalence of those sequences and which could not reasonably be expected to have occurred by random chance. Such sequence similarity with respect to polynucleotides may be determined using the publicly available bl2seq program from the BLAST suite of programs (version 2.2.5 [Nov 2002]) from NCBI (<ftp://ftp.ncbi.nih.gov/blast/>).

The similarity of polynucleotide sequences may be examined using the following unix command line parameters:

```
bl2seq -i nucleotideseq1 -j nucleotideseq2 -F F -p tblastx
```

The parameter -F F turns off filtering of low complexity sections. The parameter -p selects the appropriate algorithm for the pair of sequences. This program finds regions of similarity between the sequences and for each such region reports an "E value" which is the expected number of times one could expect to see such a match by chance in a database of a fixed reference size containing random sequences. The size of this database is set by default in the bl2seq program. For small E values, much less than one, the E value is approximately the probability of such a random match.

Variant polynucleotide sequences preferably exhibit an E value of less than 1×10^{-10} more preferably less than 1×10^{-20} , more preferably less than 1×10^{-30} , more preferably less than 1×10^{-40} , more preferably less than 1×10^{-50} , more preferably less than 1×10^{-60} , more preferably less than 1×10^{-70} , more preferably less than 1×10^{-80} , more preferably less than 1×10^{-90} and most preferably less than 1×10^{-100} when compared with any one of the specifically identified sequences.

Alternatively, variant polynucleotides of the present invention hybridize to a specified polynucleotide sequence, or complements thereof under stringent conditions.

The term "hybridize under stringent conditions", and grammatical equivalents thereof, refers to the ability of a polynucleotide molecule to hybridize to a target polynucleotide molecule (such as a target polynucleotide molecule immobilized on a DNA or RNA blot, such as a Southern blot or Northern blot) under defined conditions of temperature and salt concentration. The ability to hybridize under stringent hybridization conditions can be determined by initially hybridizing under less stringent conditions then increasing the stringency to the desired stringency.

With respect to polynucleotide molecules greater than about 100 bases in length, typical stringent hybridization conditions are no more than 25 to 30° C (for example, 10° C) below the melting temperature (T_m) of the native duplex (see generally, Sambrook *et al.*, Eds, 1987, Molecular Cloning, A Laboratory Manual, 2nd Ed. Cold Spring Harbor Press; Ausubel *et al.*, 1987, Current Protocols in Molecular Biology, Greene Publishing.). T_m for polynucleotide molecules greater than about 100 bases can be calculated by the formula $T_m = 81.5 + 0.41\% (G + C - \log(Na^+))$. (Sambrook *et al.*, Eds, 1987, Molecular Cloning, A Laboratory Manual, 2nd Ed. Cold Spring Harbor Press; Bolton and McCarthy, 1962, PNAS 84:1390). Typical stringent conditions for polynucleotide of greater than 100 bases in length would be hybridization conditions such as prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65° C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

With respect to polynucleotide molecules having a length less than 100 bases, exemplary stringent hybridization conditions are 5 to 10° C below T_m . On average, the T_m of a polynucleotide molecule of length less than 100 bp is reduced by approximately $(500/\text{oligonucleotide length})^\circ \text{C}$.

With respect to the DNA mimics known as peptide nucleic acids (PNAs) (Nielsen *et al.*, Science. 1991 Dec 6;254(5037):1497-500) T_m values are higher than those for DNA-DNA or DNA-RNA hybrids, and can be calculated using the formula described in Giesen *et al.*, Nucleic Acids Res. 1998 Nov 1;26(21):5004-6. Exemplary stringent hybridization conditions for a DNA-PNA hybrid having a length less than 100 bases are 5 to 10° C below the T_m .

Variant polynucleotides such as those in constructs of the invention encoding proteins to be expressed, also encompasses polynucleotides that differ from the specified sequences but that, as a consequence of the degeneracy of the genetic code, encode a polypeptide having similar

activity to a polypeptide encoded by a polynucleotide of the present invention. A sequence alteration that does not change the amino acid sequence of the polypeptide is a “silent variation”. Except for ATG (methionine) and TGG (tryptophan), other codons for the same amino acid may be changed by art recognized techniques, e.g., to optimize codon expression in a particular host organism.

Polynucleotide sequence alterations resulting in conservative substitutions of one or several amino acids in the encoded polypeptide sequence without significantly altering its biological activity are also contemplated. A skilled artisan will be aware of methods for making phenotypically silent amino acid substitutions (see, e.g., Bowie *et al.*, 1990, Science 247, 1306).

Variant polynucleotides due to silent variations and conservative substitutions in the encoded polypeptide sequence may be determined using the publicly available bl2seq program from the BLAST suite of programs (version 2.2.5 [Nov 2002]) from NCBI (<ftp://ftp.ncbi.nih.gov/blast/>) via the tblastx algorithm as previously described.

Polypeptide variants

The term “variant” with reference to polypeptides encompasses naturally occurring, recombinantly and synthetically produced polypeptides. Variant polypeptide sequences preferably exhibit at least 50%, more preferably at least 51%, more preferably at least 52%, more preferably at least 53%, more preferably at least 54%, more preferably at least 55%, more preferably at least 56%, more preferably at least 57%, more preferably at least 58%, more preferably at least 59%, more preferably at least 60%, more preferably at least 61%, more preferably at least 62%, more preferably at least 63%, more preferably at least 64%, more preferably at least 65%, more preferably at least 66%, more preferably at least 67%, more preferably at least 68%, more preferably at least 69%, more preferably at least 70%, more preferably at least 71%, more preferably at least 72%, more preferably at least 73%, more preferably at least 74%, more preferably at least 75%, more preferably at least 76%, more preferably at least 77%, more preferably at least 78%, more preferably at least 79%, more preferably at least 80%, more preferably at least 81%, more preferably at least 82%, more preferably at least 83%, more preferably at least 84%, more preferably at least 85%, more preferably at least 86%, more preferably at least 87%, more preferably at least 88%, more preferably at least 89%, more preferably at least 90%, more preferably at least 91%, more

preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98%, and most preferably at least 99% identity to a sequences of the present invention. Identity is found over a comparison window of at least 20 amino acid positions, preferably at least 50 amino acid positions, more preferably at least 100 amino acid positions, and most preferably over the entire length of a polypeptide of the invention.

Polypeptide sequence identity can be determined in the following manner. The subject polypeptide sequence is compared to a candidate polypeptide sequence using BLASTP (from the BLAST suite of programs, version 2.2.5 [Nov 2002]) in bl2seq, which is publicly available from NCBI (<ftp://ftp.ncbi.nih.gov/blast/>). The default parameters of bl2seq are utilized except that filtering of low complexity regions should be turned off.

Polypeptide sequence identity may also be calculated over the entire length of the overlap between a candidate and subject polynucleotide sequences using global sequence alignment programs. EMBOSS-needle (available at <http://www.ebi.ac.uk/emboss/align/>) and GAP (Huang, X. (1994) On Global Sequence Alignment. Computer Applications in the Biosciences 10, 227-235.) as discussed above are also suitable global sequence alignment programs for calculating polypeptide sequence identity.

Sequence identity may also be calculated by aligning sequences to be compared using Vector NTI version 9.0, which uses a Clustal W algorithm (Thompson et al., 1994, Nucleic Acids Research 24, 4876-4882), then calculating the percentage sequence identity between the aligned polypeptide sequences using Vector NTI version 9.0 (Sept 02, 2003 ©1994-2003 InforMax, licenced to Invitrogen).

Polypeptide variants of the present invention also encompass those which exhibit a similarity to one or more of the specifically identified sequences that is likely to preserve the functional equivalence of those sequences and which could not reasonably be expected to have occurred by random chance. Such sequence similarity with respect to polypeptides may be determined using the publicly available bl2seq program from the BLAST suite of programs (version 2.2.5 [Nov 2002]) from NCBI (<ftp://ftp.ncbi.nih.gov/blast/>). The similarity of polypeptide sequences may be examined using the following unix command line parameters:

bl2seq -i peptideseq1 -j peptideseq2 -F F -p blastp

Variant polypeptide sequences preferably exhibit an E value of less than 1×10^{-6} more preferably less than 1×10^{-9} , more preferably less than 1×10^{-12} , more preferably less than 1×10^{-15} , more preferably less than 1×10^{-18} , more preferably less than 1×10^{-21} , more preferably less than 1×10^{-30} , more preferably less than 1×10^{-40} , more preferably less than 1×10^{-50} , more preferably less than 1×10^{-60} , more preferably less than 1×10^{-70} , more preferably less than 1×10^{-80} , more preferably less than 1×10^{-90} and most preferably 1×10^{-100} when compared with any one of the specifically identified sequences.

The parameter -F F turns off filtering of low complexity sections. The parameter -p selects the appropriate algorithm for the pair of sequences. This program finds regions of similarity between the sequences and for each such region reports an "E value" which is the expected number of times one could expect to see such a match by chance in a database of a fixed reference size containing random sequences. For small E values, much less than one, this is approximately the probability of such a random match.

Conservative substitutions of one or several amino acids of a described polypeptide sequence without significantly altering its biological activity are also included in the invention. A skilled artisan will be aware of methods for making phenotypically silent amino acid substitutions (see, e.g., Bowie *et al.*, 1990, Science 247, 1306).

Constructs, vectors and components thereof

The term "genetic construct" refers to a polynucleotide molecule, usually double-stranded DNA, which may have inserted into it another polynucleotide molecule (the insert polynucleotide molecule) such as, but not limited to, a cDNA molecule. A genetic construct may contain a promoter polynucleotide such as a chimeric promoter polynucleotide of the invention including the necessary elements that permit transcribing the insert polynucleotide molecule, and, optionally, translating the transcript into a polypeptide. The insert polynucleotide molecule may be derived from the host cell, or may be derived from a different cell or organism and/or may be a synthetic or recombinant polynucleotide. Once inside the host cell the genetic construct may become integrated in the host chromosomal DNA. The genetic construct may be linked to a vector.

The term “vector” refers to a polynucleotide molecule, usually double stranded DNA, which is used to transport the genetic construct into a host cell. The vector may be capable of replication in at least one additional host system, such as *E. coli*.

The term "expression construct" refers to a genetic construct that includes the necessary elements that permit transcribing the insert polynucleotide molecule, and, optionally, translating the transcript into a polypeptide.

An expression construct typically comprises in a 5' to 3' direction:

- a) a promoter, such as a chimeric promoter polynucleotide sequence of the invention, functional in the host cell into which the construct will be transformed,
- b) the polynucleotide to be expressed, and
- c) a terminator functional in the host cell into which the construct will be transformed.

The term “coding region” or “open reading frame” (ORF) refers to the sense strand of a genomic DNA sequence or a cDNA sequence that is capable of producing a transcription product and/or a polypeptide under the control of appropriate regulatory sequences. The coding sequence is identified by the presence of a 5' translation start codon and a 3' translation stop codon. When inserted into a genetic construct, a “coding sequence” is capable of being expressed when it is operably linked to promoter and terminator sequences.

The term “operably-linked” means that the sequenced to be expressed is placed under the control of regulatory elements that include promoters, tissue-specific regulatory elements, temporal regulatory elements, enhancers, repressors and terminators.

The term “noncoding region” includes to untranslated sequences that are upstream of the translational start site and downstream of the translational stop site. These sequences are also referred to respectively as the 5' UTR and the 3' UTR. These sequences may include elements required for transcription initiation and termination and for regulation of translation efficiency. The term “noncoding” also includes intronic sequences within genomic clones.

Terminators are sequences, which terminate transcription, and are found in the 3' untranslated ends of genes downstream of the translated sequence. Terminators are important determinants of mRNA stability and in some cases have been found to have spatial regulatory functions.

The term "promoter" refers to a polynucleotide sequence capable of regulating or driving the expression of a polynucleotide sequence to which the promoter is operably linked in a cell, or cell free transcription system. Promoters may comprise cis-initiator elements which specify the transcription initiation site and conserved boxes such as the TATA box, and motifs that are bound by transcription factors.

Examples of naturally occurring promoters which may be used, in whole or in part, in production of the chimeric promoters of the invention include: the promoter of the tobacco MYB10 gene (R2R3-MYB-153; Rushton et al 2008, *Plant Physiol.* 2008 10.1104/pp.107.114041); the promoter of the Arabidopsis gene AtMYB75 (Borevitz et al, 2000, *Plant Cell* 12, 2383-2394); the promoter of the Vitamin C transferase gene (Laing et al, 2007, *PNAS*, May 2007; 104: 9534 - 9539); the promoter of the Chalcone synthase gene (Xie et al., 2003, *Science*. 2003 Jan 17;299(5605):396-9; Albert et al, 1997); the promoter of the MdTT2 gene (Genbank No. DQ267900); the promoter of the Arabidopsis AtTT2 gene (Nesi et al, 2001, *Plant Cell* 13, 2099-2114); the promoter of the Arabidopsis AtFT gene (Kardailsky et al 1999, *SCIENCE* Volume 286 Page 1962); and the promoters of fruit oxidosqualene-triterpenoid cyclases genes (Husselstein-Muller et al., 2001, *Plant Mol Biol.* Jan; 45(1):75-92.). Other plant promoters are known to those skilled in the art and are described in the scientific literature.

The applicants have isolated promoter polynucleotide sequences from apple and pear and identified a sequence motif, and variants thereof, in such promoters which strongly influence the activity of such promoters. The applicants have shown that when the sequence motif is added to a promoter, the activity of that promoter is altered, and the promoter becomes more positively regulated by certain MYB transcription factors resulting in a significant increase in expression driven by the promoter.

The invention provides a method for producing chimeric promoters comprising the sequence motif, or motifs, and variants thereof. The invention also provides such chimeric promoters and variants thereof. The invention provides genetic constructs and vectors comprising the chimeric

promoter polynucleotide sequences, and transgenic plant cells and transgenic plants comprising the chimeric promoter polynucleotide sequence, genetic constructs, or vectors of the invention.

The invention provides the opportunity to produce novel promoters with desirable activity. The invention also provides the opportunity to alter the activity of existing promoters by adding or inserting the sequence motifs, or variant thereof, to such existing promoters. Such novel or modified chimeric promoters may be regulated by certain MYB transcription factors. In this way expression of sequences operably linked to the chimeric promoters may be expressed in a desirable way and may be individually or co-ordinately regulated by the MYB transcription factors. The MYB transcription factors may be naturally expressed or may be expressed following genetic transformation.

The invention also provides methods for producing plants with modified gene expression and modified phenotype. The invention further provides plants produced by the methods of the invention.

Methods for isolating or producing polynucleotides

The polynucleotide molecules of the invention can be isolated by using a variety of techniques known to those of ordinary skill in the art. By way of example, such polynucleotides can be isolated through use of the polymerase chain reaction (PCR) described in Mullis *et al.*, Eds. 1994 *The Polymerase Chain Reaction*, Birkhauser, incorporated herein by reference. The polynucleotides of the invention can be amplified using primers, as defined herein, derived from the polynucleotide sequences of the invention.

Further methods for isolating polynucleotides of the invention, or useful in the methods of the invention, include use of all or portions, of the polynucleotides set forth herein as hybridization probes. The technique of hybridizing labeled polynucleotide probes to polynucleotides immobilized on solid supports such as nitrocellulose filters or nylon membranes, can be used to screen the genomic. Exemplary hybridization and wash conditions are: hybridization for 20 hours at 65°C in 5.0 X SSC, 0.5% sodium dodecyl sulfate, 1 X Denhardt's solution; washing (three washes of twenty minutes each at 55°C) in 1.0 X SSC, 1% (w/v) sodium dodecyl sulfate, and optionally one wash (for twenty minutes) in 0.5 X SSC, 1% (w/v) sodium dodecyl sulfate,

at 60°C. An optional further wash (for twenty minutes) can be conducted under conditions of 0.1 X SSC, 1% (w/v) sodium dodecyl sulfate, at 60°C.

The polynucleotide fragments of the invention may be produced by techniques well-known in the art such as restriction endonuclease digestion, oligonucleotide synthesis and PCR amplification.

A partial polynucleotide sequence may be used, in methods well-known in the art to identify the corresponding full length polynucleotide sequence and/or the whole gene/ and/or the promoter. Such methods include PCR-based methods, 5'RACE (Frohman MA, 1993, *Methods Enzymol.* 218: 340-56) and hybridization- based method, computer/database –based methods. Further, by way of example, inverse PCR permits acquisition of unknown sequences, flanking the polynucleotide sequences disclosed herein, starting with primers based on a known region (Triglia *et al.*, 1998, *Nucleic Acids Res* 16, 8186, incorporated herein by reference). The method uses several restriction enzymes to generate a suitable fragment in the known region of a polynucleotide. The fragment is then circularized by intramolecular ligation and used as a PCR template. Divergent primers are designed from the known region. Promoter and flanking sequences may also be isolated by PCR genome walking using a GenomeWalker™ kit (Clontech, Mountain View, California), following the manufacturers instructions. In order to physically assemble full-length clones, standard molecular biology approaches can be utilized (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed. Cold Spring Harbor Press, 1987).

It may be beneficial, when producing a transgenic plant from a particular species, to transform such a plant with a sequence or sequences derived from that species. The benefit may be to alleviate public concerns regarding cross-species transformation in generating transgenic organisms. Additionally when down-regulation of a gene is the desired result, it may be necessary to utilise a sequence identical (or at least highly similar) to that in the plant, for which reduced expression is desired. For these reasons among others, it is desirable to be able to identify and isolate orthologues of a particular gene in several different plant species. Variants (including orthologues) may be identified by the methods described.

The promoter sequences disclosed may be further characterized to identify other fragments, such as cis-elements and regions, capable of regulating to expression of operably linked sequences,

using techniques well-known to those skilled in the art. Such techniques include 5' and/or 3' deletion analysis, linker scanning analysis and various DNA footprinting techniques (Degenhardt et al., 1994 Plant Cell:6(8) 1123-34; *Directed Mutagenesis: A Practical Approach* IRL Press (1991)). Fragments include truncated versions of longer promoter sequences which may terminate (at the 3' end) at or close to the transcriptional start site. Methods for identifying the transcription start site of a promoter are well-known to those skilled in the art (discussed in Hashimoto et al., 2004, Nature Biotechnology 22, 1146-1149).

The techniques described above may be used to identify a fragment that defines essential region of the promoter that is able to confer the desired expression profile. The essential region may function by itself or may be fused to a core promoter to drive expression of an operably linked polynucleotide.

The core promoter can be any one of known core promoters such as the Cauliflower Mosaic Virus 35S or 19S promoter (U.S. Pat. No. 5,352,605), ubiquitin promoter (U.S. Pat. No. 5,510,474) the IN2 core promoter (U.S. Pat. No. 5,364,780) or a Figwort Mosaic Virus promoter (Gruber, et al. "Vectors for Plant Transformation" *Methods in Plant Molecular Biology and Biotechnology*) et al. eds, CRC Press pp.89-119 (1993)).

Promoter fragments can be tested for their utility in driving expression in any particular cell or tissue type, or at any particular developmental stage, or in response to any particular stimulus by techniques well-known to those skilled in the art. Techniques include operably-linking the promoter fragment to a reporter or other polynucleotide and measuring reporter activity or polynucleotide expressions in plants. Some of such techniques are described in the Examples section of this specification.

Methods for identifying variants

Physical methods

Variant polynucleotides may be identified using PCR-based methods (Mullis *et al.*, Eds. 1994 The Polymerase Chain Reaction, Birkhauser).

Alternatively library screening methods, well known to those skilled in the art, may be employed (Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed. Cold Spring Harbor Press, 1987). When identifying variants of the probe sequence, hybridization and/or wash stringency will typically be reduced relatively to when exact sequence matches are sought.

Computer-based methods

Polynucleotide and polypeptide variants may also be identified by computer-based methods well-known to those skilled in the art, using public domain sequence alignment algorithms and sequence similarity search tools to search sequence databases (public domain databases include Genbank, EMBL, Swiss-Prot, PIR and others). See, e.g., Nucleic Acids Res. 29: 1-10 and 11-16, 2001 for examples of online resources. Similarity searches retrieve and align target sequences for comparison with a sequence to be analyzed (i.e., a query sequence). Sequence comparison algorithms use scoring matrices to assign an overall score to each of the alignments.

An exemplary family of programs useful for identifying variants in sequence databases is the BLAST suite of programs (version 2.2.5 [Nov 2002]) including BLASTN, BLASTP, BLASTX, tBLASTN and tBLASTX, which are publicly available from (<ftp://ftp.ncbi.nih.gov/blast/>) or from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894 USA. The NCBI server also provides the facility to use the programs to screen a number of publicly available sequence databases. BLASTN compares a nucleotide query sequence against a nucleotide sequence database. BLASTP compares an amino acid query sequence against a protein sequence database. BLASTX compares a nucleotide query sequence translated in all reading frames against a protein sequence database. tBLASTN compares a protein query sequence against a nucleotide sequence database dynamically translated in all reading frames. tBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database. The BLAST programs may be used with default parameters or the parameters may be altered as required to refine the screen.

The use of the BLAST family of algorithms, including BLASTN, BLASTP, and BLASTX, is described in the publication of Altschul *et al.*, Nucleic Acids Res. 25: 3389-3402, 1997.

The “hits” to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, BLASTX, tBLASTN, tBLASTX, or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

The BLASTN, BLASTP, BLASTX, tBLASTN and tBLASTX algorithms also produce “Expect” values for alignments. The Expect value (E) indicates the number of hits one can “expect” to see by chance when searching a database of the same size containing random contiguous sequences. The Expect value is used as a significance threshold for determining whether the hit to a database indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the database screened, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in that database is 1% or less using the BLASTN, BLASTP, BLASTX, tBLASTN or tBLASTX algorithm.

Multiple sequence alignments of a group of related sequences can be carried out with CLUSTALW (Thompson, J.D., Higgins, D.G. and Gibson, T.J. (1994) CLUSTALW: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positions-specific gap penalties and weight matrix choice. *Nucleic Acids Research*, 22:4673-4680, <http://www-igbmc.u-strasbg.fr/BioInfo/ClustalW/Top.html>) or T-COFFEE (Cedric Notredame, Desmond G. Higgins, Jaap Heringa, T-Coffee: A novel method for fast and accurate multiple sequence alignment, *J. Mol. Biol.* (2000) 302: 205-217) or PILEUP, which uses progressive, pairwise alignments. (Feng and Doolittle, 1987, *J. Mol. Evol.* 25, 351).

Pattern recognition software applications are available for finding motifs or signature sequences. For example, MEME (Multiple Em for Motif Elicitation) finds motifs and signature sequences in a set of sequences, and MAST (Motif Alignment and Search Tool) uses these motifs to identify similar or the same motifs in query sequences. The MAST results are provided as a series of alignments with appropriate statistical data and a visual overview of the motifs found. MEME and MAST were developed at the University of California, San Diego.

PROSITE (Bairoch and Bucher, 1994, Nucleic Acids Res. 22, 3583; Hofmann *et al.*, 1999, Nucleic Acids Res. 27, 215) is a method of identifying the functions of uncharacterized proteins translated from genomic or cDNA sequences. The PROSITE database (www.expasy.org/prosite) contains biologically significant patterns and profiles and is designed so that it can be used with appropriate computational tools to assign a new sequence to a known family of proteins or to determine which known domain(s) are present in the sequence (Falquet *et al.*, 2002, Nucleic Acids Res. 30, 235). Prosearch is a tool that can search SWISS-PROT and EMBL databases with a given sequence pattern or signature.

Methods for producing constructs and vectors

The genetic constructs of the present invention comprise one or more polynucleotide sequences of the invention and/or polynucleotides encoding polypeptides disclosed, and may be useful for transforming, for example, bacterial, fungal, insect, mammalian or particularly plant organisms. The genetic constructs of the invention are intended to include expression constructs as herein defined.

Methods for producing and using genetic constructs and vectors are well known in the art and are described generally in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed. Cold Spring Harbor Press, 1987; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing, 1987).

Methods for producing host cells comprising constructs and vectors

The invention provides a host cell which comprises a genetic construct or vector of the invention. Host cells may be derived from, for example, bacterial, fungal, insect, mammalian or plant organisms.

Host cells comprising genetic constructs, such as expression constructs, of the invention are useful in methods well known in the art (e.g. Sambrook *et al.*, Molecular Cloning : A Laboratory Manual, 2nd Ed. Cold Spring Harbor Press, 1987 ; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing, 1987) for recombinant production of polypeptides. Such methods may involve the culture of host cells in an appropriate medium in conditions suitable for or conducive to expression of a polypeptide of the invention. The expressed recombinant

polypeptide, which may optionally be secreted into the culture, may then be separated from the medium, host cells or culture medium by methods well known in the art (e.g. Deutscher, Ed, 1990, Methods in Enzymology, Vol 182, Guide to Protein Purification).

Methods for producing plant cells and plants comprising constructs and vectors

The invention further provides plant cells which comprise a genetic construct of the invention, and plant cells modified to alter expression of a polynucleotide or polypeptide. Plants comprising such cells also form an aspect of the invention.

Methods for transforming plant cells, plants and portions thereof with polynucleotides are described in Draper *et al.*, 1988, Plant Genetic Transformation and Gene Expression. A Laboratory Manual. Blackwell Sci. Pub. Oxford, p. 365; Potrykus and Spangenburg, 1995, Gene Transfer to Plants. Springer-Verlag, Berlin.; and Gelvin *et al.*, 1993, Plant Molecular Biol. Manual. Kluwer Acad. Pub. Dordrecht. A review of transgenic plants, including transformation techniques, is provided in Galun and Breiman, 1997, Transgenic Plants. Imperial College Press, London.

The following are representative publications disclosing genetic transformation protocols that can be used to genetically transform the following plant species: Rice (Alam *et al.*, 1999, Plant Cell Rep. 18, 572); apple (Yao *et al.*, 1995, Plant Cell Reports 14, 407-412); maize (US Patent Serial Nos. 5, 177, 010 and 5, 981, 840); wheat (Ortiz *et al.*, 1996, Plant Cell Rep. 15, 1996, 877); tomato (US Patent Serial No. 5, 159, 135); potato (Kumar *et al.*, 1996 Plant J. 9, : 821); cassava (Li *et al.*, 1996 Nat. Biotechnology 14, 736); lettuce (Micheltore *et al.*, 1987, Plant Cell Rep. 6, 439); tobacco (Horsch *et al.*, 1985, Science 227, 1229); cotton (US Patent Serial Nos. 5, 846, 797 and 5, 004, 863); perennial ryegrass (Bajaj *et al.*, 2006, Plant Cell Rep. 25, 651); grasses (US Patent Nos. 5, 187, 073, 6. 020, 539); peppermint (Niu *et al.*, 1998, Plant Cell Rep. 17, 165); citrus plants (Pena *et al.*, 1995, Plant Sci.104, 183); caraway (Krens *et al.*, 1997, Plant Cell Rep, 17, 39); banana (US Patent Serial No. 5, 792, 935); soybean (US Patent Nos. 5, 416, 011 ; 5, 569, 834 ; 5, 824, 877 ; 5, 563, 04455 and 5, 968, 830); pineapple (US Patent Serial No. 5, 952, 543); poplar (US Patent No. 4, 795, 855); monocots in general (US Patent Nos. 5, 591, 616 and 6, 037, 522); brassica (US Patent Nos. 5, 188, 958 ; 5, 463, 174 and 5, 750, 871); and cereals (US Patent No. 6, 074, 877); pear (Matsuda *et al.*, 2005, Plant Cell Rep. 24(1):45-51); Prunus (Ramesh *et al.*, 2006, Plant Cell Rep. 25(8):821-8; Song and Sink 2005, Plant Cell Rep.

2006; 25(2):117-23; Gonzalez Padilla et al., 2003, Plant Cell Rep. 22(1):38-45); strawberry (Oosumi et al., 2006, Planta.; 223(6):1219-30; Folta et al., 2006, Planta. 2006 Apr 14; PMID: 16614818), rose (Li et al., 2003, Planta. 218(2):226-32), and Rubus (Graham et al., 1995, Methods Mol Biol. 1995;44:129-33). Transformation of other species is also contemplated by the invention. Suitable methods and protocols for transformation of other species are available in the scientific literature.

Methods for genetic manipulation of plants

A number of strategies for genetically manipulating plants are available (e.g. Birch, 1997, Ann Rev Plant Phys Plant Mol Biol, 48, 297). For example, strategies may be designed to increase expression of a polynucleotide/polypeptide in a plant cell, organ and/or at a particular developmental stage where/when it is normally expressed or to ectopically express a polynucleotide/polypeptide in a cell, tissue, organ and/or at a particular developmental stage which/when it is not normally expressed. Strategies may also be designed to increase expression of a polynucleotide/polypeptide in response to external stimuli, such as environmental stimuli. Environmental stimuli may include environmental stresses such as mechanical (such as herbivore activity), dehydration, salinity and temperature stresses. The expressed polynucleotide/polypeptide may be derived from the plant species to be transformed or may be derived from a different plant species.

Transformation strategies may be designed to reduce expression of a polynucleotide/polypeptide in a plant cell, tissue, organ or at a particular developmental stage which/when it is normally expressed or to reduce expression of a polynucleotide/polypeptide in response to an external stimuli. Such strategies are known as gene silencing strategies.

Genetic constructs for expression of genes in transgenic plants typically include promoters, such as promoter polynucleotides of the invention, for driving the expression of one or more cloned polynucleotide, terminators and selectable marker sequences to detect presence of the genetic construct in the transformed plant.

Exemplary terminators that are commonly used in plant transformation genetic construct include, e.g., the cauliflower mosaic virus (CaMV) 35S terminator, the *Agrobacterium tumefaciens*

nopaline synthase or octopine synthase terminators, the *Zea mays* zin gene terminator, the *Oryza sativa* ADP-glucose pyrophosphorylase terminator and the *Solanum tuberosum* PI-II terminator.

Selectable markers commonly used in plant transformation include the neomycin phosphotransferase II gene (NPT II) which confers kanamycin resistance, the aadA gene, which confers spectinomycin and streptomycin resistance, the phosphinothricin acetyl transferase (*bar* gene) for Ignite (AgrEvo) and Basta (Hoechst) resistance, and the hygromycin phosphotransferase gene (hpt) for hygromycin resistance.

Use of genetic constructs comprising reporter genes (coding sequences which express an activity that is foreign to the host, usually an enzymatic activity and/or a visible signal (e.g., luciferase, GUS, GFP) which may be used for promoter expression analysis in plants and plant tissues are also contemplated. The reporter gene literature is reviewed in Herrera-Estrella *et al.*, 1993, Nature 303, 209, and Schrott, 1995, In: Gene Transfer to Plants (Potrykus, T., Spangenberg, Eds) Springer Verlag, Berlin, pp. 325-336.

Gene silencing strategies may be focused on the gene itself or regulatory elements which effect expression of the encoded polypeptide. "Regulatory elements" is used here in the widest possible sense and includes other genes which interact with the gene of interest.

Genetic constructs designed to decrease or silence the expression of a polynucleotide/polypeptide may include an antisense copy of a polynucleotide. In such constructs the polynucleotide is placed in an antisense orientation with respect to the promoter and terminator.

An "antisense" polynucleotide is obtained by inverting a polynucleotide or a segment of the polynucleotide so that the transcript produced will be complementary to the mRNA transcript of the gene, e.g.,

5'GATCTA 3' (coding strand)
3'CUAGAU 5' mRNA

3'CTAGAT 5' (antisense strand)
5'GAUCUCG 3' antisense RNA

Genetic constructs designed for gene silencing may also include an inverted repeat. An 'inverted repeat' is a sequence that is repeated where the second half of the repeat is in the complementary strand, e.g.,

5'-GATCTA.....TAGATC-3'

3'-CTAGAT.....ATCTAG-5'

The transcript formed may undergo complementary base pairing to form a hairpin structure. Usually a spacer of at least 3-5 bp between the repeated region is required to allow hairpin formation.

Another silencing approach involves the use of a small antisense RNA targeted to the transcript equivalent to an miRNA (Llave *et al.*, 2002, Science 297, 2053). Use of such small antisense RNA corresponding to polynucleotide of the invention is expressly contemplated.

The term genetic construct as used herein also includes small antisense RNAs and other such polynucleotides useful for effecting gene silencing.

Transformation with an expression construct, as herein defined, may also result in gene silencing through a process known as sense suppression (e.g. Napoli *et al.*, 1990, Plant Cell 2, 279; de Carvalho Niebel *et al.*, 1995, Plant Cell, 7, 347). In some cases sense suppression may involve over-expression of the whole or a partial coding sequence but may also involve expression of non-coding region of the gene, such as an intron or a 5' or 3' untranslated region (UTR). Chimeric partial sense constructs can be used to coordinately silence multiple genes (Abbott *et al.*, 2002, Plant Physiol. 128(3): 844-53; Jones *et al.*, 1998, Planta 204: 499-505). The use of such sense suppression strategies to silence the expression of a sequence operably-linked to promoter of the invention is also contemplated.

The polynucleotide inserts in genetic constructs designed for gene silencing may correspond to coding sequence and/or non-coding sequence, such as promoter and/or intron and/or 5' or 3' UTR sequence, or the corresponding gene.

Other gene silencing strategies include dominant negative approaches and the use of ribozyme constructs (McIntyre, 1996, Transgenic Res, 5, 257)

Pre-transcriptional silencing may be brought about through mutation of the gene itself or its regulatory elements. Such mutations may include point mutations, frameshifts, insertions, deletions and substitutions.

Plants

The term “plant” is intended to include a whole plant or any part of a plant, propagules and progeny of a plant.

The term ‘propagule’ means any part of a plant that may be used in reproduction or propagation, either sexual or asexual, including seeds and cuttings.

A “transgenic” or transformed” plant refers to a plant which contains new genetic material as a result of genetic manipulation or transformation. The new genetic material may be derived from a plant of the same species as the resulting transgenic or transformed plant or from a different species. A transformed plant includes a plant which is either stably or transiently transformed with new genetic material.

The plants of the invention may be grown and either self-ed or crossed with a different plant strain and the resulting hybrids, with the desired phenotypic characteristics, may be identified. Two or more generations may be grown. Plants resulting from such standard breeding approaches also form part of the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the promoter polynucleotide sequence of SEQ ID NO: 5, showing the position of the repeat motifs (1, 2, 3A, 3B, 4, 5 and 6), the microsatellite (microsat) and several restriction enzyme sites.

Figure 2 shows a schematic representation of the MdMYB10 R₁ promoter from the white-fleshed cultivar with a single repeat motif (1) and the microsatellite (MS). The figure also shows schematic representation of the structure and location of the additional repeat unit composed of

repeat units 2, 3a, 3b, 4, 5 and 6 found in the promoter of the red-fleshed cultivar R₆, relative to the promoter from the white-fleshed cultivar. Example phenotypes for the MdMYB10 R₁ and R₆ promoter versions are shown to the left, *Malus x domestica* Royal Gala (i) and *Malus x domestica* niedzwetzkyana (ii).

Figure 3 shows the portion of the sequence of the promoter from the red-fleshed apple cultivar including repeat motifs 1, 2, 3a, 3b, 4, 5 and 6 and the microsatellite region.

Figure 4 shows *trans*-activation of the promoters from white-fleshed (R₁) and red-fleshed (R₆) cultivars by the MdMYB10 gene in transient tobacco transformation assays. Both promoters were infiltrated with and without MdMYB10. Error bars shown are $\pm$ S.E. of the means of 6 replicate experiments.

Figure 5 shows that amplification of a PCR product comprising the minisatellite motif serves as a marker that distinguishes white-fleshed and red-fleshed apple cultivars. A total of 87 cultivars were screened using the PCR primer pair described in Example 3. PCR products were separated on 0.9% agarose gels and stained with ethidium bromide. The figure shows the PCR amplification obtained over a subset of 10 apple varieties. Two alleles were found: a 496 bp fragment corresponding to the promoter of SEQ ID NO: 5, which was only present in red flesh varieties (lanes 1-6) and was absent in white-fleshed varieties (lanes 7-10), and a 392 bp allele present in both types of fruit. Red-fleshed varieties: 1: open-pollinated (OP) *Malus* 'Mildew Immune Seedling' 93.051 G01-048; 2: *M. x purpurea* 'Aldenhamensis'; 3: *M. pumila* var. *niedzwetzkyana*; 4: *M.* 'Prairifire'; 5: OP *M. pumila* var. *niedzwetzkyana* 'Geneva'; 6: OP *M. x domestica* 'Pomme Grise' 92.103 30-312; 7: *M. x domestica* 'Granny Smith'; 8: *M. x domestica* 'Royal Gala'; 9: *M. x domestica* 'Fuji'; 10: *M. x domestica* 'Braeburn'.

Figure 6 shows the native apple promoter containing the minisatellite induces ectopic anthocyanin accumulation. (a) Red colouration has developed around the infiltration site in the leaves of *Nicotiana tabacum* 8 days after transient transformation with R₆:MdMYB10 (i) and 35S:MdMYB10 (ii) but not with R₁. All three were co-infiltrated with 35S:MdbHLH3. (b) Regenerating Royal Gala apple callus transformed with R₆:MdMYB10. R₁ = native promoter from *Malus domestica* 'Royal Gala'. R₆ = native promoter from *Malus x pumila* var. *niedzwetzkyana*.

Figure 7 shows the interaction of the native apple promoters and MdMYB10 in the dual luciferase transient tobacco assays. To compare the transactivation activity of the apple promoters to 35S, these were co-infiltrated with the R₁ and R₆ promoter-luciferase fusions. The results provide a measure for the potential activity of the apple promoters and they show a significant increase in the case of the R₆-driven MdMYB10. R₁ = native promoter from *Malus domestica* 'Royal Gala'. R₆ = native promoter from *Malus x pumila* var. niedzwetzkyana.

Figure 8 shows the number of repeat units affects the transactivation rate. (a) Cartoon (not drawn to scale) of the different promoters with repeat units ranging from zero (R₀) to six (R₆). The two native promoters from apple are marked, R₁ as from *Malus x domestica* 'Royal gala' and R₆ from *Malus x pumila* var. niedzwetzkyana. The position of the repeat units (in black) relative to the microsatellite (grey diagonal box) is shown. R₁+ is differentiated with grey vertical shading to represent the substituted sequence replacing the spatial effect of the minisatellite. (b) Results of R₀ to R₆ promoters co-infiltrated with 35S:MdMYB10 alone (light grey bars) and with 35S:MdMYB10 and 35SMdbHLH3 (dark grey bars). Error bars shown are means $\pm$ S.E. of 6 replicate reactions.

Figure 9 shows identification of areas of the promoter critical to transactivation by deletion study. (a) Cartoon (not drawn to scale) of the different promoter deletions of R₁, (i) and R₆, (ii), denoted as Δ a - Δ d. Deleted areas are shown in white with dotted lines and the relative positions of the repeat unit R₁ to the microsatellite and minisatellite are displayed. (b) Corresponding data from promoter deletion studies with luciferase fusions of R₁, (i) and (ii), and R₆, (iii) and (iv), co-infiltrated with MdMYB10, (i) and (iii) respectively (pale grey bars) and with MdMYB10 and MdbHLH3, (ii) and (iv) respectively (dark grey bars). Error bars shown are means $\pm$ S.E. of 6 replicate reactions.

Figure 10 shows a schematic representation of the cloning of the minisatellite repeat unit (copies 1-6) from the apple MdMYB10 R₆ promoter (MdMYB10 long) into the MYB10 promoter from pear (PcMYB10(GP)) to produce the chimeric promoter PcMYB10R6(GP-R6). The MdMYB10 promoter from white-fleshed apple (MdMYB10 short) is included in the figure for reference. The position of the restriction sites (DraI and BsgI) and PCR priming sites (CB02 and RE161) is also shown.

Figure 11 shows the effect of MdMYB10 genomic and 35S:PcMYB10 constructs on luciferase reporter gene driven by PcMYB10 promoter containing or not the MdMYB10-promoter R6 repeats. Activity is expressed as a ratio of the Luciferase (LUC) to the CaMV35s-Renilla (REN) activities. Error bars represent the standard error (SE) for 4 replicates. All the promoter sequences were fused to the luciferase reporter and are abbreviated as follows: DFR, Arabidopsis DFR promoter; Md10s, MdMYB10 R1 promoter; Md10R6, MdMYB10 R6 promoter; Pc10S, PcMYB10R1 promoter and Pc10R6, PcMYB10R6 promoter. The transcription factor constructs are all driven by the CaMV35S promoter and are as follows: MdM10, MdMYB10; PcM10, PcMYB10; b33, MdbHLH33 and b2, *Arabidopsis thaliana* bHLH2.

Figure 12 shows an alignment between the sequences of the MYB10 promoters from white-fleshed apple and pear and highlights with, underlining, the conserved 23 bp repeat motif.

Figure 13 shows that other MYB10 sequences can transactivate the R6:MdMYB10 promoter in a Dual Luciferase Transient Assay in Tobacco. Leaves of *N. benthamiana* were infiltrated with pMdMYB10R1-LUC or pMdMYB10R6-LUC promoter fusions on their own or coinfiltrated with 35S:MYB and bHLH as indicated. Luminescence of LUC and REN was measured 3 days later and expressed as a ratio of LUC to REN. Error bars are the SE for 4 replicate reactions.

Figure 14 shows a schematic representation of the strategy for cloning the apple R6 domain into the PcMYB10, AtPAP1 and VitC2 promoters. The R6 domain was amplified from the 'Red Field' R6:MdMYB10 allele, digested with DraI and inserted in the PcMYB10, AtPAP1 and VitC2 promoters driving the Luciferase reporter gene at the indicated restriction sites. Each blue box represents a 23bp-single repeat, the yellow box represent the relative position of the microsatellite region.

Figure 15 shows that MdMYB10 combined with bHLH3 transactivates other MYB10 chimeric promoter fusions containing copies of the 23bp repeat count. A. Leaves of *N. benthamiana* were coinfiltrated with the MYB promoter fusions from apple, pear and Arabidopsis, either containing the apple R6 domain or not, and the MdMYB10/bHLH3 transcription factors. B. Leaves were infiltrated with the pear MYB10 promoter or the AtPAP1 promoter, either containing or not the R6 domain, and their corresponding MYB/bHLH co-factors. Luminescence of LUC and REN

was measured 3 days later and expressed as a ratio of LUC to REN. Error bars are the SE for 4 replicate reactions.

Figure 16 shows that MdMYB10 together with bHLH3 transactivates the VitC2 promoters containing the apple R6 domain in a Dual Luciferase Transient Assay. Leaves of *N. benthamiana* were coinfiltrated with the VitC2 promoter fusions from kiwifruit, either containing the apple R6 domain or not, and the MdMYB10 transcription factor alone or combined to bHLH3. In each case the presence of the R6 domain is associated to a high level of transactivation of the promoter fusion. Luminescence of LUC and REN was measured 3 days later and expressed as a ratio of LUC to REN. Error bars are the SE for 4 replicate reactions.

Figure 17 show a schematic representation of the R6 motif amplified by CB02 and RE161 primers. Also shown in boxes is the position of each 23bp repeat motif R1-R6, and the position of the DraI restriction site.

EXAMPLES

The invention will now be illustrated with reference to the following non-limiting examples.

Example 1: Isolation of the full length MdMYB10 promoter polynucleotides from white-fleshed and red-fleshed apple cultivars, and identification of additional elements within the promoter from the red-fleshed cultivar.

Isolation of genomic DNA

Genomic DNA was isolated from the leaves of a white-fleshed apple cultivar (*Malus domestica* Royal Gala) and from the leaves of a red-fleshed apple cultivar (*Malus x pumila* niedwetzkyana) using a Qiagen DNeasy Plant Mini Kit, according to the manufacturers instructions (Qiagen, Valencia, California).

Promoter isolation

A 1.7-1.8 Kb region of the upstream regulatory region of the MdMYB10 gene was isolated from the DNA of both the white-fleshed and the red-fleshed cultivar by PCR genome walking using a GenomeWalker™ kit (Clontech, Mountain View, California), following the manufacturers instructions.

The isolated promoters were sequenced by standard techniques. The sequence of the promoter from the red-fleshed cultivar is shown in SEQ ID NO: 5. The sequence of the promoter from the white-fleshed cultivar is shown in SEQ ID NO: 8.

The sequence of the MdMYB10 polypeptide is shown in SEQ ID NO: 6. The polynucleotide sequence (cDNA) encoding the MdMYB10 polypeptide is shown in SEQ ID NO: 7.

By comparing the sequences of the promoters from white-fleshed and red-fleshed apple cultivars the applicants identified a 23-base pair sequence motif found in both promoters. In the promoter from the white-fleshed cultivar, the motif is present as a single copy (with a 1bp difference versus the motif in the promoter from the red-fleshed cultivar). In the promoter from the red-fleshed cultivar the motif is present at a corresponding position, but in addition, the motif is duplicated in five tandem repeats to form a minisatellite repeat unit.

The sequence of the repeat motif is shown in SEQ ID NO: 1.

The sequence of the minisatellite unit comprising five copies of the repeat motif is shown in SEQ ID NO: 2.

Figure 1 shows the sequence of the promoter from the red-fleshed variety as shows the position of the repeated motifs. The minisatellite unit precedes a di-nucleotide microsatellite found in both promoters.

The sequence of the microsatellite is shown in SEQ ID NO: 3.

Figure 2 shows a schematic representation of promoter from the white-fleshed cultivar and shows the relative position and structure of the additional minisatellite repeat unit found in the

promoter of the red-fleshed cultivar. Minisatellites, similar to these, have been shown to have an effect on transcriptional regulation in humans (Kominato *et al.*, (1997). *J. Biol. Chem.* **272**, 25890, Lew *et al.*, (2000). *Proc. Natl. Acad. Sci. U. S. A.* **97**, 12508 and to produce phenotypic alteration in *Saccharomyces cerevisiae* (Verstrepen *et al.*, (2005) *Nat. Genet.* **37**, 986).

Example 2: Demonstration of regulation of expression of operably linked polynucleotide sequences by the promoter polynucleotides of the invention.

Dual Luciferase Assay of Transiently Transformed Tobacco Leaves

The promoter sequences for MdMYB10 from the red-fleshed and white-fleshed cultivars (SEQ ID NOs: 4 and 5 respectively) were separately inserted into the cloning site of pGreen 0800-LUC (Hellens *et al.*, 2005, R. P. Hellens, A. C. Allan, E. N. Friel EN, K. Bolitho, K. Grafton, M. D. Templeton, S. Karunairetnam, W. A. Laing, *Plant Methods* **1**:13). In the same construct, a luciferase gene from *Renilla* (REN), under the control of a 35S promoter, provided an estimate of the extent of transient expression. Activity is expressed as a ratio of LUC to REN activity. The promoter-LUC fusion was used in transient transformation by mixing 100 µl of *Agrobacterium* strain GV3101 (MP90) transformed with the reporter cassette with or without another *Agrobacterium* culture (900 µl) transformed with a cassette containing MdMYB10 fused to the 35S promoter. *Nicotiana tabacum* 'Samsun' plants were grown until at least 6 leaves were available for infiltration with *Agrobacterium*. A 10 µl loop of confluent bacterium were re-suspended in 10 ml of infiltration media (10 mM MgCl₂, 0.5 µM acetosyringone), to an OD₆₀₀ of 0.2, and incubated at room temperature without shaking for 2 h before infiltration. Approximately 150 µl of this *Agrobacterium* mixture was infiltrated at six points into a young leaf of *N. tabacum* and transient expression was analysed 3 days after inoculation. Six technical replicates of 3 mm Ø leaf discs were excised from each plant using a leaf hole-punch and buffered in Phosphate Buffer Saline (PBS). Plate-based assays were conducted using a Berthold Orion Microplate Luminometer (Berthold Detection Systems, Oak Ridge, TN, USA) according to the manufacturer's specifications for the dual luciferase assay, using the Dual Glow assay reagents (Promega, Madison, WI) for firefly luciferase and *Renilla* luciferase. Luminescence was calculated using Simplicity version 4.02 software (Berthold Detection Systems).

The results, as shown in Figure 4, show that the promoter (R₆) from the red-fleshed cultivar containing the minisatellite repeat unit drives expression of the operably linked sequence

encoding luciferase at 7 times the level of expression driven by the promoter (R₁) from the white-fleshed cultivar (from which the minisatellite repeat unit is absent) when the MdMYB10 protein is also expressed. This result demonstrates the significance of the extra sequence present in R₆ promoter (including additional copies of the repeat motif) from the red-fleshed variety.

The results also show that co-expression of the MdMYB10 transcription factor results in a 10-fold increase in expression of the luciferase sequence that is operably linked to the promoter (R₆) from the red-fleshed cultivar. The effect of MdMYB10 from the white-fleshed cultivar is much smaller. This result shows that the promoter polynucleotide of the invention is positively regulated by the MYB transcription factor MdMYB10.

Example 3: The presence of the minisatellite unit in the promoter of the invention is consistently associated with red-flesh in naturally occurring red-fleshed apple varieties.

Minisatellite region PCR amplification and sequencing

The fruit flesh (cortex) of most apple cultivars is white or off-white in colour. The skin is usually green or red, the skin reddening in response to developmental, hormonal and light signals (Ubi *et al.*, 2006, *Plant Sci.* **170**, 571). There are, however, a number of high anthocyanin, red-fleshed apples, including *Malus x pumila* niedzwetzkyana, originating from the wild-apple forests of Khazakhstan.

In apple, anthocyanin accumulation is specifically regulated by MdMYB10, with MdMYB10 transcript levels greatly elevated in red-fleshed varieties (Espley *et al.*, 2007, *Plant J.* **49**, 414).

Genomic DNA samples from several red-fleshed and white-fleshed apple cultivars listed in the Table 1 below were supplied by Charles J Simon and Philip Forsline, Agricultural Research Services USDA.

Apple genomic DNA from 19 cultivars was amplified using a pair of PCR primers located in the MdMYB10 promoter (forward: 5'-GGAGGGGAATGAAGAAGAGG-3' – SEQ ID NO: 9; reverse: 5'-TCCACAGAAGCAAACACTGAC-3' – SEQ ID NO: 10). PCR reactions were carried out in 16.5 µl volume containing 1x PCR buffer mix (Invitrogen, Carlsbad, California), 1.3 mM MgCl₂, 100 µM of each dNTP, 0.72 % formamide, 10 µM of each primer, 0.5 U of

Platinum[®] *Taq* DNA polymerase (Invitrogen) and 2 ng of genomic DNA. PCR amplifications were performed in a Hybaid PCR Express Thermal Cycler (Thermo Electron Corporation, Waltham, Massachusetts) with conditions as follows: 94°C for 2 min 45 sec followed by 40 cycles at 94°C for 55 sec, 55°C for 55 and 72°C for 1 min 39 sec, and a final elongation at 72°C for 10 min. The PCR products obtained were cloned using the TOPO TA cloning[®] kit (Invitrogen). Four clones were sequenced for each PCR product. The sequences were aligned using Vector NTI (Invitrogen).

Association of the minisatellite with the red-fleshed phenotype

Previously we have shown that MdMYB10 is linked to the red flesh and red foliage phenotype in apple (Chagné et al, 2007, *BMC Genomics*, **8**, 212). Further, PCR amplification of the promoter region from red and white-fleshed varieties consistently showed that the R₆ minisatellite was amplified in all the red phenotypes (Figure 3). We determined the association of the repeat motif with the red-fleshed phenotype by sequencing the region encompassing the minisatellite motif over 19 diverse apple varieties (11 red and 8 white flesh; Table 1). A number of sequence variations were found in the upstream region, but only the minisatellite polymorphism is perfectly associated with the elevated accumulation of anthocyanins that causes red flesh and red foliage. The same region was PCR-amplified from a further set of 68 white-fleshed apple cultivars and wild accessions taken from two collections of *Malus* species, and in each case the product corresponding to the minisatellite motif was absent (data not shown). All the white-fleshed versions tested contained only the R₁ version whilst the red-fleshed versions contained both R₁ and R₆ or R₆ only.

Table 1

Accession	Flesh colour	G/T SNP Pos 81	Minisatellite motif	A/T SNP Pos 448
<i>Malus x domestica</i> 'Babine'	Red	G:G	R ₁ :R ₆	A:T
<i>Malus x domestica</i> 'Okanagan'	Red	G:G	R ₁ :R ₆	A:T
<i>Malus x domestica</i> 'Simcoe'	Red	G:G	R ₆ :R ₆	T:T
<i>Malus x domestica</i> 'Slocan'	Red	G:T	R ₁ :R ₆	A:T
<i>Malus marjorensis</i> 'Formosa'	Red	G:T	R ₁ :R ₆	A:T
<i>Malus sieversii</i> 629319*	Red	G:G	R ₆ :R ₆	T:T
<i>Malus sieversii</i> FORM 35 (33-01)*	Red	G:T	R ₁ :R ₆	A:T
<i>Malus sieversii</i> 01P22*	Red	G:G	R ₆ :R ₆	T:T
<i>Malus sieversii</i> 3563.q*	Red	G:G	R ₆ :R ₆	T:T
<i>Malus Aldenhamii</i>	Red	T:T	R ₁ :R ₆	A:T
<i>Malus x domestica</i> 91.136 B6-77	Red	G:T	R ₁ :R ₆	A:T
<i>Malus x domestica</i> 'Close'	White	G:T	R ₁ :R ₁	A:T
<i>Malus x domestica</i> 'Mr Fitch'	White	T:T	R ₁ :R ₁	A:A
<i>Malus x domestica</i> 'Guldborg'	White	G:T	R ₁ :R ₁	A:T
<i>Malus x domestica</i> 'Alkmene'	White	T:T	R ₁ :R ₁	A:A
<i>Malus x domestica</i> 'Red Melba'	White	T:T	R ₁ :R ₁	A:A
<i>Malus x domestica</i> 'Rae Ime'	White	G:G	R ₁ :R ₁	T:T
<i>Malus x domestica</i> 'Lady Williams'	White	T:T	R ₁ :R ₁	A:A
<i>Malus x domestica</i> 'Granny Smith'	White	G:T	R ₁ :R ₁	A:A
Association test (r^2)		0.185	1	0.491

"R₁" refers to the absence of the minisatellite unit as found in the promoter from the white-fleshed Royal Gala cultivar.

"R₆" refers to the presence of the minisatellite unit as found in the promoter from the red-fleshed *Malus x pumila* niedzwetzkyana cultivar.

Given that the single repeat unit is present in the promoter from the white-fleshed, the presence of additional repeat units in the promoter from the red-fleshed cultivar are likely to account for the known increased expression level of MdMY10 and resulting anthocyanin accumulation red-fleshed apple cultivars.

Example 4: Expression of the MdMYB10 transcription factor driven by the promoter of the invention results in anthocyanin production in transiently transformed tobacco.

Previous studies have shown that when MdMYB10 was fused to 35S and co-infiltrated into *N. tabacum* with a 35S driven co-factor bHLH, a high level of anthocyanin pigmentation could be detected at the infiltration site (Espley *et al.*, 2007, The Plant Journal **49**, 414-427). The applicants therefore infiltrated *Nicotiana tabacum* with *Agrobacterium* suspensions of MdMYB10 driven by the R₁ and R₆ promoter sequences. R₁ is the native promoter from *Malus domestica* 'Royal Gala'. R₆ is the native promoter from *Malus x pumila* var. niedzwetzkyana. When R₆:MdMYB10 was co-infiltrated with 35S:MdbHLH3 a similar level of colouration was

achieved as with 35S:MdMYB10 (Figure. 6A). The applicants were unable to detect anthocyanin accumulation with the R₁:MdMYB10 infiltration, with or without 35S:MdbHLH3.

To investigate the properties of the R₆ promoter in apple, the applicants transformed Royal Gala with MdMYB10 cDNA driven by either the R₆ or R₁ promoters. Whilst the R₁ promoter is found in Royal Gala R₆ is not. It has previously been shown that when Royal Gala is transformed with 35S:MdMYB10, red callus is produced which regenerates to produce red plants (Espley *et al*, 2007, The Plant Journal **49**, 414-427). The applicants observed a similar callus phenotype when Royal Gala is transformed with R₆:MdMYB10, with bright red areas on regenerating callus (Figure 6B). However, whilst 35S:MdMYB10 was capable of driving anthocyanin accumulation in the transformed callus in the absence of light, we noted that the R₆:MdMYB10 transformants required light for the induction of pigmentation. No sustained pigmentation was seen on regenerating apple callus transformed with R₁:MdMYB10. Similarly, callus transformed with an empty vector cassette showed no pigmentation.

Example 5: Expression of the MdMYB10 transcription factor driven by the promoter of the invention can transactivate reporter gene expression at a level similar or higher than CaMV35S promoter driven expression of the MdMYB10 transcription factor.

To further investigate the effect of the promoter on MdMYB10 transcript and predicted protein levels, the applicants repeated the assay from Example 2, replacing the 35S promoter with either the R₁ or R₆ promoters. Results indicated that the high transcript abundance of MdMYB10 driven by the R₆ promoter enables transactivation of the reporter, particularly when the reporter is fused to R₆ (Figure 7). The results show a similar level of activity to the 35S promoter. With the R₁ luciferase fusion, R₆:MdMYB10 appears to exert stronger transactivation than 35S:MdMYB10. The R₁:MdMYB10 fusion did not influence transactivation to the same extent.

Example 6: The number of copies of the 23 bp repeat unit influences transcription.

A series of constructs were built, using standard molecular biology techniques, to test the effect on transcription of the number of 23 bp repeat units present in the upstream region. These constructs were based on the native promoter sequences but with repeat units ranging from one (R₁) to six (R₆) and were fused to the luciferase reporter as above (Figure 8a). To test the spatial effect that the presence of the minisatellite sequence might exert on other non-identified motifs, a

further construct (R₁+) was built where the minisatellite sequence from R₆ was replaced with non-specific DNA of the same length from a cloning vector (Promega, Madison, WI, USA). The results indicate a correlation between the number of repeat units and the activation of the promoter (Figure 8b). When co-infiltrated with 35S:MdMYB10 there is basal activity from both R₁ and R₁+ and an increasing activation from R₂ to R₆. There are numerous examples of the relationship between the anthocyanin-regulating MYB and bHLH co-factors and it has previously been shown the dependency of MdMYB10 on a co-factor bHLH in transient assays (Espley *et al*, 2007, The Plant Journal **49**, 414-427). In this assay, activation for both the R₁ and R₆ promoters is enhanced with the addition of 35S:MdbHLH3 for all the constructs tested.

Example 7: Deletion analysis of the promoter of the invention emphasises the importance of the minisatellite region, containing multiple copies of the 23 bp repeat unit, in enhancing transcription.

To define the upstream region directly responsible for transcriptional enhancement, both versions of the native promoter (R₁ and R₆) were subjected to various sequence deletion treatments (Figure 9a). The five versions for each native promoter were fused to luciferase and co-infiltrated into tobacco with 35S:MdMYB10, +/- 35S:MdbHLH3.

When the deletion versions of R₁:LUC were infiltrated with just 35S:MdMYB10, luciferase activity was barely detectable and significantly lower than the native non-deleted version (Figure 9b). Only when 35S:MdbHLH3 was co-infiltrated with 35S:MdMYB10 did luminescence rise above background. Although there is a putative bHLH binding domain at the 5' end of the isolated promoter region, when this was deleted (R₁Δa) there was still a significant increase in LUC:REN ratio with co-infiltration of the bHLH, suggesting that there may be an alternative site for bHLH binding. The R₆:LUC deletions were less affected than R₁ with activity halved for R₆Δa and R₆Δb and a lesser reduction with R₆Δc. With the restoration of the putative bHLH binding domain on both R₁Δc and R₆Δc, there is an increase in activity when 35S:MdbHLH3 is co-infiltrated.

In this assay, the R₆:LUC promoters appeared to show a lesser dependence on the bHLH for increased activity although this may be due to saturation or depletion of one or other of the co-infiltrated transcription factors. For both R₁Δd and R₆Δd there was barely detectable activity, with or without the bHLH, confirming the requirement of the 3' region for transactivation. The

data suggests that the R₆ promoter can still activate luciferase transcription in truncated form (500 bp) whereas the corresponding version of R₁ (R₁Δb) cannot.

Experimental procedures

Isolation of MdMYB10 upstream promoter region

For isolation of the upstream promoter region, genomic DNA was extracted from *Malus x domestica* 'Sciros' (Pacific Rose™, derived from a cross between 'Gala' and 'Splendour'). Nested primers were designed to the coding region of MdMYB10; primary 5'-CACTTTCCTCTCCATGAATCTCAAC-3 (SEQ ID NO: 18), and secondary 5'-CAGGTTTTTCGTTATATCCCTCCATCTC-3 (SEQ ID NO: 19). A 1.7 Kb region of upstream DNA, immediately adjacent to the transcription start site was isolated from the genomic DNA by PCR genome walking using a GenomeWalker™ kit (Clontech, Mountain View, California, USA), following the manufacturers instructions. Genomic DNA was subsequently isolated from *Malus x domestica* 'Granny Smith', *Malus x domestica* 'Royal Gala' and *Malus x pumila* var. niedzwetzkyana using forward and reverse primers 5'-ACCCTGAACACGTGGGAACCG-3 (SEQ ID NO: 20) and 5'-GCTAAGCTTAGCTGCTAGCAGATAAGAG-3 (SEQ ID NO: 21) respectively. The PCR products were cloned using the TOPO TA cloning® kit (Invitrogen, Carlsbad, California, USA) and the sequences aligned using Vector NTI (Invitrogen).

Minisatellite region PCR amplification and sequencing

Apple genomic DNA from 19 cultivars was amplified using a pair of PCR primers located in the *MYB10* promoter (forward: 5'-GGAGGGGAATGAAGAAGAGG-3' [SEQ ID NO: 22]; reverse: 5'-TCCACAGAAGCAAACACTGAC-3' [SEQ ID NO: 23]). PCR reactions were carried out in 16.5 µl volume containing 1x PCR buffer mix (Invitrogen), 1.3 mM MgCl₂, 100 µM of each dNTP, 0.72 % formamide, 10 µM of each primer, 0.5 U of Platinum *Taq* DNA polymerase (Invitrogen) and 2 ng of genomic DNA. PCR amplifications were performed in a Hybaid PCR Express Thermal Cycler (Thermo Electron Corporation, Waltham, MA, USA) with conditions as follows: 94°C for 2 min 45 sec followed by 40 cycles at 94°C for 55 sec, 55°C for 55 sec and 72°C for 1 min 39 sec, and a final elongation at 72°C for 10 min. The PCR products obtained were cloned using the TOPO TA cloning® kit (Invitrogen). Four clones were sequenced for each PCR product. The sequences were aligned using Vector NTI (Invitrogen).

Plasmid construction

Luciferase reporter constructs were derivatives of pGreen 0800-LUC (Hellens *et al.* 2005, Plant Methods **1**, 13) in which the promoter sequence for the native MdMYB10 promoter or the deletion fragments were inserted. Native promoter sequences were PCR amplified using the primers 5' – ACCCTGAACACGTGGGAACCG – 3' (SEQ ID NO: 24) and 5' – GCTAAGCTTAGCTGCTAGCAGATAAGAG – 3' (SEQ ID NO: 25) and cloned into the multi-cloning region of pGreen 0800-LUC. R₁ and R₆ promoter fragments were cloned in as native promoter sequences whilst changes to the repeat frequency for the R₂, R₃ and R₄ promoter fragments were synthesised (Geneart AG, Regensburg, Germany) and cloned into R₁ using the restriction enzymes *SpeI* and *DraI*. An inverse PCR approach was used for the R₁+ construct with the inclusion of unique restriction sites (*BamHI* and *SacI*) for the cloning of non-specific DNA (from pGEM T Easy, Promega, Madison, WI, USA) using the primers 5' – GGATCCTTCTGCACGACAACATTGACAA – 3' (SEQ ID NO: 26) and 5' – GAGCTCATGTTAGCTTTTCTATATATCGA – 3' (SEQ ID NO: 27). The pSAK construct for 35S:MdMYB10 and 35S:MdbHLH3 was as previously described (Espley *et al.*, 2007, The Plant Journal **49**, 414-427) whilst the promoter sequences were substituted for the R₁ and R₆:MdMYB10 versions. All constructs were verified by DNA sequencing.

Transactivation analysis using transformed tobacco leaves

The promoter sequences for *MdMYB10* were inserted into the cloning site of pGreen 0800-LUC (Hellens *et al.*, 2005, Plant Methods **1**, 13). In the same construct, a luciferase gene from *Renilla* (REN), under the control of a 35S promoter, provided an estimate of the extent of transient expression. Activity is expressed as a ratio of LUC to REN activity. The promoter-LUC fusions were used in transient transformation by mixing 100 µl of *Agrobacterium* strain GV3101 (MP90) transformed with the reporter cassette with or without another *Agrobacterium* culture(s) (900 µl) transformed with a cassette containing *MYB10* fused to the 35S, R₁ or R₆ promoters and MdbHLH3 fused to the 35S promoter. *Nicotiana tabacum* 'Samsun' plants were grown until at least 6 leaves were available for infiltration with *Agrobacterium*. A 10 µl loop of confluent bacterium were re-suspended in 10 ml of infiltration media (10 mM MgCl₂, 0.5 µM acetosyringone), to an OD⁶⁰⁰ of 0.2, and incubated at room temperature without shaking for 2 h before infiltration. Approximately 150 µl of this *Agrobacterium* mixture was infiltrated at six

points into a young leaf of *N. tabacum*. Transient expression was analysed three days after inoculation. Six technical replicates of 3 mm Ø leaf discs were excised from each plant using a leaf hole-punch and buffered in Phosphate Buffer Saline (PBS). Plate-based assays were conducted using a Berthold Orion Microplate Luminometer (Berthold Detection Systems, Oak Ridge, TN, USA) according to the manufacturer's specifications for the dual luciferase assay, using the Dual Glow assay reagents (Promega) for firefly luciferase and renilla luciferase. Luminescence was calculated using Simplicity version 4.02 software (Berthold Detection Systems).

Induction of anthocyanin pigmentation in tobacco

N. tabacum were grown as previously mentioned and maintained in the glasshouse for the duration of the experiment. *Agrobacterium* cultures were incubated as for the dual luciferase assay and separate strains containing the MdMYB10 gene fused to either the 35S, R₁ or R₆ promoter sequences and the MdbHLH3 gene fused to the 35S promoter were mixed (500 µl each) and infiltrated into the abaxial leaf surface. Six separate infiltrations were performed into *N. tabacum* leaves (two plants per treatment) and changes in colour were observed over an eight day period. To control for leaf-to-leaf variability, at least 2 leaves were infiltrated, and each leaf included positive (*Agrobacterium* cultures containing 35S:MdMYB10 + 35S:MdbHLH3) and negative (*Agrobacterium* with empty vector) controls.

Transformation of apple

The binary vector pSAK277 containing the *MdMYB10* cDNA driven by the R₆ or R₁ promoters was transferred into *Agrobacterium tumefaciens* strain GV3101 by the freeze-thaw method. Transgenic *Malus domestica* 'Royal Gala' plants were generated by *Agrobacterium*-mediated transformation of leaf pieces, using a method previously reported (Yao *et al.* 1995, Plant Cell Reports, **14**, 407-412).

Example 8: Isolation of the PcMYB10 promoter from pear and identification of a sequence motif analogous to the repeat motif found in apple MdMYB10 promoters.

Isolation of the MYB10 promoter from pear

Genomic DNA was isolated from the leaves of a pear cultivar (*Pyrus communis* ‘William’s Bon Chretien’) using a Qiagen DNeasy Plant Mini Kit, according to the manufacturers instructions (Qiagen, Valencia, California). Promoter sequences were isolated by PCR using the primers RE158 (5’-ACCCTGAACACGTGGGAACCG-3’, SEQ ID NO: 28) and RE159 (5’-CTCTTATCTGCTAGCAGCTAAGCTTAGC-3’, SEQ ID NO: 29).

By comparing the sequences of the MYB10 promoter from apple (Example 1) and pear, the applicants identified presence of a 23 bp motif, in the pear promoter, very similar to that found in apple MYB10 proteins.

An alignment of the MYB10 promoter from the white-fleshed apple and from pear, highlighting the 23bp motif with underlining, is shown in Figure 12.

Both the apple and pear promoters showed some positional conservation with the R1 repeat being at position -220 (from the ATG site) in apple and position -227 in pear. Similarly, the position of the microsatellite appeared to be conserved with the microsatellite in apple starting at position -253 and in pear at -259.

The applicants identified three versions of the 23 bp element, from white-fleshed apple, red-fleshed apple and pear, as summarized in Table 2 below.

Table 2. Comparison of 23bp motifs from apple and pear, highlighting variable positions

SEQ ID NO	Sequence	Species found in
1	g t t a g a c <u>t</u> g g t a g c t a <u>t</u> a a c a a	white-fleshed apple, red-fleshed apple
11	g t t a g a c <u>t</u> g g t a g c t a <u>a</u> t a a c a a	white-fleshed apple
12	g t t a g a c <u>c</u> g g t a g c t a <u>a</u> t a a c a a	pear

Percent identity between the sequences is shown in Table 3 below.

Table 3. Percent identity between 23 bp motifs from apple and pear

	SEQ ID NO: 1	SEQ ID NO: 11	SEQ ID NO: 12
SEQ ID NO: 1	100%	96%	91%
SEQ ID NO: 11		100%	96%
SEQ ID NO: 12			100%

The high degree of conservation between these three sequences, and their conserved position within the promoters, from three different sources, strongly suggest that each of the three sequences perform the same function.

Example 9: Production of a chimeric promoter with altered activity by insertion of copies of a repeated motif from the MdMYB10 promoter from red-fleshed apple into the PcMYB10 promoter from pear.

Introduction

MdMYB10 controls the accumulation of anthocyanin in apple. Transient experiments described in the Examples above have shown that the MYB10 protein is able to auto-regulate its own promoter leading to a high level of expression of a Luciferase reporter gene driven by the long version of MdMYB10 promoter (which includes the 6 repeats of a putative transcription factor binding site), when co-infiltrated with bHLH33 transcription factor. The applicants have now introduced the 6 repeats into the green pear MYB10 promoter controlling luciferase reporter gene and assessed the reporter activity in presence of PcMYB10 and MdMYB10 TFs.

Materials and methods

The green pear MYB10 promoter (SEQ ID NO: 13) was cloned in the pGreen0800LUC vector. The R6 region (SEQ ID NO: 14) of the MdMYB10 promoter was amplified using primers CB02F/RE161, digested by Dra1 and cloned in the PcMYB10 promoter at the blunted Bsg1 site (see Figure 10) to produce the recombinant chimeric promoter of SEQ ID NO: 15.

All the constructs (including MdMYB10 genomic, 35S:PcMYB10, AtbHLH2 and bHLH33 and the different LUC reporter constructs: DFR-LUC, MdMYB10short-LUC, MdMYB10long-LUC, PcMYB10short-LUC, PcMYB10R6-LUC) were transformed into GV3101 by electroporation and used to infiltrate *Nicotiana benthamiana* leaves as described previously (Hellens et al. 2005, Plant Methods 1, 13). After 5 days, leaf discs were collected and Firefly luciferase (LUC) and renilla luciferase (REN) activities were measured on a luminometer using the Dual Glow™ reagents (PROMEGA).

Results

Apple and pear MYB10 constructs, in presence of bHLH33 and bHLH2 respectively, strongly activate the DFR, MdMYB10R6 and PcMYB10R6 promoters, and only slightly activate MdMYB10R1 and PcMYB10R1 promoters. The introduction of the apple R6 repeats in the pear promoter leads to a 6-fold increase in the luciferase activity in presence of the 35S:PcMYB10 construct and an 8-fold increase in presence of the MdMYB10 genomic construct.

Example 10: The MdMYB10 promoter containing 6 copies of the 23 bp repeat unit is activated by several R2R3 transcription factor sequences.

Introduction

The effect of three MYB10 sequences (from pear [PcMYB10], strawberry [FaMYB10] and Arabidopsis [PAP1]) on two versions of the MdMYB10 promoter, R1 and R6, which contain 1 and 6 repeats of the 23 base pair repeat unit respectively, was measured using the transient transformation assay, described in previous examples, in tobacco.

Materials and methods

R1 and R6 versions of MdMYB10 native promoter are as described previously (Espley *et al.*, 2009, Plant Cell **21**, 168-183). The R1 and R6 MdMYB10 promoters fused to the luciferase reporter are as described in Example 2.

MdMYB10 and bHLH3 coding sequences have been cloned in the pSAK binary vector as described previously (Espley *et al.*, 2007, The Plant Journal **49**, 414-427). The genomic coding sequence of PcMYB10 has been isolated from WBC pear genomic DNA and cloned in the pGreenII 0029 62-SK vector under the control of the 35S promoter. AtbHLH2 (EGL3, At1g63650) coding sequence has been isolated from Arabidopsis cDNA and cloned in the pHEX binary vector under the control of the 35S promoter. FaMYB10 coding sequence (SEQ ID NO: 33) has been isolated from *Fragaria ananassa* (garden strawberry) cDNA and cloned in the pGreenII 0029 62-SK binary vector under the control of the 35S promoter (Gleave, 1992, Plant Mol Biol **20**, 1203-1207). MdMYB8 coding sequence has been isolated from *Malus domestica* 'Royal Gala' mature fruit cDNA and cloned in the pART277 binary vector (Gleave, 1992, (Gleave, 1992, Plant Mol Biol **20**, 1203-1207). The coding sequences for AtPAP1 (Accession No. **CAB09230**), AtbHLH2 (Accession No. Q9CAD0) and MdbHLH3 (Accession No. **CN934367**) were also cloned upstream of the CaMV35 promoter as described for MdMYB10 here and in Example 2.

The promoter sequences for MYB10 were inserted into the cloning site of pGreen 0800-LUC (Hellens *et al.*, 2005, Plant Methods **1**, 13) to control the expression of the LUC reporter gene. In the same construct, a luciferase gene from REN, under the control of a 35S promoter, provided an estimate of the extent of transient expression. Activity is expressed as a ratio of LUC to REN activity. The promoter-LUC fusions were used in transient transformation of *Nicotiana benthamiana*. 0.1mL of *Agrobacterium tumefaciens* strain GV3101 (MP90) transformed with the promoter-LUC cassette, was mixed with 0.45 mL of two other *Agrobacterium* cultures transformed with the 35S:MYB and 35S:bHLH constructs respectively. Infiltration of *N. benthamiana* leaf and chemiluminescence measurement are as described previously (Espley *et al.*, 2007, The Plant Journal **49**, 414-427).

Results

The results are shown in Figure 13. The results from the assay indicate that the presence of the R6 motif in the apple MYB10 promoter leads to a large increase (7 to 12-fold) in luciferase activity in presence of the different MYB10 sequences when co-infiltrated with bHLH co-factor. No significant increase in luciferase activity was measured in presence of the MdMYB8 transcription factor (Figure 13). These results show that the presence of the R6 motif confers the ability for the MdMYB10 promoter to be regulated by MdMYB10 and other R2R3 MYBs (PcMYB10, FaMYB10 and PAP1).

Example 11: Chimeric promoters produced by combining copies of the 23 bp repeat unit and naturally occurring MYB10 promoters.

Introduction

To demonstrate production of functional chimeric promoters in the invention, the R6 domain from the apple MYB10 promoter was introduced in the pear MYB10 (see SEQ ID NO: 13) and Arabidopsis PAP1 (see SEQ ID NO: 36) promoters, 275bp and 489bp upstream of the ATG respectively (Figure 15), and these constructs were assayed by the transient luminescent assay in tobacco.

Materials and methods

The MdMYB10 R1 and R6 promoters are as described in Example 10. 4.6Kb of PcMYB10 promoter (SEQ ID NO: 13) sequence was amplified from 'William Bon Chretien'(WBC) pear genomic DNA, 1.9Kb of AtPAP1 (AtMYB75, AT1G56650) promoter sequence (SEQ ID NO: 36) was amplified from Arabidopsis genomic DNA and cloned in the pGreen 0800-LUC vector (Hellens *et al.*, 2005, Plant Methods **1**, 13). The R6 domain was amplified from the 'Red Field' R6:MdMYB10 native promoter described previously (Espley *et al.*, 2009, Plant Cell **21**, 168-183), using primers CB02 5'-TGCAGAAATGTTAGACTGGTAGCTATTAAC-3' (SEQ ID NO: 30) and RE161 5'-CCAGTGACGTGCATGTCTGATATCC-3' (SEQ ID NO: 31). PCR fragment containing the R6 motif (as shown in Figure 17) was digested with DraI, gel purified and blunt-cloned in the PcMYB10 and AtPAP1 promoters at the BsgI and HindIII sites respectively to produce pPcMYB10R6-LUC and pAtPAP1R6-LUC constructs.

The sequence of the PcMYB10/R6 chimeric promoter is shown in SEQ ID NO: 15. The sequence of the AtPAP1/R6 chimeric promoter is shown in SEQ ID NO: 37.

MdMYB10 and bHLH3 coding sequences have been cloned in the pSAK binary vector as described previously (Espley *et al.*, 2007, The Plant Journal **49**, 414-427). The genomic coding sequence of PcMYB10 has been isolated from WBC pear genomic DNA and cloned in the pGreenII 0029 62-SK vector under the control of the 35S promoter. AtbHLH2 (EGL3, At1g63650) coding sequence has been isolated from Arabidopsis cDNA and cloned in the pHEX binary vector under the control of the 35S promoter.

Expression of the reporter genes under each promoter construct in the presence of the transcription factor constructs was tested in the transient assay as described in previous examples.

Results

The results are shown in Figure 15. The results indicate that the presence of the R6 motif in the pear and the Arabidopsis promoters leads to an increase in luciferase activity when apple MYB10 and bHLH3 are co-infiltrated (Figure 3). Similar results were obtained when these promoters are co-infiltrated with their corresponding MYB10 orthologs (i.e. pear promoter infiltrated with PcMYB10/bHLH2 and Arabidopsis promoter infiltrated with AtPAP1/bHLH2). These results show that functional chimeric promoters can be produced by combining copies of the 23 bp repeat unit with naturally occurring R2R3 transcription factor (MYB10) promoters. The results also demonstrate autoregulation of the chimeric promoters by the product encoded by the gene with which the natural promoters are currently associated (i.e. the MYB10 transcription factor).

Example 12: Production of a functional chimeric promoter by combining multiple copies of the 23 bp repeat unit with an unrelated naturally occurring promoter, and demonstration of regulation of the chimeric promoter by R2R3 MYB transcription factors.

Introduction

The apple R6 motif was introduced into the promoter region of the VitC2 gene of *A. eriantha* 221bp upstream of the 5'UTR (694bp upstream of the ATG) (Figure 14) and the construct was assayed as described in previous examples, in tobacco. VitC2 is a GDP-L-galactose guanyltransferase found to be a rate limiting step in ascorbic acid biosynthesis (Bulley *et al.*, 2009, J Exp Bot **60**, 765-778).

Materials and methods

2.1Kb of VitC2 promoter sequence (SEQ ID NO: 38) was amplified from *Actinidia eriantha* genomic DNA (Laing *et al.*, 2007, Proc Natl Acad Sci USA **104**, 9534-9539), and cloned in the pGreen 0800-LUC vector (Hellens *et al.*, 2005, Plant Methods **1**, 13). The R6 domain (SEQ ID NO: 14) was amplified from the 'Red Field' R6:MdMYB10 native promoter described previously (Espley *et al.*, 2009, Plant Cell **21**, 168-183), using primers CB02 5'-TGCAGAAATGTTAGACTGGTAGCTATTAAC-3' (SEQ ID NO: 30) and RE161 5'-CCAGTGACGTGCATGTCTGATATCC-3' (SEQ ID NO: 31). PCR fragment containing the R6 motif (as shown in Figure 17) was digested with DraI, gel purified and blunt-cloned into the VitC2 promoters at the HpaI site to produce the pVitC2R6-LUC construct. Two tandem insertions of the R6 motifs were cloned in the VitC2 promoter to produce pVitC2R12-LUC. The sequence of the chimeric Vit C/R6 promoter is shown in SEQ ID NO: 39. The sequence of the chimeric VitC2/R12 promoter is shown in SEQ ID NO: 40. MdMYB10 and bHLH3 coding sequences have been cloned in the pSAK binary vector as described previously (Espley *et al.*, 2007, The Plant Journal **49**, 414-427).

Expression of the reporter genes under each promoter construct in the presence of the transcription factor constructs was tested in the transient assay as described in previous examples.

Results

The results are shown in Figure 16. The results indicate that the presence of the R6 motif in the VitC2 promoter leads to a significant increase in luciferase activity (up to 10-fold) when MdMYB10 and bHLH3 are co-infiltrated (Figure 16). Interestingly, a higher number of repeats (R12) further increases the level of activation by MdMYB10 alone, although this effect is not seen when MdMYB10 and bHLH3 are co-infiltrated.

The above Examples illustrate practice of the invention. It will be appreciated by those skilled in the art that numerous variations and modifications may be made without departing from the spirit and scope of the invention.

SUMMARY OF SEQUENCES:

SEQ ID NO:	Sequence type	Information	Species
1	polynucleotide	23 bp sequence motif, version 1	<i>Malus domestica</i> and <i>Malus domestica</i> <i>niedwetzkyana</i>
2	polynucleotide	minisatellite repeat unit, from MdMYB10 promoter from red-fleshed cultivar <i>Malus x domestica</i> niedwetzkyana, including repeat motifs 2, 3A, 3B, 4, 5 and 6	<i>Malus domestica</i> <i>niedwetzkyana</i>
3	polynucleotide	microsatellite	<i>Malus domestica</i> <i>niedwetzkyana</i>
4	polynucleotide	region of MdMYB10 promoter from red-fleshed cultivar <i>Malus x domestica</i> niedwetzkyana including minisatellite repeat unit, microsatellite and repeat unit 1	<i>Malus domestica</i> <i>niedwetzkyana</i>
5	polynucleotide	whole MdMYB10 promoter from red-fleshed cultivar <i>Malus x domestica</i> niedwetzkyana	<i>Malus domestica</i> <i>niedwetzkyana</i>
6	polypeptide	MdMYB10	<i>Malus domestica</i>
7	polynucleotide	MdMYB10 coding region	<i>Malus domestica</i>
8	polynucleotide	whole MdMYB10 promoter from white-fleshed cultivar <i>Malus domestica</i> Royal Gala	<i>Malus domestica</i>
9	polynucleotide	forward primer	artificial
10	polynucleotide	reverse primer	artificial
11	polynucleotide	23 bp sequence motif, version 2	<i>Malus domestica</i>
12	polynucleotide	23 bp sequence motif, version 3	<i>Pyrus communis</i>
13	polynucleotide	whole pear PcMYB10 promoter	<i>Pyrus communis</i>
14	polynucleotide	apple minisatellite sequence that was inserted into pear (PcMYB10), Arabidopsis (PAP1) and kiwifruit (VitC2) promoters	<i>Malus domestica</i> <i>niedwetzkyana</i>

SEQ ID NO:	Sequence type	Information	Species
15	polynucleotide	Chimeric apple/pear promoter	artificial
16	polypeptide	Pear PcMYB10	<i>Pyrus communis</i>
17	polynucleotide	Pear PcMYB10 coding sequence	<i>Pyrus communis</i>
18	polynucleotide	Primer	artificial
19	polynucleotide	Primer	artificial
20	polynucleotide	Primer	artificial
21	polynucleotide	Primer	artificial
22	polynucleotide	Primer	artificial
23	polynucleotide	Primer	artificial
24	polynucleotide	Primer	artificial
25	polynucleotide	Primer	artificial
26	polynucleotide	Primer	artificial
27	polynucleotide	Primer	artificial
28	polynucleotide	Primer	artificial
29	polynucleotide	Primer	artificial
30	polynucleotide	Primer	artificial
31	polynucleotide	Primer	artificial
32	polypeptide	Strawberry FaMYB10	<i>Fragaria ananassa</i>
33	polynucleotide	Strawberry FaMYB10 coding sequence	<i>Fragaria ananassa</i>
34	polypeptide	Arabidopsis PAP1	<i>Arabidopsis thaliana</i>
35	polynucleotide	Arabidopsis PAP1 coding sequence	<i>Arabidopsis thaliana</i>
36	polynucleotide	Arabidopsis PAP1 promoter	<i>Arabidopsis thaliana</i>
37	polynucleotide	Chimeric PAP1 R6 promoter	artificial
38	polynucleotide	Kiwifruit VitC2 promoter	<i>Actinidia eriantha</i>

SEQ ID NO:	Sequence type	Information	Species
39	polynucleotide	Chimeric VitC2 R6 promoter	artificial
40	polynucleotide	Chimeric VitC2 R6 promoter	artificial
41	polynucleotide	consensus motif	artificial
42	polynucleotide	consensus motif	artificial

CLAIMS:

1. A method for producing a chimeric promoter polynucleotide capable of controlling transcription of an operably linked polynucleotide in a plant cell or plant, wherein the method comprises combining:
 - a) at least one sequence motif comprising a sequence with at least 70% identity to SEQ ID NO:1, 11 or 12, and
 - b) another polynucleotide sequence.
2. The method of claim 1 in which the at least one sequence motif in a) comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 1.
3. The method of claim 1 in which the at least one sequence motif in a) comprises the sequence of SEQ ID NO:41.
4. The method of claim 1 in which the at least one sequence motif in a) comprises the sequence of SEQ ID NO:42.
5. The method of any of claims 1 to 4 in which at least one sequence motif in a) comprises the sequence of SEQ ID NO: 1.
6. The method of any of claims 1 to 4 in which at least one sequence motif in a) comprises the sequence of SEQ ID NO: 11.
7. The method of any of claims 1 to 4 in which at least one sequence motif in a) comprises the sequence of SEQ ID NO: 12.
8. The method of any preceding claim in which at least one of the sequence motifs is interrupted by at least one of the other sequence motifs.
9. The method of any preceding claim in which the sequence motif in a) is part of a promoter polynucleotide sequence that naturally occurs in a plant.

10. The method of any preceding claim in which the polynucleotide in b) is a promoter polynucleotide sequence.
11. The method of any preceding claim in which the polynucleotide in b) is a promoter polynucleotide sequence that naturally occurs in a plant.
12. The method of claim 10 or 11 in which the promoter polynucleotide in b) comprises a sequence with at least 70% identity to one of the sequences of SEQ ID NO:13, 36 and 38.
13. The method of claim 10 or 11 in which the promoter polynucleotide comprises one of the sequences of SEQ ID NO:13, 36 and 38.
14. The method of any preceding claim in which chimeric promoter is produced by combining:
 - a) a sequence with at least 70% identity to the sequence of SEQ ID NO:14, and
 - b) a sequence with at least 70% identity to one of the sequences of SEQ ID NO:13, 36 and 38.
15. The method of any preceding claim in which chimeric promoter is produced by combining:
 - a) the sequence of SEQ ID NO:14, and
 - b) one of the sequences of SEQ ID NO:13, 36 and 38.
16. A chimeric promoter produced by the method of any one of claims 1 to 15.
17. A chimeric promoter polynucleotide capable of controlling transcription of an operably linked polynucleotide in a plant cell or plant, wherein the promoter polynucleotide comprises:
 - a) at least one sequence motif comprising a sequence with at least 70% identity to SEQ ID NO:1, 11 or 12
 - b) another polynucleotide sequence.
18. The chimeric promoter of claim 16 in which the at least one sequence motif in a) comprises a sequence with at least 70% identity to the sequence of SEQ ID NO: 1.
19. The chimeric promoter of claim 16 in which the at least one sequence motif in a) comprises the sequence of SEQ ID NO:41.

20. The chimeric promoter of claim 16 in which the at least one sequence motif in a) comprises the sequence of SEQ ID NO:42.
21. The chimeric promoter of any of claims 16 to 20 in which the at least one sequence motif in a) comprises the sequence of SEQ ID NO: 1.
22. The chimeric promoter of any of claims 16 to 20 in which the at least one sequence motif in a) comprises the sequence of SEQ ID NO: 11.
23. The chimeric promoter of any of claims 16 to 20 in which the at least one sequence motif in a) comprises the sequence of SEQ ID NO: 12.
24. The chimeric promoter of any of claims 16 to 23 in which the at least one of the sequence motifs is interrupted by at least one other of the sequence motifs.
25. The chimeric promoter of any of claims 16 to 24 in which the at least one sequence motif in a) is part of a promoter polynucleotide sequence that naturally occurs in a plant.
26. The chimeric promoter of any of claims 16 to 25 in which the polynucleotide in b) is a promoter polynucleotide sequence.
27. The chimeric promoter of any of claims 16 to 26 in which the polynucleotide in b) is a promoter polynucleotide sequence that naturally occurs in a plant.
28. The chimeric promoter of any of claims 16 to 27 in which the naturally occurring promoter polynucleotide comprises a sequence with at least 70% identity to one of the sequences of SEQ ID NO:13, 36 and 38.
29. The chimeric promoter of any of claims 16 to 28 in which the naturally occurring promoter polynucleotide comprises one of the sequences of SEQ ID NO:13, 36 and 38.
30. The chimeric promoter of any of claims 16 to 29 comprising:
- a) a sequence with at least 70% identity to the sequence of SEQ ID NO:14, and
 - b) a sequence with at least 70% identity to one of the sequences of SEQ ID NO:13, 36 and 38.

31. The chimeric promoter of any of claims 16 to 30 comprising:
- a) the sequence of SEQ ID NO:14, and
 - b) at least one of the sequences of SEQ ID NO:13, 36 and 38.
32. The chimeric promoter of any of claims 16 to 31 comprising a sequence with at least 70% identity to SEQ ID NO:15.
33. The chimeric promoter of any of claims 16 to 31, wherein the chimeric promoter polynucleotide is modulated by a MYB transcription factor.
34. The chimeric promoter of any of claims 16 to 31, wherein chimeric promoter polynucleotide is positively modulated, or activated, or up-regulated by the MYB transcription factor.
35. The chimeric promoter claim 33 or 34, wherein the MYB transcription factor comprises an R2R3 DNA binding domain.
36. The chimeric promoter claim 33 or 34, wherein the MYB transcription factor comprises a sequence with at least 70% identity to any one of the sequences of SEQ ID NO: 6, 17, 32 and 34.
37. The chimeric promoter claim 33 or 34, wherein the MYB transcription factor comprises one of the sequences of SEQ ID NO: 6, 17, 32 and 34.
38. The chimeric promoter claim 33 or 34, wherein the chimeric promoter polynucleotide is capable of controlling transcription of an operably linked polynucleotide sequence constitutively in substantially all tissues of a plant.
39. The chimeric promoter claim 33 or 34, wherein the chimeric promoter polynucleotide is capable of controlling transcription of an operably linked polynucleotide sequence in any plant, plant cell, or plant tissue in which the MYB transcription factor is expressed.
40. The chimeric promoter of any one of claims 16 to 39 comprising a sequence with at least 70% identity to any one of SEQ ID NO: 15, 37, 39 and 40.

41. The chimeric promoter of any one of claims 16 to 39 comprising the sequence of any one of SEQ ID NO:15, 37, 39 and 40.
42. A genetic construct comprising a chimeric promoter polynucleotide of any one of claims 16 to 39.
43. The genetic construct of claim 42, in which the chimeric promoter polynucleotide is operably linked to a polynucleotide sequence to be expressed.
44. A host cell transformed with the chimeric promoter polynucleotide of any one of claims 16 to 39.
45. A plant cell or plant transformed with the chimeric promoter polynucleotide of any one of claims 16 to 39.
46. A plant cell or plant transformed with a genetic construct of claim 42 or 43.
47. The plant cell plant cell or plant of claim 45 or 46, that is also transformed with a polynucleotide or genetic construct for expressing a MYB transcription factor that modulates expression of the chimeric promoter polynucleotide.
48. The plant cell or plant of claim 45 or 46, which naturally expresses the MYB transcription factor.
49. The plant cell or plant of claim 47 or 48, in which the MYB transcription factor comprises an amino acid sequence with at least 70% identity to one of the sequences of SEQ ID NO: 6, 17, 32 and 34.
50. The plant cell or plant of claim 47 or 48, in which the MYB transcription factor comprises the amino acid sequence of one of the sequences of SEQ ID NO: 6, 17, 32 and 34.
51. A method for producing a plant cell or plant with modified expression of at least one polynucleotide, the method comprising transformation of the plant cell or plant with a chimeric promoter polynucleotide of any one of claim 16 to 39.

52. The method of claim 51 in which the plant cell or plant has a modified phenotype, relative to the plant cell or plant in the non-transformed state.
53. The method of claim 51 or 52, in which the plant cell or plant is transformed with a genetic construct of claim 42 or 43.
54. The method of any one of claims 51 to 53, in which the plant cell or plant is also transformed with a polynucleotide or genetic construct capable of expressing a MYB transcription factor that modulates expression of the chimeric promoter polynucleotide.
55. The method of any one of claims 51 to 53, in which the plant cell or plant naturally expresses the MYB transcription factor.
56. The method of claim 54 or 55, in which the MYB transcription factor comprises an amino acid sequence with at least 70% identity to one of the sequences of SEQ ID NO: 6, 17, 32 and 34.
57. The method of claim 54 or 55, in which the MYB transcription factor comprises the amino acid sequence of one of the sequences of SEQ ID NO: 6, 17, 32 and 34.
58. A plant cell or plant produced by the method of any one of claims 51 to 57.
59. A seed, propagule, progeny, part, fruit or harvested material of the plant of any one of claims 45 to 50 and 58.
60. The seed, propagule, progeny, part, fruit or harvested material of claim 59 comprising a chimeric promoter polynucleotide of any one of claims 16 to 39.

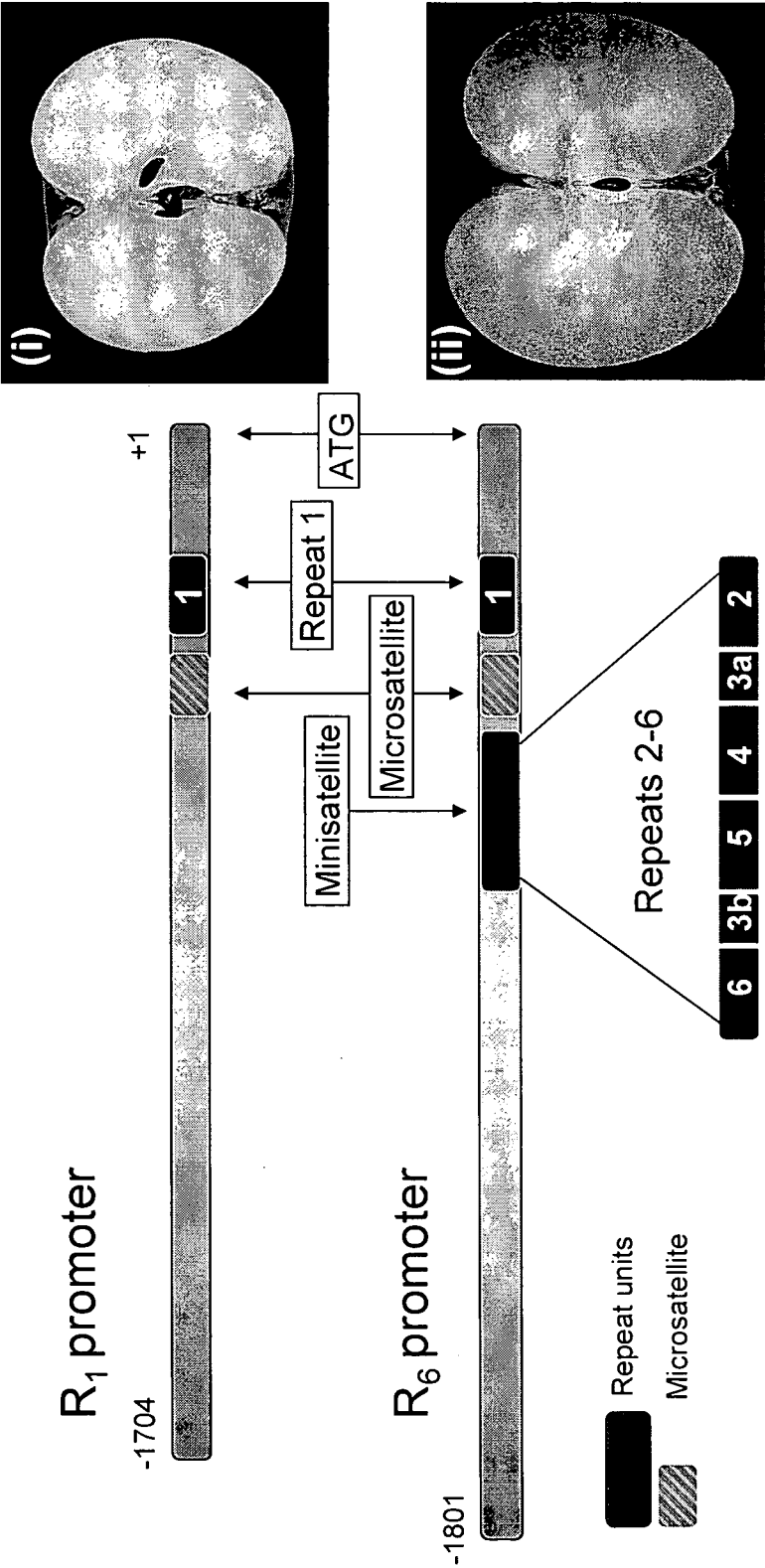
Figure 1

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1      TACCTTGAAC AGTGGGGAAC CGGCCGGTTT GTAACAGACT GAGATAGGTC CGTTCTATT TCTTAAAAAC CCAACACCCG CTACGTTCCA TTTATAAAGC
101    ATGGACTTG TCCACCCCTTG GCCGGCAAA CATTTCTGA CTCTATCAG GCTATCCAG GCTGTGGGC GATCGAAGGT ABATATTTGC
      GGTCGGCTG GTCCCTCCAA CTTTGAGCCC GGCTGACTT GTGCCACTC CTAACATAA CCATATAAAA ACCAAGATT CCCTTCATC TTTACACAT
201    CCAGCGAGAC CAGGAGGTT GAACTCGG CCGAGCTGAA CAGGCTGAG GATTGATTT TGTATTTTAA GGGAAAGTAG AAGTGTGTA
      ATCACCTTAC TTTCACAAA CAATTCAACA CAATCAAC ACATCAAC ATCATCAGT CACTAATAA GACAACCTTC ATAAGGGTTG
301    TAGTGAATG AAAGTTGTT GTTAAGTTGT TAGTGTGTT TATTAGTTGG TAGTCTAGT ATATAGTGA CAGTATATT CTGTGGAAG TATCCCAAC
      CCGTAGTTCT CTACTTGAA TCCAAATTGC TAGCATTTGA ACCCTAAGT ACACACAAA ACATAAAGT TATGCAATG AATCTAGGT
401    GGATCAAGA CTCACACTT AGGTTACAG ATCGTAACAT TCGGATCAA TGCTGTGTT TGTATTGAA CTCGTTGAAG ATAGCTATTC TATAGATCCCA
      TTGGAATAA CTCACAGAA CCTAACAGA AATAATATC TGGACGGTT AACGGCTTC AACGAAGA TCGCTTCGT TCCAAAGCT GTTGAGTGC CTGTGTTAT
501    AAACCTGATT GAGTTGTCTT GGAUTGTCT TTATTATAAG ACCTGCGAA TTGCTTAGG TTGCTTCTGT TCCAAAGCT GTTGAGTGC CTGTGTTAT
      GGAAGAGGA TATAACCAT TCAAGGAAT CCATCTTAG ATAGGCATA GTCCCCAAT ACGGATTAAC CAGTGAGAA CATAGGCCAT CTGATAGCGT
601    CCTTTCCCT ATATTGTTA AGTTGCTTTA GTAGAAATC TTATCGGTA CAGGGGTTA TGCTAATTG TGCTAATTG GATGCGGTA GACTATCGCA
      GGTCCCGCAA GACAGTTAAC CAAGTAGAC CACCGATGGT ATATGTGAC CAAGTAAGA GTCACTTAA ATGTAGATTA ACCACGTGA GTTAAATTA
      CCAGGGGTT CTGTCAATTG GTTCATCTG GTTCATCTGT CACTGGGATT TACATCTAAT TGGTGCACCT CAATTTAATT
      EcoRI
701    CRAAGCTGAA CCACCTATGA AAATAATGTA AGCTGAAT CTAGAGAG AATTCTTGCT CTAGGGACA AATGATTTTC GTATGCCATA GTGTTTTTTT
      GTTCCGACTT GGTGATACT TTTATTACAT TCGGACTTTA GAATCTCTC TTAAGAACA GATCCCTGT TTAATAAAG CATACGGATT CACAAAAAAA
      HindIII
801    AGTGACAGTA AACTAAGATT TGAGTACAGA GACATTAAC TGTGTGAAG CTTAGTGAGT TGAAGCAGCT AGCCAATTAT ATTGACCAAT
      TCACTGTCT TTGATTCTAA ACTCATGCT CTGTAATTGA CTCTAAGTGA GAACACTTTC GAATCACTCA ACTTCGTGCA TCGGTTAATA TAACCTGTTA
901    GGTTAGGTG TAGGCTCTAA ACTTCCGTAG TACGTTTGT CAGCAATATA GTGGGGTGC CGCAAAATGC AGACAGTAGC AATAAATAC GGCCTAGGAT
      CACAATCCAC ATCGCAGATT TGAAGGCATC CTCAAAACAT GTGCTTATAT CACCCCGACG CGGTTTACG TCTGTCAATG TTATTTAATG CCGGATCCCTA
1001  TTCTCCTCT TTTTCTTCTA TTCCATTCCA TCCATCTCTC TCACATCTCT TATTTGCTT TTCTCTTCT ATAAAAAT AATAAAGAT GTTAATGTAA
      AAGAGAGGA AAAAAAAGC AAGTAAGGT AGGTAAGAG ATAAACAGA AAGCAAGA TTATTTTAA TTATATTCTA CAATTACATT
1101  CTTGACCGTG ACTATTCAA TAGGAGGGA ATGAAGAGA GGGAAAAA ATCTTACTC GTTAAATTAC AAGCAACAC TTTTTTTT
      GAACCTGGAC TGAATAGTTT ATCTCCCT TACTTCTCT CCGTTTTT CTCTCTCTC TTAGGATGAG GCATTTAATG TTCGTTGTG AAAAAAAA
      SpeI
1201  TTTGGACAAG CAGAAGCAA CAAACACTTG AAAAAGCAGC GAAAGCATCA TAAAGGTATC TTATGTGTT TGTGTAACT AGTTACACGA
      AAACCTGTTT GTCTTCGTTT GTTTGTGAC TTTTTCGTG CTTCGTACT ATTTCCATAG AATACCACA GTTCTACAC ACAACATTGA TCAATGTCT
      SacII
1301  TTCTGCATTC ACATTTCATAG AATGTGCTTT TGAATATTAT ATTACAGCTA GAGAAATTTA TGCCCTGGGA TTGATTTCC TACCGCGTG TCAATGTTGT
      AAGACGTAAG TGTAAGTATC TTACACGAAA ACTTATAATA TAAATCTCAT CTCTTAAAT ACGGGACCT AACTAAAGG ATGGCGCCAC AGTTACARCA
      Repeat 3A
      Repeat 4
      Repeat 5
      Repeat 6
      Repeat 3B
1401  CGTGCGAATA TGTTAGACTG GTAGCTATTA ACAAGTTAGA CTGGTTAGAC TGGTAGCTAT TAACAAGTTA GACTGGTAGC TATTAAACAC TGGTAGCTAT
      GCACGTCTTT ACAATCTGAC CATCGATAAT TGTTCAAICT GACCAATCTG ACCATCGATA ATTGTTCAAT CTGACCATCG ATATTGTTG ACCATCGATA
      Repeat 3B
      Repeat 1
      Repeat 2
      Repeat 3
      Repeat 4
      Repeat 5
      Repeat 6
      Repeat 3B
1501  TAACAAGTTA GACTGGTAGC TATTAAACA GTAGACTGIG TGTGTGTG TATTTCACAA GTTAGACTGG TAGCTATTAA CAACTGTGG AATGTTTTAA
      ATGTTTCAAT CTGACCATCG AATAATGTTT AATCTGACAC ACACACACAT AATAAGTGT CAACTGACC ATCGATAAT GTTGACAACT TTACAAAAAT
1601  ACTGTGCTGT GTTCTCTTCT GTGGATATCA GACATGCACG TCACGTGGCT TGTAAAGTTA ATTAGGCCGA TGGTATCCAT AGCGTTAAGC TCATGGCAAA
      TGAACAGTCA CAAACGAAGA CACCTATAGT CTGTAGCTGC AGTGACCGA ACATCTAAT TAACTCCGGT ACCATAGGTA TCGCAATTGC AGTACCGTTT
      HindIII
1701  CACACTCTAA TTATATATAA TGGTAGCTAG GTGTCTTTCT GGAGTCTATG AAGTGGGTAG CAGGCAAAAG ATAAGCTAAG CTTAGCTGCT AGCAGATAAG
      GTGTGAGATT AATATATATT ACCATCGATC CACAGAAAAG CUTCAGATAC TTCACCATC GTCCGTTTC TATTGATTC GAATCGACGA TCGTCTATTTC
      AG
      TC

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Figure 2



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Figure 3

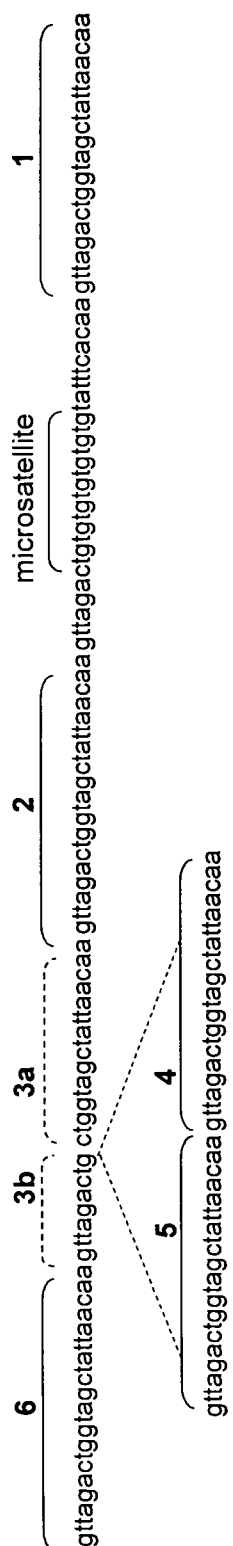
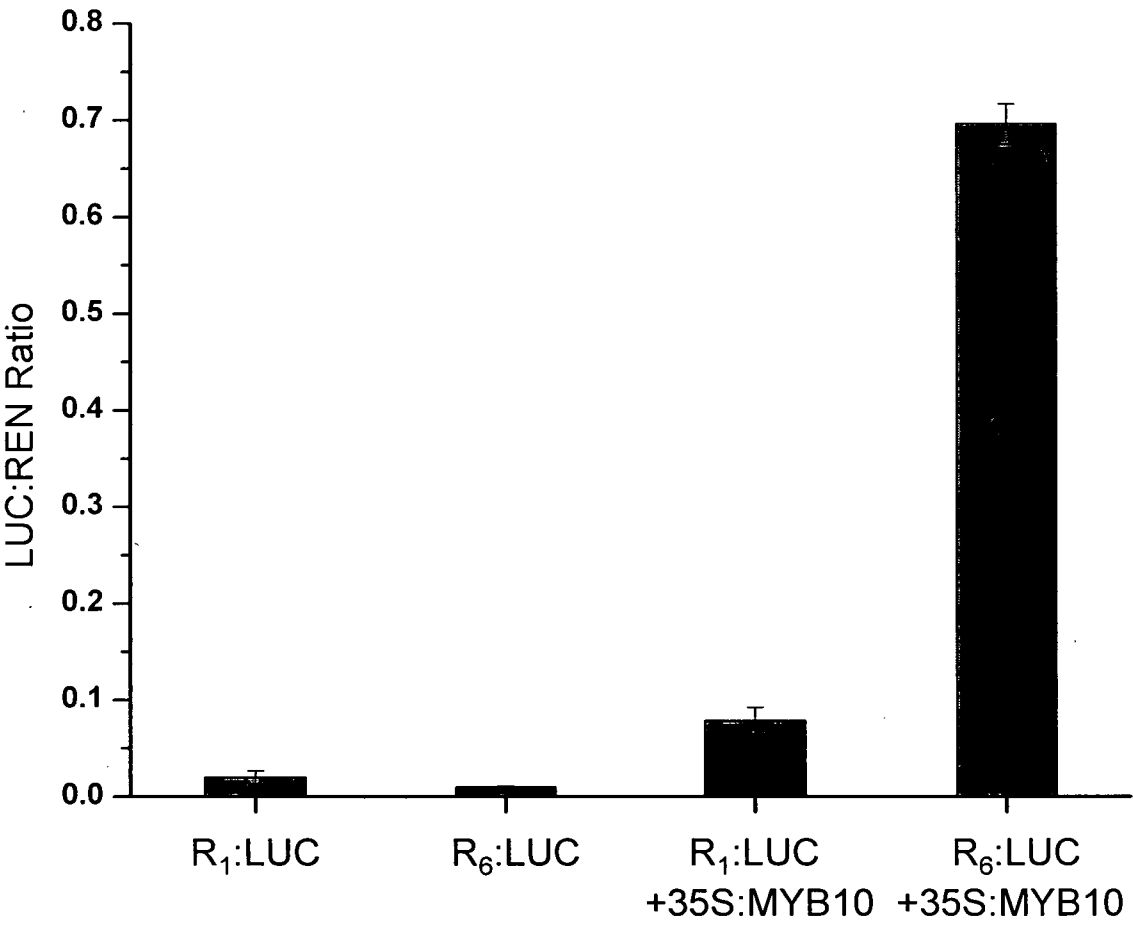
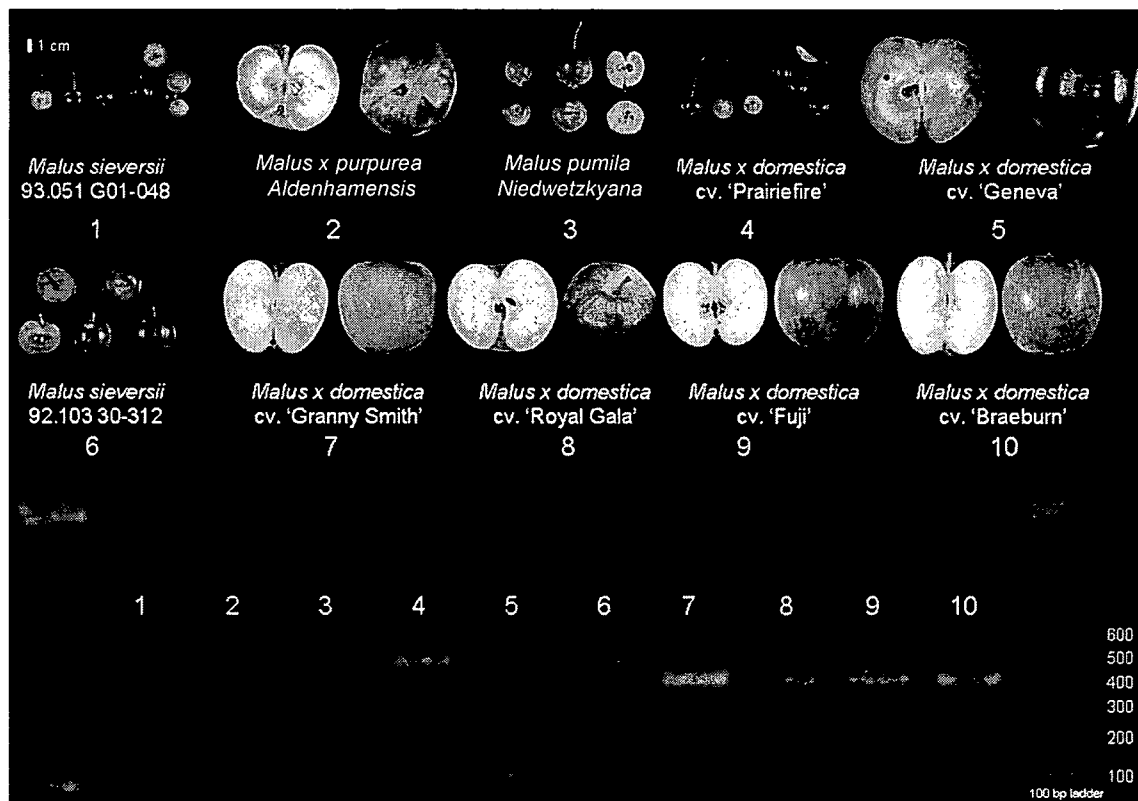


Figure 4



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Figure 5



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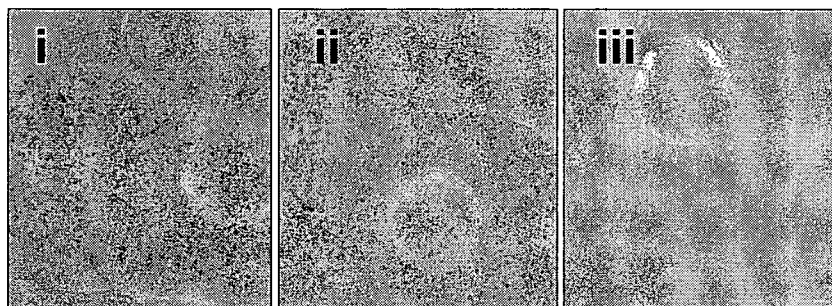
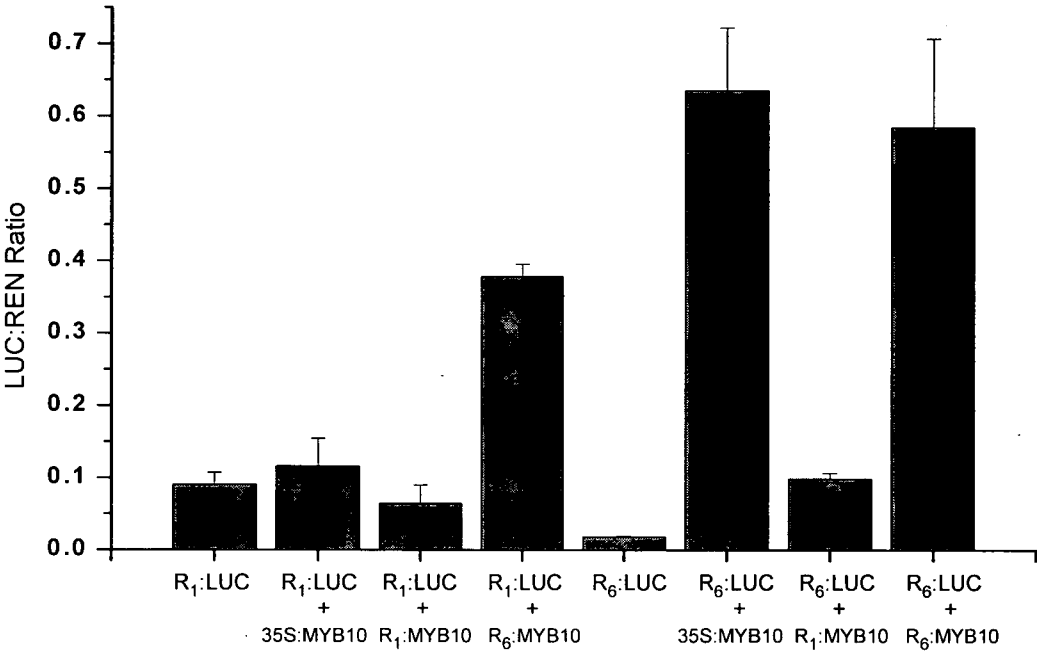
Figure 6**(a)****(b)**

Figure 7



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Figure 8

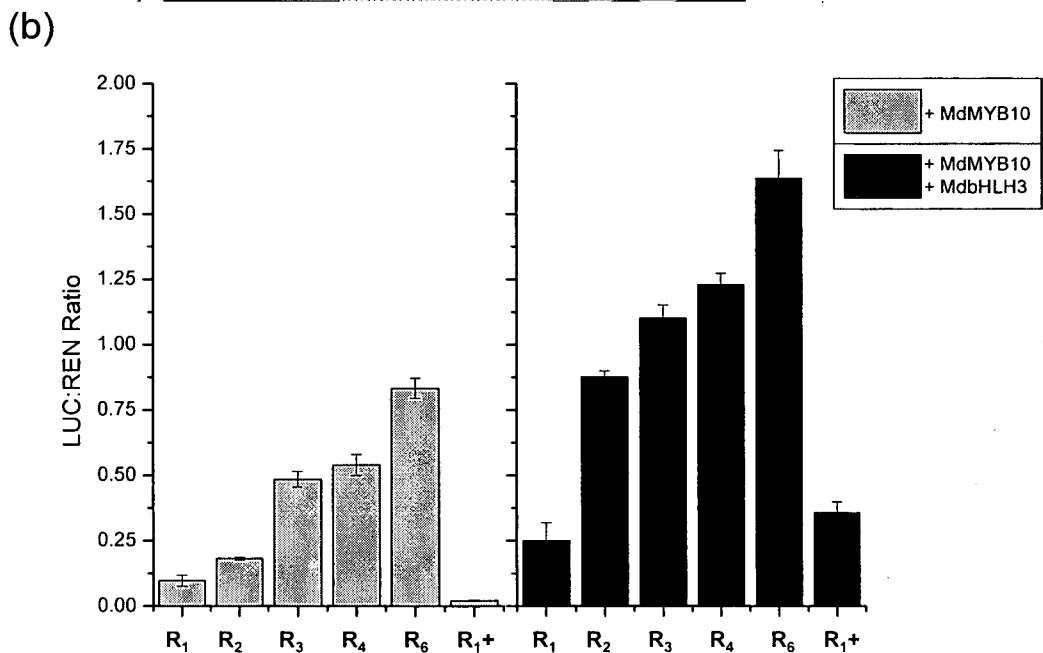
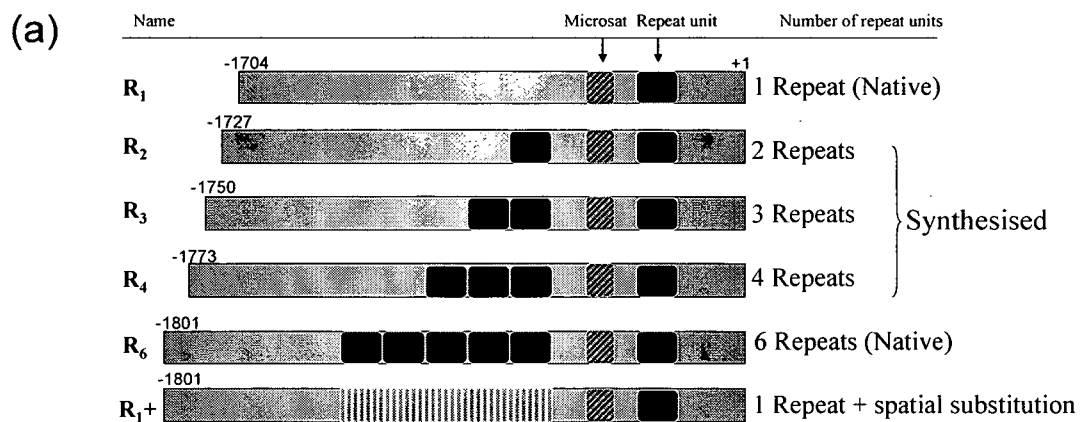
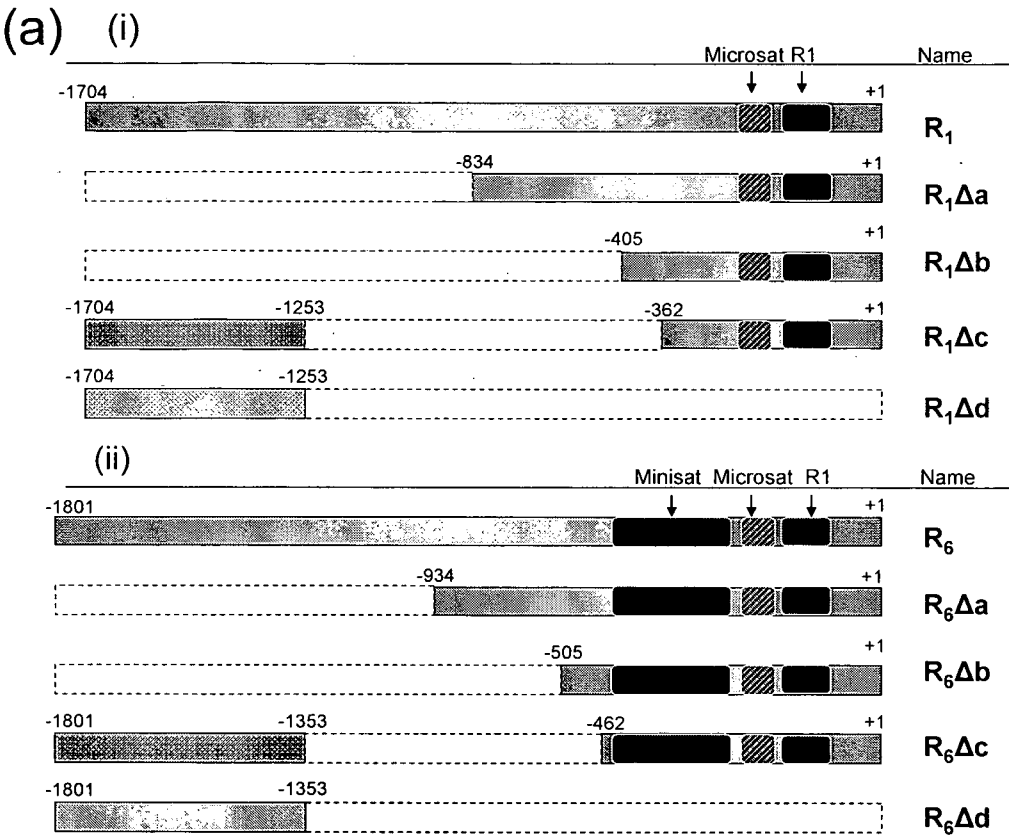
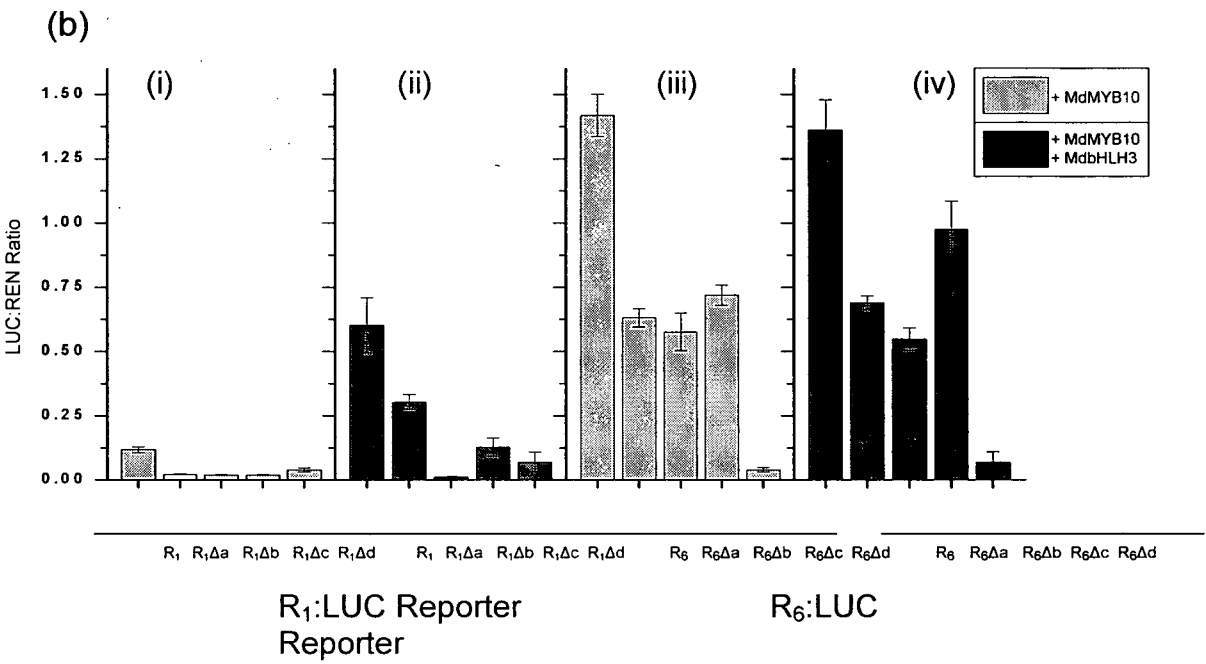


Figure 9a



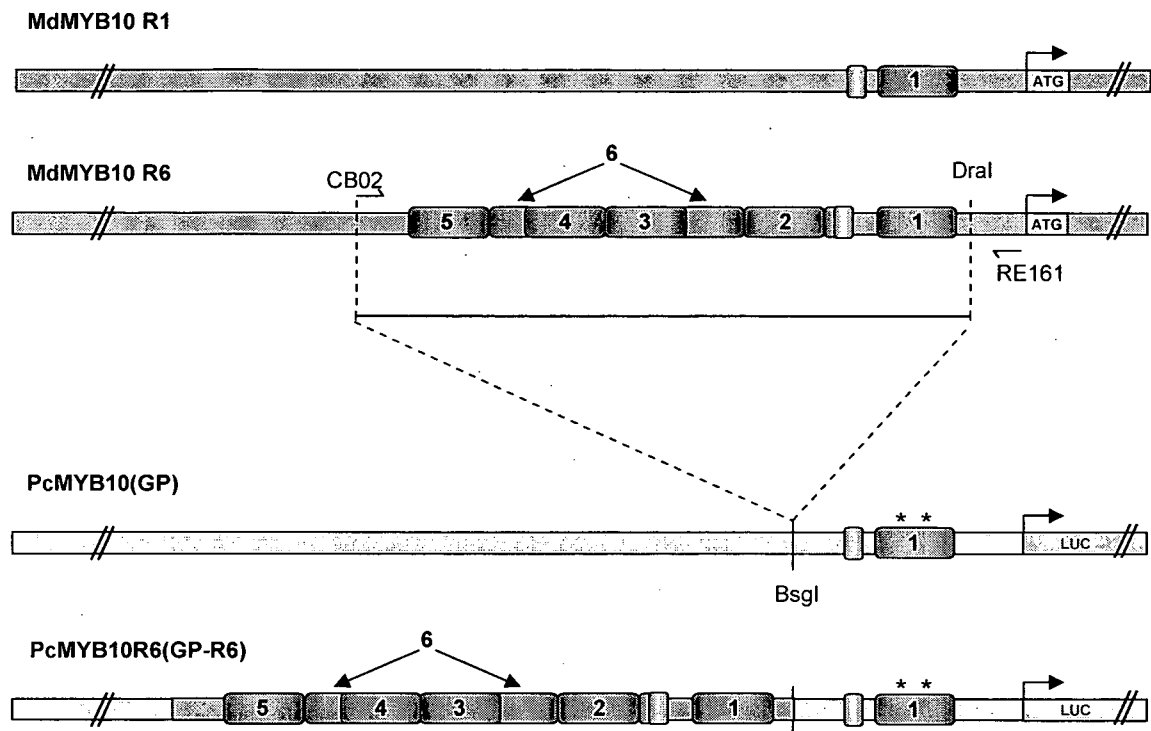
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Figure 9b



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Figure 10



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Figure 11

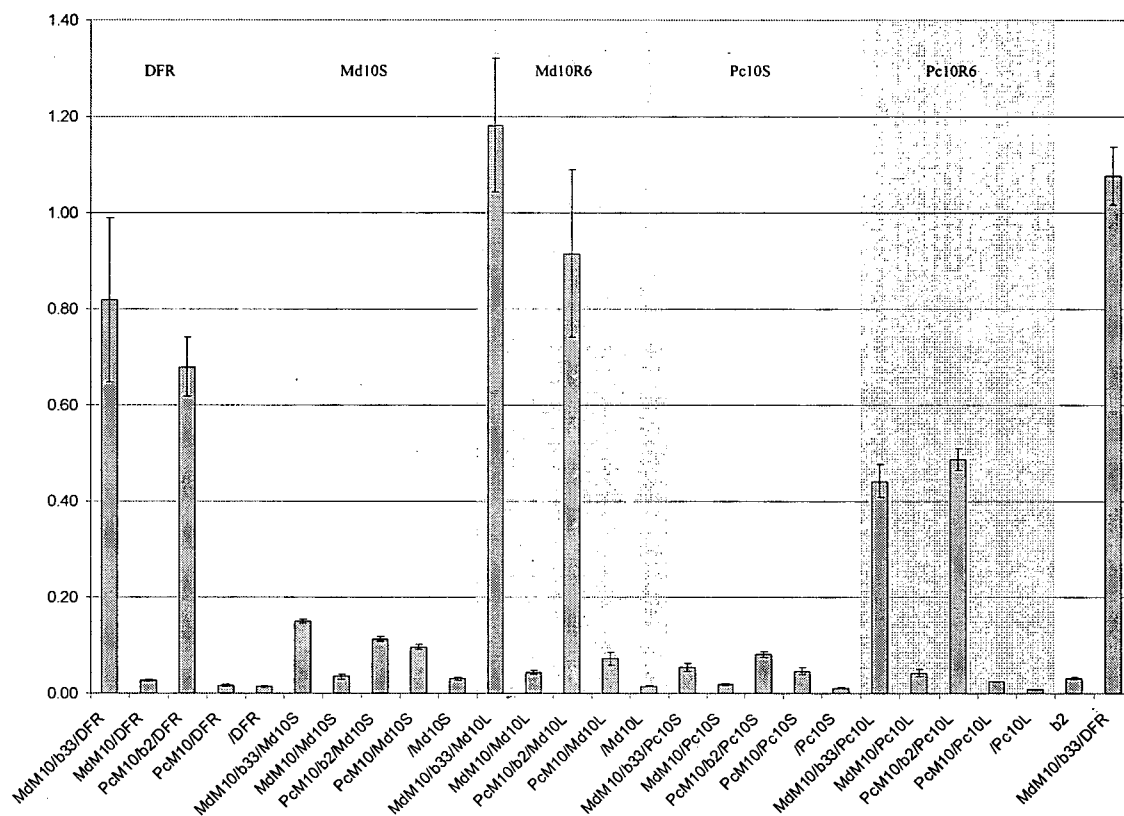


Figure 12

	1		50
GP3-3_pear_promoter	GGTGTGAGG GGGAGTGTTG AAGATCAACA CCAGCCCAAT TGGTGTGTTGT		
MdMYB10_Promoter_(short)			
	51		100
GP3-3_pear_promoter	GTTGAAGTGT AATCTTGCCT TGGCCCAAGA TGGATCGAAC CCATGGACAA		
MdMYB10_Promoter_(short)			
	101		150
GP3-3_pear_promoter	AGAAATATCC ATACACATGC TAGAAAATTC TAGCAAAGTT CAAGTTGGTG		
MdMYB10_Promoter_(short)	ATGAGCT CACCCTG...		
	151		200
GP3-3_pear_promoter	GAACAGTTTA GAA..GAATG GTGAGGAGAA GGCATCCACA ...CCATCTG		
MdMYB10_Promoter_(short)	.AACACGTGG GAACCGGCCC GTTTGTAACC GACTGAGATA GGTCCGGTTC		
	201		250
GP3-3_pear_promoter	TATCAATTAA GAAGACTAAG TGAGAGTGAG AAGTAGGAGT AGTCTTGTGA		
MdMYB10_Promoter_(short)	TATTTCTTAA AAACCC.AAC ACCCGCTATG TTCTATTTAT AAACGGGTCC		
	251		300
GP3-3_pear_promoter	GGAGTGTGAG TGGTCTAAAG TTTGTCTCTA GAAAGAGTGA GTGTCATAGC		
MdMYB10_Promoter_(short)	GGTCTG...G TCCCTCCAAC TTTGAGCCCG GCTCGACTT. GTGCCCACTC		
	301		350
GP3-3_pear_promoter	TTCAAATAGT GTCTTTGAGA GTTTGTGTGC TATAATATTT TGTGAGTTAA		
MdMYB10_Promoter_(short)	CTAAACTAAA CCATATAAAA ACCAAGAT.. ..TTCCCTTT TCTTCTTTCA		
	351		400
GP3-3_pear_promoter	TACAAGTAAT TGTTTACTTG TGTTGTCTCT CCAACACTTG TGTTAAAGTT		
MdMYB10_Promoter_(short)	CACATATCAC .GTTACTTTC CAACAACAAT TCAACAATCA CAACAAA...		
	401		450
GP3-3_pear_promoter	GTGTACTCTA AGTTTTCCCC AACATATATC ACTTCACTAA TAAAGACAAC		
MdMYB10_Promoter_(short)	...TAATCAA CCA..TCAAG ATCATATATC ACGTCACTAA TAAAGACAAC		
	451		500
GP3-3_pear_promoter	CTTCGTAAGG GTTGCCGTAG TTCTCTACTT GAAATCCAAT TATCTAGCAT		
MdMYB10_Promoter_(short)	CTTCACAAGG GTTGTCGTAG TTCTCTACTG GAAATCCAAT TGTCTAGCAT		
	501		550
GP3-3_pear_promoter	TGTAACCCTA AGTTACAGAC ACAAACATAA ACTTGAGCAA CTTCTATGCA		
MdMYB10_Promoter_(short)	TGTAACCCTA AGTTACAGAC ACAAACATAA ACTTGAGCAA CTTCTATGCA		
	551		600
GP3-3_pear_promoter	TAAGAATCTA GGGTTTCAGA CTAACCTCAAT GGAACCTAAC AAGAAATAAT		
MdMYB10_Promoter_(short)	TAAGAATCTG GGGTTTTGGA CTAACCTCAAC AGAACCTAAC AAGAAATAAT		
	601		650
GP3-3_pear_promoter	ATCC.GGACC GCT.AACGAT GCATCCAATC GAAGACAAGG TTTCGGAC.A		
MdMYB10_Promoter_(short)	ATTCTGGACC GCTTAACG.. GAATCCAA.C GAAGACAAGG TTTCGGACCA		
	651		700
GP3-3_pear_promoter	CTCAACGGAA CAAATAAGGG AAAAGGATAT AAACCACTCA ACGAAGTTCA		
MdMYB10_Promoter_(short)	CTCAACGGAA CAAATAAGGG AAAGGGATAT AAACCATTCA ACGAAATCCA		

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	701				750
GP3-3_pear_promoter	TCTCTAGAAT	ACGTATAGTC	.CCCAATACG	GATTAACCAA	GTGAGAACAT
MdMYB10_Promoter_(short)	TCTTTAGAAT	ACGCATAGTC	TCCCAATACG	GATTAACCAA	GTGAGAACAT
	751				800
GP3-3_pear_promoter	ACACCATCTA	ATAGCATGGT	CCTGCAAGAT	AGATAACTAG	GTAGGACCAC
MdMYB10_Promoter_(short)	ACGCCATCTG	ATAGCGTGGT	CCCGCAAGAC	AGATAACCAA	GTAGGACCAC
	801				850
GP3-3_pear_promoter	CGATGGTATA	ATGTGACCAA	GTAAGTAGTG	ACCCTAAATG	TAGATTAACC
MdMYB10_Promoter_(short)	CGATGGTATA	ATGTGACCAA	GTAAGCAGTG	ACCCTAAATG	TAGATTAACC
	851				900
GP3-3_pear_promoter	AAGTGGAGTT	AAATTTAGAA	TGCATATGCA	CCCTACCCCC	CCAAGACAGA
MdMYB10_Promoter_(short)	ACATGGAGTT	AAATTA...A			
	901				950
GP3-3_pear_promoter	CTAACCAGGC	AGAACCATAT	GCATTCCCCC	AATAGTGTGG	TTCCTTAATG
MdMYB10_Promoter_(short)					
	951				1000
GP3-3_pear_promoter	CAGATTGACA	AGGCGGAACC	ACCTATGAAA	ATAATGTAAC	TAGGTAGGGC
MdMYB10_Promoter_(short)	CA	AGGCTGAACC	ACCTATGAAA	ATAATGTAA.	
	1001				1050
GP3-3_pear_promoter	CCGACGAATA	TCTATTGCCT	GAAATCTTAG	GAGAGAATTC	TTGCTCTAGG
MdMYB10_Promoter_(short)		GCCT	GAAATCTTAG	GAGAGAATTC	TTGCTCTAGG
	1051				1100
GP3-3_pear_promoter	GGACAAATGA	TTTTCGTATG	CCTAAGTATT	TTTTATTTAG	TGACAGTAAA
MdMYB10_Promoter_(short)	GGACAAATGA	TTTTCGTATG	CCTAAGTGTT	TTTT...TAG	TGACAGTAAA
	1101				1150
GP3-3_pear_promoter	CTAAGATTTG	AGTACAGAGA	CATTAAGTGA	GATTGACTCT	TGTGAAAGCT
MdMYB10_Promoter_(short)	CTAAGATTTG	AGTACAGAGA	CATTAAGTGA	GATTGACTCT	TGTGAAAGCT
	1151				1200
GP3-3_pear_promoter	TAGTGAGTTG	AAGCACTTAG	GCCAATTATA	TTGAGCAATG	TGTTAGGTGT
MdMYB10_Promoter_(short)	TAGTGAGTTG	AAGCACGTAG	GCCAATTATA	TTGAGCAATG	TGTTAGGTGT
	1201				1250
GP3-3_pear_promoter	AGCGTCTAAA	CTTCCGTAGG	AGTTTTTTAC	AACAAGATAG	TGGGGGTGCC
MdMYB10_Promoter_(short)	AGCGTCTAAA	CTTCCGTAGG	AGTTTTGTAC	AGCAATATAG	TGGGGGTGCC
	1251				1300
GP3-3_pear_promoter	GCAAAATGCA	GACAGTAGCA	ATAAATTACG	GGCTAGGATT	ATCTCCCCTC
MdMYB10_Promoter_(short)	GCAAAATGCA	GACAGTAGCA	ATAAATTACG	GGCTAGGATT	TTCTCCTCTT
	1301				1350
GP3-3_pear_promoter	GTTTTTTTGT	TCCATTCCAT	CCCTTCCTCT	CACATTCTCT	ATTTTGTCTT
MdMYB10_Promoter_(short)	TTTTTTTCGT	TCCATTCCAT	CCATTCCCTCT	CACATTTTTT	ATTTTGTCTT
	1351				1400
GP3-3_pear_promoter	TCTTTTCTA	AAAAAAATTA	ATATAAGATG	TTGATATAGC	TTAACCGGGA
MdMYB10_Promoter_(short)	TCTCTTCTA	TAAAAAATTA	ATATAAGATG	TTAATGTAAC	TTGACCGTGA
	1401				1450
GP3-3_pear_promoter	CCGTTCAAAT	AAGAGGGGAA	GGAAGAAGAG	GAAAAAAGAA	AGAGAGGAAG
MdMYB10_Promoter_(short)	CTATTCAAAT	AGGAGGGGAA	TGAAGAAGAG	GGAAAAAA.	GG...
	1451				1500
GP3-3_pear_promoter	GAAGAAGAGG	AAAAAAGAGG	GGAAGAAGAG	GGAAGAAGATT	TTACTTTATA

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MdMYB10_Promoter_(short)  ....A..... .....GAGA. ....ATC CTA CTACTCCATA

                                1501                                1550
GP3-3_pear_promoter      AATTACAAGC AGACACTTTT TGTTTTTTTT TTTTTTTGAC AAGGAGAAGC
MdMYB10_Promoter_(short) AATTACAAGC AAACACTTT. ....TTTTT TTTTTTTGAC AAGCAGAAGC

                                1551                                1600
GP3-3_pear_promoter      AAACAAACAC TTGAAAAAGC AGCGAAAGCA GGCTAAAGGT ATCTTATGGT
MdMYB10_Promoter_(short) AAACAAACAC TTGAAAAAGC AGCGAAAGCA TGATAAAGGT ATCTTATGGT

                                1601                                1650
GP3-3_pear_promoter      GGTCAAAGAT GTGTGTTGTA ACTAGTTACA CGATTCTGCC TTCACATTCA
MdMYB10_Promoter_(short) GGTCAAAGAT GTGTGTTGTA ACTAGTTACA CGATTCTGCA TTCACATTCA

                                1651                                1700
GP3-3_pear_promoter      TAGAATGTGC TTTTGAATAT TATATTACAG CTAGAGAATT TGATGTCTTA
MdMYB10_Promoter_(short) TAGAATGTGC TTTTGAATAT TATATTACAG CTAGAGAATT TTATGCCCTG

                                1701                                1750
GP3-3_pear_promoter      GGA..... .....A TGTTGTCGTG CAGAAATGTC AGCTTTTCTA
MdMYB10_Promoter_(short) GGATTGATTT CCCTTGTCAA TGTTGTCGTG CAGAAATGTT AGCTTTTCTA

                                1751                                1800
GP3-3_pear_promoter      TATATAGCGT GTGTGT.... .....ATTT CACAAGTTAG ACCGGTAGCT
MdMYB10_Promoter_(short) TATATCGAGT GTGTGTGTGT GTGTGTATTT CACAAGTTAG ACTGGTAGCT

                                1801                                1850
GP3-3_pear_promoter      AATAACAACT GTTGAAATGT TTCAAACGTG TCACTGTTTG CTTCTGTGGA
MdMYB10_Promoter_(short) AATAACAACT GTTGAAATGT TTAAACTTG TCAGTGTGTTG CTTCTGTGGA

                                1851                                1900
GP3-3_pear_promoter      TATCAGACAT GCACGTCACT GGCCTTGGAA GATTAATTAG TCCGATGGTA
MdMYB10_Promoter_(short) TATCAGACAT GCACGTCACT GGCCTTGTA GATTAATTAG GCCGATGGTA

                                1901                                1950
GP3-3_pear_promoter      TCCATAGCGT TAACGTCATG GCAAACACAC TCTAAATATA TATATATATA
MdMYB10_Promoter_(short) TCCATAGCGT TAATGTCATG GCAAACACAC TCTAATTATA TAT..A....

                                1951                                2000
GP3-3_pear_promoter      TAATGGTAGC TAGGTGTCTT TCTGGAGT.. ATGAAGTGGG TAGCAGGCAA
MdMYB10_Promoter_(short) ..ATGGTAGC TAGGTGTCTT TCTGGAGTGT ATGAAGTGGG TAGCAGGCAA

                                2001                                2038
GP3-3_pear_promoter      AAGATAAGCT AAGTTTAGCT GCTAGCAGAT ACGAGATG
MdMYB10_Promoter_(short) AAGAATAGCT AAGCTTAGCT GCTAGCAGAT AAGAGATG

```

Figure 13

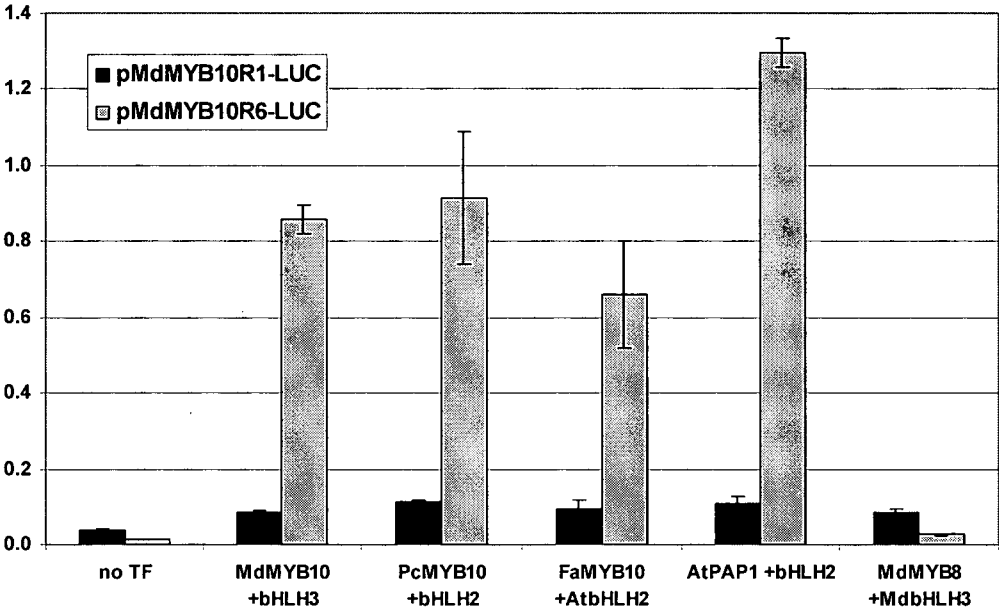


Figure 14

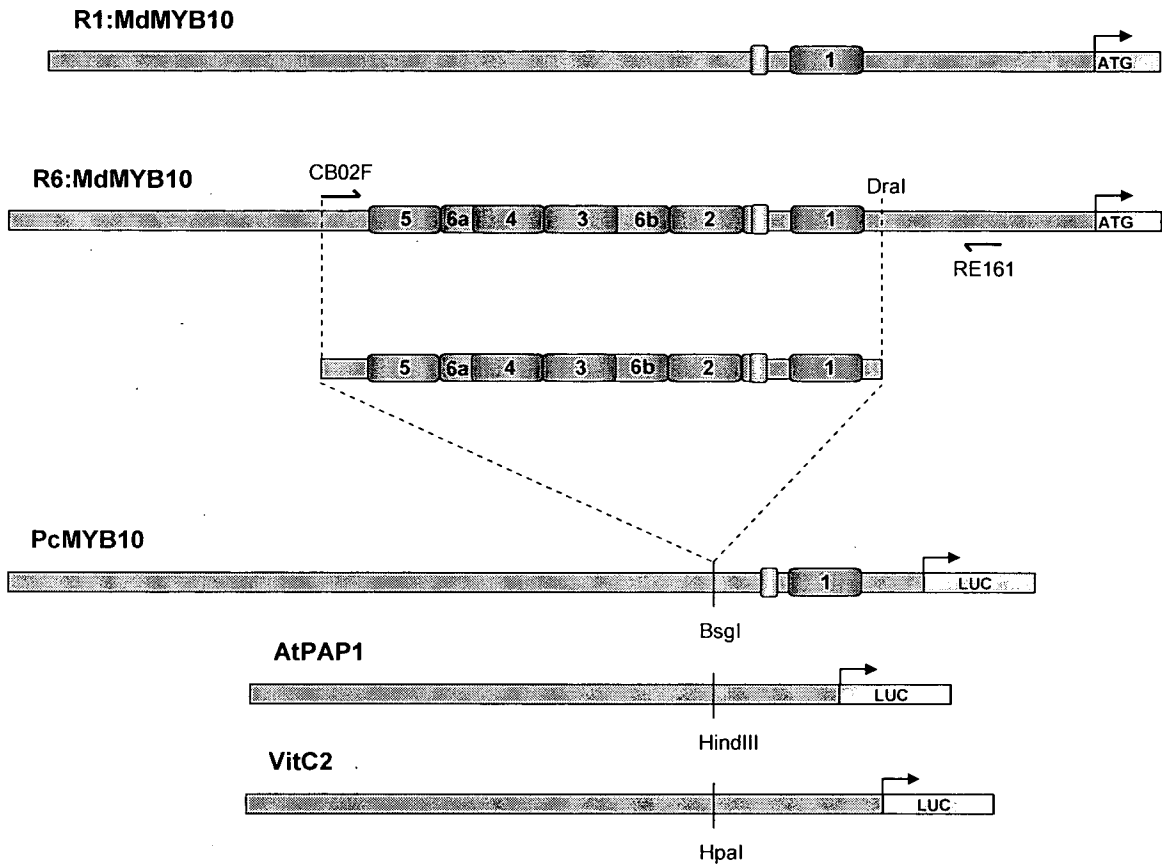


Figure 15

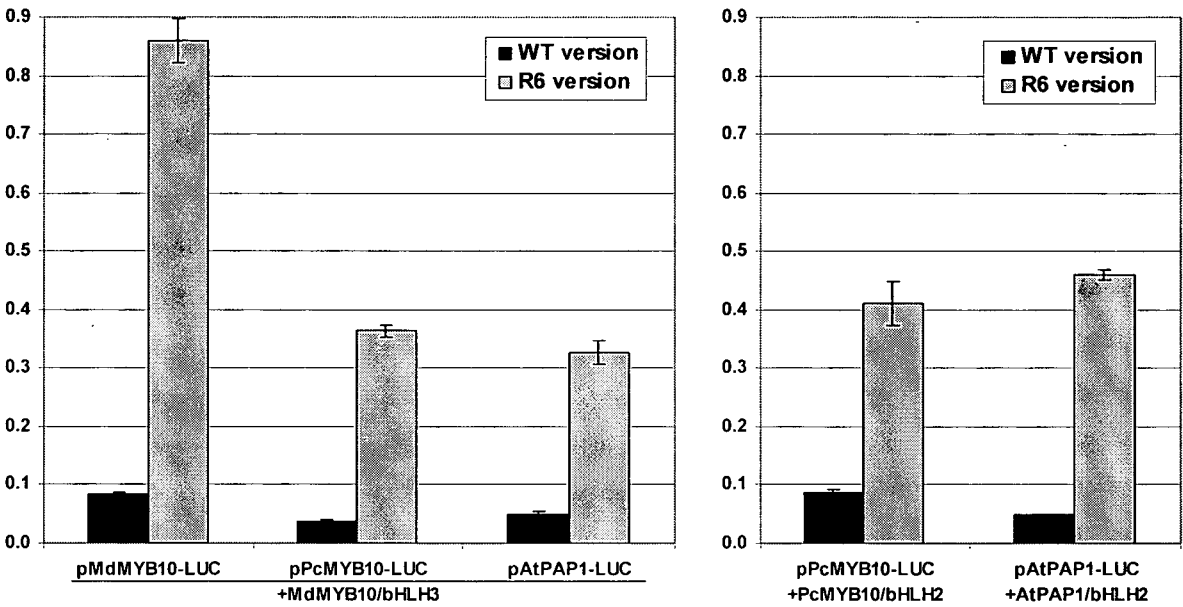


Figure 16

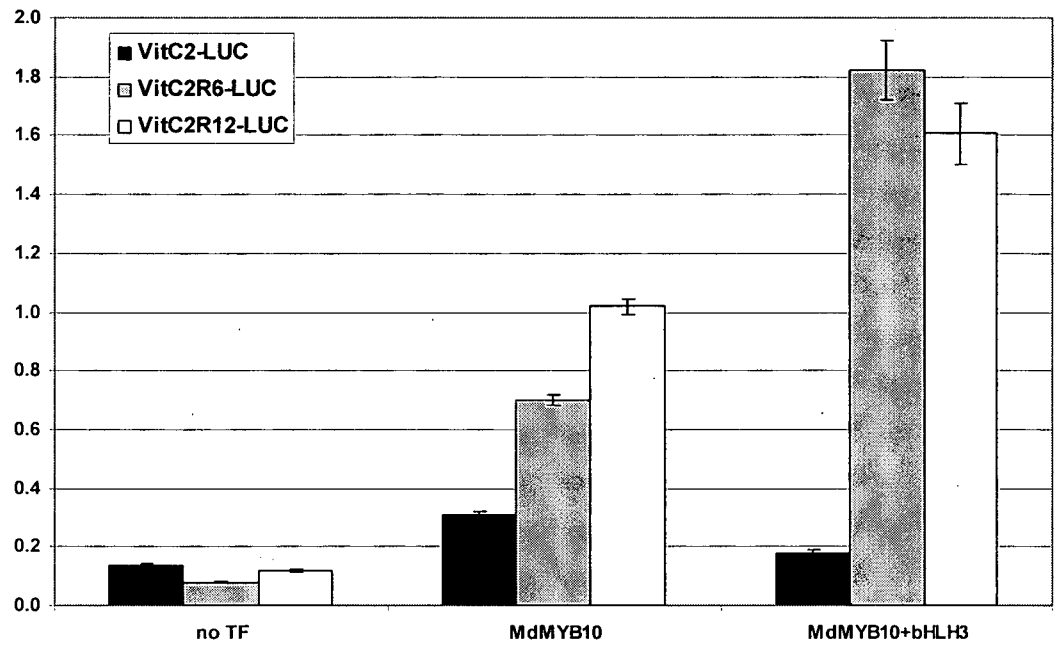
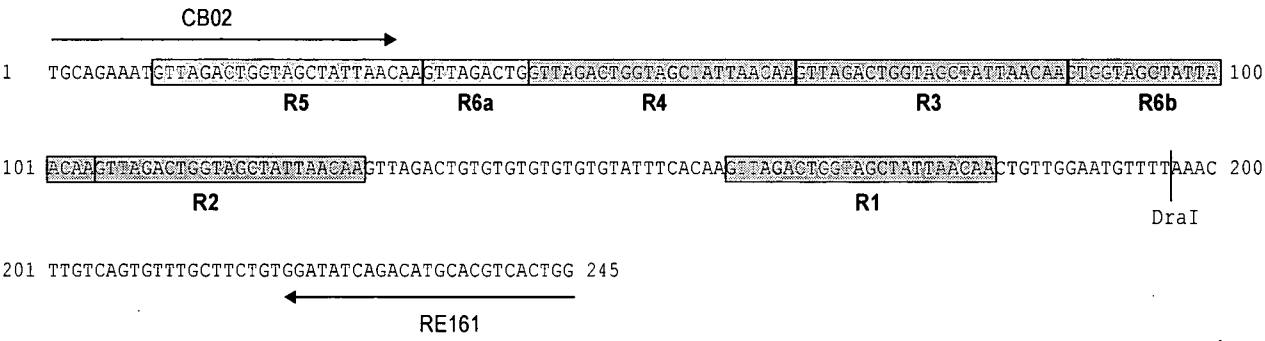


Figure 17



INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ2009/000076

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl.

C12N 15/82 (2006.01) Int. Cl.

A01H 1/00 (2006.01)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

GenomeQuest: SEQ ID NOs: 1, 11, 12, 41, 42, 13, 14, 36, 38, 15, 37, 39, and 40

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2007/0118921 A1 (Boukharov A. et al.), 24 May 2007 (see [0031], [0039], [0061], [0081], [0134], [0119]-[0122])	1-11, 16-27, 42-46, 48-53, 55-60
X	US 2007/0209085 A1 (Wu K. et al.), 6 September 2007 (see e.g. Abstract, [0144]-[0146])	1, 3-11, 16- 27, 42-46, 48- 53, 55-60
A	US 2004/0009476 A9 (Harper J.F. et al.), 15 January 2004 (see e.g. [0017], [0023], [0078], SEQ ID NO: 5311)	40-46, 48-53, 56-60
A	US 2007/0016976 A1 (Katagiri F. et al.), 18 January 2007 (see e.g. [0024], [0026], [0058], SEQ ID NO: 2241)	40-46, 48-53, 56-60

☒ Further documents are listed in the continuation of Box C☒ See patent family annex

* Special categories of cited documents:	
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"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search
30 September 2009

Date of mailing of the international search report 07 OCT 2009

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ2009/000076

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Takos A.M. et al. Light-Induced Expression of a MYB Gene Regulates Anthocyanin Biosynthesis in Red Apples. Plant Physiology, 2006, vol. 142, pp. 1216-1232 (see e.g. NCBI Accession DQ886414, DQ886415, DQ886416 entries/annotations)	32, 40-41 49-50, 56-57

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.

PCT/NZ2009/000076

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

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		US	2008072354	US	2008104730	US	2008114160
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INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.

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	WO	9945046	WO	9945047	WO	9945049	
	WO	9967414	WO	2009021041			
US	2007209085	US	2006141495				
US	2004009476	AU	86811/01	CA	2420555	EP	1313867
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		WO	0216655				
US	2007016976	NONE					
Due to data integration issues this family listing may not include 10 digit Australian applications filed since May 2001.							
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