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(54) **GENE EXPRESSION CONSTRUCT**

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(57) **ABSTRACT**

Provided are novel nucleic acid molecule encoding modified HAP1 DNA-binding domains. Also provided are novel reporter genes based on GFP and extension. The materials provided by the invention may be used in a variety of methods of activating genes having HAP1 upstream activation sequences in plants, which methods can be used to co-ordinate or investigate gene expression, optionally in conjunction with GAL4-regulated expression, and also in novel "enhancer" traps.

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Figure 1

mHAP1-A

AAGCTTGGATCCAACAATGTCCTCCGACTCGTCCAAGATCAAGAGGAAGCGGAACCGCATCC
CGCTCAGCTGCACCATCTGCCGGAAGAGGAAGGTCAAGTGGGACAAGC

mHAP1-B

TCAGGCCGCACTGCCAGCAGTGCACCAAGACCGGGGTGGCCCACCTCTGCCACTACATGGAG
CAGACCTGGGCCGAGGAGGCCGAGAAGGAGTTGCTGAAGGACAACGAGTT

mHAP1-C

GAAGAAGCTCAGGGAGCGGTGAAGTCCTTGGAGAAGACCCTCTCCAAGGTGCACTCCTCCC
CGTCGTCCAACCTCCACGGCCCCCCCCGACCGACGTCAGCCTGGGGGACGAGCTC

mHAP1-D

GGCAGTGCGGCCTGAGCTTGTGCACTTGA

mHAP1-E

TCCCTGAGCTTCTTCAACTCGTTGTCCTTC

mHAP1-5'

CGGCAAGCTTGGATCCAACAATG

mHAP1-3'

CCCGGAGCTCGTCCCCAGGCTG

Figure 2a

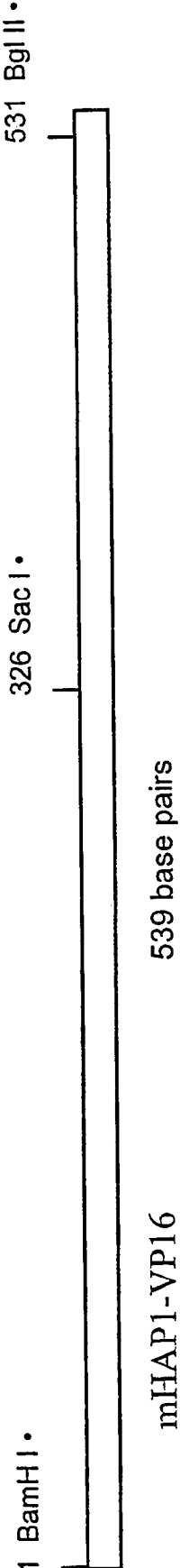


Figure 2b

<p>17/1</p> <p>atg tct tca gat tcg tcc aag atc aag agg aag cgt aac aga att ccg ctc agt tgc acc atg tcC tcC gaC tcg tcc aag atc aag agg aag cgG aac CgC atC ccg ctc agC tgc acc M S S D S S K I K R K R N R I P L S C T</p>	<p>47/11</p>	<p>HAP1 mHAP1</p>
<p>77/21</p> <p>att tgt cgg aaa agg aaa gtc aaa tgt gac aaa ctc aga cca cac tgc cag cag tgc act atC tgC cgg aaG agg aaG gtc aaG tgC gac aaG ctc agG ccG cac tgc cag cag tgc acC I C R K R K V K C D K L R P H C Q Q C T</p>	<p>107/31</p>	<p>HAP1 mHAP1</p>
<p>137/41</p> <p>aaa act ggg gta gcc cat ctc tgc cac tac atg gaa cag acc tgg gca gaa gag gca gag aaG acC ggg gtG gcc caC ctc tgc cac tac atg gaG cag acc tgg gcC gaG gag gcC gag K T G V A H L C H Y M E Q T W A E E A E</p>	<p>167/51</p>	<p>HAP1 mHAP1</p>
<p>197/61</p> <p>aaa gaa ttg ctg aag gac aac gaa tta aag aag ctt agg gag cgc gta aaa tct tta gaa aaG gaG ttg ctg aag gac aac gaG ttG aag aag ctC agg gag cgc gtG aaG tcC ttG gaG K E L L K D N E L K K L R E R V K S L E</p>	<p>227/71</p>	<p>HAP1 mHAP1</p>
<p>257/81</p> <p>aag act ctt tct aag gtg cac tct tct cct tcg tct aac tcc aag acC ctC tcC aag gtg cac tcC tcC ccG tcg tcC aac tcc K T L S K V H S S P S S N S</p>	<p>287/91</p>	<p>HAP1 mHAP1</p>

Figure 3a

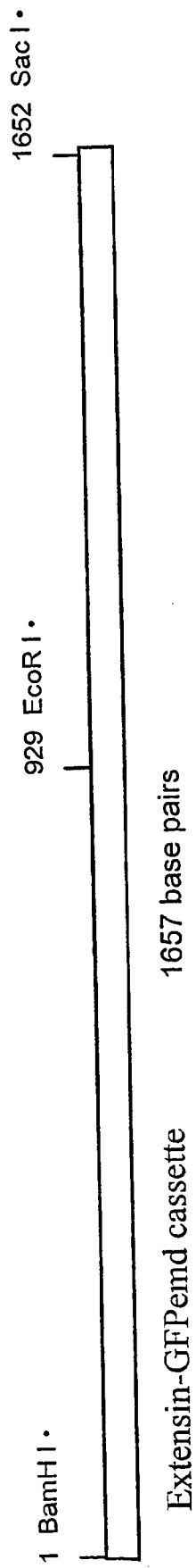


Figure 4

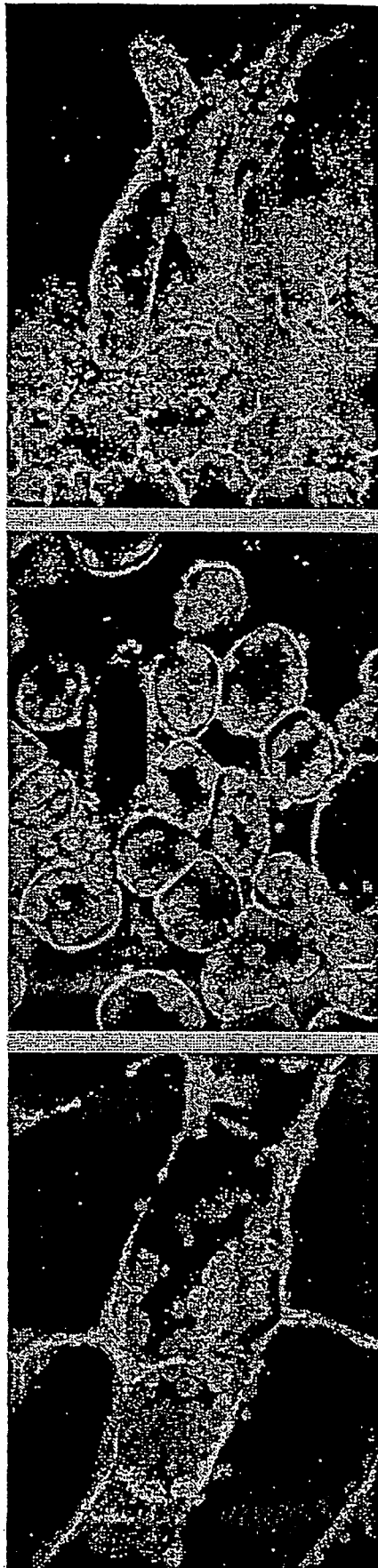
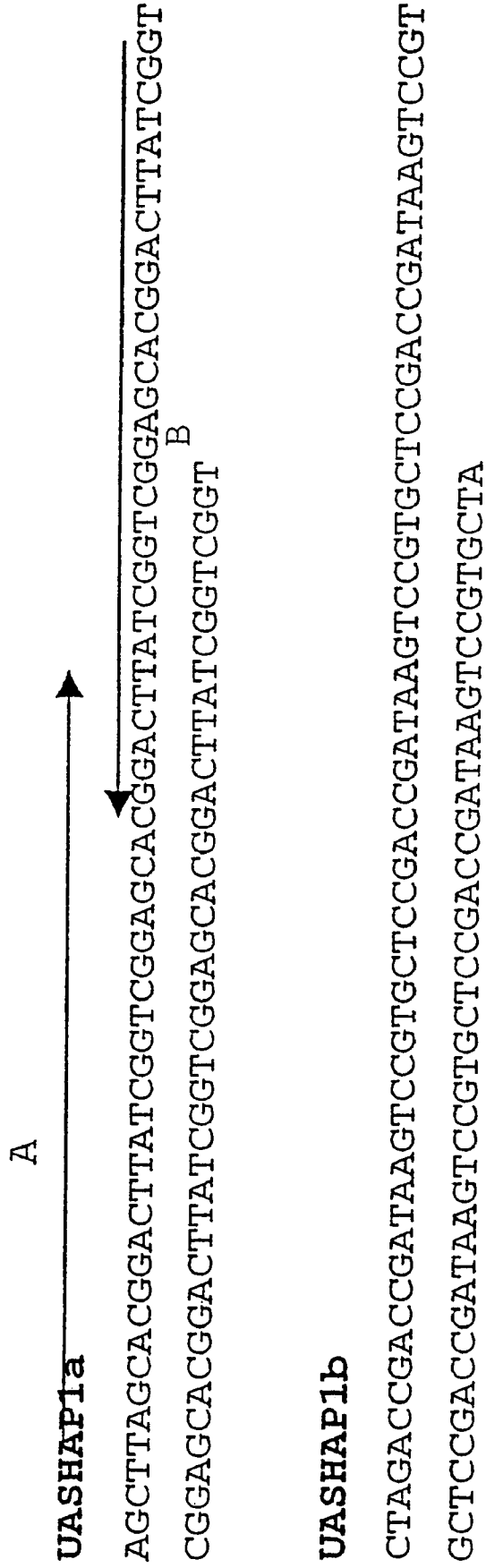


Figure 5



GENE EXPRESSION CONSTRUCT

TECHNICAL FIELD

[0001] The present invention relates generally to methods and materials for use in achieving and detecting gene expression, particularly localised expression of genes in a plant, and the detection of gene expression in a plant.

PRIOR ART

[0002] Developing multicellular tissues or organs generally demonstrate a capacity for self-organisation. For example, wounded tissues generally respond in a robust and coordinated fashion to allow repair, and local induction events can initiate prolonged and coordinated developmental processes. These types of developmental plasticity and functional autonomy are particularly evident in plant tissues. The basic features of a plant's body plan are established during embryogenesis, however its final form results from the continued growth of meristems and the formation of organs throughout its life, often in a modular and indeterminate fashion. Plant cells are constrained by rigid cell walls and are generally non-motile, so there is the clear possibility that cell fates within a meristem are determined by lineage. However, evidence from plant chimera and wounding studies have demonstrated a more important role for cell-cell interactions during fate determination (reviewed in Steeves & Sussex, *Patterns in Plant Development*, 1989) and laser ablation of cells within the *Arabidopsis* root meristem has shown that after the death of a cell, a neighbouring cell can be triggered to divide and compensate for the loss (van der Berg et al., *Nature* 378:62-65, 1995). It is likely that positional information during plant development is obtained via cell-cell contact, and that the coordination and fate of cells within a developing meristem may be determined by a network of local cellular interactions. The present inventors have chosen the *Arabidopsis* root meristem as a model system for investigating intercellular interactions. The root meristem possesses indeterminate growth and has a simple and transparent architecture. *Arabidopsis* is genetically amenable, and one can routinely generate transgenic lines for work with the intact organism.

[0003] However, in order to dissect and engineer local cell-cell interactions, it is crucial that one can (i) clearly visualise individual cells inside living meristems and (ii) have the means to perturb them. Over the past several years, the present inventors have developed a set of genetic and optical techniques which enable the manipulation and visualisation of cells within living plants.

[0004] In order to genetically manipulate cells during meristem development, the inventors have previously devised a scheme for targeted gene expression, which is based on a method widely used in *Drosophila* (Brand and Perrimon, *Development* 118:401-415, 1993). PCT/GB97/00406 describes a method using a highly modified transcription factor derived from the yeast GAL4 protein to form *Arabidopsis* plant lines that display localised expression of the foreign transcription factor, which can be used to trigger the ectopic expression of any other chosen gene at a particular time and place during the growth of the plant. The expression of the transcription factor can be followed using GFP as a reporter gene.

[0005] However, this system has a number of problems, one of which that it is limited in its application to the

activation of a single chosen gene or the simultaneous activation of different genes within the same cell types, but does not allow the activation of different genes in different cell types and/or at different times within the same plant.

[0006] Thus it can be seen that another modified transcription factor which could be used in conjunction with or as an alternative to GAL4 would provide a valuable contribution to the art.

[0007] In order to visualise plant cells in transgenic plants, the gene encoding jellyfish green fluorescent protein (GFP) has been adapted for use as a reporter gene. The wild-type GFP cDNA is not expressed in *Arabidopsis*. The present inventors have extensively modified the *gfp* gene to remove a cryptic intron, to introduce mutations that confer improved folding and spectral properties and to alter the subcellular localisation of the protein. All of these alterations have been incorporated into a single modified form of the gene (*mgfp5-ER*) which can be routinely used for monitoring gene expression and marking cells in live transgenic plants (Siemering et al., *Current Biology* 6:1653-1663, 1996; Haseloff et al., *PNAS* 94:2122-2127, 1997).

[0008] Fluorescence microscopy techniques for high resolution observation of living cells have been developed. The expression of GFP within an organism produces an intrinsic fluorescence that colours normal cellular processes, and high resolution optical techniques can be used non-invasively to monitor the dynamic activities of these living cells. Using coverslip-based culture vessels, specialised microscope objectives and the optical sectioning properties of the confocal microscope, it is possible to monitor simply and precisely both the arrangement of living cells within a meristem, and their behaviour through long time-lapse observations. Further, the present inventors have recently constructed cyan and yellow emitting GFP variants that can be distinguished from the green fluorescent protein during confocal microscopy. These colour variants have enabled simultaneous imaging of different tagged proteins in living cells (Haseloff, J., "GFP variants for multispectral imaging of living cells", in *Methods in Cell Biology*, Vol. 58, Kay, S. and Sullivan, K. Eds. Academic Press (1999).

[0009] However, the usefulness of reporter proteins such as GFP is limited by the fact that, when plant tissues are cleared and stained for detailed 3-Dimensional analysis, reporter proteins such as GFP are lost from the tissues.

[0010] Thus it can be seen that a robust insoluble reporter protein would provide a valuable contribution to the art.

DISCLOSURE OF THE INVENTION

[0011] In a first aspect of the present invention there is provided an isolated nucleic acid, expressible in a plant cell, encoding at least an effective portion of a HAP1 DNA-binding domain, wherein the sequence has an A/T base content substantially reduced compared to the wild-type sequence.

[0012] "Effective Portion"

[0013] An effective portion of the DNA-binding domain is a portion sufficient to retain most (i.e. over 50%) of the DNA-binding activity of the full length DNA-binding domain. Preferably the "effective portion" comprises amino acid residues 1 to 94 of the yeast polypeptide, which we have

found to be the minimal amount required to retain DNA binding activity. Typically, the “effective portion” will comprise at least 60% of the full-length sequence of the DNA-binding domain.

[0014] “A/T Base Content”

[0015] The A/T content of the wild-type yeast sequence encoding the DNA-binding domain of HAP1 is about 54%. The % A/T base content of the sequence of the invention encoding the effective portion of the HAP1 should be taken to be substantially reduced when it is less than 45%. Preferably, it will be less than 40%, most preferably it is 39%.

[0016] Preferably, the encoded polypeptide will have the identical amino acid sequence to the wild-type HAP1 polypeptide shown in **FIG. 2b** (bottom line). However, on the other hand, the encoded polypeptide may comprise an amino acid sequence which differs by one or more amino acid residues from the amino acid sequence shown in **FIG. 2b** (bottom line).

[0017] Nucleic acid encoding at least an effective portion of a HAP1 DNA-binding domain which is an amino acid sequence mutant, variant or derivative of the amino acid sequence shown in **FIG. 2b**, wherein the nucleic acid sequence has an A/T base content substantially reduced compared to the wild-type sequence is therefore included within the scope of the present invention.

[0018] A peptide which is an amino acid sequence variant, derivative or mutant of an amino acid sequence of a peptide may comprise an amino acid sequence which shares greater than about 60% sequence identity with the sequence of the amino acid sequence shown in **FIG. 2b** (bottom line), greater than about 70%, greater than about 80%, greater than about 90% or greater than about 95%. The sequence may share greater than about 70% similarity, greater than about 80% similarity, greater than about 90% similarity or greater than about 95% similarity with the amino acid sequence shown in **FIG. 2b** (bottom line).

[0019] For amino acid “homology”, this may be understood to be similarity (according to the established principles of amino acid similarity, e.g. as determined using the algorithm GAP (as described below) or identity).

[0020] Amino acid similarity is generally defined with reference to the algorithm GAP (Genetics Computer Group, Madison, Wis.). GAP uses the Needleman and Wunsch algorithm to align two complete sequences that maximizes the number of matches and minimizes the number of gaps. Generally, the default parameters are used, with a gap creation penalty=12 and gap extension penalty=4. Use of GAP may be preferred but other algorithms may be used, e.g. BLAST (which uses the method of Altschul et al. (1990) J. Mol. Biol. 215: 405-410), FASTA (which uses the method of Pearson and Lipman (1988) PNAS USA 85: 2444-2448), or the Smith-Waterman algorithm (Smith and Waterman (1981) J. Mol. Biol. 147: 195-197), generally employing default parameters.

[0021] Similarity allows for “conservative variation”, i.e. substitution of one hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as arginine for lysine, glutamic for aspartic acid, or glutamine for asparagine.

[0022] In a preferred embodiment, the nucleic acid of the invention comprises the nucleic acid sequence of modified HAP1 (labelled mHAP1—middle line of **FIG. 2b**), which sequence has a substantially reduced A/T content relative to the wild-type yeast sequence which is shown in the top line of **FIG. 2b**, labelled HAP1 (substantially reduced base content is defined above).

[0023] In a preferred embodiment, the nucleic acid encoding the portion of HAP1 binding domain is fused to a nucleic acid sequence, said sequence being structural (e.g. encoding functional polypeptides) and/or regulatory. Preferably, said sequence encodes a transcriptional activator. The transcriptional activator may be the activation domain of the HAP1 protein, in which case the sequence encoding the HAP1 transcriptional activator should be optimised for expression in plants, by, for example, reducing the A/T content thereof. Alternatively, the transcriptional activator may be any transcriptional activator known by the skilled person to be active in plants. In such cases, the sequence of the invention thus encodes a chimeric polypeptide. In a preferred embodiment, the transcriptional activator domain is that of the herpes simplex virus (HSV) VP-16 (Greaves and O’Hare, J. Virol 63 1641-1650, (1989)). Preferably, the sequence comprises the nucleic acid sequence of VP16 shown in **FIG. 2c** (from nucleotide 293 onwards, i.e., the part of the top line of sequence which is in upper case). Thus in a preferred embodiment of the invention, there is provided a chimeric polypeptide comprising the nucleic acid sequence of the mHAP1-VPI6 chimera shown in **FIG. 2c** (i.e., the entire nucleotide sequence of **FIG. 2c** (top line)).

[0024] Other suitable transcriptional activation domains include certain peptides encoded by the *E. coli* genomic DNA fragments (Ma and Ptashne, Cell 51 113-119 (1987)) or synthetic peptides designed to form amphiphilic α -helix. (Giniger and Ptashne Nature 330 670-672 (1987)). A common requirement for suitable transcriptional activation domains is the need for excess charge (Gill and Ptashne, Cell 51 113-119 (1987), Estruch et al Nucl. Acids Res. 22 3983-3989 (1994)). Using this criteria, the skilled person is able to select or synthesise sequences which encode transcriptional activation activity in plants.

[0025] In a further aspect of the present invention, there is provided a nucleic acid construct, comprising the nucleic acid defined above.

[0026] Preferred Vectors

[0027] In one aspect of the present invention, the nucleic acid construct is in the form of a recombinant and preferably replicable vector. “Vector” is defined to include, inter alia, any plasmid, cosmid, phage or *Agrobacterium* binary vector in double or single stranded linear or circular form which may or may not be self transmissible or mobilizable, and which can transform a prokaryotic or eukaryotic host either by integration into the cellular genome or exist extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication).

[0028] Generally speaking, those skilled in the art are well able to construct vectors and design protocols for recombinant gene expression. Suitable vectors can be chosen or constructed, containing appropriate regulatory sequences, including promoter sequences, terminator fragments, polyadenylation sequences, enhancer sequences, marker genes

and other sequences as appropriate. For further details see, for example, *Molecular Cloning: a Laboratory Manual*: 2nd edition, Sambrook et al, 1989, Cold Spring Harbor Laboratory Press or *Current Protocols in Molecular Biology*, Second Edition, Ausubel et al. eds., John Wiley & Sons, 1992.

[0029] A vector including nucleic acid according to the present invention need not include a promoter or other regulatory sequence, particularly if the vector is to be used to introduce the nucleic acid into cells for recombination into the genome.

[0030] Preferably the nucleic acid in the vector is under the control of, and operably linked to, an appropriate promoter or other regulatory elements for transcription in a host cell such as a microbial, e.g. bacterial, or plant cell. The vector may be a bi-functional expression vector which functions in multiple hosts. In the case of genomic DNA, this may contain its own promoter or other regulatory elements and in the case of cDNA this may be under the control of an appropriate promoter or other regulatory elements for expression in the host cell.

[0031] By "promoter" is meant a sequence of nucleotides from which transcription may be initiated of DNA operably linked downstream (i.e. in the 3' direction on the sense strand of double-stranded DNA).

[0032] "Operably linked" means joined as part of the same nucleic acid molecule, suitably positioned and oriented for transcription to be initiated from the promoter. DNA operably linked to a promoter is "under transcriptional initiation regulation" of the promoter.

[0033] Thus this aspect of the invention provides a gene construct, preferably a replicable vector, comprising a promoter operably linked to a nucleic acid provided by the present invention, for example, the sequence encoding the HAP1 DNA-binding domain.

[0034] Particularly of interest in the present context are nucleic acid constructs which operate as plant vectors. Specific procedures and vectors previously used with wide success upon plants are described by Guerinéau and Mullineaux (1993) (*Plant transformation and expression vectors*. In: *Plant Molecular Biology Labfax* (Croy R R D ed) Oxford, BIOS Scientific Publishers, pp 121-148). Suitable vectors may include plant viral-derived vectors (see e.g. EP-A-194809).

[0035] Preferred Promoters

[0036] Preferably the promoter to be used in the construct is an "enhancer dependent" (or naïve) promoter, which requires the presence of a suitable enhancer sequence and appropriate transcription factors to cause substantial levels of transcription. Such naïve promoters correspond to the TATA box region of known plant promoters. "Plant promoters" should be understood to refer to promoters (e.g. viral or bacterial) active in a plant cell. The naïve promoter is in competent relationship with the sequence encoding the HAP1 DNA binding domain and transcription activation domain such that if the promoter is inserted into a plant host cell genome in functional relationship with an enhancer sequence and required transcription factors, the promoter will direct expression of the HAP1 DNA-binding domain in a tissue specific manner.

[0037] Reporter Genes

[0038] In preferred embodiments of the invention, a reporter gene operably linked to a HAP1 upstream activation sequence (UAS) is provided, such that the reporter gene will be expressed in response to synthesis of the transcriptional activator discussed above. The reporter gene may be present as part of a nucleic acid construct comprising the nucleic acid encoding an effective portion of a HAP1 DNA-binding domain. Alternatively, the reporter gene may be present in another nucleic acid construct.

[0039] The reporter gene may be any suitable reporter gene known to the skilled person as being active in plants. Use of a reporter gene facilitates determination of the UAS activity by reference to protein production. The reporter gene preferably encodes an enzyme which catalyses a reaction which produces a detectable signal, preferably a visually detectable signal, such as a coloured product. Many examples are known, including β -galactosidase and luciferase. β -galactosidase activity may be assayed by production of blue colour on substrate, the assay being by eye or by use of a spectro-photometer to measure absorbance. Fluorescence, for example that produced as a result of luciferase activity, may be quantitated using a spectrophotometer. Radioactive assays may be used, for instance using chloramphenicol acetyltransferase, which may also be used in non-radioactive assays. The presence and/or amount of gene product resulting from expression from the reporter gene may be determined using a molecule able to bind the product, such as an antibody or fragment thereof. The binding molecule may be labelled directly or indirectly using any standard technique.

[0040] Those skilled in the art are well aware of a multitude of possible reporter genes and assay techniques which may be used to determine UAS activity. Any suitable reporter/assay may be used and it should be appreciated that no particular choice is essential to or a limitation of the present invention.

[0041] In preferred embodiments of the invention, the reporter gene is GFP. The *gfp* gene may be the wild-type *Aequorea victoria* gene, or may be modified in any conventional way. For example, in a preferred embodiment, the *gfp* gene is *mgfp5-ER*, which has a cryptic intron removed, and has mutations which confer improved folding and spectral properties and altered subcellular localisation of the protein (Siemering et al., *Current Biology* 6:1653-1663, 1996; Haseloff et al., *PNAS* 94:2122-2127, 1997).

[0042] However, although GFP (wild-type and modified forms) provides a convenient method of marking cells, clearing and staining of plant tissues normally result in loss of the green fluorescent protein from the tissues. For example, after treatment with even gentle clearing agents such as 50% ethanol or 50% glycerol, the protein becomes dislodged from treated cells.

[0043] The present inventors have overcome this problem by developing a new robust surface marker for visualisation of plant cells utilising GFP fused to an extensin protein (see below). Thus, in preferred embodiments of the invention, the reporter gene comprises the GFP extensin reporter gene fusion as described below.

[0044] Host Plants

[0045] In a further aspect of the invention, the invention provides a plant, plantlet or part thereof (e.g. a plant host cell or cell line) comprising a nucleic acid construct of the invention.

[0046] In preferred embodiments, the construct will have become stably integrated into a plant cell genome. In particular, the invention provides a plurality of plants, plantlets or parts thereof comprising a library, each plant or part thereof comprising a stably maintained nucleic acid sequence encoding an effective portion of the HAP1 DNA-binding domain as defined above. Preferably, the nucleic acid construct will be incorporated into the genome of plant cells present in the library. The library may be of any plant of interest to the skilled person. Suitable plants include maize, rice, tobacco, petunia, carrot, potato and *Arabidopsis*. Where the term “plant” is referred to hereinafter, unless context demands otherwise, it will be understood that the invention applies also to plantlets or parts of plants.

[0047] Each plant, plantlet or part thereof may have a particular pattern of expression of the integrated reporter gene. Thus, introduction of a further gene, having a HAP1-responsive UAS into the cells will result in the expression of the introduced gene in the same temporal/spatial pattern as the reporter gene, enabling expression of a gene of interest in selected tissues and/or at selected times.

[0048] Uses of Constructs of the Invention

[0049] In a preferred embodiment of the invention, the nucleic acid construct can be used in an “enhancer trap assay” to identify plant enhancer sequences (Sundaresan et al, *Genes and Dev.* 9 1797-1810). In such cases, the nucleic acid construct will preferably comprise right and left Ti-DNA, to enable random, stable insertion into the genome of a plant host cell.

[0050] As well as nucleic acid constructs for use in “enhancer trap assays”, the invention further provides a method of identifying a plant “enhancer” nucleic acid sequence, comprising the steps of:

[0051] transforming a plant cell host with a nucleic acid construct comprising a naïve promoter sequence and a sequence encoding an effective portion of an HAP1 binding domain fused to a transcription activating domain, under the control of said naïve promoter sequence,

[0052] wherein, when said plant is transformed with said construct such that the promoter is in functional relationship with a host cell enhancer sequence, the promoter will direct expression of said HAP1 binding domain operably linked to a transcription activating domain in the presence of “enhancer” transcription factors.

[0053] Thus the expression of said HAP1 binding domain operably linked to a transcription activating domain will indicate the presence of such an “enhancer” sequence. Optionally, the method includes the further step of identifying the position and nucleic acid sequence of the enhancer sequence.

[0054] For example, this may be performed by standard inverse PCR (I-PCR) or TAIL-PCR amplification of flank-

ing sequences (see Sambrook & Russell, *Molecular Cloning: a laboratory manual*. 3rd edition, CSHL press 2001: sections 4.75 (TAIL-PCR), 8-81 (I-PCR)).

[0055] The nucleic acid construct of the invention may thus also be used to control expression of an heterologous gene in a plant or part thereof. Thus in a further aspect of the present invention, there is provided a method of controlling expression of a gene of interest in a plant or part thereof comprising the steps of:

[0056] introducing the gene of interest into a plant or part thereof, said gene of interest having an HAP1 responsive upstream activation sequence,

[0057] said plant or part thereof comprising a nucleic acid sequence encoding an effective portion of an HAP1 binding domain fused to a transcription activating domain, under the control of said naïve promoter such that expression of a transcriptional activator from said sequence is limited to those cell types in which a naïve promoter sequence is in functional relationship with a host cell enhancer sequence;

[0058] wherein binding of said transcriptional activator to said upstream activator sequence causes transcriptional activation of the gene of interest.

[0059] The nucleic acid of the invention enables the activation of different genes of interest in different cell types and/or at different times within the same plant, particularly wherein the nucleic acid encoding at least an effective portion of a HAP1 DNA-binding domain is used in conjunction with nucleic acid encoding a modified GAL4 transcription factor, for example that described in WO97/30164, the expression of each gene of interest being under the operable control of a different transcription factor.

[0060] Thus, included within the scope of the present invention is a method of independently controlling expression of a first and a second gene of interest in a plant comprising the steps of:

[0061] introducing the first gene of interest into a plant or part thereof, said first gene of interest having an HAP1 responsive upstream activation sequence;

[0062] introducing the second gene of interest into a plant or part thereof, said second gene of interest having a GAL4 responsive upstream activation sequence;

[0063] said plant or part thereof comprising a first nucleic acid sequence, which encodes a HAP1 transcriptional activator and a second nucleic acid sequence, which encodes a GAL4 transcriptional activator;

[0064] wherein binding of said HAP1 transcriptional activator to said upstream activator sequence causes transcriptional activation of the first gene of interest and binding of said GAL4 transcriptional activator to said upstream activator sequence causes transcriptional activation of the second gene of interest.

[0065] In this way, where the expression of the HAP1 transcriptional activator and the GAL4 transcriptional activator are each independently under the control of a different naïve promoter sequence, expression of each transcriptional

activator is limited to those cell types in which the naïve promoter sequence is in functional relationship with a host cell enhancer sequence.

[0066] Moreover, using the nucleic acid construct of the invention, the simultaneous expression of a number of genes of interest may be controlled. Thus, in a further aspect of the invention, there is provided a method of co-ordinating the expression of a plurality of genes of interest in a plant or part thereof, comprising the steps of introducing the genes of interest into a plant or part thereof,

[0067] said genes of interest each being under the control of an HAP1 responsive upstream activation sequence and said plant or part thereof comprising a nucleic acid sequence of the invention capable of expressing an HAP1 transcriptional activator,

[0068] wherein binding of said HAP1 transcriptional activator to said upstream activator sequence causes transcriptional activation of the genes of interest.

[0069] The plurality of genes may all be associated with a single UAS, which facilitates their introduction into the plant or part thereof. Alternatively, one or more genes may be operably linked to a respective UAS.

[0070] Using the nucleic acid construct of the invention in conjunction with a nucleic acid construct encoding a GAL4 transcriptional activator, the expression of a first group of genes may be coordinated and the expression of a second group of genes may be co-ordinated, wherein each group of genes is expressed in different cell-types and/or at different times.

[0071] The gene or genes of interest may be any target gene or genes, the expression of which the researcher wishes to study. In preferred embodiments, the gene or genes of interest may be developmental genes or may encode one or more toxins. For example, a gene of interest may encode a toxin such as the A-chain of diphtheria toxin (DTA) and thus the method may be used to kill specific cells, for example, within the root meristem. Other genes of interest may encode one or more cell cycle regulatory proteins, in which case expression of such gene or genes may be used to drive misexpression of such proteins and activate or inhibit particular cell divisions e.g. within the root meristem. The gene or genes of interest may encode homeodomain proteins and thus the effect of their ectopic expression on cell fate determination may be studied.

[0072] The gene of interest may be of unknown function. Using the methods of the invention, the function of a gene of interest may be determined by comparing the phenotype of plants, or parts thereof in which the gene of interest is expressed with the phenotype of plants or parts thereof in which it is not expressed. Thus the invention extends to a method of determining the function of a gene of interest comprising the steps of:

[0073] introducing a gene of interest into a plant or part thereof, said gene of interest having an HAP1 responsive upstream activation sequence;

[0074] said plant or part thereof comprising a nucleic acid sequence, which encodes a HAP1 transcriptional activator;

[0075] wherein binding of said HAP1 transcriptional activator to said upstream activator sequence causes transcriptional activation of the gene of interest;

[0076] comparing the phenotype of said plant or part thereof in which said gene of interest is expressed with a second plant or part thereof in which said gene of interest is not expressed.

[0077] The gene or genes of interest may be “introduced” into the plant or part thereof using any conventional technique, for example, using any one of the vectors described above. Conveniently, the gene of interest is introduced using *Agrobacterium* mediated transformation.

[0078] In preferred embodiments of the methods of the invention, a reporter gene having an HAP1 responsive upstream activation sequence is provided, such that binding of said transcriptional activator to said upstream activator sequence causes transcriptional activation of the reporter gene. The reporter gene may be any suitable reporter gene, details of which are given above. Preferably, the reporter gene will be the extensin-GFP fusion gene described below.

[0079] Extensin-GFP Reporter Gene Construct

[0080] As described above, conventional cell markers utilising GFP suffer from the disadvantage that, during clearing of the tissues, the GFP is often lost to at least some degree. The present inventors have overcome this problem by developing a new robust surface marker for visualisation of plant cells utilising GFP.

[0081] This aspect of the invention is based on the inventors’ demonstration that, when a coding sequence encoding GFP is fused to the coding sequence of the carrot extensin gene, the resulting expressed extensin-GFP fusion protein results in a bright marker resistant to clearing techniques which normally result in complete loss of GFP from treated tissues. Thus in a preferred embodiment of the present invention, the reporter gene construct is an extensin-GFP reporter gene.

[0082] Indeed the extensin-GFP reporter gene fusion forms a separate aspect of the present invention. Thus, this aspect of the present invention provides a gene fusion, expressible in a plant cell, comprising a nucleic acid sequence encoding a green fluorescent protein operably linked to a nucleic acid sequence encoding at least an effective portion of extensin.

[0083] An effective portion of extensin is a portion sufficient to retain most (i.e. over 50%) of the activity of the full length carrot extensin. Typically, the “effective portion” will comprise at least 60% of the full-length sequence of the carrot extensin. Wild-type extensin is involved in cell wall expansion in plants, other cell wall expansion proteins may be used, as would be understood by the person skilled in the art.

[0084] In a preferred embodiment, the nucleic acid sequence encoding the green fluorescent protein is the nucleic acid sequence of GFP shown in FIG. 3b (uppercase nucleic acid sequence) and/or the nucleic acid sequence encoding the extensin protein is the nucleic acid sequence of extensin shown in FIG. 3b (lowercase amino acid sequence). The gene fusion preferably comprises the a nucleic acid molecule having the entire sequence shown in FIG. 3b.

[0085] In one aspect of the present invention, the gene fusion is in the form of a recombinant and preferably

replicable vector. Details of suitable vectors are those described above for the nucleic acid construct of the invention.

[0086] The extensin-GFP gene fusion is preferably part of a construct in which it is in operable relationship with an upstream activation sequence or promoter, the activation of which by an activation domain of a transcription factor causes expression of the extensin-GFP gene fusion.

[0087] In a further aspect of the invention, the invention provides a plant, plantlet or part thereof (e.g. a plant host cell or cell line) comprising the extensin-GFP gene fusion of the invention. In preferred embodiments, the extensin-GFP gene fusion will have become stably integrated into a plant cell genome.

[0088] Uses of Extensin-GFP Gene Fusion and Fusion Protein

[0089] The extensin-GFP gene fusion may be used in any of the applications for which a reporter gene may be routinely used, including those described above for "Reporter Genes".

[0090] In particular, the extensin-GFP gene fusion may be used to visualise specific patterns of cell-wall-localised expression in assays and methods as described herein.

[0091] Thus, for example, the invention provides the use of the extensin-GFP gene fusion of the invention in an enhancer trap assay. In a preferred embodiment, the "enhancer trap" assay is the "enhancer trap" assay described above. In such an assay, the extensin-GFP gene fusion is in operable relationship with an upstream activation sequence or promoter, the activation of which by an activation domain of an HAP1 binding domain operably linked to a transcription activating domain causes expression of the extensin-GFP gene fusion and thus enables the visualisation of expression of the HAP1 transcription factor.

[0092] Further included within the scope of the invention is the use of the extensin-GFP gene fusion in a method of cell sorting including the step of screening plants, plantlets, parts or cells thereof for extensin-GFP expression and selecting those plants, plantlets, parts or cells thereof which express GFP-extensin-GFP.

[0093] The cells expressing the extensin-GFP protein may be isolated using methods known to the skilled person, e.g. using antibody based sorting methods. For example, to isolate cell-types expressing extensin-GFP protein in a plant, e.g. *Arabidopsis*, from those not expressing the extensin-GFP protein, tissues from the transgenic plant may be treated with one or more enzymes e.g. pectinase, to liberate cells, followed by incubation with anti-GFP antibody coated magnetic particles. The purity of the magnetically isolated cells may be checked by fluorescence microscopy.

[0094] The same technique could be useful for studying the protein components of specific cell types, for example using antibody assays or fluorescent 2D gel display techniques. If unfixed cells are used, biochemical activities may be assayed. In addition, it is envisaged that sequential selection for different epitopes may be used to isolate cellular subpopulations. For example, if a cell wall GFP marker provided an epitope for the selection of certain cell types, a second independent marker could be used to select

an even more specific sub-population (e.g. using a marker for a natural cell wall component).

[0095] Screening for Reporter Gene Expression in Plants

[0096] Expression of a reporter gene may be monitored using any suitable technique known to the person skilled in the art. For example, for the screening of shoots and roots of transgenic plantlets in which the reporter protein is a fluorescent protein such as GFP or the extensin-GFP of the invention, expression can be screened directly using epifluorescence microscopy, to, for example, monitor expression in developing meristems.

[0097] For the monitoring of expression of fluorescent proteins, multispectral dynamic imaging may be used. Such confocal microscope based methods allow high resolution observation of living cells. The expression of GFP within an organism produces an intrinsic fluorescence that colours normal cellular processes, and high resolution optical techniques can be used non-invasively to monitor the dynamic activities of these living cells. Using coverslip-based culture vessels, specialised microscope objectives and the optical sectioning properties of the confocal microscope, it is possible to monitor simply and precisely both the arrangement of living cells within a meristem, and their behaviour through long timelapse observations (see <http://www.plantsci.cam.ac.uk/Haseloff>). Further, the use of cyan and yellow emitting GFP variants that can be distinguished from the green fluorescent protein during confocal microscopy enable simultaneous imaging of different tagged proteins in living cells.

[0098] As a further or alternative screen, a second screen may be used on adult transgenic plants, in which parts of the plants such as the flowers or siliques are dissected and the fluorescence of parts monitored. Such screens are particularly useful for identifying expression patterns in embryos and floral parts, in which GFP may not be expressed in plantlets.

[0099] The invention will now be further described with reference to the following non-limiting Figures and Examples. Other embodiments of the invention will occur to those skilled in the art in the light of these.

FIGURES

[0100] FIG. 1 shows oligonucleotides for construction of mHAP1 DNA binding domain.

[0101] FIG. 2a shows a schematic diagram of the mHAP1-VP16 synthetic transcription activator chimeric gene

[0102] FIG. 2b shows the nucleic acid sequence of wild-type HAP1 (top line—labelled HAP1); the nucleic acid sequence of modified HAP1 (middle line—labelled mHAP1); and the encoded amino acid sequence (bottom line)

[0103] FIG. 2c shows the nucleic acid sequence (top line) of the mHAP1-VP16 synthetic transcription activator chimeric gene, in which the HAP1 sequence is the modified sequence (running from the 5' terminus to position 292); the VP19 nucleic acid sequence runs from position 293 onwards and is shown in upper case); and the amino acid sequence of the synthetic transcription activator chimeric protein is shown in the bottom line.

[0104] FIG. 3a shows a schematic diagram of the extensin-GFP gene fusion.

[0105] FIG. 3b shows the coding sequence of the extensin-GFP fusion of FIG. 3a in the top line and the encoded amino acid sequence in the bottom line. Extensin nucleotide sequence is shown in lower case and the GFP nucleotide sequence is shown in uppercase.

[0106] FIG. 4 shows expression of an extensin-GFP gene fusion in transgenic *Arabidopsis*. A 35S-extensin-GFP construction was introduced into *Arabidopsis* using *Agrobacterium* mediated transformation. Confocal optical sections of transformed plantlets are shown. Chlorophyll autofluorescence is seen in the red channel.

[0107] FIG. 5 shows oligonucleotides used in construction of a HAP1 DNA binding site.

EXAMPLES

Example 1

Construction of the Modified HAP1-VP16 Gene

[0108] The yeast HAP1 protein is a member of a family of zinc-finger (Cys₄) transcription factors which are limited to fungi, and homologues have not been found in plants to date. Yeast genes have a high A/T content and are often poorly expressed in *Arabidopsis* due to aberrant post-transcriptional processing. A synthetic gene which has an elevated G/C content, and in which the DNA binding domain is fused to the highly active and G/C-rich transcription activator domain of VP16, was constructed:

[0109] Three long oligonucleotides, mHAP1-A, B & C (shown in FIG. 1) were made using automated synthesis on solid supports. The oligonucleotides encoded the predicted DNA binding domain of HAP1 protein with modified codon usage. Codon usage was modified according to the following criteria:

[0110] (i) GC content was increased

[0111] (ii) splice junction consensus sequences were avoided

[0112] (iii) the resultant amino acid sequence encoded by the nucleic acid was unchanged.

[0113] Oligonucleotides mHAP1-D and E (FIG. 1) contained complementary sequence corresponding to the junctions of the three longer oligonucleotides. The synthetic oligonucleotides were purified by polyacrylamide gel electrophoresis and phosphorylated after incubation with ATP and T4 polynucleotide kinase. The oligonucleotides were then mixed and heated at 94° C. for 1 min and annealed at 60° C. for 5 min. After cooling, the sample was treated with T4 DNA ligase to produce a small quantity of single-strand DNA corresponding to the mHAP1 DNA binding domain. This was then used as a template for PCR amplification with oligonucleotides mHAP1-5' and 3' (FIG. 1).

[0114] FIG. 2a shows in diagrammatic form the mHAP1-VP16 synthetic transcription activator chimeric gene (FIG. 2c entire sequence). The DNA sequence, encoding, in the 5' portion (bases 1 to 292), the modified HAP1 DNA binding domain (see also FIG. 2b middle sequence) and encoding, in the 3' portion (bases 293-533), the transcriptional activa-

tion domain from HSV VP16, is shown as the top sequence of FIG. 2c with the encoded amino acid sequence shown below. The SacI restriction endonuclease site within the gene is marked.

[0115] The wild-type sequence of the HAP1 binding domain (see the top sequence of FIG. 2b) is shown above for comparison of the A/T %. The wild-type HAP1 DNA binding domain DNA sequence is A/T rich.

Example 2

Construction of Insoluble GFP Marker

[0116] A variant of GFP was fused to the coding sequence of a carrot extensin. PCR amplification was used to obtain a copy of the extensin gene, isolated from carrots purchased in Cambridge market square. The carrot gene was genetically fused to a variant of green fluorescent protein obtained from Packard Biosciences (Meridian, Conn. (GFPemd)).

[0117] A schematic diagram of the extensin-GFP gene fusion is shown in FIG. 3a with the coding sequence shown in FIG. 3b (top line), the encoded amino acid sequence is shown below in the bottom line of FIG. 3b. Extensin sequence is in lower case and GFP sequence is in uppercase.

Example 3

Expression of Extensin GFP Gene Fusion in Transgenic *Arabidopsis*

[0118] a) Construction of the 35S-Extensin-GFP Construct.

[0119] A variant of GFP was fused to the coding sequence of a carrot extensin. PCR amplification was used to obtain a copy of the gene, isolated from carrots purchased in Cambridge market square. The carrot gene was genetically fused to a variant of green fluorescent protein obtained from Packard Bioscience (GFPemd (emerald)). Expression of this gene fusion in transgenic *Arabidopsis* tissues results in the decoration of cell walls with bright fluorescence.

[0120] Construction of the GFP-Extensin Gene

[0121] The following oligonucleotides were synthesised, and used as primers for the PCR amplification of the carrot extensin gene.

CarExt5
GGC GGA TCC AAC AAT GGG AAG AAT TGC TAG AGG CTC

CarExt3
GGC GGA TTC GTA GTG GTG AGG AGG AGG AGG TGA CGT

[0122] Template carrot DNA was isolated using a Qiagen DNA extraction kit (UK—QIAGEN Ltd., Boundary Court, Gatwick Road, Crawley, West Sussex, RH10 9AX), and 1 microgram of isolated carrot DNA was used in a PCR reaction with VENT polymerase (New England Biolabs), (30 cycles: 92° C. 30 sec, 60° C. 30 sec, 72° C. 60 sec). The amplified product was purified by 1% agarose gel electrophoresis, and digested with the restriction endonucleases BamH1 and EcoR1. The cut fragment was then ligated into a plasmid vector that contained a GFP gene with an EcoR1 restriction fused to the N-terminus of the coding sequence, Haseloff, J., Siemerling, K. R., Prasher, D. C. and Hodge, S

Removal of a cryptic intron and subcellular localization of green fluorescent protein are required to mark transgenic Arabidopsis plants brightly. Proc. Natl. Acad. Sci. USA. 94, 2122-2127 (1997). The resulting plasmid contained a translational fusion between carrot extensin and the GFPemd gene (Packard Bioscience).

[0123] FIG. 3a shows a schematic diagram of the extensin-GFP gene fusion. The extensin sequences lie between the BamH1 and EcoR1 sites, and the GFP sequences lie between the EcoR1 and Sac1 sequences.

[0124] This reporter gene has been tested by insertion into plant transformation vectors, and expressed in transgenic *Arabidopsis* plants behind a constitutive CaMV 35S promoter, and as part of a HAP1-based enhancer trap vector. Bright, cell wall localised fluorescence results in both cases.

[0125] b) Transformation of *Arabidopsis thaliana*

[0126] *Arabidopsis thaliana* was transformed using the method given in PCT/GB97/00406.

[0127] Expression of the extensin-GFP gene fusion in transgenic *Arabidopsis* tissues results in the decoration of cell walls with bright fluorescence (FIG. 4). Extensin becomes covalently linked to the cell wall matrix, and the GFP-extensin marker is resistant to various clearing techniques that normally result in complete loss of the protein from treated tissues. For example, the cell wall bound signal is retained after glycerol infiltration.

Example 4

Construction of a HAP1 Promoter for Use in Plants

[0128] An optimised multimeric binding site for HAP 1 was synthesised and cloned behind a GFP promoter. Oligonucleotides used in the construction of the binding site are shown in FIG. 5 (UASHAP1a and UASHAP1b).

[0129] The oligonucleotides were phosphorylated using polynucleotide kinase, annealed, and ligated into the Hind III-Xba I sites of a UAS_{GAL4} containing vector. The oligonucleotide sequences replaced the UAS_{GAL4} with the appropriate UAS_{HAP1} sequences—already positioned upstream of a plant TATA box and GFP reporter gene.

Example 5

Construction of HAP1-GFP Enhancer Trap Vector

[0130] An enhancer trap vector was constructed using the modified HAP1-VP16 gene positioned with a minimal (naïve) promoter and the extensin GFP gene fusion as described above.

[0131] The PCR product produced as described in Example 1 was cut with BamH1 and Sac1 restriction endonucleases and purified after electrophoresis through a 1.5% LGT agarose gel.

[0132] The plasmid pCMVGal65 (Cousens et al., EMBO J. 8:2337-2342, 1989) was used as a source of the VP16 sequence. A SacI-KpnI fragment, which encodes the activation domain of the herpes simplex virus VP16 protein, had been previously fused to a modified form of the GAL4 DNA binding domain (Haseloff and Hodge, U.S. Pat. No. 6,255, 558 B1) within a plant enhancer-trap vector, pET-15 (GAL4-GFP). The GAL4 sequence was excised from the pET-15

vector by restriction endonuclease digestion with BamH1 and Sac1, and replaced by ligation with the amplified mHAP1 sequence (see construction of extensin-GFP gene).

[0133] The mHAP1-VP16 gene was directly assayed for activity in transformed *Arabidopsis* plants by *Agrobacterium*-mediated transformation (Valvekens et al. Proc. Natl. Acad. Sci. USA 85:5536-5540, 1988).

Example 6

Enhancer Trap Screen

[0134] The vector was used to transform *Arabidopsis thaliana* using *Agrobacterium* mediated transformation as described in Example 3. In this way, large numbers of transgenic calli are regenerated, induced to form roots and shoots and are directly screened by epifluorescence microscopy for extensin-GFP expression in the developing meristems.

[0135] A suitable protocol is as follows:

[0136] (1) 20-100 transgenic *Arabidopsis* seed were placed in a 1.5 ml microfuge tube and washed for about 1 min with 1 ml of ethanol.

[0137] (2) Seeds were then incubated with 1 ml of a surface sterilising solution containing 1% (w/v) sodium hypochlorite and 0.1% (v/v) NP40 detergent, for 15 min at room temperature.

[0138] (3) The seeds were then washed three times with 1 ml of sterile water, and transferred by pipette to agar plates containing GM medium (Valvekens, D., Van Montagu, M and Van Lijsebettens, M. (1988) *Agrobacterium tumefaciens*-mediated transformation of *Arabidopsis thaliana* root explants by using kanamycin selection. *Proceedings of the National Academy of Sciences U.S.A.* 85:5536-5540).

1x Murashige and Skoog basal medium with Gamborgs B5 vitamins (Sigma)
 1% sucrose
 0.5 g/l 2-(N-morpholino)ethanesulfonic acid (MES)
 0.8% agar
 (adjusted to pH 5.7 with 1M KOH)
 25 mg/l kanamycin was added if antibiotic selection of transgenic seedlings was necessary.

[0139] These procedures were performed in a laminar flow hood.

[0140] Alternatively, for extended timelapse imaging of roots, sterile seeds were sown in coverslip based vessels (Nunc) which comprised 4 wells, each containing about 400 μ l of low gelling temperature agarose with GM medium. The roots of these plants grow down through the media and then along the surface of the coverslip. The roots are then ideally positioned for high resolution microscopic imaging through the base of the vessel.

[0141] (4) Sealed plates or vessels were incubated for 1-3 days in the dark at 4° C., and then transferred to an artificially lit growth room at 23° C. for germination.

[0142] (5) *Arabidopsis* seedlings germinate after 3 days, and can be used for microscopy for several weeks. Root and shoot tissues can be directly scored for GFP expression

using an inverted fluorescence microscope (Leitz DM-IL) fitted with filter sets suitable for UV (Leitz-D; excitation filter 355-425 nm, dichroic mirror 455 nm, longpass emission filter 460 nm) and blue (Leitz-13; excitation filter 450-490 nm, dichroic mirror 510 nm, longpass emission filter 520 nm) light excitation of GFP. Roots, which grow along the base of the petri dish can be observed directly by epifluorescence microscopy through the clear plastic base. Shoot tissues were directly observed in inverted dishes by using one or two 7 mm threaded extension tubes with a 4× objective (EF 4/0.12), that gave greater working distances. Epifluorescence images were captured in Adobe Photoshop using a Sony DXC-930P 3-chip CCD video camera and F100-MPU integrating frame store, connected to a Nu Vista+ video digitiser in an Apple Macintosh computer.

[0143] GFP-expressing *Arabidopsis* seedlings were removed from agar media, and simply mounted in water under glass coverslips for microscopy. Growing roots could also be directly viewed through coverslip based vessels. Specimens were examined using a BioRad MRC-600 laser-scanning confocal microscope equipped with a 25 m W krypton-argon or argon ion laser and filter sets suitable for the detection of fluorescein and texas red dyes (BioRad filter blocks K1/K2 with krypton-argon ion laser, and A1/A2 with argon ion laser). We routinely use a Nikon 60x PlanApo N. A. 1.2 water immersion objective to minimise loss of signal through spherical aberration at long working distances. For the collection of timelapse images, the laser light source was attenuated by 99% using a neutral density filter, the confocal aperture was stopped down and single scans were collected at two second intervals. The large data files were transferred to an Apple Macintosh computer, and the programs PicMerge and 4DTurnaround were used with Adobe Photoshop and Premiere to produce QuickTime movies for display and analysis.

[0144] GFP fluorescence can be seen from 4 days after *Agrobacterium* inoculation, depending on the expression pattern. The plantlets exhibiting fluorescence can be used to construct a library of transformed plants.

Example 7

Transactivation

[0145] mHAP1-VP16 expression within these lines can be used to direct the expression of a chosen gene at a precise time and place within the organism. The inventors have produced transgenic plants which maintain regulatory proteins or toxins, silent behind a HAP1-responsive promoter. These genes can now be activated in specific cells by crossing to a chosen mHAP1-VP16 expressing line.

[0146] A stable transformed line HJR1 of *Arabidopsis thaliana*, which forms part of the library described above, expresses modified GFP (under the influence of the mHAP1-VP16 activator) in the cells of the extreme root tip. Similar lines have also been produced which carry a localised cyan fluorescent protein, driven by the mHAP1-VP16 gene.

[0147] Using standard techniques, the line is crossed with another *Arabidopsis* line which comprises a silently maintained GUS reporter gene under operable control of a HAP1-responsive UAS. The plantlets obtained from the cross express GUS under the influence of the HAP1-VP16 transcriptional activator. The pattern of expression is the same as that for the GFP reporter gene in the parent cell line (i.e. at the extreme root tip). Thus the modified HAP1 DNA binding domain sequence enables the expression of chosen genes of interest (e.g. GUS) in a predictable pattern and enables simultaneous expression of a plurality of genes of interest (e.g. GFP and GUS).

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ctc agt tgc acc att tgt cgg aaa agg aaa gtc aaa tgt gac aaa ctc      96
Leu Ser Cys Thr Ile Cys Arg Lys Arg Lys Val Lys Cys Asp Lys Leu
             20             25             30

aga cca cac tgc cag cag tgc act aaa act ggg gta gcc cat ctc tgc     144
Arg Pro His Cys Gln Gln Cys Thr Lys Thr Gly Val Ala His Leu Cys
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His Tyr Met Glu Gln Thr Trp Ala Glu Glu Ala Glu Lys Glu Leu Leu
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Lys Asp Asn Glu Leu Lys Lys Leu Arg Glu Arg Val Lys Ser Leu Glu
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Arg Pro His Cys Gln Gln Cys Thr Lys Thr Gly Val Ala His Leu Cys
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His Tyr Met Glu Gln Thr Trp Ala Glu Glu Ala Glu Lys Glu Leu Leu
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Lys Asp Asn Glu Leu Lys Lys Leu Arg Glu Arg Val Lys Ser Leu Glu
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Arg Pro His Cys Gln Gln Cys Thr Lys Thr Gly Val Ala His Leu Cys
 35 40 45

cac tac atg gag cag acc tgg gcc gag gag gcc gag aag gag ttg ctg 192
His Tyr Met Glu Gln Thr Trp Ala Glu Glu Ala Glu Lys Glu Leu Leu
 50 55 60

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Lys Asp Asn Glu Leu Lys Lys Leu Arg Glu Arg Val Lys Ser Leu Glu
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Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly Glu
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tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt gag cag 480
Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu Gln
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Arg Pro His Cys Gln Gln Cys Thr Lys Thr Gly Val Ala His Leu Cys
           35           40           45
His Tyr Met Glu Gln Thr Trp Ala Glu Glu Ala Glu Lys Glu Leu Leu
           50           55           60
Lys Asp Asn Glu Leu Lys Lys Leu Arg Glu Arg Val Lys Ser Leu Glu
           65           70           75           80
Lys Thr Leu Ser Lys Val His Ser Ser Pro Ser Ser Asn Ser Thr Ala
           85           90           95
Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly Glu
           100          105          110
Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp
           115          120          125
Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His Asp
           130          135          140
Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu Gln
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Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly
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<222> LOCATION: (1)..(1641)

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 1           5           10           15

ttg ctt gta gta ttg gtg tca ctc aat ttg gct tcc gaa acc aca gct      96
Leu Leu Val Val Leu Val Ser Leu Asn Leu Ala Ser Glu Thr Thr Ala
           20           25           30

aaa tac act tac tcc tct cca cca cct ccc gag cat tct cct cca ccg      144
Lys Tyr Thr Tyr Ser Ser Pro Pro Pro Glu His Ser Pro Pro Pro
           35           40           45

ccg gag cat tct cct cct ccg cct tac cac tac gaa tcc ccg ccc ccg      192
Pro Glu His Ser Pro Pro Pro Pro Tyr His Tyr Glu Ser Pro Pro Pro
           50           55           60

cct aaa cat tct cca cca cca cct aca ccg gtt tac aag tac aag tct      240
Pro Lys His Ser Pro Pro Pro Pro Thr Pro Val Tyr Lys Tyr Lys Ser
           65           70           75           80

cca ccg cct cct atg cat tct cct cca ccg cct tat cat ttt gag tct      288
Pro Pro Pro Pro Met His Ser Pro Pro Pro Pro Tyr His Phe Glu Ser
           85           90           95

cca cct cca cca aaa cat tct cca cca cca cca acg ccg gtt tac aag      336
Pro Pro Pro Pro Lys His Ser Pro Pro Pro Pro Thr Pro Val Tyr Lys
           100          105          110

tac aaa tct cca cca cca cct aaa cat tct cct gca cca gtg cat cat      384

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Tyr	Lys	Ser	Pro	Pro	Pro	Pro	Lys	His	Ser	Pro	Ala	Pro	Val	His	His		
		115						120					125				
tat	aaa	tac	aag	tct	cca	cca	cca	cca	aca	ccg	gtt	tat	aag	tat	aaa	432	
Tyr	Lys	Tyr	Lys	Ser	Pro	Pro	Pro	Pro	Thr	Pro	Val	Tyr	Lys	Tyr	Lys		
	130						135				140						
tct	cca	cca	cca	cca	aag	cat	tct	cct	gca	cca	gaa	cat	cac	tat	aag	480	
Ser	Pro	Pro	Pro	Pro	Lys	His	Ser	Pro	Ala	Pro	Glu	His	His	Tyr	Lys		
145					150					155					160		
tac	aag	tct	cca	cca	cca	cct	aag	cat	ttt	cct	gca	cca	gaa	cat	cac	528	
Tyr	Lys	Ser	Pro	Pro	Pro	Pro	Lys	His	Phe	Pro	Ala	Pro	Glu	His	His		
					165				170						175		
tat	aag	tac	aag	tac	aag	tct	cca	cca	cca	cca	aca	ccg	gtc	tac	aag	576	
Tyr	Lys	Tyr	Lys	Tyr	Lys	Ser	Pro	Pro	Pro	Pro	Thr	Pro	Val	Tyr	Lys		
	180							185					190				
tat	aaa	tct	cca	cca	cct	cca	aca	ccg	gtc	tac	aag	tac	aag	tct	cca	624	
Tyr	Lys	Ser	Pro	Pro	Pro	Pro	Thr	Pro	Val	Tyr	Lys	Tyr	Lys	Ser	Pro		
	195						200					205					
cca	cca	ccc	aag	cat	tct	ccc	gca	cca	gta	cac	cat	tac	aag	tac	aag	672	
Pro	Pro	Pro	Lys	His	Ser	Pro	Ala	Pro	Val	His	His	Tyr	Lys	Tyr	Lys		
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tct	cca	cca	cca	cca	act	cca	ggt	tat	aaa	tct	cca	cca	cca	ccc	gaa	720	
Ser	Pro	Pro	Pro	Pro	Thr	Pro	Val	Tyr	Lys	Ser	Pro	Pro	Pro	Pro	Glu		
225					230					235					240		
cat	tcc	cca	cca	cca	cca	aca	ccg	gtc	tac	aaa	tac	aag	tct	cca	cca	768	
His	Ser	Pro	Pro	Pro	Pro	Thr	Pro	Val	Tyr	Lys	Tyr	Lys	Ser	Pro	Pro		
				245					250					255			
cca	cca	atg	cac	tct	cca	cca	cca	cca	aca	cca	ggt	tac	aag	tac	aag	816	
Pro	Pro	Met	His	Ser	Pro	Pro	Pro	Pro	Thr	Pro	Val	Tyr	Lys	Tyr	Lys		
		260							265				270				
tct	ccg	cca	cca	cca	atg	cac	tct	ccc	cca	cca	cca	ggt	tac	tct	cca	864	
Ser	Pro	Pro	Pro	Pro	Met	His	Ser	Pro	Pro	Pro	Pro	Val	Tyr	Ser	Pro		
		275					280						285				
cca	cca	ccc	aaa	cat	cac	tac	tcc	tat	acg	tca	cct	cct	cct	cct	cac	912	
Pro	Pro	Pro	Lys	His	His	Tyr	Ser	Tyr	Thr	Ser	Pro	Pro	Pro	Pro	His		
		290				295					300						
cac	tac	gaa	ttc	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	960	
His	Tyr	Glu	Phe	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val		
305					310					315					320		
ccc	atc	ctg	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	1008	
Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser		
				325					330					335			
gtg	tcc	ggc	gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	1056	
Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu		
			340					345					350				
aag	ttc	atc	tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	1104	
Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu		
		355					360					365					
gtg	acc	acc	ttg	acc	tac	ggc	gtg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	1152	
Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp		
		370				375					380						
cac	atg	aag	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	1200	
His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr		
385					390					395					400		
gtc	cag	gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	1248	
Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr		
				405					410					415			
cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	1296	

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Tyr Lys Ser Pro Pro Pro Pro Lys His Phe Pro Ala Pro Glu His His
 165 170 175
 Tyr Lys Tyr Lys Tyr Lys Ser Pro Pro Pro Pro Thr Pro Val Tyr Lys
 180 185 190
 Tyr Lys Ser Pro Pro Pro Pro Thr Pro Val Tyr Lys Tyr Lys Ser Pro
 195 200 205
 Pro Pro Pro Lys His Ser Pro Ala Pro Val His His Tyr Lys Tyr Lys
 210 215 220
 Ser Pro Pro Pro Pro Thr Pro Val Tyr Lys Ser Pro Pro Pro Pro Glu
 225 230 235 240
 His Ser Pro Pro Pro Pro Thr Pro Val Tyr Lys Tyr Lys Ser Pro Pro
 245 250 255
 Pro Pro Met His Ser Pro Pro Pro Pro Thr Pro Val Tyr Lys Tyr Lys
 260 265 270
 Ser Pro Pro Pro Pro Met His Ser Pro Pro Pro Pro Val Tyr Ser Pro
 275 280 285
 Pro Pro Pro Lys His His Tyr Ser Tyr Thr Ser Pro Pro Pro Pro His
 290 295 300
 His Tyr Glu Phe Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
 305 310 315 320
 Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
 325 330 335
 Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
 340 345 350
 Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
 355 360 365
 Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp
 370 375 380
 His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
 385 390 395 400
 Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
 405 410 415
 Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
 420 425 430
 Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
 435 440 445
 Leu Glu Tyr Asn Tyr Asn Ser His Lys Val Tyr Ile Thr Ala Asp Lys
 450 455 460
 Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu
 465 470 475 480
 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 485 490 495
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
 500 505 510
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
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 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 530 535 540
 Tyr Lys
 545

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gtcggagcac ggacttatcg gtcggagcac ggacttatcg gtcggt                                106

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      binding site

<400> SEQUENCE: 16

ctagaccgac cgataagtcc gtgctccgac cgataagtcc gtgctccgac cgataagtcc      60
gtgctccgac cgataagtcc gtgctccgac cgataagtcc gtgcta                                106

<210> SEQ ID NO 17
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ggcggatcca acaatgggaa gaattgctag aggctc                                          36

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<400> SEQUENCE: 18

ggcggattcg tagtggtgag gaggaggagg tgacgt                                          36

```

1. An isolated nucleic acid molecule comprising a modified HAP1 DNA-binding domain nucleotide sequence encoding at least an effective portion of a HAP1 DNA-binding domain,

characterised in that said modified nucleotide sequence has an A/T base content substantially reduced compared to the wild-type sequence such as to be expressible in a plant cell.

2. A nucleic acid molecule as claimed in claim 1 wherein the effective portion comprises amino acid residues 1 to 94 of the yeast HAP1 HAP1 polypeptide.

3. A nucleic acid molecule as claimed in claim 1 wherein the % A/T base content of the modified nucleotide sequence is less than 45%.

4. A nucleic acid molecule as claimed in claim 1 wherein the effective portion of a HAP1 DNA-binding domain has the amino acid sequence of **FIG. 2b** (bottom line).

5. A nucleic acid molecule as claimed in claim 4 wherein the

modified nucleotide sequence has the sequence of **FIG. 2b** (middle line)

6. A nucleic acid molecule as claimed in claim 1 wherein the modified nucleotide sequence is fused to a second nucleotide sequence which encodes a transcriptional activator domain such as to encode a HAP1 transcriptional activator.

7. A nucleic acid molecule as claimed in claim 6 wherein the transcriptional activator domain is selected from the activation domain of the HAP1 protein or herpes simplex virus (HSV) VP-16.

8. A nucleic acid molecule as claimed in claim 7 wherein the modified nucleotide sequence and the second nucleotide sequence encode the amino acid sequence of the mHAP1-VPI6 chimera shown in **FIG. 2c** (bottom line).

9. A nucleic acid molecule as claimed in claim 8 wherein the modified nucleotide sequence and second nucleotide sequence consist of the sequence shown in **FIG. 2c** (top line).

10. A recombinant vector which comprises the nucleic acid of claim 1.

11. A vector as claimed in claim 10 which is a plant vector comprising right and left Ti-DNA, to enable stable insertion into the genome of a plant host cell.

12. A vector as claimed in claim 10 wherein the nucleic acid is operably linked to a promoter for transcription in a host cell, wherein the promoter is optionally an inducible promoter.

13. A vector as claimed in claim 12 wherein the promoter is an enhancer dependent promoter such that if the promoter is inserted into a plant host cell genome in functional relationship with an enhancer sequence and required transcription factors, the promoter will direct expression in a tissue specific manner.

14. A vector as claimed in claim 10 further comprising a reporter nucleotide sequence consisting of a reporter gene operably linked to a HAP1 upstream activation sequence.

15. A vector as claimed in claim 14 wherein the reporter gene encodes a reporter polypeptide capable of generating a visually detectable signal.

16. A vector as claimed in claim 15 wherein the visually detectable signal can be monitored by multispectral dynamic imaging.

17. A vector as claimed in claim 15 wherein the reporter polypeptide is a wild-type of modified GFP.

18. A vector as claimed in claim 17 wherein the modified GFP is encoded by mgfp5-ER.

19. A vector as claimed in claim 17 wherein the modified GFP is a GFP extensin reporter gene fusion.

20. A vector as claimed in claim 19 wherein the GFP extensin reporter gene fusion is as claimed in any one of claims 39 to 42.

21. A composition of matter comprising a pair vectors, which vectors are:

- (i) a vector as claimed in any one of claims 10 to 13,
- (ii) a vector comprising a nucleic acid which includes a reporter nucleotide sequence consisting of a reporter gene operably linked to a HAP1 upstream activation sequence,

which reporter nucleotide sequence is as described in any one of claims 14 to 20.

22. A method which comprises the step of introducing the vector or pair of vectors of claim 10 into a host plant cell, and optionally causing or allowing recombination between the vector or vectors and the plant cell genome such as to transform the host cell.

23. A plant cell containing or transformed with the vector or pair of vectors of claim 10.

24. A method for producing a transgenic plant, which method comprises the steps of:

- (a) performing a method as claimed in claim 22,
- (b) regenerating a plant from the transformed plant cell.

25. A transgenic plant which is obtainable by the method of claim 24, or which is a clone, or selfed or hybrid progeny or other descendant of said transgenic plant, which in each case includes a nucleic acid of any one of claims 1 to 9.

26. A plant as claimed in claim 25 which has integrated therein a reporter nucleotide sequence consisting of a reporter gene operably linked to a HAP1 upstream activation sequence

which reporter nucleotide sequence is as described in any one of claims 14 to 20.

27. A population of plants as claimed in claim 26 wherein the integrated reporter gene differs between said plants, plantlets or parts thereof.

28. A method comprising introducing a gene of interest into the plant or plants of claim 26

which gene of interest is operable linked to a HAP1 upstream activation sequence,

such that the pattern of expression of the gene of interest is the same as that of the reporter gene.

29. A method as claimed in claim 28 wherein the gene of interest is introduced and thereby trans-activated by crossing.

30. A method as claimed in claim 28 wherein the gene of interest is introduced by means of a plant vector.

31. A method of identifying a plant enhancer nucleic acid sequence, comprising the steps of:

- (i) transforming a plant cell host with a vector as claimed in claim 13,
- (ii) observing said plant expression of said HAP1 binding domain, and
- (iii) optionally, characterising the position and/or nucleic acid sequence of the enhancer sequence.

32. A method of controlling expression of a gene of interest in a plant, the method comprising the steps of:

- (i) providing a plant comprising a nucleic acid encoding a HAP1 transcriptional activator as defined in claim 6 under the control of a naïve promoter such that expression of the HAP1 transcriptional activator is limited to those cell types in which a naïve promoter sequence is in functional relationship with a host cell enhancer sequence and required transcription factors,
- (ii) introducing the gene of interest into said plant or part thereof, said gene of interest having an HAP1 responsive upstream activation sequence,

wherein binding of said HAP1 transcriptional activator to said upstream activator sequence causes transcriptional activation of the gene of interest.

33. A method as claimed in claim 32 wherein the gene of interest encodes a toxin.

34. A method as claimed in claim 32 wherein the gene of interest is of unknown function.

35. A method of determining the function of a gene of interest comprising the steps of:

- (i) performing a method as claimed in claim 34,
- (ii) comparing the phenotype of said plant or part thereof in which said gene of interest is expressed with a second plant or part thereof in which said gene of interest is not expressed.

36. A method of independently controlling expression of a first and a second gene of interest in a plant comprising the steps of:

- (i) providing a plant comprising a nucleic acid encoding a HAP1 transcriptional activator as defined in claim 6, and a second nucleic acid sequence, which encodes a GAL4 transcriptional activator;
- (ii) introducing the first gene of interest into a plant or part thereof, said first gene of interest having a HAP1 responsive upstream activation sequence;

introducing the second gene of interest into a plant or part thereof, said second gene of interest having a GAL4 responsive upstream activation sequence;

wherein binding of said HAP1 transcriptional activator to said upstream activator sequence causes transcriptional activation of the first gene of interest and binding of said GAL4 transcriptional activator to said upstream activator sequence causes transcriptional activation of the second gene of interest.

37. A method of coordinating the expression of a plurality of genes of interest in a plant or part thereof, comprising the steps of:

- (i) providing a plant comprising a nucleic acid encoding a HAP1 transcriptional activator as defined in claim 6, and a second nucleic acid sequence, which encodes a GAL4 transcriptional activator;
- (ii) introducing the genes of interest into a plant or part thereof, said genes of interest each being under the control of an HAP1 responsive upstream activation sequence,

wherein binding of said HAP1 transcriptional activator to said upstream activator sequence causes transcriptional activation of the genes of interest.

38. A method as claimed in claim 37 wherein the plurality of genes are associated with a single upstream activator sequence.

39. An isolated nucleic acid molecule comprising a reporter gene nucleotide sequence, which reporter gene encodes a green fluorescent protein linked to an effective portion of extensin.

40. A nucleic acid as claimed in claim 39 wherein the effective portion comprises at least 60% of the full-length sequence of a carrot extensin polypeptide.

41. A nucleic acid as claimed in claim 40 wherein the reporter gene nucleotide sequence encodes the amino acid sequence of **FIG. 3b** (bottom line).

42. A nucleic acid as claimed in claim 41 wherein the reporter gene nucleotide sequence has the sequence of **FIG. 3a** (top line).

43. A recombinant vector which comprises the nucleic acid of claim 39.

44. A vector as claimed in claim 43 which is a plant vector comprising right and left Ti-DNA to enable stable insertion into the genome of a plant host cell.

45. A vector as claimed in claim 43 wherein the nucleic acid is operably linked to a promoter for transcription in a host cell, wherein the promoter is optionally an inducible promoter.

46. A vector as claimed in claim 43 wherein the reporter gene is operably linked to a HAP1 upstream activation sequence to form a reporter nucleotide sequence consisting.

47. A method which comprises the step of introducing the vector of claim 43 into a host plant cell, and optionally causing or allowing recombination between the vector and the plant cell genome such as to transform the host cell.

48. A plant cell containing or transformed with a vector of claim 43.

49. A method for producing a transgenic plant, which method comprises the steps of:

- (a) performing a method as claimed in claim 48,
- (b) regenerating a plant from the transformed plant cell.

50. A transgenic plant which is obtainable by the method of claim 49, or which is a clone, or selfed or hybrid progeny or other descendant of said transgenic plant, which in each case includes a nucleic acid of any one of claims 39 to 42.

51. A method of cell sorting including the step of screening plants, plantlets, parts or cells thereof for expression of a nucleic acid of claim 39, and selecting those plants, plantlets, parts or cells thereof which express said nucleic acid.

52. An isolated polypeptide encoded by the nucleic acid of claim 39.

53. An isolated polypeptide encoded by the nucleic acid of claim 1.

* * * * *