

DESCRIPTION

METHOD FOR CONTROLLING FLOWERING TIME OF PLANT

BACKGROUND OF THE INVENTION

5 Field of the Invention

The present invention relates to a method for controlling flowering time of plant using a chemical substance.

Description of the Related Art

10 Flowering time of a plant is influenced by extrinsic factors such as photoperiod, temperature, and nutritional status, in addition to species-specific intrinsic factors. Accordingly, it is necessary to use special facilities such as a light irradiation device and a temperature control device
15 for controlling environmental conditions in order to control flowering time of a plant, which raises cost problems. In addition, seeding time or a cultivation area is limited depending on a species, imposing a huge obstacle for improving productivity.

20 Recently, various genes involved in controlling flowering time in plant have been identified (Science 286, 1960-1962, 1999) and transgenic plants having altered flowering time have been produced by introducing those genes. In most of the plants, a foreign gene controlling flowering
25 time is expressed under the control of a constitutive promoter which is constantly expressed.

In order to control flowering time of a transgenic plant by inducing expression of an introduced foreign gene which

controls flowering time, an inducible system which has a high induction ratio and can be precisely regulated is required. That is, required is an inducible system which can decrease the expression of a foreign gene of interest to a low level under a non-inducible condition but can activate the expression of the foreign gene of interest under an inducible condition. A copper ion inducible system, which is one of the systems known as an inducible system, uses an inexpensive inducing agent and can be used in the field (Proc Natl Acad Sci 90, 4567-45712, 1993). However, the conventionally known copper ion inducible system has a problem that, expression of a foreign gene under non-inducing condition cannot be inhibited to a sufficient low level, expression of a foreign gene under inducing condition cannot be activated to a sufficient high level, and a copper ion as an inducing agent should be treated at a high concentration for a long period of time, resulting in significant toxic effects (Current Opin Plant Biol 6, 169-177, 2003).

SUMMARY OF THE INVENTION

It is an object of the present invention to provide a method of controlling flowering time of a transgenic plant in a copper ion-dependent manner, by inducing the expression of a foreign gene which controls flowering time using an inducible system that can induce the expression of the foreign gene at a high induction ratio.

The present invention provides:

1. a method for controlling flowering time of a plant,

which comprises bringing a plant into contact with copper ions, wherein the plant has been transformed with the following DNA constructs (i) and (ii):

(i) a first DNA construct comprising a nucleotide
5 sequence encoding a chimeric transcription factor, wherein the chimeric transcription factor comprises the following a) and b) as operably linked elements:

a) a DNA-binding domain of a first transcription factor that is capable of being activated by copper ion, and

10 b) a transcriptional activation domain of at least one second transcription factor that is different from the first transcription factor; and

(ii) a second DNA construct encoding a heterologous gene which controls flowering time of a plant, wherein the gene is
15 under the control of a heterologous promoter capable of being stimulated by the chimeric transcription factor of (i) in the presence of copper ion

(hereinafter, sometimes, referred to as the present controlling method);

20 2. the method according to the item 1, wherein the chimeric transcription factor further comprises as the operably linked elements a transcriptional activation domain of the first transcription factor;

3. the method according to the item 1 or 2, wherein the
25 first transcription factor is selected from the group consisting of:

(1) a eukaryote transcription factor which is capable of being activated by copper ion,

(2) a yeast transcription factor which is capable of being activated by copper ion, and

(3) a transcription factor derived from the yeast ACE1 which is capable of being activated by copper ion;

5 4. the method according to any of the items 1 to 3, wherein the second transcription factor is selected from the group consisting of:

(1) a transcription factor of a virus,

(2) a transcription factor of a virus belonging to

10 Simplex virus genus,

(3) a transcription factor of Herpes simplex virus, and

(4) the VP16 transcription factor of Herpes simplex virus;

15 5. the method according to any of the items 1 to 4, wherein the heterologous gene which controls flowering time of a plant is selected from the group consisting of:

(1) a plant gene controlling flowering time,

(2) an angiosperm gene controlling flowering time,

(3) a dicotyledonous gene controlling flowering time,

20 (4) a Cruciferous gene controlling flowering time,

(5) an *Arabidopsis thaliana* gene controlling flowering time, and

(6) a flowering-time controlling gene derived from the *Arabidopsis thaliana* FT gene;

25 6. the method according to any of the items 1 to 5, wherein the first DNA construct further comprises a promoter which is capable of functioning in plant cells and is operably linked to the nucleotide sequence encoding the chimeric

transcription factor;

7. a set of the following DNA constructs (i) and (ii):

(i) a first DNA construct comprising a nucleotide sequence encoding a chimeric transcription factor, wherein the chimeric transcription factor comprises the following a) and b) as operably linked elements:

a) a DNA-binding domain of a first transcription factor that is capable of being activated by copper ion, and

b) a transcriptional activation domain of at least one second transcription factor that is different from the first transcription factor; and

(ii) a second DNA construct encoding a heterologous gene which controls flowering time of a plant, wherein the gene is under the control of a heterologous promoter capable of being stimulated by the chimeric transcription factor of (i) in the presence of copper ion

(hereinafter, sometimes, referred to as the present DNA constructs);

8. the set of the DNA constructs according to the item 7, wherein the chimeric transcription factor further comprises as the operably linked elements a transcriptional activation domain of the first transcription factor;

9. the set of the DNA constructs according to the item 7 or 8, wherein the first transcription factor is selected from the group consisting of:

(1) a eukaryote transcription factor which is capable of being activated by copper ion,

(2) a yeast transcription factor which is capable of

being activated by copper ion, and

(3) a transcription factor derived from the yeast ACE1 which is capable of being activated by copper ion;

10 10. the set of the DNA constructs according to any of the items 7 to 9, wherein the second transcription factor is selected from the group consisting of:

(1) a transcription factor of a virus,

(2) a transcription factor of a virus belonging to Simplex virus genus,

10 (3) a transcription factor of Herpes simplex virus, and

(4) the VP16 transcription factor of Herpes simplex virus;

15 11. the set of the DNA constructs according to any of the items 7 to 10, wherein the heterologous gene which controls flowering time of a plant is selected from the group consisting of:

(1) a plant gene controlling flowering time,

(2) an angiosperm gene controlling flowering time,

(3) a dicotyledonous gene controlling flowering time,

20 (4) a Cruciferous gene controlling flowering time,

(5) an *Arabidopsis thaliana* gene controlling flowering time, and

(6) a flowering-time controlling gene derived from the *Arabidopsis thaliana* FT gene;

25 12. the set of the DNA constructs according to any of the items 7 to 11, wherein the first DNA construct further comprises a promoter which is capable of functioning in plant cells and is operably linked to the nucleotide sequence

encoding the chimeric transcription factor;

13. a plant transformed with the set of DNA constructs of any of the items 7 to 11 (hereinafter, sometimes, referred to as the present transformed plant); and

5 14. a method of producing a transgenic plant with a copper-inducible control of flowering time comprising:

introducing the set of DNA constructs of any of the items 7 to 11 into a plant cell,

regenerating a plant from the plant cell,

10 selecting a plant comprising the DNA constructs, and growing the plant under conditions that allow copper-inducible control of flowering time.

According to the present invention, a method for
15 controlling flowering time of a transgenic plant in a copper ion-inducible manner is provided, wherein a heterologous gene which controls flowering time has been introduced to the plant. Thus, regardless of an environment, seeding time or cultivation area, flowering can be induced at any desired time
20 so that systematic harvest and shipping based on precisely estimated needs, efficient production of F_1 hybrid seeds, prevention of gene leakage from a genetically-engineered crop, efficient production of leaf vegetables or root vegetables, improvement of productivity for flowers and ornamental plants,
25 efficient breed improvement based on reduced period between generations, increased harvest amount, and the like may be expected to be achieved.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a schematic view illustrating the structures of T-DNA regions of copper ion-inducible sGFP gene expression vectors and a copper ion-inducible FT gene expression vector.

5 The symbol "*" in Fig. 1 shows a mutation-introduced region of the as-1 site.

Fig. 2 shows difference in flowering time of the recombinant *Arabidopsis thaliana* in which the copper ion-inducible FT gene expression vector has been introduced.

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DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

Herein below, the present invention will be described in more detail.

The present DNA constructs can be used for inducing in
15 chemical substance-dependent manner expression of a heterologous gene which controls flowering time of a plant.

The present DNA constructs can be constructably prepared so as to comprise:

(i) a first DNA construct comprising a nucleotide
20 sequence encoding a chimeric transcription factor (hereinafter, sometimes, referred to as the present chimeric transcription factor), wherein the chimeric transcription factor comprises the following a) and b) as operably linked elements:

a) a DNA-binding domain of a first transcription factor
25 that is capable of being activated by copper ion, and

b) a transcriptional activation domain of at least one second transcription factor that is different from the first transcription factor; and

(ii) a second DNA construct encoding a heterologous gene which controls flowering time of a plant (hereinafter, sometimes, referred to as the present flowering-time control gene), wherein the gene is under the control of a heterologous promoter capable of being stimulated by the chimeric transcription factor of (i) in the presence of copper ion.

An "expression cassette" described below indicates a DNA construct which can express a structural gene, such as the present flowering-time control gene, comprised in the construct in a host cell. Examples of the expression cassette include a DNA construct in which a promoter and a terminator are operably linked respectively to the upstream and the downstream of a structural gene.

The present chimeric transcription factor can be activated by copper ions and can induce the transcription of the present flowering-time control gene. In the absence of copper ions, the present chimeric transcription factor is in an inactive form, and therefore transcription of the present flowering-time control gene is not substantially induced. In the presence of copper ions, the present chimeric transcription factor is converted into an active form, and therefore can induce the transcription of the present flowering-time control gene.

A transcription factor generally contains a DNA binding domain and a transcriptional activation domain. The transcriptional activation domain has a function to recruit mediators for a RNA polymerase complex in a host plant cell

and activate the transcription of a target gene.

In the present invention, the present chimeric transcription factor comprises as operably linked elements

5 a) a DNA-binding domain of a first transcription factor that is capable of being activated by copper ion and

b) a transcriptional activation domain of at least one second transcription factor that is different from the first transcription factor.

10 The present chimeric transcription factor may further comprise as the operably linked elements a transcriptional activation domain of the first transcription factor. That is, examples of the present chimeric transcription factor also include a chimeric transcription factor comprises as operably linked elements

15 a-1) a DNA-binding domain and a transcriptional activation domain of a first transcription factor that is capable of being activated by copper ion, and

b) a transcriptional activation domain of at least one second transcription factor that is different from the first
20 transcription factor.

The present chimeric transcription factor can induce the expression of the present flowering-time control gene at a high induction ratio because of its structural feature that it comprises a transcriptional activation domain of at least one
25 second transcription factor that is different from the first transcription factor. In order to control the flowering time of the present transformed plant, higher ratio for inducing the expression of the present flowering-time control gene is

preferable.

Examples of the "first transcription factor" include a transcription factor selected from the group consisting of:

- 5 (1) a eukaryote transcription factor which is capable of being activated by copper ion,
- (2) a yeast transcription factor which is capable of being activated by copper ion, and
- (3) a transcription factor derived from the yeast ACE1
- 10 (activating copper-metallothionein expression 1) which is capable of being activated by copper ion.

Examples of the first transcription factor also include AMT1 of *Candida glabrata* (J Biol Chem, 268, 12512-12518, 1993), CRF1 of *Yarrowia lipolytica* (J Biol Chem, 277, 37359-37368, 15 2002), a transcription factor which can induce the expression of the corn SOD gene cluster in a copper ion-dependent manner (Biochemistry, 42, 1508-1516, 2003).

The "second transcription factor" is a transcription factor different from the first transcription factor as 20 described above and a transcriptional activation domain of the second transcription factor allows the present chimeric transcription factor to induce the expression of the present flowering-time control gene at a high induction ratio.

25 Examples of the "second transcription factor" include a transcription factor selected from the group consisting of:

- (1) a transcription factor of a virus,
- (2) a transcription factor of a virus belonging to

Simplex virus genus,

(3) a transcription factor of Herpes simplex virus, and

(4) the VP16 transcription factor of Herpes simplex virus (Genes Dev 2(6), 718-29, 1998).

5 Examples of the second transcription factor also include GAL4 transcription factor (Cell 51(1), 121-126, 1987), and an artificially synthesized peptide AH (Chem Biol 8(6), 583-592, 2001) having an ability of activating transcription.

10 A "heterologous gene which controls flowering time of a plant" utilized (i.e., the present flowering-time control gene) can be a gene which promotes flowering or a gene which delays flowering. Preferably, it is appropriately selected in accordance with the intended use. That is, the term "controls
15 flowering time" for the present controlling method means either to promote flowering or to delay flowering, depending on the nature of the present flowering-time control gene.

 Examples of a gene which promotes flowering include FT, CO, GI, SOC1, AGL24, LD, FCA, FUL, LFY, AP1, TSF, and FD genes
20 and also include any genes which can promote flowering. In addition, genes which promote flowering include dominant-negative mutants, antisense genes and RNAi-inducing genes for genes which delay flowering as described below. It is preferable that genes which integrate pathways each relating
25 to determination of flowering time be used, the pathways including photoperiod-dependent promotion pathway, autonomous promotion pathway, vernalization-dependent promotion pathway and gibberellin-dependent promotion pathway, and the genes

including FT, SOCI and LFY genes. It is more preferable that FT gene, which may be involved in the production of florigen, and homologous genes thereof be used.

Examples of a gene which delays flowering include FLC,
5 FRI, PIE1, TFL2, VIP1-7, LHY, SVP, SPA, and CDF1 genes and also include any genes which can delay flowering. In addition, genes which delay flowering include dominant-negative mutants, antisense genes and RNAi-inducing genes for genes which promote flowering as described above. It is preferable that
10 dominant-negative mutants, antisense genes or RNAi-inducing gene for genes which integrate pathways each relating to determination of flowering time be used, the pathways including photoperiod-dependent promotion pathway, autonomous promotion pathway, vernalization-dependent promotion pathway
15 and gibberellin-dependent promotion pathway, and the genes including FT, SOCI and LFY genes. It is more preferable that dominant-negative mutants, antisense genes or RNAi-inducing gene for FT gene and homologous genes thereof be used.

Specifically, the FT gene of *Arabidopsis thaliana*
20 (Science 286, 1960-1962, 1999) has been known and its homologous gene was identified as Hd3a gene in rice (Science 316, 1033-1036, 2007). Genes homologous to *Arabidopsis* FT gene have also been identified from morning glory, orange, poplar, barley, grape, apple and the like. In addition to the
25 *Arabidopsis* FT gene, many genes which control flowering time have been identified from various plant species. Some of the genes controlling flowering time can function across plant species. While it is preferable that a flowering-time control

gene originating from a host plant species into which the gene will be introduced, a flowering-time control gene originating from other plant species may also be used, without limitation, if the gene can control flowering time in a host plant species of interest.

More detailed information regarding the above-described genes which controls flowering time is given in some review articles (for example: Genes Dev 21,2371-84, 2007; and Bioessays 26, 363-373, 2004).

Examples of the present flowering-time control gene include a heterologous gene selected from the group consisting of:

- (1) a plant gene controlling flowering time,
- (2) an angiosperm gene controlling flowering time,
- (3) a dicotyledonous gene controlling flowering time,
- (4) a Cruciferous gene controlling flowering time,
- (5) an *Arabidopsis thaliana* gene controlling flowering time, and
- (6) a flowering-time controlling gene derived from the *Arabidopsis thaliana* FT gene.

FT gene is an abbreviation of a Flowering Locus T gene, and means a gene encoding a factor that positively functions in flowering-time control. Expression of FT gene increases at a sieve part of fibrovascular bundle in response to length of day, and then the expressed FT moves to a top of a stem and interacts with a bZIP type transcription factor called FD expressed on a top of the stem, thereby inducing flowering

(Genes Dev 21, 2371-2384, 2007).

In the present invention, the present flowering-time control gene is under the control of a heterologous promoter capable of being stimulated by the present chimeric transcription factor in the presence of copper ion. Specifically, in the present flowering-time control gene, a heterologous promoter sequence capable of being stimulated by the present chimeric transcription factor in the presence of copper ion (hereinafter, sometimes, referred to as the present promoter sequence) is operably linked in sense or antisense orientation to a coding sequence of the gene. Any sequence can be used as the present promoter sequence as far as the present flowering-time control gene can be expressed in the host cells under inducible conditions. Preferably, for example, there can be mentioned a promoter sequence containing MRE sequences of yeast (Proc Natl Acad Sci 90, 4567-4571, 1993). Specifically, there is mentioned a promoter sequence in which MRE sequences of yeast are repeatedly located upstream of a TATA sequence of a commonly used promoter. In the present flowering-time control gene, no 5'-untranslated sequence of a foreign gene is required to be inserted between the promoter sequence and the coding sequence. For example, the promoter sequence and the coding sequence may be substantially directly linked.

Preferred examples of the present DNA constructs include a DNA construct in which the first DNA construct further

comprises a promoter which is capable of functioning in plant cells and is operably linked to the nucleotide sequence encoding the chimeric transcription factor. Examples of the promoter include a commonly used promoter described below.

5 The commonly used promoter described above can be a constitutive promoter, a tissue-specific promoter or an inducible promoter that induce transcription by certain stimulation. Preferably, it is appropriately selected in accordance with the intended use.

10 Examples of the constitutive promoter include CaMV 35S promoter, PG10-90 (US Patent No.6187996), ubiquitin promoter (International Publication No.01/094394), actin promoter (International Publication No.00/070067) and the like. Further, examples of the tissue-specific promoter include
15 soybean seed glycinin promoter (EP Publication No.0571741), prolamine promoter (International Publication No.2004/056993), kidney bean seed phaseolin promoter (International Publication No.91/013993), rape seed napin promoter (International Publication No. 91/013972), *Arabidopsis thaliana* Sultr2;2
20 promoter (Plant J 23,171-82, 2000), and *Agrobacterium rolC* promoter (Physiol 115,1599-1607, 1997).

 Preferred examples of the present DNA constructs also include a gene DNA construct in which the first DNA construct further comprises a terminator which is capable of functioning
25 in plant cells and is operably linked to the nucleotide sequence encoding the chimeric transcription factor. Examples of the terminator include NOS terminator, CR16 terminator (US Patent No.7202083), and soybean seed glycinin terminator (EP

The present DNA constructs can be constructably prepared so as to contain the respective elements (i) and (ii) described above. That is, it can be constructed so as to contain the respective elements (i) and (ii) on a single vector, or it can be constructed by using two vectors so as to contain the element (i) on one vector and to contain the element (ii) on the other vector.

Such vector can be constructed by using a conventional genetic engineering method. In addition, when the present DNA constructs are constructed by using two vectors, it is possible that the above (i) is constructed as a first vector and the above (ii) is constructed as a second vector, for example.

The present DNA constructs are introduced, for example, into a host plant and induce expression of the present DNA constructs. The introduction of the present DNA constructs into a host plant can be carried out according to a conventional genetic engineering technique, according to a method applicable to each host plant.

Specifically, the present DNA constructs can be introduced by using a single vector that is constructed so as to contain the respective elements (i) and (ii) described above, or those can be introduced by mixing the first vector that is constructed so as to contain the above (i) with the second vector that is constructed so as to contain the above

(ii). In addition, to a host plant in which part of the present DNA constructs has been introduced by using any of the first vector or the second vector, the rest of the present DNA constructs can be further introduced by using the remaining
5 vector. In addition, the present DNA constructs can be introduced into a host plant by crossbreeding between a plant in which part of the present DNA constructs has been introduced by using the first vector and a plant in which the other part of the present DNA constructs has been introduced
10 by using the second vector. It is also possible that multiple kinds of the second vector are constructed using multiple kinds of flowering-time controlling genes and obtained DNA constructs are introduced thereto to simultaneously induce the expression of multiple kinds of genes which controls flowering
15 time.

As the method of introducing the present DNA constructs, there can be used various known methods such as Agrobacterium method, particle gun method, electroporation method, calcium
20 phosphate method, and virus vector method.

Examples of the host plant include species important for agriculture and gardening, or useful in genetics such as genome analysis. Further, the host plant includes arbitrary
25 plant species. Examples thereof include soybean, pea, kidney bean, alfalfa, Lotus japonicus, clover, peanut, sweet pea, walnut, tea, cotton, pepper, cucumber, water melon, pumpkin, squash, melon, radish, rapeseed, canolla, beet, lettuce,

cabbage, broccoli, cauliflower, Arabidopsis, tobacco, eggplant,
potato, sweet potato, taro, artichoke, tomato, spinach,
asparagus, carrot, sesame, endive, chrysanthemum, geranium,
antirrhinum, carnation, pink, sweet oleander, Bouvardia,
5 Gypsophilla, gerbera, Russell prairie gentian, tulip, Mathiola
incana, Limonium, cyclamen, Saxifraga stolonifera, swamp
chrysanthemum, violet, rose, cherry, apple, strawberry,
Japanese apricot, orange, Japanese quince, azalea, Barbados
nut, gentian, cosmos, morning-glory, sunflower, ginkgo,
10 Japanese cedar, Japanese cypress, poplar, pine, Sequoia, oak,
water lily, Eucommia, beech, rice, wheat, barley, rye, oat,
corn, maize, green onion, garlic, lily, Tiger lily, orchid,
gladiolus and pineapple.

15 In the present controlling method, the present
transformed plant is brought into contact with copper ions.
Examples of the contact method include a method of adding
copper ions to a medium or nutrient solution when the present
transformed plant is cultivated in the medium or
20 hydroponically cultivated (specifically, the concentration of
copper ions is 1 μM to 24 mM, for example). Further, when the
present transformed plant is cultivated in soil, a method in
which copper ions can be applied to the soil or to the stems
and leaves of the present transformed plant (specifically, the
25 amount of copper ions is from 1 nmol/plant to 2.4 mmol/plant,
and the concentration of copper ions is 1 μM to 24 mM, for
example) can be mentioned. Depending on types of host plants
and specific condition of use, an appropriate method is

preferably selected. In the present controlling method, it is required to penetrate copper ion into plant cells wherein induced expression of a flowering-time controlling gene is expected. For the purpose of this penetration, for example, a preparation of a complex of copper ion to be applied can be used. Alternatively, a copper agent for agriculture applications such as Bordeaux (Sumitomo Chemical Co., Ltd.), G-fine (Yashima Chemical Industry Co., Ltd.), Tomono Z-Bordeaux (Tomono Agrica Co., Ltd.), Ridomilpulus (Nihon Nohyaku Co., Ltd.), Highcopper (Sumitomo Chemical Co., Ltd.), CUPRAVIT forte (Bayer CropScience Corporation), Kocide Bordeaux (DuPont Corporation), Kinondo (Agro Kanesho Co., Ltd.) or Yonepon (Yonezawa Chemical Co., Ltd.); or a copper agent to be used as food additives such as copper gluconate (Wako Pure Chemical Industries, Ltd.) can be employed by adjusting to a desired concentration. Further, a spreading agent can be mixed when a preparation or an agent is applied.

The contact of the present transformed plant with copper ion described above may be carried out by applying a mixture of copper ions and fertilizer or a conventional agricultural pest control agent such as insecticide, fungicide, herbicide and plant growth regulator. The contact of the present transformed plant with copper ion may also be carried out when the present transformed plants are irrigated.

25

The DNA constructs used for the present controlling method is, for example, the present DNA constructs as described above. Further, the transcription factor used for

the present controlling method is the present chimeric transcription factor as described above, and it is activated by copper ions. Further, the gene which controls plant flowering time that is used for the present controlling method
5 is the present flowering-time control gene as described above, and its transcription is induced by the present chimeric transcription factor that is activated by copper ions. In addition, the transcriptional activation domain that is used for the present controlling method is the transcriptional
10 activation domain as described above, and it is contained in the present chimeric transcription factor that can be activated by copper ions.

The present transformed plant is a transgenic plant which is obtained by introducing the present DNA constructs
15 thereto, as described above.

When the present flowering-time control gene is a gene for promoting flowering, by introducing the present DNA constructs to a plant having a difficulty in flowering or no
20 flowering due to a mutation introduced to a flowering promotion gene, RNAi, or overexpression of a gene which delays flowering, etc., more precise control of flowering time can be achieved. On the other hand, when the present flowering-time control gene is a gene for delaying flowering, by introducing
25 the present DNA constructs to a plant having precocious flowering due to a mutation introduced to a flowering delay gene, RNAi, or overexpression of a gene which promotes flowering, etc., more precise control of flowering time can be

achieved.

The present invention is not limited to each embodiment described above. Within the scope described in the claims, various modifications can be made, and an embodiment which is
5 obtained by appropriate combination of technical means that is separately described in different embodiments is also within the technical scope of the present invention.

10 EXAMPLES

Herein below, the present invention will be described in more detail by way of examples. However, the present invention is not limited thereto.

Example 1 (Construction of an introduction vector)

15 (1) Construction of transcription factor gene expression cassettes

A genomic DNA was extracted from budding yeast (*Saccharomyces cerevisiae* strain AH22) cultured with shaking at 30°C in a YPD medium (1% yeast extract, 2% polypeptone, 2% glucose) for 2 days by using a genome DNA extraction kit "Gen-
20 torukun" (Takara Bio, Inc.). By using the extracted genome DNA as a template, an ACE1 transcription factor gene was amplified by PCR using two kinds of specific primers (ACE1-1F, ACE1-1RC). The amplified ACE1 transcription factor gene was
25 cloned into pBI221 (Clontech) by replacing a GUS gene of pBI221 by the amplified ACE1 transcription factor gene to prepare p35S-ACE1-NOS. Next, a NOS terminator contained in the p35S-ACE1-NOS was replaced by a CR16 terminator (US Patent

No.7202083) to prepare p35S-ACE1-CR.

Seeds of recombinant *Arabidopsis thaliana* (No.N70016), which had been purchased from NASC (Nottingham Arabidopsis Stock Centre), were plated on a modified MS agar medium (MS inorganic salts, B5 vitamin, 2% sucrose, 0.8% agar). From the true leaves of the recombinant *Arabidopsis thaliana* which had been grown for three weeks at 23°C, genomic DNA was extracted by using a kit for extracting plant genomic DNA, "DNeasy Plant mini kit (QIAGEN)." Using the extracted genomic DNA as a template, PCR was carried out by using two kinds of specific primers (VP16-1F, VP16-1RC) to amplify the gene for transcriptional activation domain (VP16AD) of transcription factor VP16 of a Herpes simplex virus. The amplified VP16AD gene was subjected to TA cloning into pCR2.1 (Invitrogen) to prepare pCR2.1-VP16AD. Using the pCR2.1-VP16AD as a template, PCR was carried out by using two specific kinds of primers (VP16-2F, VP16-2RC) and mutation was introduced into SacI site in the VP16AD gene to prepare pCR2.1-VP16AD(dSacI). Then, using the pCR2.1-VP16AD(dSacI) as a template, PCR was carried out by using two kinds of specific primers (VP16-3F, VP16-3RC) to add an XhoI site to the 5'-terminal, and SacI site to the 3'-terminal of the VP16AD(dSacI) gene. Furthermore, using the pCR2.1-VP16AD(dSacI) as a template, PCR was carried out by using two kinds of specific primers (VP16-4F, VP16-3RC) to add an BglII site to the 5'-terminal, and SacI site to the 3'-terminal of the VP16AD(dSacI) gene.

Using p35S-ACE1-CR as a template, PCR was carried out by using two kinds of specific primers (ACE1-1F, ACE1-2RC) to

remove the termination codon of the ACE1 transcription factor gene and to add XhoI site thereto. To the downstream of the ACE1 transcription factor gene to which XhoI site had been added to the 3'-terminal, VP16AD (dSacI) gene in which XhoI site had been added to the 5'-terminal was ligated in frame. As a result, p35S-ACE1/VP16AD-CR was prepared. Further, p35S-ACE1-CR was treated with the restriction enzymes BglII and SacI to cut out ACE1AD gene. To the downstream of the ACE1DBD transcription factor gene that lacks ACE1AD gene, VP16AD(dSacI) gene in which BglII site had been added to the 5'-terminal was ligated in frame to replace the ACE1AD gene by the VP16AD(dSacI) gene. As a result, p35S-ACE1DBD/VP16AD-CR was prepared.

ACE1-1F : 5'-atggatccatggtcgtaattaacggg-3' (SEQ ID NO:1)
 15 ACE1-1RC : 5'-tggagctcttattgtgaatgtgagttatg-3' (SEQ ID NO:2)
 ACE1-2RC : 5'-aactcgagttgtgaatgtgagttatg-3' (SEQ ID NO:3)
 VP16-1F : 5'-acggctccaccgaccgacgtc-3' (SEQ ID NO:4)
 VP16-1RC : 5'-ctaccaccgtactcgtcaattc-3' (SEQ ID NO:5)
 VP16-2F : 5'-ggacgaactccacttagacgg-3' (SEQ ID NO:6)
 20 VP16-2RC : 5'-ccgtctaagtggagttcgtcc-3' (SEQ ID NO:7)
 VP16-3F : 5'-tactcgagtcaacggctccaccgaccgacgt-3' (SEQ ID NO:8)
 VP16-3RC : 5'-aagagctcttaccaccgtactcgtcaattccaag-3' (SEQ ID NO:9)
 VP16-4F : 5'-taagatctatcaacggctccaccgaccgacgt-3' (SEQ ID NO:10)
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(2) Construction of an expression cassette for sGFP gene
 An sGFP gene was cut out from the plasmid CaMV35S-

sGFP(S65T)-NOS3' ("Experimental protocol for observation of a plant cell", edited by Fukuda Hiroo et al., 1997, Shujunsha, ISBN 4-87962-170-6), and cloned into pBI221 by using an adaptors NS-1F and NS-1RC and replacing a GUS gene of pBI221
5 by the sGFP gene to prepare p35S-sGFP. A region from -830bp to -91bp of CaMV35S promoter that is contained in p35S-sGFP was replaced by synthetic oligonucleotides MRE-1F and MRE-1RC to prepare pMRE/35S(-90)-sGFP.

The pMRE/35S(-90)-sGFP was treated with the restriction
10 enzyme EcoRV, and then dephosphorylated by using "Calf intestine Alkaline Phosphatase" (TAKARA BIO). Then, the blunt-ended and phosphorylated synthetic oligonucleotides MRE-1F and MRE-1RC were inserted thereto by using "Blunting Kination Ligation kit" (TAKARA BIO) to arrange MRE sequences
15 repeatedly twice in the forward direction. The portion in which the MRE sequence is repeated twice was cut out, and then was blunt-ended according to the method same as described above, and inserted again into EcoRV site. As a result, pMRE4/35S(-90)-sGFP in which MRE sequence is repeatedly
20 aligned four times in the forward direction was prepared.

In addition, using pBI221 as a template, PCR was carried out by using two kinds of specific primers (46bp-1F, 46bp-1RC) to amplify a DNA fragment containing a region from -46bp to -1bp of CaMV35S promoter. The amplified DNA fragment was
25 substituted for the region encompassing from -90bp to -1bp of CaMV35 promoter, which is located downstream of the MRE sequence that had been repeatedly aligned four times in the forward direction in the pMRE4/35S(-90)-sGFP, to give

pMRE4/35S(-46)-sGFP.

Meanwhile, a replacement was carried out with a sequence in which a mutation had been introduced to an as-1 site present in the region encompassing from -90bp to -1bp of CaMV35S promoter (Benfey PN & Chua NH, 1990, Science 250, 959-966). First, genomic DNA was extracted from *Arabidopsis thaliana* (No. N70016) purchased from NASC. Using the extracted genomic DNA as a template, PCR was carried out by using two kinds of specific primers (90m-1F, 90m-1RC). Then, 35S(-90m) sequence containing a mutation at an as-1 site was subjected to TA cloning into pCR2.1 (Invitrogen) to prepare pCR2.1-35S(-90m). Using pCR2.1-35S(-90m) as a template, PCR was carried out by using two kinds of specific primers (90m-2F, 90m-2RC) to add EcoRV site to the 5'-terminal and XbaI site to the 3'-terminal. The resulting DNA fragment was substituted for the region encompassing from -90bp to -1bp of CaMV35S promoter, which is located downstream of the MRE sequence that had been repeatedly aligned four times in the forward direction in the pMRE4/35S(-90)-sGFP, to give pMRE4/35S(-90m)-sGFP.

Each of the pMRE4/35S(-46)-sGFP and the pMRE4/35S(-90m)-sGFP was treated with the restriction enzyme HindIII, blunt-ended and phosphorylated by using "Blunting Kination Ligation kit", and then synthetic oligonucleotides KXS-1F and KXS-1RC were inserted thereto to prepare pKXS-MRE4/35S(-46)-sGFP or pKXS-MRE4/35S(-90m)-sGFP.

NS-1F: 5'-ggccgcgagctcagt-3' (SEQ ID NO:11)

NS-1RC: 5'-gactgagctcgc-3' (SEQ ID NO:12)

MRE-1F: 5' -
agcttagcgatgcggtcttttccgctgaaccggtccagcaaaaaagactagat-3' (SEQ
ID NO:13)

MRE-1RC: 5' -atctagtcttttttgctggaacgggttcagcggaaaagacgcacgcta-
5 3' (SEQ ID NO:14)

46bp-1F: 5' -tagatatcgcaagacccttcctctatataagg-3' (SEQ ID
NO:15)

46bp-1RC: 5' -atcctctagagtcccccggtgttc-3' (SEQ ID NO:16)

90m-1F: 5' -gctatgaccatgattacgccaaagcttg-3' (SEQ ID NO:17)

10 90m-1RC: 5' -cattgttatatctccttggtatccgtcg-3' (SEQ ID NO:18)

90m-2F: 5' -tagatatctccacgtccataagggac-3' (SEQ ID NO:19)

90m-2RC: 5' -aatctagactgcaggtcgtcctctcca-3' (SEQ ID NO:20)

KXS-1F: 5' -ggtagctcgagtcgac-3' (SEQ ID NO:21)

KXS-1RC: 5' -gtcgactcgaggtacc-3' (SEQ ID NO:22)

15

(3) Construction of an expression cassette for FT gene

Seeds of *Arabidopsis thaliana* (*Arabidopsis thaliana*
ecotype Columbia) were plated on a modified MS agar medium (MS
inorganic salts, B5 vitamin, 2% sucrose, 0.8% agar), and grown
20 at 23°C for three weeks. The obtained plant was then
transplanted to a pot already filled with culture soil and
cultivated in an artificial weather chamber. Two weeks after
the transplantation, total RNA was extracted from the flower
bud and true leaf of the plant by using a plant RNA extracting
25 kit "RNeasy Plant Mini Kit" (QIAGEN). With the extracted
total RNA, cDNA was synthesized by using a cDNA synthesis kit
"ReverTra Ace" (TOYOBO). Using the synthesized cDNA as a
template, PCR was carried out by using two kinds of specific

primers (FT-1F, FT-1RC) to amplify FT gene (GenBank Accession Number AB027504). Then, the amplified FT gene was substituted for GUS gene of pBI221 (Clontech). Using thus obtained plasmid as a template, fusion PCR was carried out by using six
5 kinds of specific primers (FT-2F, FT-2RC, FT-3F, FT-3RC, FT-4F, FT-1RC). As a result, a mutation without causing amino acid substitution was introduced at the BamHI site and EcoRI site present in the FT gene, and also an XbaI site at the 5'-terminal was changed to a BamHI site. The resulting modified
10 FT gene was substituted for sGFP gene of pKXS-MRE4/35S(-90m)-sGFP to prepare pKXS-MRE4/35S(-90m)-FT.

FT-1F: 5'-taatctagaatgtctataaaatataagagaccctc-3' (SEQ ID NO:23)

FT-1RC: 5'-atagagctcctaaagtcttcttctcctccg-3' (SEQ ID NO:24)

15 FT-2F: 5'-taaggatccatgtctataaaatataagagaccctc-3' (SEQ ID NO:25)

FT-2RC: 5'-gaacatctggatcgaccataaccaaagta-3' (SEQ ID NO:26)

FT-3F: 5'-tacttttggttatggtcgatccagatgttc-3' (SEQ ID NO:27)

FT-3RC: 5'-gacacgatgaataacctgcagtggga-3' (SEQ ID NO:28)

FT-4F: 5'-tcccactgcaggtattcatcgtgtc-3' (SEQ ID NO:29)

20

(4) Linking an expression cassette for transcription factor gene to an expression cassette for sGFP gene or to an expression cassette for FT gene

Plasmids p35S-ACE-CR, p35S-ACE1DBD/VP16AD-CR, and p35S-
25 ACE1/VP16AD-CR, containing expression cassettes for transcription factor gene, were treated with the restriction enzymes HindIII and EcoRI to cut out the expression cassettes for transcription factor gene. Plasmids pKXS-MRE4/35S(-46)-

sGFP and pKXS-MRE4/35S(-90m)-sGFP containing expression cassettes for sGFP gene and pKXS-MRE4/35S(-90m)-FT containing an expression cassette for FT gene were treated with the restriction enzymes KpnI and EcoRI to cut out the expression cassettes for sGFP gene and the expression cassette for FT gene, respectively.

An expression cassette for GUS gene contained in pBI121 (Clontech) was replaced by synthetic oligonucleotides HEK-1F and HEK-1RC to prepare pBI121-HEK. The pBI121-HEK was then treated with the restriction enzymes HindIII and KpnI. To the pBI121-HEK which had been treated with HindIII and KpnI, each one of the expression cassettes for transcription factor gene, and each one of the expression cassettes for sGFP gene or the expression cassette for FT gene, which had been cut out as described above, were ligated to obtain binary vectors in each of which the expression cassette for transcription factor gene and the expression cassette for sGFP gene or the expression cassette for FT gene are ligated at each terminator side (see, Fig. 1). A vector derived from p35S-ACE1-CR and pKXS-MRE4/35S(-46)-sGFP was referred to as vector (a), a vector derived from p35S-ACE1DBD/VP16AD-CR and pKXS-MRE4/35S(-46)-sGFP was referred to as vector (b), a vector derived from p35S-ACE1/VP16AD-CR and pKXS-MRE4/35S(-46)-sGFP was referred to as vector (c), a derived from p35S-ACE1/VP16AD-CR and pKXS-MRE4/35S(-90m)-sGFP was referred to as vector (d), and a vector derived from p35S-ACE1/VP16AD-CR and pKXS-MRE4/35S(-90m)-FT was referred to as vector (e).

HEK-1F: 5'-agcttgaattcgctcgacggtacctaggacgagctc-3' (SEQ ID NO:30)

HEK-1RC: 5'-aattgagctcgctcctaggtaccgctcgacgaattca-3' (SEQ ID NO:31)

5

Example 2 (Analysis of GFP accumulation amount in recombinant tobacco cultured cells)

(1) Preparation and selection of recombinant tobacco cultured cells

10 Each of vectors (a), (b), (c) and (d) produced in Example 1 was introduced into tobacco cultured cells (BY-2) by using gold particles of 1.0 μ m in diameter coated with each of these vectors according to a particle gun method (Morikawa Hiromichi et al, 1992, Plant Cell Engineering, Vol.4 No.1
15 p.47-52, Shujunsha Co., Ltd.). The DNA amount per 1.0 mg of gold particles was adjusted to 0.1 μ g. On the 3rd to 5th days after gene introduction operation, the tobacco cell suspension cultures subjected to gene introduction were spread on a modified MS agar medium (MS inorganic salts, 3% sucrose, 1 μ M
20 2,4-D, 1 mg/L thiamin HCl, 100 mg/L myo-inositol, 200 mg/L KH_2PO_4 , 0.8% agar) containing 30 mg/L of kanamycin. After culturing for one month, cell mass exhibiting resistance to 30 mg/L kanamycin was selected and the selected cell masses were again cultured for 4 to 8 weeks while they are transferred to
25 a new agar medium every one or two weeks. The condition for culture was at 23 to 25°C in a dark place.

(2) Analysis of GFP accumulation amount using a

fluorescent plate reader

The obtained cell mass was transplanted onto modified MS agar medium (MS inorganic salts, 3% sucrose, 1 μ M 2,4-D, 1 mg/L thiamin HCl, 100 mg/L myo-inositol, 200 mg/L KH_2PO_4 , 0.8% agar) containing 100 μ M CuSO_4 as an inducible expression treatment group to carry out a treatment for induced expression of a target heterologous gene by copper ion (hereinafter, sometimes, referred to as the inducible expression treatment). Additionally, as a non-inducible expression treatment group, a modified MS agar medium not containing CuSO_4 was used.

Three days after the inducible expression treatment, the cell mass was examined under a fluorescent microscope (Nikon) to determine the fluorescent emission state of GFP.

The cell mass confirmed with the increased fluorescent emission of GFP was frozen in liquid nitrogen. Then, to the frozen cells, glass beads (0.25 to 0.5 mm) and an extraction buffer (1 $\times$ PBS (-), 5 mM DTT, 1 mM PMSF, 0.1% protease inhibitor cocktail) were added, followed by disruption treatment using a disruption device, "Mixer Mill" (QIAGEN). The resulting disruption product was centrifuged by a table centrifugal machine at 15000 rpm, 4°C for five minutes to obtain the supernatant, which was used as a protein extraction solution. Subsequently, the protein extraction solution was diluted appropriately with 1 $\times$ PBS (-), and the fluorescence intensity of GFP in the obtained diluted solution was determined by using a multi label counter "Wallac 1420 ARVOMX" (Perkin Elmer). Meanwhile, as a standard sample, a dilution

obtained by diluting recombinant GFP (Cosmo Bio) with 1×PBS (-
) was used. From the measured fluorescence intensity, GFP
conversion amount per unit amount of soluble proteins was
obtained. Further, by subtracting the corresponding value for
5 the control wild-type cell mass as background value, the GFP
accumulation amount was calculated. In addition, the protein
concentration in the protein extraction solution was
quantified according to the Bradford method.

In Table 1, a quantification result of GFP accumulated
10 in the recombinant tobacco cultured cells, in which sGFP gene
expression vector that can be induced by copper ions is
introduced, is summarized. Induction ratio indicates the
ratio of accumulated amount of GFP in the inducible expression
treatment group compared to the accumulated amount of GFP in
15 the non-inducible expression treatment group.

For the recombinant tobacco cultured cells into which
the vector (a) has been introduced, the accumulated amount of
GFP in the inducible expression treatment group was two times
higher than that of GFP in the non-inducible expression
20 treatment group (hereinafter, sometimes also referred to as
"induction ratio for the recombinant tobacco cultured cells
into which the vector (a) has been introduced). For the
recombinant tobacco cultured cells into which the vector (b)
has been introduced in which ACE1AD of the ACE1 transcription
25 factor has been replaced by VP16AD, the accumulated amount of
GFP in the inducible expression treatment group was four times
higher than that of GFP in the non-inducible expression
treatment group (hereinafter, sometimes also referred to as

"induction ratio for the recombinant tobacco cultured cells into which the vector (b) has been introduced), and it was recognized that it was improved two times compared to the induction ratio of the recombinant tobacco cultured cells into which the vector (a) has been introduced.

Meanwhile, for the recombinant tobacco cultured cells into which the vector (c) has been introduced in which VP16AD has been added to the ACE1 transcription factor, the accumulated amount of GFP in the inducible expression treatment group was eighteen times higher than that of GFP in the non-inducible expression treatment group (hereinafter, sometimes also referred to as "induction ratio for the recombinant tobacco cultured cells into which the vector (c) has been introduced), and it was recognized that it was improved nine times compared to the induction ratio of the recombinant tobacco cultured cells into which the vector (a) was introduced.

Still further, for the recombinant tobacco cultured cells into which the vector (d) has been introduced in which 35S(-90m) sequence having a mutation at as-1 site is used, the accumulated amount of GFP in the inducible expression treatment group was eighteen times higher than that of GFP in the non-inducible expression treatment group (hereinafter, sometimes also referred to as "induction ratio for the recombinant tobacco cultured cells into which the vector (d) has been introduced), and it was recognized that it was improved nine times compared to the induction ratio of the recombinant tobacco cultured cells into which the vector (a)

has been introduced.

Table 1

Vector	GFP (ng/μg protein)		Induction ratio	Improvement ratio
	Non-inducible expression treatment group	Inducible expression treatment group		
(a)	0.5	1.0	2	1
(b)	1.1	4.2	4	2
(c)	0.8	14.2	18	9
(d)	0.6	10.8	18	9

Example 3 (Flowering induction in recombinant

5 *Arabidopsis thaliana*)

(1) Preparation and selection of recombinant *Arabidopsis thaliana*

The vector (e) prepared in Example 1 was introduced into *Agrobacterium* (*Agrobacterium tumefaciens* strain C58C1). The
10 resulting *Agrobacterium* was cultured in a LB agar medium (0.5% yeast extract, 1.0% bactotrypton, 0.5% saline, 1% agar) containing 50 mg/L kanamycin, 100 mg/L ampicillin, and 100 mg/L rifampicin, and a drug-resistant colony was selected to obtain recombinant *Agrobacterium*. *Arabidopsis* (*Arabidopsis*
15 *thaliana* ecotype Columbia) was infected by the obtained recombinant *Agrobacterium* according to the method described in Model Plant Laboratory Manual (edited by Iwabuchi Masaki et al, 2000, Springer-Verlag Tokyo Co., Ltd., ISBN 4-431-70881-2 C3045) to introduce genes. After T₁ seeds collected from the
20 *Arabidopsis* subjected to gene introduction, the seeds were plated and grown on a modified MS agar medium (MS inorganic salts, B5 vitamin, 1% sucrose, 0.8% agar) containing 20 mg/L

of Benlate, 200 mg/L of Claforan, and 25 mg/L kanamycin to select a plant individual resistant to kanamycin. The selected plant individual was transplanted to a pot in which culture soil was previously placed, and grown in an artificial weather chamber to obtain T₂ seeds. After the obtained T₂ seeds were plated and grown on a modified MS agar medium (MS inorganic salts, B5 vitamin, 2% sucrose, 0.8% agar) containing 25 mg/L kanamycin, a plant line which produces the kanamycin-resistant individual plant in 3:1 ratio at 5% significance level according to chi-square test was selected. Meanwhile, the condition for cultivating the plant included 23 hours of light period and 1 hour of dark period at 23 to 25°C.

(2) Flowering induction in recombinant *Arabidopsis thaliana*

With respect to the selected line, T₂ seeds were plated on a modified MS agar medium (MS inorganic salts, B5 vitamin, 2% sucrose, 0.8% agar). After incubating the individual plant for 11 days under the condition including 23 hours of light period and 1 hour of dark period at 23 to 25°C, the resulting plant was transplanted to a modified MS agar medium (MS inorganic salts, B5 vitamin, 2% sucrose, 0.8% agar) containing 50 µM CuSO₄, to carry out a treatment for inducible expression of a heterologous gene of interest by copper ions (hereinafter, sometimes referred to as inducible expression treatment). In addition, as a non-inducible expression treatment group, a modified MS agar medium not containing CuSO₄ was used.

Six hours after the inducible expression treatment, the

individual plant was transferred to the modified MS agar medium (MS inorganic salts, B5 vitamin, 2% sucrose, 0.8% agar) not containing CuSO_4 . Five days after the inducible expression treatment, observation of the individual plant was carried out.

5 As a result, it was found that flowering was induced earlier in the inducible expression treatment group compared to non-inducible expression treatment group (see, Fig. 2).

10 According to the present invention, a method for control of flowering time in a transgenic plant in a copper-inducible manner is provided, wherein a heterologous gene which controls flowering time has been introduced to the transgenic plant.

WHAT IS CLAIMED IS:

1. A method for controlling flowering time of a plant,
which comprises bringing a plant into contact with copper ions,
5 wherein the plant has been transformed with the following DNA
constructs (i) and (ii):

(i) a first DNA construct comprising a nucleotide
sequence encoding a chimeric transcription factor, wherein the
chimeric transcription factor comprises the following a) and
10 b) as operably linked elements:

a) a DNA-binding domain of a first transcription factor
that is capable of being activated by copper ion, and

b) a transcriptional activation domain of at least one
second transcription factor that is different from the first
15 transcription factor; and

(ii) a second DNA construct encoding a heterologous gene
which controls flowering time of a plant, wherein the gene is
under the control of a heterologous promoter capable of being
stimulated by the chimeric transcription factor of (i) in the
20 presence of copper ion.

2. The method according to claim 1, wherein the chimeric
transcription factor further comprises as the operably linked
elements a transcriptional activation domain of the first
25 transcription factor.

3. The method according to claim 1 or 2, wherein the
first transcription factor is selected from the group

consisting of:

(1) a eukaryote transcription factor which is capable of being activated by copper ion,

(2) a yeast transcription factor which is capable of being activated by copper ion, and

(3) a transcription factor derived from the yeast ACE1 which is capable of being activated by copper ion.

4. The method according to any of claims 1 to 3, wherein the second transcription factor is selected from the group consisting of:

(1) a transcription factor of a virus,

(2) a transcription factor of a virus belonging to Simplex virus genus,

(3) a transcription factor of Herpes simplex virus, and

(4) the VP16 transcription factor of Herpes simplex virus.

5. The method according to any of claims 1 to 4, wherein the heterologous gene which controls flowering time of a plant is selected from the group consisting of:

(1) a plant gene controlling flowering time,

(2) an angiosperm gene controlling flowering time,

(3) a dicotyledonous gene controlling flowering time,

(4) a Cruciferous gene controlling flowering time,

(5) an *Arabidopsis thaliana* gene controlling flowering time, and

(6) a flowering-time controlling gene derived from the

Arabidopsis thaliana FT gene.

6. The method according to any of claims 1 to 5, wherein the first DNA construct further comprises a promoter which is
5 capable of functioning in plant cells and is operably linked to the nucleotide sequence encoding the chimeric transcription factor.

7. A set of the following DNA constructs (i) and (ii):
10 (i) a first DNA construct comprising a nucleotide sequence encoding a chimeric transcription factor, wherein the chimeric transcription factor comprises the following a) and b) as operably linked elements:

a) a DNA-binding domain of a first transcription factor
15 that is capable of being activated by copper ion, and

b) a transcriptional activation domain of at least one second transcription factor that is different from the first transcription factor; and

(ii) a second DNA construct encoding a heterologous gene
20 which controls flowering time of a plant, wherein the gene is under the control of a heterologous promoter capable of being stimulated by the chimeric transcription factor of (i) in the presence of copper ion.

25 8. The set of the DNA constructs according to claim 7, wherein the chimeric transcription factor further comprises as the operably linked elements a transcriptional activation domain of the first transcription factor.

9. The set of the DNA constructs according to claim 7 or 8, wherein the first transcription factor is selected from the group consisting of:

5 (1) a eukaryote transcription factor which is capable of being activated by copper ion,

(2) a yeast transcription factor which is capable of being activated by copper ion, and

(3) a transcription factor derived from the yeast ACE1
10 which is capable of being activated by copper ion.

10. The set of the DNA constructs according to any of claims 7 to 9, wherein the second transcription factor is selected from the group consisting of:

15 (1) a transcription factor of a virus,

(2) a transcription factor of a virus belonging to Simplex virus genus,

(3) a transcription factor of Herpes simplex virus, and

(4) the VP16 transcription factor of Herpes simplex
20 virus.

11. The set of the DNA constructs according to any of claims 7 to 10, wherein the heterologous gene which controls flowering time of a plant is selected from the group

25 consisting of:

(1) a plant gene controlling flowering time,

(2) an angiosperm gene controlling flowering time,

(3) a dicotyledonous gene controlling flowering time,

(4) a Cruciferous gene controlling flowering time,
(5) an *Arabidopsis thaliana* gene controlling flowering
time, and
(6) a flowering-time controlling gene derived from the
5 *Arabidopsis thaliana* FT gene.

12. The set of the DNA constructs according to any of
claims 7 to 11, wherein the first DNA construct further
comprises a promoter which is capable of functioning in plant
10 cells and is operably linked to the nucleotide sequence
encoding the chimeric transcription factor.

13. A plant transformed with the set of DNA constructs
of any of claims 7 to 11.
15

14. A method of producing a transgenic plant with a
copper-inducible control of flowering time comprising:
introducing the set of DNA constructs of any of the
items 7 to 11 into a plant cell,
20 regenerating a plant from the plant cell,
selecting a plant comprising the DNA constructs, and
growing the plant under conditions that allow copper-
inducible control of flowering time.

SEQUENCE LISTING

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<120> METHOD FOR CONTROLLING FLOWERING TIME OF PLANT

<130> S21491

<150> JP2008-225711

<151> 2008-09-03

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