DESCRIPTION

PROCESS FOR PRODUCING ROSE WITH MODIFIED COLOR

Technical Field

The present invention relates to a new method for producing a rose with altered petal colors. More specifically, it relates to a method for producing a rose by artificially inhibiting the endogenous metabolic pathway of rose, and expressing the gene coding for pansy flavonoid 3',5'-hydroxylase and the gene coding for dihydroflavonol reductase which reduces dihydromyricetin.

Background Art

Flower petals perform the role of attracting pollinators such as insects and birds, which transport plant pollen, and therefore flower colors, shapes, patterns and odors have evolved in tandem with pollinators (Honda, T. et al., Gendai Kagaku, May, 25-32(1998)). Probably as a result of this, it is rare for a single species of flower to exhibit several different colors, and for example, rose or carnation varieties exhibiting violet to blue colors do not exist, while iris or gentian varieties exhibiting bright red colors do not exist. Because flower color is the most important aspect of petals for purposes of appreciation as well, flowers of different colors have traditionally been bred by crossbreeding. The rose, known as the "queen of flowers" and having high commercial value, has also been crossbred throughout the world.

For example, the current yellow rose cultivar was created by crossbreeding of *Rosa foetida*, originating from western Asia, with a non-yellow rose variety. However, because flower color is determined by the genetic capacity of the plant, there has been a limit to the flower colors that can currently be produced in cross-bred strains whose available genetic sources are

restricted (Tanaka et al. Plant Cell Physiol. 39, 1119-1126, 1998; Mol et al. Curr. Opinion Biotechnol. 10, 198-201 1999). Among these, the cultivation of blue roses has been thought impossible and has been considered the "holy grail" of colors (Oba, H., "Bara no Tanjo", 1997, Chukoshinsho; Suzuki, M., "Shokubutsu Bio no Mahou: Aoi Bara mo Yume dewanakunatta", 1990, Kodansha Bluebacks; Saisho, H., "Aoi Bara", 2001, Shogakkan).

Although "blue rose" varieties currently exist, these are actually pale violet roses. The first improved variety of "blue rose" by crossbreeding is said to have been the light-violet shaded grey-colored "Grey Pearl" created in 1945. The light-violet pink-colored "Staring Silver" was later created in 1957, and these varieties were crossed to produce several pale violet roses such as "Blue Moon" (1964) and "Madam Violet" (1981). These pale violet roses and other roses were then utilized in further breeding to create light-grey-colored roses such as "Seiryu" (1992) and "Blue Heaven" (2002), which were hailed as new types of "blue roses".

However, these flower colors are not actually blue but merely greyish-dull pink, and despite many years of breeding efforts, there is still no example of a truly "blue" rose. In horticultural industry, the group of colors from violet to blue is generally considered "blue" according to the RHSCC (The Royal Horticultural Society Colour Chart). It is an aim of the present invention to create rose plants having flower colors falling within the "violet group", "violet-blue" group and "blue group" according to the Royal Horticultural Society Colour Chart.

Flower colors derive mainly from the three compound groups of anthocyanins, carotenoids and betalains, but it is the anthocyanins, having the widest absorption wavelength range (from orange to blue), that are responsible for blue color. Anthocyanins belong to the flavonoid family and are biosynthesized by the metabolic

pathway shown in Fig. 1. Anthocyanins are normally localized in the vacuoles of epithelial cells. The color shade of anthocyanins (i.e. flower color) depends largely on the structure of the anthocyanins, with more numerous hydroxyl groups on the B ring resulting in a bluer color. Hydroxylation of the B ring is catalyzed by flavonoid 3'-hydroxylase (F3'H) and flavonoid 3',5'-hydroxylase (F3'5'H). Absence of F3'H and F3'5'H activity leads to synthesis of pelargonidin (orange to red colors), presence of F3'H activity leads to synthesis of cyanidin (red to rouge colors) and presence of F3'5'H activity leads to synthesis of delphinidin (violet color).

These anthocyanidins are modified with sugars and acyl groups to produce an assortment of anthocyanins. Generally speaking, a larger number of modifying aromatic acyl groups correlates to bluer anthocyanins. Anthocyanins also produce quite different colors depending on the vacuole pH and the copresent flavonols and flavones or metal ions (Saito, N., Tanpakushitsu Kakusan Kouso, 47 202-209, 2002; Broullard and Dangles, In the flavonoids: Advances in Research since 1986 (Ed. by Harborne) Capmann and Hall, London pp.565-588; Tanaka et al. Plant Cell Physiol. 39 1119-1126, 1998; Mol et al., Trends in Plant Science 3, 212-217, 1998; Mol et al., Curr. Opinion Biotechnol. 10, 198-201 1999).

Rose flower petal anthocyanins are derivatives of pelargonidin, cyanidin and peonidin, whereas no delphinidin derivatives are known (Biolley and May, J. Experimental Botany, 44, 1725-1734 1993; Mikanagi Y., Saito N., Yokoi M. and Tatsuzawa F. (2000) Biochem. Systematics Ecol. 28:887-902). This is considered to be the main reason for the lack of blue roses. Existing roses have been created by crossbreeding of crossable related rose species (*R. multiflora*, *R. chinensis*, *R. gigantean*, *R. moschata*, *R. gallica*, *R. whichuraiana*, *R. foetida*, etc.).

The fact that no blue rose has been achieved in

spite of repeated efforts at crossbreeding is attributed to the lack of delphinidin production ability by rose-related varieties. Production of delphinidin in rose petals would require expression of F3'5'H in the petals as mentioned above, but F3'5'H is believed to be non-expressed in the petals of rose and rose-related varieties. Thus, it is likely impossible to obtain a blue rose by accumulating delphinidin in the petals through crossbreeding. It is known that trace amounts of the blue pigment rosacyanin are found in rose petals and its chemical structure has been determined (Japanese Unexamined Patent Publication No. 2002-201372), but no reports are known regarding augmentation of rosacyanin to create a blue rose, and no findings have been published on the rosacyanin biosynthesis pathway or the relevant enzymes or genes.

Examples of blue or violet colors produced by biological organisms also include indigo plant-produced indigo (for example, Appl. Microbiol. Biotechnol. Feb. 2003, 60(6):720-5) and microbially-produced violacein (J. Mol. Microbiol. Biotechnol. Oct. 2000 2(4):513-9; Org. Lett., Vol.3, No.13, 2001, 1981-1984), and their derivation from tryptophan and their biosynthetic pathways have been studied.

Blue pigments based on gardenia fruit-derived iridoid compounds (S. Fujikawa, Y. Fukui, K. Koga, T. Iwashita, H. Komura, K. Nomoto, (1987) Structure of genipocyanin G1, a spontaneous reaction product between genipin and glycine. Tetrahedron Lett. 28 (40), 4699-700; S. Fujikawa, Y. Fukui, K. Koga, J. Kumada, (1987), Brilliant skyblue pigment formation from gardenia fruits, J. Ferment. Technol. 65 (4), 419-24) and lichen-derived azulenes (Wako Pure Chemical Industries Co., Ltd.) are also known, but no reports are known of expressing these in plant flower petals to produce blue-colored flowers.

It has been expected that a blue rose could be created by transferring the F3'5'H gene expressed by

other plants into rose and expressing it in rose petals (Saisho, H., "Aoi Bara", 2001, Shogakkan). The F3'5'H gene has been obtained from several plants including petunia, gentian and *Eustoma russellianum* (Holton et al. Nature 366, 276-279, 1993; Tanaka et al. Plan Cell Physiol. 37, 711-716 1996; WO93/18155). There are also reports of transformed varieties of rose (for example, Firoozababy et al. Bio/Technology 12:609-613 (1994); US 5480789; US 5792927; EP 536,327 A1; US 20010007157 A1).

Actual transfer of the petunia F3'5'H gene into rose has also been reported (WO93/18155, WO94/28140).

However, it has not been possible to obtain a blue rose, and it is believed that obtaining a blue rose will require a modification which alters the metabolism of flower pigments suited for rose.

On the other hand, it has been confirmed that transfer of the F3'5'H gene into red carnation, which produces pelargonidin instead of delphinidin, leads to accumulation of both pelargonidin and delphinidin, but that the flower color is only altered to a slightly purplish red (WO94/28140). This result suggests that it is not possible to obtain a "blue" carnation simply by expression of F3'5'H, and that it is necessary to inhibit the metabolic pathway to endogenous synthesis of pelargonidin by carnation.

In order to avoid competition with the carnation endogenous metabolic pathway (reduction of dihydrokaempferol (DHK) by dihydroflavonol reductase (DFR)), a variety lacking DFR was selected from among white carnations. The F3'5'H gene and petunia DFR (which is known to efficiently reduce dihydromyricetin (DHM) without reducing DHK) gene were transferred into carnation. This resulted in one case of successfully obtaining a recombinant carnation with a delphinidin content of about 100% and a blue-violet flower color previously not found in carnation (Tanpakushitsu Kakusan Kouso, Vol.47, No.3, p225, 2002). Thus, further

modification was necessary to realize a blue carnation flower, in addition to accumulating delphinidin by expression of the F3'5'H gene.

DFR has already been cloned from several plants (petunia, tobacco, rose, *Torenia*, snapdragon, transvaal daisy, orchid, barley, corn, etc.) (Meyer et al., Nature 330, 677-678, 1987; Helariutta et al., Plant Mol. Biol. 22, 183-193 1993; Tanaka et al., Plant Cell Physiol. 36, 1023-1031; Johnson et al., Plant J. 19, 81-85, 1999). Substrate specificity of the DFR gene differs depending on the plant variety, and it is known that the petunia, tobacco and orchid DFR genes cannot reduce DHK, whereas the petunia DFR gene most efficiently reduces DHM among the dihydroflavonols (Forkmann et al., Z. Naturforsch. 42c, 1146-1148, 1987; Johnson et al. Plant J. 19, 81-85, 1999). Nevertheless, no cases have been reported for expression of these DFR genes in rose.

As a means of avoiding competition with the endogenous metabolic pathway or between the enzyme and the exogenous gene-derived enzyme such as F3'5'H, as mentioned above, the gene may be transferred into a variety lacking the gene. Also, it is known that expression of the target gene can be artificially inhibited by deletion methods involving homologous recombination of the target gene, but because of the low frequency of homologous recombination and the limited number of suitable plant varieties, this has not been implemented in practice (for example, Nat. Biotechnol. 2002, 20:1030-4).

Inhibition methods on the transcription level include the antisense method using antisense RNA transcripts for mRNA of the target gene (van der Krol et al., Nature 333, 866-869, 1988), the sense (cosuppression) method using transcripts of RNA equivalent to mRNA of the target gene (Napoli et al., Plant Cell 2, 279-289, 1990) and a method of using duplex RNA transcripts corresponding to mRNA of the target gene

(RNAi method; Waterhouse et al., Pro. Natl. Acad. Sci. USA 95, 13959-13964, 1998).

Numerous successful examples of these three methods have been published. For rose, cosuppression of chalcone synthase (CHS) gene which is necessary for synthesis of anthocyanins was reported to successfully alter flower color from red to pink (Gutterson HortScience 30:964-966 1995), but this CHS suppression is incomplete and therefore it has not been possible to totally suppress anthocyanin synthesis to obtain a white flower stock.

Patent document 1: Japanese Unexamined Patent Publication No. 2002-201372

Patent document 2: WO93/18155

Patent document 3: USP 5480789

Patent document 4: USP 5792927

Patent document 5: EP 536 327 A1

Patent document 6: US 20010007157 A1

Patent document 7: WO94/28140

Non-patent document 1: Honda T. et al. Gendai Kagaku, May, 25-32(1998)

Non-patent document 2: Tanaka et al. Plant Cell Physiol. 39, 1119-1126, 1998

Non-patent document 3: Mol et al. Curr. Opinion Biotechnol. 10, 198-201 1999

Non-patent document 4: Oba, H., "Bara no Tanjo", 1997, Chukoshinsho

Non-patent document 5: Suzuki, M., "Shokubutsu Bio no Mahou: Aoi Bara mo Yume dewanakunatta", 1990, Kodansha Bluebacks

Non-patent document 6: Saisho, H., "Aoi Bara", 2001, Shogakkan

Non-patent document 7: Saito, N., Tanpakushitsu Kakusan Kouso, 47 202-209, 2002

Non-patent document 8: Broullard et al. In the flavonoids: Advances in Research since 1986 (Ed by Harborne) Capmann and Hall, London pp565-588

Non-patent document 9: Tanaka et al. Plant Cell

Physiol. 39 1119-1126, 1998

Non-patent document 10: Mol et al, Trends in Plant Science 3, 212-217 1998

Non-patent document 11: Mol et al. Curr. Opinion Biotechnol. 10, 198-201 1999

Non-patent document 12: Biolley and May, J. Experimental Botany, 44, 1725-1734 1993

Non-patent document 13: Mikanagi Y, et al. (2000) Biochem Systematics Ecol. 28:887-902

Non-patent document 14: Appl. Microbiol. Biotechnol. 2003 Feb;60(6):720-5

Non-patent document 15: J. Mol. Microbiol. Biotechnol. 2000 Oct; 2 (4): 513-9

Non-patent document 16: Org. Lett., Vol. 3, No. 13, 2001, 1981-1984

Non-patent document 17: S. Fujikawa, et al. (1987) Tetrahedron Lett. 28 (40), 4699-700

Non-patent document 18: S. Fujikawa, et al. (1987) J. Ferment. Technol. 65 (4), 419-24

Non-patent document 19: Holton et al. Nature 366, 276-279, 1993

Non-patent document 20: Tanaka et al. Plant Cell Physiol. 37, 711-716 1996

Non-patent document 21: Firoozababy et al. Bio/Technology 12: 609-613 (1994)

Non-patent document 22: Tanpakushitsu Kakusan Kouso, Vol.47, No.3, p225, 2002

Non-patent document 23: Meyer et al. Nature 330, 677-678, 1987

Non-patent document 24: Helariutta et al. Plant Mol. Biol. 22 183-193 1993

Non-patent document 25: Tanaka et al. Plant Cell Physiol. 36, 1023-1031

Non-patent document 26: Johnson et al. Plant J. 19, 81-85, 1999

Non-patent document 27: Forkmann et al. Z. Naturforsch. 42c, 1146-1148, 1987

Non-patent document 28: Nat Biotechnol 2002, 20:1030-4

Non-patent document 29: van der Krol et al. Nature 333, 866-869, 1988

Non-patent document 30: Napoli et al. Plant Cell 2, 279-289, 1990

Non-patent document 31: Waterhouse et al. Pro. Natl. Acad. Sci. USA 95, 13959-13964 1998

Non-patent document 32: Gutterson HortScience 30:964-966 1995

Non-patent document 33: Suzuki, S., "Bara, Hanazufu", Shogakkann, p.256-260, 1990

Disclosure of the Invention

As mentioned above, rose flower colors have been successfully altered by transferring the F3'5'H gene into rose and expressing it in the petals. In carnation, the F3'5'H gene and petunia DFR gene have been expressed in DFR-deficient varieties to create blue-violet carnations. However, a "blue rose" has not yet been created. It is therefore an object of the present invention to provide a rose which blossoms with a blue flower.

The invention thus provides (1) a method for producing a rose characterized by artificially suppressing the rose endogenous metabolic pathway and expressing the pansy gene coding for flavonoid 3',5'-hydroxylase.

The invention further provides (2) a method for producing a rose characterized by artificially suppressing the rose endogenous metabolic pathway, and expressing the pansy gene coding for flavonoid 3',5'-hydroxylase and the gene coding for dihydroflavonol reductase.

The invention still further provides (3) a method for producing a rose characterized by artificially suppressing expression of rose endogenous dihydroflavonol reductase, and expressing the pansy gene coding for

flavonoid 3',5'-hydroxylase and the gene coding for dihydroflavonol reductase derived from a plant other than rose.

The invention still further provides (4) a method for producing a rose characterized by artificially suppressing expression of rose endogenous flavonoid 3'-hydroxylase and expressing the pansy gene coding for flavonoid 3',5'-hydroxylase.

The aforementioned pansy gene coding for flavonoid 3',5'-hydroxylase is, for example, the gene listed as SEQ ID NO: 1 or SEQ ID NO: 3. The gene coding for dihydroflavonol reductase is preferably derived from iris, *Nierembergia*, petunia, orchid, gentian or *Eustoma russellianum*.

The invention still further provides (5) a rose obtained by the production method according to any one of (1) to (4) above, or a progeny or tissue thereof having the same properties as the rose.

The invention still further provides (6) a rose obtained by the production method according to any one of (1) to (4) above, or a progeny or tissue thereof, wherein the petal color of the rose is violet, blue-violet or blue.

The invention further provides (7) a rose according to (6) above, or a progeny or tissue thereof, wherein the petal color of the rose belongs to the "Violet group", "Violet-Blue" group or "Blue group" according to the Royal Horticultural Society Colour Chart (RHSCC).

The invention further provides (8) a rose according to (7) above, or a progeny or tissue thereof, wherein the petal color of the rose belongs to "Violet group" 85a or 85b according to the Royal Horticultural Society Colour Chart (RHSCC).

Brief Description of the Drawings

Fig. 1 shows the flavonoid biosynthesis pathway. CHS: Chalcone synthase, CHI: Chalcone isomerase

FNS: Flavone synthase, F3H: Flavanone 3-hydroxylase
F3'H: Flavonoid 3'-hydroxylase
F3'5'H: Flavonoid 3'5'-hydroxylase, FLS: Flavonol synthase
DFR: Dihydroflavonol 4-reductase
ANS: Anthocyanidin synthase, AS: Aurone synthase
C2'GT: Chalcone 2'-glucosyl transferase
Fig. 2 shows the structure of plasmid pBERD1.
Fig. 3 shows the structure of plasmid pBPDBP2.
Fig. 4 shows the structure of plasmid pBPDBP8.
Fig. 5 shows the structure of plasmid pSPB461.
Fig. 6 shows the structure of plasmid pSPB472.
Fig. 7 shows the structure of plasmid pSPB130.
Fig. 8 shows the structure of plasmid pSPB919.
Fig. 9 shows the structure of plasmid pSPB920.
Fig. 10 shows the structure of plasmid pSPB1106.

Best Mode for Carrying Out the Invention

Several reasons may be postulated for a lack of blue color in rose even with production of delphinidin. The stability, solubility and color of anthocyanins varies depending on modification with acyl groups and sugars. Specifically, it is known that an increased number of aromatic acyl groups results in greater blueness. Also, formation of complexes between flavonol and flavone copigments and anthocyanins produce a blue color and shift the maximum absorption wavelength toward the longer wavelength end while also increasing the absorbance. Anthocyanin color is also dependent on pH. Since a lower pH tends toward redness and a more neutral pH produces blueness, the flower color depends on the pH of the vacuoles in which the anthocyanins are localized. In addition, formation of metal chelates in the copresence of metal ions such as Al^{3+} and Mg^{2+} can significantly affect flower color as well. Trial and error and assiduous research led to the proposal for a modification whereby the proportion of delphinidin in flower petals is

increased.

First, it was attempted to create a blue rose by the same method used to create a blue-violet carnation. Specifically, it was attempted to analyze white rose variety 112 and identify a DFR-deficient line, but unlike carnation, no completely DFR-deficient line could be obtained. This is presumably due to the fact that carnation is diploid while ordinarily cultivated rose is tetraploid, such that it is difficult to find a line deficient in a single gene.

Next, the pansy F3'5'H gene and petunia DFR gene were transferred into the white flower variety Tineke and accumulation of delphinidin was detected, but the amount was minimal and a blue rose was not obtained.

According to the present invention, the DFR gene, an enzyme participating in the rose endogenous flavonoid synthesis pathway, is artificially suppressed by a gene engineering technique, and the pansy F3'5'H gene is expressed while a dihydromyricetin-reducing DFR gene is also expressed, in order to increase the delphinidin content to roughly 80-100% of the total anthocyanidins in the flower petals, thereby allowing realization of a blue rose.

The dihydromyricetin-reducing DFR genes used in this case were derived from iris (*Iridaceae*), *Nierembergia* (*Solanaceae*) and petunia (*Solanaceae*), but as other dihydromyricetin-reducing DFR gene sources there may be mentioned non-pelargonidin-accumulating plants such as tobacco (Solanaceae), cyclamen (Primulaceae), delphinium (*Ranunculaceae*), orchid (*Orchidaceae*), gentian (*Gentianaceae*), *Eustoma russellianum* (*Gentianaceae*) and the like (Forkmann 1991, Plant Breeding 106, 1-26; Johnson et al., Plant J. 1999, 19, 81-85). The DFR genes used for the present invention are genes that preferentially reduce dihydromyricetin.

According to the invention, the flavonoid 3'-hydroxylase (F3'H) gene, an enzyme participating in the

rose endogenous flavonoid synthesis pathway, is artificially suppressed by a gene engineering technique, and the pansy F3'5'H gene is expressed, in order to increase the delphinidin content to roughly 80-100% of the total anthocyanidins in the flower petals, thereby allowing realization of a blue rose.

The roses obtained according to the invention have hitherto non-existent flower colors, and the invention can provide roses with flower colors belonging not only to the red-purple group, purple group and purple-violet group but also to the violet group, violet-blue group and blue group, according to the Royal Horticultural Society Colour Chart.

Examples

The present invention will now be explained in greater detail by the following examples. Unless otherwise specified, the molecular biological protocols used were based on Molecular Cloning (Sambrook and Russell, 2001, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York).

Example 1. Flower color measuring method

The flower petal color shade was evaluated by measurement using a CM2022 spectrophotometric colorimeter (Minolta Japan) with a 10° visual field and a D65 light source, and analysis using SpectraMagic color control software (Minolta Japan). The Royal Horticultural Society Colour Chart (RHSCC) number is the nearest color as compared against Color Classification System Version 2.1.1 (The Japan Research Institute Co., Ltd.; Japanese Unexamined Patent Publication No. 2002-016935), based on the color value (CIE L*a*b* color system) obtained by visual discrimination and measurement with the device mentioned above. This system may be used for objective selection of the nearest RHSCC number.

Upon measuring the color shades of flower petals of cultivars conventionally referred to as "blue roses" and

determining the nearest colors according to the RHSCC by this method, it was determined that Blue Moon and Madam Violet were 186d (Greyed-Purple group), Lavande was 186c (Greyed-Purple group), Seiryu was 189d (Greyed-Green group) and Blue Heaven was 198d (Greyed-Green group). These cultivars are called blue roses but are classified in "Grey" groups according to RHSCC number and therefore do not exhibit the blue color which is the object of the present invention.

Example 2. Flavonoid analysis

1) Extraction of flower petal color

A 0.5 g portion of freeze-dried rose petals was subjected to extraction in 4 ml of 50% acetonitrile (CH_3CN) containing 0.1% TFA for 20 minutes under ultrasonic vibration and then filtered with a 0.45 μm filter. High-performance liquid chromatography (HPLC) of the anthocyanins in the extract was conducted under the following conditions. Isocratic elution was carried out using an RSpak DE-413L (4.6 mmϕ x 25 cm, Shoko Co., Ltd.) column with a flow rate of 0.6 ml/min, and a mobile phase at a linear concentration gradient of 10%→50% CH_3CN/H_2O containing 0.5% trifluoroacetic acid (TFA) for 15 minutes followed by 50% CH_3CN/H_2O containing 0.5% TFA for 10 minutes. Detection was performed using an SPD-M10A photodiode array detector (Shimadzu Laboratories), with detection in the wavelength range of 600-250 nm and calculation of the abundance ratio of each anthocyanin based on the 520 nm absorbance area.

2) Anthocyanidin analysis

A 0.2 ml portion of the filtrate was dried completely under reduced pressure in a glass test tube and dissolved in 0.2 ml of 6N hydrochloric acid (HCl), and subjected to hydrolysis at 100°C for 20 minutes. The hydrolyzed anthocyanidins were extracted with 0.2 ml of 1-pentanol, and the organic layer was analyzed by HPLC

under the following conditions. The column used was an ODS-A312 (6 mmϕ x 15 cm, YMC Co., Ltd.), and elution was performed at a flow rate of 1 ml/min using a $CH_3COOH:CH_3OH:H_2O$ = 15:20:65 solution as the mobile phase.

Detection was performed by spectral measurement at 600-400 nm using an SPD-M10A photodiode array detector (Shimadzu Laboratories), identification based on absorption maximum (λmax) and retention time (RT), and quantitation based on 520 nm absorbance area. The retention time and λmax of delphinidin and cyanidin under these HPLC conditions were 4.0 min, 5.2 min and 534 nm, 525 nm, respectively. Delphinidin hydrochloride and cyanidin hydrochloride purchased from Funakoshi Co., Ltd. were used as samples for identification and quantitation.

3) Flavonol analysis

A 0.2 ml portion of the flower petal-extracted filtrate was dried to hardness under reduced pressure in a 1.5 ml Eppendorf tube and dissolved in 0.2 ml of 0.1 M potassium phosphate buffer (KPB) at pH 4.5, and then 6 units of β-glucosidase (Shinnihon Kagaku Co., Ltd.) and 1 unit of naringenase (Sigma Chemical Co., MO, USA) were added and the mixture was kept at 30°C for 16 hours. After the reaction, 0.2 ml of 90% CH_3CN was added to the enzyme reaction solution to terminate the reaction. The solution was filtered with a 0.45 μm filter and subjected to HPLC under the following conditions.

Isocratic elution was carried out using a Develosil C30-UG-5 (4.6 mmϕ x 15 cm, Nomura Chemical Co., Ltd.) column with a flow rate of 0.6 ml/min, and a mobile phase at a linear concentration gradient of 18%→63% CH_3CN/H_2O containing 0.1% TFA for 10 minutes followed by 63% CH_3CN/H_2O containing 0.1% TFA for 10 minutes. Detection was performed using an SPD-M10A photodiode array detector, with detection in the wavelength range of 400-250 nm. The R.T. and λmax of kaempferol and quercetin under these conditions were 11.6 min, 365 nm and 10.3

min, 370 nm, respectively. Kaempferol and quercetin purchased from Funakoshi Co., Ltd. were used as samples for quantitation based on the A330 nm area.

Example 3. pH measurement method

Approximately 2 g of rose petals frozen at -80°C for 1 hour or longer was pressed with a homogenizer to obtain the petal juice. The pH was measured by connecting a 6069-10C microelectrode (Horiba Laboratories) to a pH meter (F-22, Horiba Laboratories).

Example 4. Transformation of rose

Several methods have been reported for transformation of roses (for example, Firoozababy et al. Bio/Technology 12:609-613 (1994); US 5480789; US 5792927; EP 536,327 A1; US 20010007157 A1), and transformation may be carried out by any of these techniques. Specifically, rose calli taken from aseptic seedling leaves were immersed for 5 minutes in a bacterial suspension of *Agrobacterium tumefaciens* Ag10 (Lazo et al., Bio/Technology 9:963-967, 1991), the excess bacterial suspension was wiped off with sterile filter paper, and the calli were transferred to subculturing medium and cocultivated for 2 days in a dark room.

After subsequently rinsing with MS liquid medium containing 400 mg/L carbenicillin, the calli were transferred to selection/elimination medium prepared by adding 50 mg/L kanamycin and 200 mg/L carbenicillin to subculturing medium. Upon repeating transfer and cultivation of the portions which grew normally in selection medium without growth inhibition, the kanamycin-resistant calli were selected out. The kanamycin-resistant transformed calli were cultivated in redifferentiation medium containing 50 mg/L kanamycin and 200 mg/L carbenicillin to obtain kanamycin-resistant shoots. The obtained shoots were rooted in 1/2MS medium and then habituated. The habituated plants were potted and then cultivated in a closed greenhouse until blooming.

Example 5. Obtaining rose flavonoid gene

A cDNA library derived from Kardinal rose variety flower petals was screened using the petunia DFR gene (described in WO96/36716) as the probe, to obtain rose DFR cDNA was which designated as pCGP645. The details have already been reported (Tanaka et al., Plant Cell Physiol. 36, 1023-1031 1995).

Likewise, the same library was screened with the petunia chalcone synthase-A (CHS-A) gene (Koes et al., Gene (1989) 81, 245-257) and the anthocyanidin synthase (ANS) gene (Martin et al., Plant J., (1991) 1, 37-49) according to a publicly known procedure (Tanaka et al., Plant Cell Physiol. 36, 1023-1031 1995), to obtain rose chalcone synthase (CHS) and anthocyanidin synthase (ANS) homologs which were designated as pCGP634 and pCGP1375, respectively. The nucleotide sequence for rose CHS is listed as SEQ ID NO: 5, and the nucleotide sequence for rose ANS is listed as SEQ ID NO: 6.

Example 6. Screening for white rose

For creation of a blue cultivar by gene recombination, cultivars lacking only the DFR gene may be selected, in order to avoid competition between the endogenous anthocyanin synthesis pathway and the introduced genes (particularly the F3'5'H gene), and the petunia DFR gene and F3'5H gene transferred into those cultivars (WO96/36716).

A screening was conducted among the numerous existing white rose varieties, for those lacking only the DFR gene and normally expressing other anthocyanin biosynthesis enzyme genes. The cause of flower color whitening is believed to be occasional mutation or deletion of structural genes involved in anthocyanin biosynthesis, and occasional loss of transcription regulating factors which control transcription of structural genes involved in anthocyanin biosynthesis. Roses lacking DFR gene mRNA were examined according to the method described in WO96/36716.

First, 112 primarily white rose lines were analyzed for flavonoid composition of the flower petals by the method described in Example 1, and lines with high accumulation of flavonols were selected. The pH of each petal juice was then measured and 80 cultivars with relatively high pH values were chosen as primary candidates.

RNA was then extracted from petals of these cultivars. The RNA extraction was accomplished by a publicly known method (Tanaka et al., Plant Cell Physiol. 36, 1023-1031, 1995). The obtained RNA was used to examine the presence or absence of mRNA corresponding to the rose DFR gene (Tanaka et al., Plant Cell Physiol. 36, 1023-1031, 1995) and the rose anthocyanidin synthase (ANS) gene. RT-PCR was performed and eight cultivars (WKS-11, 13, 22, 36, 43, White Killarney, Tsuru No.2, Tineke) having low endogenous expression of DFR mRNA and normal ANS mRNA levels were selected.

RT-PCR was carried out with a Script First-strand Synthesis System for RT-PCR (Invitrogen) using RNA obtained from petals of each cultivar. The DFR mRNA was detected using DFR-2F (5'-CAAGCAATGGCATCGGAATC-3') (SEQ ID NO: 13) and DFR-2B (5'-TTTCCAGTGAGTGGCGAAAGTC-3') (SEQ ID NO: 14) primers, and the ANS mRNA was detected using ANS-2F (5'-TGGACTCGAAGAACTCGTCC-3') (SEQ ID NO: 15) and ANS-2B (5'-CCTCACCTTCTCCCTTGTT-3') (SEQ ID NO: 16) primers.

These eight cultivars showed lower levels of DFR mRNA and normal levels of ANS mRNA in Northern blotting (Table 1), and their cultivating properties were excellent. Two of the transformable cultivars (Tineke, WKS36) were decided on for actual transfer of the delphinidin-producing construct.

Table 1

Cultivar name	Flavonols (mg/g petal)			pH	RT-PCR		
	Q	K	Total		DFR	CHS	ANS
WKS-36	0.082	8.095	8.177	4.81	-	+	+
White Killarney	1.343	6.113	7.456	4.7	+	+	+
Tsuru No.2	0.715	5.188	5.903	4.7	+	+	+
WKS-11	2.028	0.475	2.503	4.51	+	+	+
Tineke	0.097	4.337	4.434	4.45	-	+	+
WKS-13	0.320	3.993	4.313	4.45	-	+	+
WKS-22	0.145	10.469	10.614	4.41	-	+	+
WKS-43	0.045	2.104	2.149	4.07	-	+	+

+: mRNA detected at same level as colored rose (Rote Rose cultivar)

-: mRNA detected at lower level than colored rose (Rote Rose cultivar)

Q: Quercetin, K: kaempferol

Example 7. Transfer of rose DFR gene into Tineke

Plasmid pE2113 (Mitsuhara et al., Plant Cell Physiol. 37, 49-59, 1996) comprises the enhancer sequence repeat-containing cauliflower mosaic virus 35S (E1235S) promoter and the nopaline synthase terminator. This plasmid was digested with SacI and the ends were blunted using a Blunting Kit (Takara). The DNA fragment was ligated with an 8 bp SalI linker (Takara) and the obtained plasmid was designated as pUE5.

Plasmid pUE5 was digested with HindIII and EcoRI to obtain an approximately 3 kb DNA fragment, which was introduced into pBin19 (Bevan M., Binary Agrobacterium Vector for plant transformation. Nucl. Acid Res. 12. 8711-21, 1984) previously digested with HindIII and EcoRI, to obtain plasmid pBE5. Next, pCGP645 was digested with BamHI and XhoI to obtain a DNA fragment containing full-length rose DFR cDNA. This was ligated with pBE5 digested with BamHI and XhoI to construct pBERD1 (Fig. 2). The plasmid was transferred into

Agrobacterium tumefaciens Ag10.

Plasmid pBERD1 (Fig. 2) was transferred into the white rose cultivar "Tineke", and 18 transformants were obtained. Flower color was altered in six of the obtained transformants. Pigment analysis of two plants in which a clear color change from white to pink was observed confirmed accumulation of cyanidin and pelargonidin in both (Table 2). These results suggested that the Tineke cultivar is a cultivar lacking the DFR gene.

Table 2

Plant No.	Cya (mg/g)	Pel (mg/g)
1	0.014	0.005
2	0.014	0.006

Cya: Cyanidin, Pel: Pelargonidin

Example 8. Transfer of pansy F3'5'H gene (#18) and petunia DFR gene into Tineke

RNA was extracted from young budding pansy (Black Pansy variety) petals by the method of Turpen and Griffith (BioTechniques 4:11-15, 1986), and Oligotex-dT (Qiagen) was used for purification of polyA$^+$RNA. This polyA$^+$RNA and a λZAPII/GigapackII Cloning Kit (Stratagene) were used to construct a cDNA library from the young budding pansy petals. After transferring approximately 100,000 pfu of phage plaques grown on an NZY plate onto a Colony/PlaqueScreen (DuPont), treatment was conducted by the manufacturer's recommended protocol. The plaques were ^{32}P-labeled and screened using petunia Hf1cDNA (pCGP602, Holton et al., Nature, 366, p276-279, 1993) as the probe.

The membrane was subjected to pre-hybridization for 1 hour at 42°C in hybridization buffer (10% (v/v) formamide, 1 M NaCl, 10% (w/v) dextran sulfate, 1% SDS), and then the ^{32}P-labeled probe was added to 1 x 10^6 cpm/ml

and hybridization was performed for 16 hours at 42°C. The membrane was then rinsed for 1 hour in 2xSSC, 1% SDS at 42°C, fresh rinsing solution was exchanged, and rinsing was again performed for 1 hour. The rinsed membrane was exposed on a Kodak XAR film together with an intensifying screen, and the hybridization signal was detected.

The results of cDNA analysis demonstrated that the two obtained cDNA had high identity with petunia Hf1. The two cDNA types were designated as pansy F3'5'H cDNA, BP#18 (pCGP1959) and BP#40 (pCGP1961). The nucleotide sequence for #18 is listed as SEQ ID NO: 1, and its corresponding amino acid sequence is listed as SEQ ID NO: 2, the nucleotide sequence for #40 is listed as SEQ ID No. 3, and its corresponding amino acid sequence is listed as SEQ ID NO: 4. BP#18 and BP#40 have 82% identity on the DNA level. Also, BP#18 and BP#40 both exhibit 60% identity with petunia Hf1 and 62% identity with petunia Hf2 (Holton et al., Nature, 366, p276-279, 1993), on the DNA level.

Separately, plasmid pUE5 was digested with EcoRI and the ends were blunted using a Blunting Kit (Takara), and the obtained DNA fragment was ligated with an 8 bp HindIII linker (Takara), producing a plasmid which was designated as pUE5H. There was recovered an approximately 1.8 kb DNA fragment obtained by subjecting plasmid pCGP1959 containing pansy F3'5'H #18 cDNA to complete digestion with BamHI and partial digestion with XhoI. The plasmid obtained by ligation of this with pUE5H digested with BamHI and XhoI was designated as pUEBP18.

Separately, a DNA fragment containing petunia DFR cDNA was recovered by digestion of pCGP1403 (WO96/36716) with BamHI and XhoI, and this DNA fragment was ligated with pBE5 that had been digested with BamHI and XhoI, to prepare pBEPD2. Next, pUEBP18 was partially digested with HindIII and an approximately 2.8 kb DNA fragment was recovered containing the E1235S promoter, pansy F3'5'H

#18 cDNA and the nos terminator. This fragment was ligated with a DNA fragment obtained by partial digestion of pBEPD2 with HindIII to obtain a binary vector plasmid pBPDBP2 (Fig. 3). This plasmid was introduced into *Agrobacterium tumefaciens* Ag10.

Plasmid pBPDBP2 (Fig. 3) was transferred into the white rose cultivar "Tineke", and 40 transformants were obtained. Flower color was altered in 23 of the obtained transformants, and pigment analysis confirmed accumulation of delphinidin in 16 of the 19 analyzed transformants (Table 3). The delphinidin content was 100% at maximum (average: 87%), but the maximum amount of pigment was very low at 0.035 mg per gram of petals and the flower color was only altered from RHS Color Chart 158d (Yellow-White group) to 56a (Red group) or 65b (Red-Purple group), while no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained.

Table 3

Plant No.	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	87	0.002	0.000	0.000	0.058	0.354
2	100	0.004	0.000	0.338	0.059	1.921
3	82	0.002	0.001	0.203	0.039	1.382
4	100	0.003	0.000	0.245	0.050	1.840
5	76	0.005	0.001	0.000	0.280	3.288
6	0	0.000	0.000	0.000	0.098	0.409
7	0	0.000	0.001	0.000	0.101	0.358
8	0	0.000	0.001	0.000	0.030	2.277
9	83	0.013	0.003	0.000	0.117	0.841
10	85	0.011	0.002	0.000	0.104	3.300
11	84	0.020	0.004	0.000	0.168	3.137
12	91	0.025	0.002	0.294	0.119	1.252
13	90	0.028	0.003	0.000	0.075	1.912
14	91	0.014	0.001	0.000	0.152	2.667
15	90	0.035	0.004	0.000	0.086	1.616
16	83	0.023	0.005	0.000	0.117	2.267
17	91	0.014	0.001	0.000	0.113	0.825
18	76	0.003	0.001	0.000	0.085	2.351
19	82	0.005	0.001	0.000	0.054	1.616

Del: delphinidin, M: Myricetin

Example 9. Transfer of pansy F3'5'H gene (#40) and petunia DFR gene into Tineke

Plasmid pE2113 (Mitsuhara et al., Plant Cell Physiol. 37, 49-59, 1996) was digested with HindIII and XbaI to obtain an approximately 800 bp DNA fragment, which was ligated with pBin19 (Bevan M., Binary Agrobacterium Vector for plant transformation. Nucl. Acid Res. 12. 8711-21, 1984) previously digested with HindIII and XbaI. The obtained plasmid was designated as pCGP1391. Another plasmid, pCGP669 (WO94/21840), contains the petunia chalcone synthase A (CHS-A) gene promoter. This plasmid was digested with EcoRI, blunted and then digested with HindIII.

The approximately 700 bp DNA fragment was ligated with pCGP1391 that had been digested with HindIII and SnaBI, and the obtained plasmid was designated as

pCGP1707. Also, there was recovered an approximately 1.8 kb DNA fragment obtained by subjecting plasmid pCGP1961 containing pansy F3'5'H #40 cDNA to complete digestion with BamHI and partial digestion with XhoI. The plasmid obtained by ligation of this with pUE5H digested with BamHI and XhoI was designated as pUEBP40. Plasmid pUEBP40 was digested with EcoRV and XbaI and an approximately 5.5 kb DNA fragment was recovered.

This fragment was ligated with an approximately 700 bp fragment obtained by digesting plasmid pCGP1707 with HindIII, blunting the ends and further digesting with XbaI, to obtain plasmid pUFBP40. Next, pUFBP40 was partially digested with HindIII and an approximately 3.4 kb DNA fragment was recovered containing the cauliflower 35S promoter enhancer, CHS-A promoter, pansy F3'5'H #40 cDNA and the nos terminator. This fragment was ligated with a DNA fragment obtained by partial digestion of pBEPD2 with HindIII to obtain a binary vector plasmid pBPDBP8 (Fig. 4). This plasmid was introduced into *Agrobacterium tumefaciens* Ag10.

Plasmid pBPDBP8 (Fig. 4) was transferred into the white rose cultivar "Tineke", and 53 transformants were obtained. Flower color was altered in 17 of the obtained transformants, and pigment analysis confirmed accumulation of delphinidin in 8 of the 9 analyzed transformants (Table 4). The delphinidin content was 93% at maximum (average: 79%), but the maximum amount of pigment was very low at 0.014 mg per gram of petals and the flower color was only altered from RHS Color Chart 158d (Yellow-White group) to 56a (Red group) or 65b (Red-Purple group), while no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained. This suggested that the Tineke variety is not a variety lacking only the DFR gene.

Table 4

Plant No.	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	0	0.000	0.001	0.000	0.018	2.023
2	9	0.001	0.006	na	na	na
3	93	0.011	0.001	0.000	0.036	2.724
4	86	0.007	0.001	0.000	0.076	2.957
5	71	0.013	0.006	0.000	0.073	2.503
6	87	0.014	0.002	0.000	0.058	3.390
7	78	0.005	0.002	0.000	0.049	1.241
8	47	0.004	0.004	0.000	0.070	1.800
9	78	0.004	0.001	0.000	0.029	2.326

na: no analysis/measurement

Example 10. Transfer of pansy F3'5'H gene (#18) and petunia DFR gene into WKS36

Plasmid pBPDBP2 (Fig. 3) was transferred into the white rose "WKS36", and 138 transformants were obtained. Flower color was altered in 10 of the obtained transformants, and accumulation of delphinidin was confirmed in all of the plants (Table 5). The delphinidin content was 91% at maximum (average: 60%), but the maximum amount of pigment was very low at 0.033 mg per gram of petals and the flower color was only altered to very light pink, while no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained. This suggested that the WKS36 variety is not a variety lacking only the DFR gene.

Table 5

Plant No.	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	60	0.008	0.005	0.381	0.169	2.291
2	40	0.006	0.009	0.633	0.486	2.911
3	54	0.005	0.005	0.654	0.336	3.460
4	43	0.016	0.021	0.000	0.656	2.469
5	53	0.009	0.008	0.404	0.325	2.397
6	53	0.004	0.003	0.498	0.251	2.768
7	45	0.013	0.016	0.000	0.381	1.537
8	83	0.004	0.001	0.000	0.156	1.632
9	80	0.033	0.008	0.000	0.557	3.766
10	91	0.013	0.000	0.000	0.184	2.610

Example 11. Transfer of pansy F3'5'H gene (#18) and petunia DFR gene into WKS36

A plasmid obtained by replacing the AscI site of plasmid pUCAP (van Engelen et al., Transgenic Research 4, 288-290, 1995) with PacI linker was designated as pUCPP. Separately, an expression cassette prepared by linking the rose chalcone synthase promoter, pansy F3'5'H #18 cDNA and nos terminator was obtained in the following manner.

Chromosomal DNA was extracted from young leaves of the Kardinal rose cultivar (Tanaka et al., Plant Cell Physiol. 36, 1023-1031, 1995). An approximately 100 μg portion of DNA was partially digested with Sau3AI, and approximately 20-kb DNA fragments were recovered by sucrose density gradient.

These were ligated with lambda phage EMBL3 (for example, Stratagene) that had been digested with BamHI, and a chromosomal DNA library was prepared by the manufacturer's recommended protocol. The library was screened by a publicly known method (Tanaka et al., Plant Cell Physiol. 36, 1023-1031, 1995) using rose chalcone synthase cDNA (DNA database: GenBank Accession No. AB038246) as the probe. Among the obtained chalcone

synthase chromosome clones, there existed lambda CHS20 which included an approximately 6.4 kb DNA sequence upstream from the start codon of chalcone synthase. The approximately 2.9 kb DNA fragment obtained by digestion of lambda CHS20 with HindIII and EcoRV includes the chalcone synthase promoter region.

This fragment was ligated with a fragment obtained by digestion of pUC19 (Yanisch-Perron C et al., Gene 33:103-119, 1985) with HindIII and SmaI. This was designated as pCGP1116. The sequence of the chalcone synthase promoter region included therein is listed as SEQ ID NO: 21. An approximately 2.9 kb DNA fragment obtained by digestion of pCGP1116 with HindIII and KpnI was ligated with a DNA fragment obtained by digestion of pJB1 (Bodeau, Molecular and genetic regulation of Bronze-2 and other maize anthocyanin genes. Dissertation, Stanford University, USA, 1994) with HindIII and KpnI to obtain pCGP197.

Separately, an approximately 300 bp DNA fragment containing the nopaline synthase terminator, obtained by digestion of pUE5 with SacI and KpnI, was blunted and linked with pBluescriptSK- which had been digested with EcoRV and BamHI and blunted. A plasmid of those obtained in which the 5' end of the terminator was close to the SalI site of pBluescriptSK- was designated as pCGP1986. A DNA fragment obtained by digesting pCGP1986 with XhoI, blunting the ends and further digesting with SalI was linked with a DNA fragment obtained by digesting pCGP197 with HindIII, blunting the ends and further digesting with SalI, to obtain pCGP2201.

Next, a DNA fragment obtained by digesting pCGP2201 with SalI and blunting the ends was linked with an approximately 1.7 kb DNA fragment (containing the pansy flavonoid 3',5'-hydroxylase gene) obtained by digesting pCGP1959 with BamHI and KpnI and blunting the ends. A plasmid of those obtained in which the rose chalcone synthase promoter had been inserted in a direction

allowing transcription of the pansy flavonoid 3',5'-hydroxylase gene in the forward direction was designated as pCGP2203. Plasmid pCGP2203 was recovered by digestion with HindIII and SacI. The DNA fragment was cloned at the HindIII and SacI sites of pUCPP, and the resulting plasmid was designated as pSPB459. Next, plasmid pE2113 was digested with SnaBI and a BamHI linker (Takara) was inserted to obtain a plasmid designated as pUE6.

An approximately 700 bp DNA fragment obtained by digestion of pUE6 with HindIII and BamHI was linked with an approximately 2.2 kb DNA fragment obtained by digestion of pCGP1405 (WO96/36716) with BamHI and BglII and with the binary vector pBinplus (van Engelen et al., Transgenic Research 4, 288-290, 1995) digested with HindIII and BamHI, to obtain pSPB460. An approximately 5 kb DNA fragment obtained by digestion of pSPB459 with PacI was introduced into the PacI site of pSPB460 to obtain pSPB461 (Fig. 5) having the petunia DFR and pansy F3'5'H #18 genes linked in the forward direction on the binary vector. This plasmid is modified for constitutive expression of the petunia DFR gene in plants and specific transcription of the pansy F3'5'H #18 gene in flower petals. The plasmid was transferred into *Agrobacterium tumefaciens* Ag10.

Plasmid pSPB461 (Fig. 5) was transferred into the white rose "WKS36", and 229 transformants were obtained. Flower color was altered in 16 of the obtained transformants, and accumulation of delphinidin was confirmed in all 12 of the pigment-analyzed plants (Table 6). The delphinidin content was 79% at maximum (average: 58%), but the amount of pigment was very low at 0.031 mg per gram of petals and the flower color was only altered to very light pink, while no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained. This suggested that the WKS36 variety is not a variety lacking only the DFR gene.

Table 6

Plant No.	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	39	0.002	0.004	0.000	0.414	3.744
2	52	0.006	0.005	0.000	0.465	3.363
3	27	0.002	0.005	0.000	0.342	3.703
4	58	0.014	0.010	0.000	0.430	2.780
5	62	0.008	0.005	0.498	0.281	2.189
6	72	0.002	0.001	0.000	0.193	2.391
7	71	0.010	0.004	0.000	0.152	4.021
8	79	0.031	0.008	0.403	0.215	2.660
9	26	0.004	0.011	0.000	0.249	2.331
10	54	0.007	0.006	0.000	0.299	2.085
11	74	0.017	0.006	0.145	0.248	3.505
12	74	0.013	0.005	0.000	0.229	2.005

Example 12. Transfer of pansy F3'5'H gene (#18), petunia DFR gene and perilla anthocyanin 3-glucoside acyltransferase gene into WKS36

A gene comprising a start codon added to the perilla hydroxycinnamoyl CoA: anthocyanin 3-glucoside acyltransferase (3AT) gene was designated as pSAT208F (Yonekura-Sakakibara et al., Plant Cell Physiol. 41, 495-502, 2000). An approximately 3.9 kb DNA fragment obtained by digestion of pSPB580 (PCT/AU03/00079) with BamHI and XhoI was linked with an approximately 1.8 kb DNA fragment obtained by digestion of pSAT208F with BamHI and XhoI.

The obtained plasmid was digested with AscI, and a DNA fragment was recovered containing the E1235S promoter, the perilla 3AT gene and the petunia phospholipid transfer protein terminator. The DNA fragment was inserted into the AscI site of pSPB461 to obtain plasmid pSPB472 (Fig. 6) having the perilla 3AT, petunia DFR and pansy F3'5'H #18 gene transcription directions in the forward direction. This plasmid is modified for constitutive expression of the perilla 3AT

gene and the petunia DFR gene in plants and specific transcription of the pansy F3'5'H #18 gene in flower petals. The plasmid was transferred into *Agrobacterium tumefaciens* Ag10.

Plasmid pSPB472 (Fig. 6) was transferred into the white rose "WKS36", and 75 transformants were obtained. Flower color was altered in four of the obtained transformants, and accumulation of delphinidin was confirmed in all three of the pigment-analyzed plants (Table 7). The delphinidin content was 67% at maximum (average: 49%), but the amount of pigment was very low at 0.011 mg per gram of petals and the flower color was only altered to very light pink, while no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained. This suggested that the WKS36 variety is not a variety lacking only the DFR gene.

Table 7

Plant No.	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	32	0.003	0.006	0.219	0.236	1.972
2	67	0.011	0.005	0.520	0.329	3.234
3	46	0.006	0.007	0.000	0.579	3.874

Thus, despite screening of several white roses, it was not possible to obtain a cultivar lacking only the DFR gene. In other words, it was not possible to obtain a blue rose by the method for creation of blue carnation (WO94/28140).

Example 13. Inhibition of rose DFR gene by cosuppression

Plasmid pBERD1 was transferred into the pale violet rose "Lavande", and 26 transformants were obtained. However, none of the plants exhibited altered flower color, suggesting that it is difficult to inhibit the

rose endogenous DFR gene by cosuppression.

Example 14. Screening for colored roses

Cultivars for creation of blue roses were then selected from among colored roses. After visually selecting 136 lines from colored rose cultivars with relatively blue shades, 89 of the lines were subjected to pigment analysis. The values obtained for the examined colored roses are shown in Tables 8 to 10.

Table 8

Name	Cya (mg/g)	Pel (mg/g)	Peo (mg/g)	Q (mg/g)	K (mg/g)
Lavande	0.078	0.000	0.000	0.451	0.078
Madam Violet	0.055	0.000	0.000	1.780	0.189
Vol de Nuit	0.317	0.003	0.000	2.661	0.316
Blue Moon	0.049	0.000	0.000	1.341	0.119
Seiryu	0.015	0.000	0.000	3.030	1.300
WKS077	1.875	0.008	0.000	1.430	0.247
WKS078	0.211	0.000	0.000	1.286	0.133
WKS079	2.864	0.003	0.000	1.030	0.106
WKS080	0.040	0.000	0.000	0.362	0.047
WKS081	0.032	0.000	0.000	4.480	1.563
WKS082	0.074	0.000	0.000	2.400	0.196
WKS083	0.018	0.405	0.000	0.146	0.962
WKS084	0.055	0.000	0.000	1.269	0.159
WKS087	0.032	0.000	0.000	0.797	0.134
WKS089	0.030	0.000	0.000	1.484	0.317
WKS090	1.571	0.007	0.000	1.346	0.339
WKS091	0.045	0.169	0.000	0.186	0.899
WKS092	0.038	0.002	0.000	1.358	0.135
WKS095	0.015	0.000	0.000	2.945	0.255
WKS096	0.024	0.000	0.000	2.032	0.349
WKS097	0.991	0.002	0.000	1.659	0.185
WKS100	0.051	0.000	0.000	1.410	0.615
WKS101	0.424	0.000	0.000	2.194	0.482
WKS104	0.066	0.000	0.000	2.347	0.424
WKS107	1.202	0.004	0.000	3.134	0.460
WKS114	0.429	0.000	0.000	3.509	0.541
WKS116	0.026	0.000	0.000	3.440	0.868
WKS117	0.027	0.000	0.000	0.227	0.149
WKS121	0.669	0.006	0.000	1.336	0.453
WKS123	0.487	0.003	0.000	3.663	0.826

Peo: Peonidin

Table 9

Name	Cya (mg/g)	Pel (mg/g)	Peo (mg/g)	Q (mg/g)	K (mg/g)
WKS124	0.022	0.045	0.000	0.192	2.012
WKS125	0.187	0.002	0.000	0.349	0.089
WKS126	0.544	0.002	0.000	2.226	0.895
WKS127	1.609	0.008	0.006	2.278	0.528
WKS128	1.844	0.003	0.007	2.576	0.409
WKS129	1.645	0.002	0.006	0.450	0.160
WKS130	1.332	0.008	0.005	1.599	0.525
WKS131	0.582	0.002	0.001	2.460	0.567
WKS132	1.101	0.006	0.000	0.298	0.208
WKS133	2.773	0.003	0.000	1.263	0.230
WKS133	3.487	0.011	0.023	0.414	0.108
WKS134	1.084	0.001	0.002	2.777	0.413
WKS135	0.241	0.007	0.001	0.803	0.113
WKS136	0.637	0.000	0.003	1.451	0.062
WKS137	1.208	0.014	0.002	1.034	1.027
WKS138	1.955	0.006	0.000	3.857	0.855
WKS139	0.285	0.003	0.000	1.363	0.538
WKS140	0.075	0.000	0.000	0.291	0.097
WKS141	0.197	0.000	0.000	0.358	0.045
WKS142	1.906	0.029	0.106	1.890	1.860
WKS143	1.125	0.027	0.020	1.596	1.129
WKS144	2.685	0.484	0.000	0.160	0.184
WKS145	0.948	0.006	0.000	3.086	1.222
WKS146	3.108	0.047	0.000	0.228	0.398
WKS147	0.593	0.003	0.004	3.619	0.924
WKS148	0.059	0.000	0.000	3.113	0.466
WKS149	1.101	0.013	0.000	1.481	1.866
WKS150	0.498	0.562	0.000	0.061	0.156
WKS151	0.947	1.073	0.000	0.038	0.227
WKS152	0.303	1.599	0.000	0.015	0.464

Peo: Peonidin

Table 10

Name	Cya (mg/g)	Pel (mg/g)	Peo (mg/g)	Q (mg/g)	K (mg/g)
WKS153	1.178	0.796	0.000	0.020	0.179
WKS154	0.219	0.659	0.000	0.007	0.265
WKS155	0.547	0.006	0.000	1.274	0.073
WKS156	0.851	0.005	0.000	1.139	0.238
WKS157	0.955	0.555	0.000	0.133	1.315
WKS158	0.634	0.005	0.000	0.526	0.219
WKS159	0.106	0.320	0.000	0.034	0.959
WKS160	0.750	0.005	0.000	2.283	0.768
WKS161	0.262	0.419	0.000	0.197	1.115
WKS162	0.039	0.564	0.000	0.041	0.447
WKS163	0.184	0.002	0.000	0.756	0.105
WKS164	0.918	0.012	0.000	1.954	2.832
WKS165	0.097	0.604	0.000	0.026	0.197
WKS166	0.116	0.015	0.000	0.488	0.566
WKS167	0.647	0.002	0.000	2.507	0.499
WKS168	1.109	0.029	0.000	1.797	2.328
WKS169	0.070	0.003	0.000	0.208	1.369
Baby Faurax	2.247	0.022	0.058	4.518	0.580
Indigo	0.891	0.006	0.000	5.781	3.820
Intermezzo	0.040	0.000	0.000	1.075	0.443
James Veitch	1.281	0.004	0.002	2.087	0.923
Lagoon	0.053	0.000	0.000	2.887	0.315
Magenta	0.126	0.000	0.000	1.062	0.191
MRS COLVILLE	1.666	0.012	0.000	3.500	2.940
Mme. Isaac Pereire	0.629	0.003	0.000	1.021	0.105
Mme. de La Roche-Lambert	0.869	0.005	0.000	4.994	2.794
Roseraie de L'hay	0.364	0.005	1.256	0.156	0.077
Rose de Rescht	1.348	0.004	0.000	4.027	0.842
Rose du Roi a Fleurs Pourpres	2.556	0.017	0.000	0.968	0.411

Peo: Peonidin

Example 15. Transfer of pansy F3'5'H gene (#40) and *Torenia* anthocyanin 5-acyltransferase gene into Lavande

Modification of anthocyanins with aromatic acyl groups can stabilize the anthocyanins and produce a bluer color (for example, WO96/25500). The following experiment was conducted with the goal of producing acylated delphinidin-type anthocyanins.

RNA was obtained from *Torenia* Summer Wave flower petals, and polyA$^+$RNA was prepared therefrom. A cDNA library was prepared from the polyA$^+$RNA with λZAPII (Stratagene) as the vector, using a directional cDNA library preparation kit (Stratagene) according to the manufacturer's recommended protocol. The major anthocyanin of *Torenia* is modified with an aromatic acyl group at the 5-position glucose (Suzuki et al., Molecular Breeding 2000 6, 239-246), and therefore anthocyanin acyltransferase is expressed in *Torenia* petals.

Anthocyanin acyltransferase includes the conserved amino acid sequence Asp-Phe-Gly-Trp-Gly-Lys, and corresponding synthetic DNA can be used as primer to obtain the anthocyanin acyltransferase gene (WO96/25500). Specifically, 10 ng of single-stranded cDNA synthesized for construction of the *Torenia* cDNA library was used as template, and 100 ng of ATC primer (5'-GA(TC)TT(TC)GGITGGGGIAA-3', I: inosine) (SEQ ID NO: 17) and 100 ng of oligo dT primer (5'-TTTTTTTTTTTTTTTTCTCGAG-3') (SEQ ID NO: 18) were used as primers for PCR with Taq polymerase (Takara, Japan), under the manufacturer's recommended conditions.

The PCR was carried out in 25 cycles of reaction with one cycle consisting of 1 minute at 95°C, 1 minute at 55°C and 1 minute at 72°C. The approximately 400 bp DNA fragment that was obtained was recovered with Gene Clean II (BIO,101. Inc.) according to the manufacturer's recommended protocol, and was subcloned in pCR-TOPO. Determination of the nucleotide sequence revealed a sequence homologous to the gentian acyltransferase gene (Fujiwara et al., 1998, Plant J. 16 421-431). The nucleotide sequence was determined by the Dye Primer method (Applied Biosystems), using Sequencer 310 or 377 (both by Applied Biosystems).

The DNA fragment was labeled with DIG using a DIG-labeling detection kit (Japan Roche), and used for

screening of a *Torenia* cDNA library by plaque hybridization according to the manufacturer's recommended protocol. Twelve of the obtained positive signal clones were randomly selected, the plasmids were recovered, and their nucleotide sequences were determined. These exhibited high homology with anthocyanin acyltransferase. The total nucleotide sequence of the cDNA in the clone designated as pTAT7 was determined. The nucleotide sequence is listed as SEQ ID NO: 7, and the corresponding amino acid sequence is listed as SEQ ID NO: 8.

After digesting pBE2113-GUS (Mitsuhara et al., Plant Cell Physiol. 37, 49-59, 1996) with SacI, the ends were blunted and an 8 bp XhoI linker (Takara) was inserted. An approximately 1.7 kb DNA fragment obtained by digesting pTAT7 with BamHI and XhoI was inserted at the BamHI and XhoI sites of this plasmid, to obtain pSPB120. After digesting pSPB120 with SnaBI and BamHI, the ends were blunted and ligation was performed to obtain pSPB120'. Separately, plasmid pCGP1961 containing pansy F3'5'H #40 cDNA was completely digested with BamHI and then partially digested with XhoI to obtain an approximately 1.8 kb DNA fragment which was recovered and ligated with pUE5H previously digested with BamHI and XhoI, to obtain a plasmid which was designated as pUEBP40.

After digesting pUEBP40 with SnaBI and BamHI, the ends were blunted and ligation was performed to obtain pUEBP40'. This plasmid pUEBP40' was partially digested with HindIII to obtain an approximately 2.7 kb DNA fragment which was recovered and linked with a DNA fragment obtained by partial digestion of pSPB120' with HindIII. Of the obtained plasmids, a binary vector having the neomycin phosphotransferase gene, pansy F3'5'H #40 gene and *Torenia* 5AT gene linked in that order in the same direction from the right border sequence on the binary vector, was designated as pSPB130 (Fig. 7). This plasmid is modified for constitutive expression of the

pansy F3'5'H #40 gene and the *Torenia* 5AT gene in plants and specific transcription of the genes in the flower petals. The plasmid was transferred into *Agrobacterium tumefaciens* Ag10.

Plasmid pSPB130 (Fig. 7) was transferred into the pale violet rose variety "Lavande", and 41 transformants were obtained. Accumulation of delphinidin was confirmed in 20 of the 32 pigment-analyzed plants (Tables 11 and 12). The delphinidin content was 71% at maximum (average: 36%). The flower color was altered from RHS Color Chart 186c (Greyed-Purple group) to 79d (Purple group). The proportion of acylated anthocyanins was only about 30% of the total anthocyanins. Upon spectral measurement of the acylated anthocyanins, the maximum absorption wavelength had shifted toward longer wavelength by 4 nm from delphinidin 3,5-diglucoside, but because of the low proportion among the total anthocyanins, no clear effect was achieved for the flower color.

Table 11

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	0	9	0.005	0.050	na	na	na
2	0	11	0.009	0.069	na	na	na
3	0	10	0.010	0.087	na	na	na
4	0	22	0.028	0.102	na	na	na
5	5	51	0.073	0.069	na	na	na
6	4	57	0.093	0.069	na	na	na
7	5	48	0.039	0.042	na	na	na
8	13	0	0.000	0.065	na	na	na
9	17	9	0.006	0.062	na	na	na
10	26	0	0.000	0.104	na	na	na
11	17	67	0.074	0.036	na	na	na
12	0	0	0.000	0.131	na	na	na
13	0	0	0.000	0.083	na	na	na
14	6	48	0.084	0.092	na	na	na
15	0	20	0.020	0.081	na	na	na
16	42	13	0.020	0.131	0.000	0.637	0.020
17	32	36	0.032	0.058	na	na	na
18	7	0	0.000	0.146	na	na	na
19	0	0	0.000	0.069	na	na	na
20	0	0	0.000	0.142	na	na	na
21	0	0	0.000	0.080	na	na	na

na: no analysis/measurement

Table 12

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
22	0	0	0.000	0.069	na	na	na
23	0	0	0.000	0.057	na	na	na
24	18	4	0.006	0.149	na	na	na
25	17	4	0.008	0.208	na	na	na
26	0	0	0.000	0.188	na	na	na
27	0	0	0.000	0.078	na	na	na
28	17	67	0.090	0.044	na	na	na
29	17	71	0.057	0.024	na	na	na
30	16	40	0.040	0.059	na	na	na
31	21	70	0.082	0.036	0.305	0.062	0.008
32	18	62	0.066	0.040	na	na	na

na: no analysis/measurement

Example 16. Transfer of pansy F3'5'H gene (#40) and

Torenia anthocyanin 5-acyltransferase gene into WKS100

Plasmid pSPB130 (Fig. 7) was transferred into the pale violet rose variety "WKS100", and 146 transformants were obtained. Accumulation of delphinidin was confirmed in 56 of the 63 pigment-analyzed plants (Tables 13-15). The delphinidin content was 95% at maximum (average: 44%). The flower color was altered from RHS Color Chart 56d (Red group) to 186d (Greyed-Purple group). However, no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained.

Table 13

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	20	75	0.036	0.012	0.000	2.944	0.974	0.322
2	16	51	0.027	0.027	0.000	1.685	1.734	0.512
3	13	50	0.024	0.024	0.000	0.000	1.382	1.912
4	23	50	0.037	0.037	0.000	na	na	na
5	9	25	0.013	0.033	0.005	na	na	na
6	10	26	0.034	0.097	0.000	na	na	na
7	13	65	0.053	0.028	0.000	1.936	1.184	0.760
8	13	65	0.044	0.024	0.000	1.622	1.065	0.562
9	14	62	0.033	0.021	0.000	2.096	1.444	0.710
10	14	95	0.137	0.008	0.000	0.000	0.156	1.097
11	10	62	0.036	0.022	0.000	2.025	1.194	0.799
12	5	59	0.054	0.038	0.000	2.194	1.289	0.783
13	9	43	0.033	0.044	0.000	2.542	1.803	0.734
14	9	50	0.030	0.031	0.000	0.020	1.971	0.741
15	1	70	0.066	0.028	0.000	1.652	1.659	0.867
16	0	20	0.008	0.023	0.008	0.308	2.632	1.463
17	1	63	0.068	0.040	0.000	2.037	2.128	1.554
18	21	51	0.037	0.035	0.000	2.659	1.936	1.002
19	0	0	0.000	0.095	0.000	na	na	na
20	0	0	0.000	0.037	0.000	na	na	na
21	0	23	0.026	0.086	0.003	0.182	4.554	3.083
22	4	71	0.110	0.044	0.000	3.265	1.643	1.341
23	12	65	0.051	0.025	0.002	1.356	0.888	0.387
24	6	58	0.038	0.027	0.000	2.374	2.016	0.809
25	5	52	0.044	0.040	0.000	2.651	2.546	1.108

na: no analysis/measurement

Table 14

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
26	6	64	0.033	0.019	0.000	2.707	1.546	0.605
27	16	0	0.000	0.041	0.000	na	na	na
28	16	13	0.007	0.050	0.000	0.249	3.359	1.459
29	12	7	0.007	0.095	0.000	na	na	na
30	15	9	0.007	0.069	0.000	na	na	na
31	15	8	0.007	0.081	0.000	na	na	na
32	7	7	0.007	0.094	0.000	na	na	na
33	13	10	0.006	0.055	0.000	na	na	na
34	14	46	0.078	0.090	0.002	na	na	na
35	7	8	0.007	0.078	0.000	na	na	na
36	3	48	0.045	0.039	0.010	3.050	2.304	1.326
37	2	39	0.029	0.046	0.000	na	na	na
38	1	55	0.073	0.059	0.000	1.608	2.138	1.015
39	1	33	0.030	0.063	0.000	na	na	na
40	2	59	0.050	0.035	0.000	3.651	2.727	1.076
41	17	15	0.011	0.061	0.000	na	na	na
42	0	0	0.000	0.048	0.002	na	na	na
43	3	17	0.009	0.046	0.000	na	na	na
44	40	32	0.027	0.058	0.000	na	na	na
45	2	0	0.000	0.031	0.000	na	na	na
46	2	0	0.000	0.038	0.000	na	na	na
47	1	8	0.004	0.048	0.000	na	na	na
48	19	57	0.046	0.034	0.000	2.626	2.165	0.900
49	10	59	0.047	0.032	0.000	1.737	1.901	1.054
50	2	70	0.057	0.024	0.000	1.545	0.880	0.694

na: no analysis/measurement

Table 15

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
51	4	10	0.006	0.056	0.000	na	na	na
52	16	12	0.006	0.039	0.002	na	na	na
53	34	84	0.156	0.030	0.000	5.100	1.056	0.511
54	32	89	0.131	0.017	0.000	3.907	0.803	0.431
55	29	89	0.098	0.013	0.000	3.687	0.453	0.226
56	21	83	0.083	0.017	0.000	2.679	0.817	0.431
57	14	8	0.007	0.082	0.000	na	na	na
58	9	44	0.034	0.041	0.002	2.258	2.054	0.672
59	7	51	0.040	0.038	0.000	2.246	2.151	0.765
60	0	7	0.008	0.111	0.000	na	na	na
61	1	48	0.069	0.073	0.000	1.558	1.730	0.565
62	13	0	0.000	0.036	0.000	na	na	na
63	16	14	0.005	0.029	0.000	na	na	na

na: no analysis/measurement

Example 17. Transfer of pansy F3'5'H gene (#40) and *Torenia* anthocyanin 5-acyltransferase gene into WKS116

Plasmid pSPB130 (Fig. 7) was transferred into the pale violet rose variety "WKS116", and 282 transformants were obtained. Accumulation of delphinidin was confirmed in 33 of the 36 pigment-analyzed plants (Tables 16 and 17). The delphinidin content was 80% at maximum (average: 73%). The flower color was altered from RHS Color Chart 196d (Greyed-Green group) to 186d (Greyed-Purple group). However, no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained.

Table 16

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	1.8	78	0.015	0.004	0.746	0.753	0.507
2	12.7	78	0.097	0.028	1.826	2.352	1.572
3	5.9	78	0.030	0.009	1.000	1.452	0.934
4	0.0	76	0.030	0.010	0.813	0.990	0.480
5	2.6	72	0.038	0.015	1.279	1.835	0.832
6	0.0	72	0.019	0.007	0.839	0.983	0.642
7	3.1	75	0.033	0.011	1.131	1.476	0.877
8	1.9	75	0.028	0.009	0.761	0.977	0.466
9	2.6	76	0.034	0.011	na	na	na
10	2.7	73	0.031	0.011	na	na	na
11	4.4	77	0.033	0.010	1.001	1.003	0.618
12	7.0	74	0.035	0.012	0.849	0.945	0.577
13	9.3	74	0.025	0.009	na	na	na
14	3.2	80	0.044	0.011	1.045	0.959	0.545
15	4.5	75	0.031	0.010	1.115	1.256	0.729
16	10.5	71	0.028	0.012	1.055	1.155	0.670
17	1.7	51	0.016	0.016	0.330	1.537	1.052
18	10.5	77	0.112	0.033	2.008	2.976	2.216
19	0.0	0	0.000	0.010	na	na	na
20	0.0	30	0.007	0.015	na	na	na
21	na	56	0.013	0.010	0.197	1.960	1.463
22	4.4	47	0.006	0.007	na	na	na
23	3.6	77	0.026	0.008	na	na	na

na: no analysis/measurement

Table 17

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
24	7.2	82	0.028	0.006	1.295	1.272	0.805
25	3.5	83	0.035	0.007	na	na	na
26	17.4	26	0.009	0.025	na	na	na
27	39.3	91	0.101	0.010	3.499	0.563	0.178
28	28.2	85	0.047	0.005	na	na	na
29	0.0	0	0.000	0.025	na	na	na
30	10.4	89	0.092	0.012	na	na	na
31	1.9	0	0.000	0.036	na	na	na
32	5.8	76	0.027	0.009	na	na	na
33	16.8	88	0.066	0.009	na	na	na
34	10.5	87	0.103	0.015	na	na	na
35	13.7	38	0.021	0.034	na	na	na
36	18.3	95	0.051	0.003	na	na	na

na: no analysis/measurement

Example 18. Transfer of pansy F3'5'H gene (#40) and *Torenia* anthocyanin 5-acyltransferase gene into WKS124

Plasmid pSPB130 (Fig. 7) was transferred into the pale orange rose variety "WKS124", and 50 transformants were obtained. Accumulation of delphinidin was confirmed in 13 of the 15 pigment-analyzed plants (Table 18). The delphinidin content was 95% at maximum (average: 82%). The flower color was altered from RHS Color Chart 52d (Red group) to 71c (Red-Purple group). However, no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained.

Table 18

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	0.6	0	0.000	0.013	0.069	na	na	na
2	35.5	75	0.256	0.051	0.034	0.066	0.093	1.190
3	43.0	78	0.385	0.068	0.041	0.039	0.046	1.197
4	44.2	85	0.811	0.120	0.028	0.106	0.094	1.021
5	na	86	0.907	0.123	0.024	0.219	0.066	0.852
6	4.6	0	0.000	0.023	0.075	na	na	na
7	7.9	90	1.498	0.169	0.008	0.905	0.143	0.679
8	8.4	90	1.403	0.146	0.008	0.971	0.145	0.827
9	26.7	88	0.521	0.066	0.003	0.623	0.108	0.853
10	21.9	89	0.504	0.058	0.003	0.636	0.098	0.727
11	26.0	85	0.928	0.145	0.019	0.424	0.152	0.455
12	3.8	95	1.017	0.058	0.000	1.161	0.140	0.262
13	11.6	84	0.939	0.156	0.025	0.748	0.128	0.262
14	38.5	69	0.166	0.071	0.007	0.000	0.059	0.776
15	27.1	55	0.137	0.040	0.074	0.000	0.021	2.330

na: no analysis/measurement

Example 19. Transfer of pansy F3'5'H gene (#40) and *Torenia* anthocyanin 5-acyltransferase gene into WKS132

Plasmid pSPB130 (Fig. 7) was transferred into the bright red rose variety "WKS132", and 24 transformants were obtained. Accumulation of delphinidin was confirmed in 6 of the 7 pigment-analyzed plants (Table 19). The delphinidin content was 43% at maximum (average: 12%). The flower color was altered from RHS Color Chart 57a (Red-Purple group) to 66a (Red-Purple group). However, no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained.

Table 19

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)
1	1.8	0.4	0.008	1.872	0.009
2	1.0	0.0	0.000	1.409	0.010
3	21.3	11.4	0.237	1.841	0.007
4	6.8	42.5	0.461	0.619	0.006
5	7.6	9.5	0.204	1.936	0.011
6	na	1.3	0.016	1.227	0.007
7	23.7	5.4	0.081	1.407	0.005

Example 20. Transfer of pansy F3'5'H gene (#40) and *Torenia* anthocyanin 5-acyltransferase gene into WKS133

Plasmid pSPB130 (Fig. 7) was transferred into the dark red-violet rose variety "WKS133", and 16 transformants were obtained. Accumulation of delphinidin was confirmed in all eight of the pigment-analyzed plants (Table 20). The delphinidin content was 34% at maximum (average: 11%). The flower color was altered from RHS Color Chart 53a (Red group) to 61a (Red-Purple group). However, no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained.

Table 20

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	Peo (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	10.3	23.7	1.322	4.253	0.009	0.004	0.691	0.792	0.133
2	11.8	33.8	1.192	2.324	0.005	0.003	0.621	0.422	0.093
3	6.1	12.9	0.009	0.060	0.000	0.000	0.102	0.500	0.048
4	3.8	9.1	0.363	3.627	0.005	0.008	na	na	na
5	15.8	2.0	0.078	3.774	0.009	0.000	0.045	0.939	0.472
6	11.5	2.7	0.135	4.771	0.011	0.005	0.046	0.576	0.034
7	13.3	3.0	0.180	5.800	0.009	0.009	0.100	0.937	0.179
8	12.2	3.5	0.161	4.470	0.009	0.009	0.068	0.738	0.148

na: no analysis/measurement

Example 21. Transfer of pansy F3'5'H gene (#40) and *Torenia* anthocyanin 5-acyltransferase gene into WKS137

Plasmid pSPB130 (Fig. 7) was transferred into the dark red-violet rose variety "WKS137", and 20 transformants were obtained. Accumulation of delphinidin was confirmed in all 17 of the pigment-analyzed plants (Table 21). The delphinidin content was 1.3% at maximum (average: 0.4%). No alteration in flower color was observed from RHS Color Chart 61b (Red-Purple group).

Table 21

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	Peo (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	0.5	0.3	0.008	2.821	0.037	0.000	na	na	na
2	0.8	0.3	0.010	3.384	0.051	0.000	na	na	na
3	0.4	0.3	0.005	1.982	0.014	0.000	na	na	na
4	0.6	0.2	0.008	3.344	0.057	0.000	na	na	na
5	0.7	0.4	0.011	3.145	0.035	0.000	na	na	na
6	0.7	1.3	0.025	2.919	0.040	0.003	na	na	na
7	0.4	0.3	0.008	2.820	0.045	0.000	na	na	na
8	0.5	0.4	0.010	2.467	0.042	0.000	na	na	na
9	0.7	0.2	0.010	3.836	0.024	0.000	na	na	na
10	0.1	0.5	0.008	1.743	0.016	0.000	na	na	na
11	0.7	0.4	0.011	2.593	0.027	0.003	na	na	na
12	0.6	0.3	0.007	2.393	0.022	0.000	0.048	3.026	2.812
13	1.4	0.2	0.009	3.756	0.065	0.000	na	na	na
14	0.7	0.4	0.008	2.149	0.024	0.001	na	na	na
15	0.8	0.5	0.007	2.281	0.041	0.000	na	na	na
16	0.5	0.5	0.007	1.314	0.014	0.000	na	na	na
17	1.0	0.2	0.007	2.892	0.051	0.000	na	na	na

na: no analysis/measurement

Example 22. Transfer of pansy F3'5'H gene (#40) and *Torenia* anthocyanin 5-acyltransferase gene into WKS140

Plasmid pSPB130 (Fig. 7) was transferred into the pale violet rose variety "WKS140", and 197 transformants were obtained. Accumulation of delphinidin was confirmed in 37 of the 45 pigment-analyzed plants (Tables 22 and 23). The delphinidin content was 94% at maximum (average: 47%). The flower color was altered from RHS Color Chart 186d (Greyed-Purple group) to 79d (Purple group). However, no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained.

Table 22

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	3.5	0.0	0.000	0.090	na	na	na
2	2.5	0.0	0.000	0.093	0.096	2.429	0.246
3	5.5	63.5	0.061	0.035	0.688	1.090	0.106
4	13.2	17.7	0.013	0.059	na	na	na
5	5.4	11.6	0.017	0.129	na	na	na
6	3.6	12.3	0.011	0.078	na	na	na
7	13.6	11.7	0.009	0.069	na	na	na
8	4.1	22.3	0.012	0.041	0.057	1.950	0.492
9	3.3	0.0	0.000	0.071	na	na	na
10	2.6	18.6	0.017	0.076	na	na	na
11	4.2	18.6	0.012	0.052	0.130	3.101	1.172
12	6.5	25.0	0.026	0.079	0.251	2.300	0.592
13	1.3	0.0	0.000	0.062	0.000	2.200	0.552
14	22.7	85.4	0.261	0.045	1.649	0.943	0.126
15	20.9	57.4	0.093	0.069	0.481	1.418	0.182
16	16.4	39.9	0.052	0.078	na	na	na
17	15.2	50.8	0.074	0.072	na	na	na
18	6.1	22.6	0.036	0.111	0.148	2.152	0.279
19	2.7	0.0	0.000	0.033	na	na	na
20	9.1	52.6	0.041	0.037	na	na	na
21	4.4	46.2	0.075	0.087	na	na	na
22	8.5	34.7	0.040	0.075	0.195	1.847	0.394
23	11.0	30.9	0.018	0.040	0.155	1.106	0.142
24	13.4	46.8	0.056	0.063	na	na	na
25	2.8	5.1	0.006	0.107	na	na	na

na: no analysis/measurement

Table 23

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
26	4.1	6.8	0.007	0.098	na	na	na
27	31.4	93.4	0.252	0.018	1.434	0.361	0.052
28	13.4	86.7	0.101	0.016	1.237	1.740	0.499
29	32.3	94.2	0.200	0.012	0.862	0.131	0.029
30	13.0	89.7	0.176	0.020	0.553	0.289	0.026
31	12.3	87.1	0.150	0.022	1.007	0.674	0.135
32	6.7	9.9	0.009	0.086	na	na	na
33	11.5	67.4	0.108	0.052	na	na	na
34	5.0	11.2	0.014	0.110	0.074	2.588	0.659
35	12.5	79.7	0.088	0.022	1.192	1.185	0.574
36	15.0	83.4	0.065	0.013	1.478	1.147	0.570
37	1.8	0.0	0.000	0.068	na	na	na
38	1.3	44.3	0.105	0.132	0.582	3.259	1.232
39	2.5	73.6	0.114	0.041	na	na	na
40	14.0	85.3	0.165	0.028	1.881	1.035	0.180
41	0.5	4.3	0.006	0.144	na	na	na
42	9.9	53.3	0.040	0.035	0.373	1.038	0.164
43	33.5	87.4	0.275	0.040	1.851	0.701	0.148
44	1.3	0.0	0.000	0.073	na	na	na
45	1.5	0.0	0.000	0.062	na	na	na

na: no analysis/measurement

Example 23. Transfer of pansy F3'5'H gene (#40) and *Torenia* anthocyanin 5-acyltransferase gene into WKS77

Plasmid pSPB130 (Fig. 7) was transferred into the dark red-purple rose variety "WKS77", and 35 transformants were obtained. Accumulation of delphinidin was confirmed in all 17 of the pigment-analyzed plants (Table 24). The delphinidin content was 57% at maximum (average: 33%). The flower color was altered from RHS Color Chart 57a (Red-Purple group) to 71a (Red-Purple group). However, no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained.

Table 24

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	6.2	42.5	1.153	1.552	0.008	0.484	0.679	0.196
2	7.6	38.6	0.618	0.979	0.005	0.267	0.465	0.094
3	3.9	40.4	0.706	1.030	0.011	1.266	1.768	0.722
4	2.0	46.9	0.372	0.417	0.004	0.363	0.608	0.276
5	5.4	40.6	0.540	0.784	0.005	1.077	1.809	0.645
6	2.0	44.7	1.078	1.325	0.009	0.516	1.034	0.382
7	2.1	46.5	0.398	0.453	0.005	0.353	0.792	0.569
8	5.8	39.7	0.647	0.980	0.005	0.425	0.706	0.183
9	4.7	40.0	0.844	1.268	0.000	0.310	0.764	0.199
10	7.6	39.7	1.345	2.033	0.009	0.350	0.635	0.119
11	14.1	2.9	0.068	2.274	0.013	na	na	na
12	12.8	6.9	0.126	1.688	0.009	na	na	na
13	12.7	4.2	0.109	2.468	0.012	0.060	1.541	0.366
14	13.0	20.9	0.704	2.669	0.000	0.407	2.502	0.694
15	19.3	43.5	1.011	1.308	0.007	0.357	0.843	0.276
16	19.6	6.1	0.092	1.414	0.010	0.120	1.740	0.477
17	22.8	56.6	1.068	0.814	0.004	0.604	0.503	0.126

na: no analysis/measurement

Example 24. Transfer of pansy F3'5'H gene (#40) and *Torenia* anthocyanin 5-acyltransferase gene into WKS82

Plasmid pSPB130 (Fig. 7) was transferred into the pale violet rose variety "WKS82", and 89 transformants were obtained. Accumulation of delphinidin was confirmed in all 44 of the pigment-analyzed plants (Tables 25 and 26). The delphinidin content was 91% at maximum (average: 49%). The flower color was altered from RHS Color Chart 186d (Greyed-Purple group) to 80c (Purple-Violet group). However, no color of the Violet group, Violet-Blue group or Blue group according to the RHSCC was achieved and the target blue rose could not be obtained.

Table 25

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	10.5	52.3	0.055	0.050	0.000	0.430	0.883	0.083
2	15.9	62.5	0.091	0.054	0.000	0.570	0.549	0.030
3	15.9	36.6	0.044	0.076	0.000	0.622	2.221	0.102
4	6.8	40.0	0.023	0.034	0.000	0.247	0.986	0.172
5	15.0	82.9	0.087	0.018	0.000	5.451	0.403	0.042
6	na	89.7	0.072	0.008	0.000	0.853	0.163	0.062
7	9.5	89.5	0.101	0.012	0.000	0.719	0.144	0.019
8	14.7	11.4	0.012	0.090	0.000	na	na	na
9	11.6	29.3	0.024	0.059	0.000	na	na	na
10	8.7	15.2	0.010	0.053	0.000	na	na	na
11	7.9	59.0	0.046	0.032	0.000	0.580	0.619	0.022
12	8.5	55.6	0.060	0.048	0.000	1.318	1.615	0.165
13	13.9	42.3	0.026	0.035	0.000	0.603	1.094	0.052
14	10.1	10.3	0.008	0.073	0.000	na	na	na
15	10.6	18.8	0.018	0.079	0.000	na	na	na
16	9.3	11.7	0.009	0.066	0.000	na	na	na
17	14.3	76.2	0.112	0.035	0.000	3.741	1.587	0.377
18	12.7	76.7	0.101	0.031	0.000	1.608	0.656	0.075
19	9.8	71.7	0.057	0.022	0.000	1.403	0.455	0.041
20	5.3	14.1	0.011	0.068	0.000	0.132	2.999	0.720
21	3.5	18.5	0.008	0.035	0.000	na	na	na
22	7.7	23.1	0.017	0.055	0.000	0.141	0.929	0.034
23	5.4	19.0	0.015	0.065	0.000	0.297	4.128	1.350

na: no analysis/measurement

Table 26

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
24	1.1	42.1	0.036	0.050	0.000	0.609	2.929	0.679
25	22.7	91.0	0.079	0.008	0.000	0.964	0.218	0.018
26	6.1	61.3	0.048	0.030	0.000	0.490	0.468	0.029
27	8.7	91.3	0.097	0.009	0.000	2.053	0.339	0.123
28	9.4	59.9	0.060	0.040	0.000	1.537	1.631	0.422
29	5.5	51.2	0.040	0.038	0.000	0.688	0.723	0.038
30	5.1	61.4	0.056	0.032	0.003	0.637	0.537	0.087
31	7.0	53.3	0.037	0.032	0.000	0.706	1.032	0.051
32	5.7	58.1	0.071	0.051	0.000	1.592	1.478	0.220
33	4.3	64.6	0.092	0.050	0.000	0.849	0.753	0.035
34	6.4	61.7	0.042	0.026	0.000	0.477	0.468	0.023
35	8.9	58.8	0.048	0.034	0.000	0.646	0.928	0.063
36	6.2	11.6	0.007	0.057	0.000	0.094	1.132	0.066
37	7.1	51.2	0.038	0.036	0.000	0.911	1.135	0.079
38	5.8	50.8	0.029	0.028	0.000	0.868	1.105	0.096
39	5.5	47.0	0.027	0.023	0.007	1.366	1.632	0.105
40	4.9	67.0	0.044	0.022	0.000	0.795	0.586	0.051
41	na	61.1	0.053	0.033	0.000	1.310	1.466	0.259
42	9.6	71.0	0.074	0.030	0.000	0.460	0.337	0.023
43	1.2	27.6	0.009	0.024	0.000	na	na	na
44	5.2	13.8	0.013	0.078	0.000	na	na	na

na: no analysis/measurement

Example 25. Transfer of pansy F3'5'H gene (#40) and *Torenia* anthocyanin 5-acyltransferase gene into WKS91

Plasmid pSPB130 (Fig. 7) was transferred into the light orange rose variety "WKS91", and 10 transformants were obtained. Accumulation of delphinidin was confirmed in only one of the two pigment-analyzed plants (Table 27). The delphinidin content was 2% at maximum. No alteration in flower color was observed from RHS Color Chart 43c (Red group).

Table 27

Plant No.	Acylation (%)	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)
1	0.7	0.0	0.000	0.090	0.307
2	0.0	1.8	0.006	0.040	0.295

Example 26. Expression of pansy F3'5'H gene (#40) and iris DFR gene and suppression of rose endogenous DFR gene in Lavande

RNA was obtained from blue iris petals of cut flowers, and polyA$^+$RNA was prepared therefrom. A cDNA library was prepared from the polyA$^+$RNA with λZAPII (Stratagene) as the vector, using a cDNA library preparation kit (Stratagene) according to the manufacturer's recommended protocol. An iris DFR gene fragment was prepared by the same method as reported for obtaining gentian DFR gene fragment (Tanaka et al. Plant Cell Physiol. 37, 711-716 1996).

The approximately 400 bp DNA fragment obtained was recovered with Gene Clean according to the manufacturer's recommended protocol, and was subcloned in pCR-TOPO. Determination of the nucleotide sequence revealed a sequence homologous to the rose DFR gene. The DNA fragment was used for screening of the iris cDNA library,

and iris DFR cDNA including the full-length amino acid sequence was obtained. The total nucleotide sequence of the cDNA in the clone designated as pSPB906 was determined. The nucleotide sequence is listed as SEQ ID NO: 9, and the corresponding amino acid sequence is listed as SEQ ID NO: 10.

Next, an approximately 3.9 kb DNA fragment obtained by digestion of pSPB580 with BamHI and XhoI was linked with an approximately 1.5 kb DNA fragment obtained by digestion of pSPB906 with BamHI and XhoI, and the obtained plasmid was designated as pSPB909.

A vector for transcription of double-stranded RNA for the rose DFR cDNA in plants was prepared in the following manner. An approximately 3.5 kb DNA fragment (including Mac1 promoter, rose DFR cDNA and mas terminator) obtained by partial digestion of pCGP1364 (Tanaka et al., Plant Cell Physiol. (1995) 36, 1023-1031) with PstI was inserted at the PstI site of pUC19 (Yanisch-Perron C et al., Gene 33:103-119, 1985) to obtain plasmids, among which a plasmid having the HindIII site of pUC19 near the MacI promoter was designated as pCGP1394.

Next, an approximately 1.4 kb DNA fragment obtained by digestion of pCGP1394 with HindIII and SacII was ligated with an approximately 1.9 kb DNA fragment obtained by digestion of pCGP1394 with PstI, blunting of the ends and further digestion with SacII, and with a binary vector fragment obtained by digestion of pBinPLUS with SacI, blunting of the ends and further digestion with HindIII, to obtain pSPB185. Plasmid pSPB185 was digested with XbaI, blunted and ligated with a SalI linker to obtain pSPB521. An approximately 700 bp DNA fragment obtained by digestion of pUE6 with HindIII and BamHI was ligated with a binary vector DNA fragment obtained by digestion of pSPB521 with HindIII and SacI and with a GUS gene fragment obtained by digestion of pE2113 with BamHI and SacI, to obtain pSPB528.

Plasmid pSPB528 is a binary vector having a structural gene inserted between the enhancer-containing cauliflower mosaic virus 35S promoter and the manopine synthase terminator, which is expressible in plants. Also, in order to shorten the 5'-end non-translated sequence of rose DFR cDNA in pCGP645, plasmid pCGP645 was digested with SmaI and PvuI, blunted and re-ligated to obtain pCGP645s.

The 5'-end sequence of rose DFR cDNA was obtained by PCR amplification using pCGP645s as the template and a reverse primer and the synthetic primer RDF310 (5'-CCCTCGAGCCCTTGATGGCCTCGTCG-3') (SEQ ID NO: 19) as the primers, and was cloned in pCRTOPO. The DNA nucleotide sequence was determined and absence of errors by PCR was confirmed. This plasmid was designated as pSPB569. Also, a rose DFR cDNA 5'-end sequence with a different length was obtained by amplification using pCGP645s as the template and a reverse primer and the synthetic primer RDF830 (5'-GGGTCGACGCGGCCCTCTGCTTTCGG-3') (SEQ ID NO: 20) as the primers, and was cloned in pCRTOPO. The DNA nucleotide sequence was determined and absence of errors by PCR was confirmed.

This plasmid was designated as pSPB570. A binary vector DNA fragment obtained by digestion of pSPB528 with BamHI and SacI, and an approximately 0.3 kb DNA fragment obtained by digestion of pSPB569 with SacI and XhoI, were ligated with a DNA fragment obtained by digestion of pSPB570 with BamHI and SalI, to obtain pSPB572. This vector is designed for transcription of double-stranded RNA for rose DFR cDNA in plants.

Plasmid pUE6 was digested with SacI and blunted, and a SalI linker was inserted to obtain pUE8. A DNA fragment obtained by digesting pUE8 with HindIII and EcoRI was introduced at the HindIII and EcoRI sites of pBinPLUS to obtain plasmid pSPB189. An approximately 3.7 kb DNA fragment obtained by digestion of pSPB189 with BamHI and SalI was ligated with an approximately 1.8 kb

DNA fragment obtained by complete digestion of pCGP1961 with BamHI followed by partial digestion with XhoI, to obtain plasmid pSPB567. After PacI digestion and dephosphorylation treatment of pSPB572, it was linked with an approximately 2.8 kb DNA fragment obtained by digestion of pSPB567 with PacI, and a plasmid with transcription of the nptII gene and pansy F3'5'H #40 in the same direction was selected and designated as pSPB905.

After AscI digestion and dephosphorylation treatment of pSPB905, it was linked with an approximately 2.5 kb DNA fragment obtained by digestion of pSPB909 with AscI, and a plasmid with transcription of the iris DFR gene in the same direction as the nptII gene was obtained and designated as pSPB919 (Fig. 8). This plasmid is expected to allow transcription of the iris DFR gene and pansy F3'5'H #40 gene in rose, while suppressing expression of the rose DFR gene due to transcription of double-stranded RNA. The plasmid was transferred into *Agrobacterium tumefaciens* Ag10.

Plasmid pSPB919 (Fig. 8) was transferred into the pale violet rose variety "Lavande", and 87 transformants were obtained. Accumulation of delphinidin was confirmed in 31 of the 38 pigment-analyzed plants (Tables 28 and 29). The delphinidin content was 100% at maximum (average: 76%). The flower color was altered from RHS Color Chart 186c (Greyed-Purple group) to 85a,b (Violet group).

RNA was extracted from rose petals in the same manner as explained above, and after separating the RNA by agarose gel electrophoresis, it was transferred onto Hybond N (Amersham) (for example, Tanaka et al., 1995). The mRNA was detected using a DIG Northern Starter Kit (Roche) by the manufacturer's recommended protocol. The rose DFR mRNA was detected using pCGP645 (Tanaka et al., Plant Cell Physiol. 36, 1023-1031, 1995) as template and a T7 primer transcript as the probe.

Detection of pansy F3'5'H #40 mRNA was accomplished using pCGP1961 as template and a T7 primer transcript as the probe. Detection of iris DFR mRNA was accomplished using pSPB906 as template and a T7 primer transcript as the probe. Pansy F3'5'H #40 and iris DFR gene mRNA were detected in the altered-color roses. On the other hand, rose DFR mRNA was significantly reduced compared to the host and a band was detected at the low molecular weight position, indicating decomposition of the rose DFR mRNA.

Table 28

Plant No.	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	0.0	0.000	0.105	0.036	0.856	0.038
2	0.0	0.000	0.125	na	na	na
3	0.0	0.000	0.091	0.023	0.851	0.101
4	0.0	0.000	0.116	0.000	1.336	0.087
5	0.0	0.000	0.048	na	na	na
6	88.5	0.086	0.011	1.626	1.187	0.411
7	90.8	0.089	0.009	0.797	1.548	0.087
8	84.0	0.046	0.009	0.163	0.699	0.016
9	87.8	0.062	0.009	0.193	0.760	0.022
10	89.3	0.072	0.009	0.210	0.575	0.033
11	91.5	0.049	0.005	0.398	0.805	0.050
12	91.5	0.032	0.003	0.100	0.811	0.014
13	85.7	0.040	0.007	0.092	0.497	0.012
14	64.9	0.040	0.021	0.263	0.327	0.015
15	88.3	0.041	0.005	na	na	na
16	66.4	0.011	0.006	0.036	1.221	0.030
17	79.7	0.008	0.002	0.030	0.765	0.009
18	100.0	0.010	0.000	0.048	1.343	0.067
19	95.9	0.040	0.002	0.159	0.136	0.004
20	65.4	0.016	0.008	0.090	1.244	0.048
21	18.8	0.011	0.049	0.048	0.855	0.020
22	0.0	0.000	0.110	0.000	1.274	0.079
23	0.0	0.000	0.140	0.000	1.952	0.200

na: no analysis/measurement

Table 29

Plant No.	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
24	41.4	0.102	0.144	0.265	0.417	0.015
25	34.3	0.042	0.081	0.167	0.429	0.024
26	34.6	0.023	0.043	na	na	na
27	41.4	0.082	0.116	0.232	0.385	0.019
28	37.7	0.046	0.076	0.254	0.429	0.018
29	36.1	0.032	0.057	0.151	0.235	0.042
30	97.2	0.052	0.002	0.208	0.088	0.004
31	93.0	0.038	0.003	0.347	0.137	0.007
32	98.2	0.101	0.002	0.339	0.258	0.029
33	91.3	0.039	0.004	na	na	na
34	91.9	0.041	0.004	0.332	0.120	0.007
35	96.8	0.052	0.002	na	na	na
36	96.7	0.084	0.003	0.342	0.168	0.010
37	88.0	0.014	0.002	0.076	1.000	0.029
38	84.5	0.016	0.003	0.074	1.121	0.025

na: no analysis/measurement

Example 27. Expression of pansy F3'5'H gene (#40) and *Nierembergia* DFR gene, and suppression of rose endogenous DFR gene in Lavande

RNA was obtained from petals of the *Nierembergia hybrida* cultivar Fairy Bell Patio Light Blue (Suntory Flowers Co., Ltd.), and polyA$^+$RNA was prepared therefrom. A cDNA library was prepared from the polyA$^+$RNA with λZAPII (Stratagene) as the vector, using a cDNA library synthesis kit (Stratagene) according to the manufacturer's recommended protocol. The cDNA library was screened using DIG-labeled petunia DFR cDNA (from pCGP1405).

The screening conditions were according to the plaque hybridization method using a DIG-labeling system, according to the manufacturer's recommended protocol. However, the formaldehyde concentration was 30% for the pre-hybridization and hybridization buffers, and hybridization was carried out overnight at 37°C. The membrane was rinsed at 55°C in 5xSSC containing 1% SDS.

Plasmids were recovered from 20 plaques among the numerous positive signals, and their nucleotide sequences were determined using Reverse Primer (Takara). These exhibited high homology with the DFR genes of other plants including petunia. The total nucleotide sequence of the cDNA in the clone designated as pSPB709 was determined. The nucleotide sequence is listed as SEQ ID NO: 11, and the corresponding amino acid sequence is listed as SEQ ID NO: 12

An approximately 3.9 kb DNA fragment obtained by digestion of pSPB580 with BamHI and XhoI was linked with an approximately 1.5 kb DNA fragment obtained by digestion of pSPB709 with BamHI and XhoI, to obtain plasmid pSPB910. After AscI digestion and dephosphorylation treatment of pSPB910, it was linked with an approximately 2.5 kb DNA fragment obtained by digestion of pSPB910 with AscI, and a plasmid with transcription of the *Nierembergia* DFR gene in the same direction as the nptII gene was obtained and designated as pSPB920 (Fig. 9). This plasmid is expected to allow transcription of the *Nierembergia* DFR gene and pansy F3'5'H #40 gene in rose, while suppressing expression of the rose DFR gene due to transcription of double-stranded RNA. The plasmid was transferred into *Agrobacterium tumefaciens* Ag10.

Plasmid pSPB920 (Fig. 9) was transferred into the pale violet rose variety "Lavande", and 56 transformants were obtained. Accumulation of delphinidin was confirmed in 23 of the 24 pigment-analyzed plants (Table 30). The delphinidin content was 100% at maximum (average: 43%). The flower color was altered from RHS Color Chart 186c (Greyed-Purple group) to 85b (Violet group).

Table 30

Plant No.	Del content (%)	Del (mg/g)	Cya (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	69.5	0.025	0.002	0.081	2.265	0.066
2	85.4	0.024	0.004	0.114	1.355	0.032
3	71.8	0.006	0.002	0.043	0.781	0.027
4	100.0	0.012	0.000	0.414	0.283	0.030
5	88.2	0.015	0.002	0.506	0.126	0.030
6	100.0	0.013	0.000	0.430	0.123	0.008
7	33.3	0.019	0.038	na	na	na
8	37.3	0.012	0.020	na	na	na
9	48.2	0.012	0.013	na	na	na
10	18.9	0.011	0.049	0.053	1.023	0.022
11	39.7	0.037	0.056	0.120	1.157	0.035
12	9.4	0.010	0.095	na	na	na
13	11.0	0.008	0.062	na	na	na
14	24.4	0.017	0.054	0.128	1.852	0.181
15	12.4	0.015	0.102	na	na	na
16	89.7	0.089	0.010	0.530	1.424	0.165
17	15.4	0.006	0.035	na	na	na
18	22.3	0.006	0.019	0.018	1.286	0.038
19	10.4	0.007	0.058	0.039	1.673	0.045
20	28.3	0.006	0.015	0.028	0.932	0.025
21	35.2	0.015	0.028	0.105	0.743	0.028
22	16.0	0.010	0.052	na	na	na
23	0.0	0.000	0.018	0.013	1.764	0.027
24	13.7	0.007	0.042	0.033	1.469	0.041

na: no analysis/measurement

Example 28. Inheritance of traits to progeny

Cross-breeding was carried out using a transformant (LA/919-2-13) obtained by transfer of pSPB919 (Fig. 8) into the pale violet rose variety "Lavande" as the pollen parent and non-recombinant WKS77 or WKS133 as the maternal parent (Suzuki, S., "Bara, Hanazufu", Shogakkann, p.256-260, 1990). Fruit was collected on the 100th day after pollination. Seed production was accomplished by first peeling the fruit, harvesting the achene, peeling the achene, and then removing the germ and embedding it on moistened filter paper in a dish. The water used for seed production was sterilized water

containing 1 ml/l PPM™ (Plant Preservative Mixture, Plant Cell Technology, Inc.) and 50 mg/l kanamycin, and seedlings were raised by potting only the normally budded plants.

Accumulation of delphinidin was confirmed in all 40 of the pigment-analyzed transformant progeny (Tables 31 and 32). The delphinidin content was 99% at maximum (average: 46%).

Table 31

Plant No.	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	Peo (mg/g)
1	89.8	0.494	0.056	0.000	0.000
2	96.1	3.900	0.153	0.005	0.000
3	55.9	0.836	0.660	0.000	0.000
4	24.6	0.041	0.127	0.000	0.000
5	23.5	1.108	3.605	0.009	0.002
6	25.9	0.191	0.545	0.003	0.000
7	0.5	0.013	2.552	0.012	0.002
8	75.8	0.283	0.090	0.000	0.000
9	95.9	1.420	0.061	0.000	0.000
10	30.8	0.862	1.841	0.007	0.105
11	13.3	0.068	0.441	0.004	0.000
12	23.9	0.529	1.667	0.023	0.000
13	43.7	0.280	0.362	0.000	0.000
14	19.3	0.035	0.145	0.000	0.000
15	0.6	0.008	1.418	0.021	0.000
16	20.8	0.048	0.183	0.000	0.000
17	92.5	2.257	0.177	0.007	0.000
18	66.4	2.496	1.247	0.015	0.000
19	42.4	0.369	0.497	0.004	0.000
20	75.6	0.597	0.183	0.010	0.000
21	19.6	0.271	1.103	0.008	0.000
22	71.0	0.107	0.044	0.000	0.000
23	0.6	0.006	0.850	0.004	0.000

Table 32

Plant No.	Del content (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	Peo (mg/g)
24	16.7	0.053	0.263	0.000	0.000
25	71.8	0.211	0.083	0.000	0.000
26	18.6	0.177	0.769	0.003	0.000
27	1.3	0.009	0.652	0.004	0.000
28	59.7	0.183	0.124	0.000	0.000
29	39.6	0.124	0.187	0.003	0.000
30	21.4	0.187	0.684	0.003	0.000
31	0.6	0.005	0.763	0.004	0.000
32	38.8	0.226	0.353	0.003	0.000
33	50.5	0.154	0.151	0.000	0.000
34	28.0	0.267	0.682	0.003	0.000
35	83.9	0.204	0.039	0.000	0.000
36	64.9	0.380	0.205	0.000	0.000
37	78.8	0.239	0.064	0.000	0.000
38	97.4	0.614	0.016	0.000	0.000
39	98.7	0.805	0.011	0.000	0.000
40	54.9	0.083	0.068	0.000	0.000

Example 29. Expression of pansy F3'5'H #40 gene and iris DFR gene and suppression of rose endogenous DFR gene in WKS140

Plasmid pSPB919 was transferred into the pale violet rose variety "WKS140", and 89 transformants were obtained. Accumulation of delphinidin was confirmed in 74 of the 79 pigment-analyzed plants. The delphinidin content was 100% at maximum (average: 68%). The flower color was altered from RHS Color Chart 186d (Greyed-Purple group) to primarily 84c (Violet group).

Table 33

Plant No.	Del (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)
1	0.0%	0.0000	0.0423	0.0000
2	89.9%	0.0242	0.0027	na
3	90.0%	0.0245	0.0027	na
4	88.6%	0.0093	0.0012	na
5	43.5%	0.0042	0.0054	na
6	91.2%	0.0118	0.0011	na
7	81.2%	0.0027	0.0006	na
8	81.0%	0.0173	0.0041	na
9	73.9%	0.0733	0.0259	na
10	62.9%	0.0321	0.0190	na
11	91.9%	0.0962	0.0084	na
12	99.1%	0.1606	0.0015	na
13	94.7%	0.0588	0.0033	na
14	100.0%	0.0839	0.0000	na
15	0.0%	0.0000	0.0005	na
16	98.4%	0.0296	0.0005	na
17	80.4%	0.1748	0.0451	na
18	94.6%	0.0190	0.0000	na
19	0.0%	0.0000	0.0714	na
20	34.3%	0.0099	0.0191	na
21	30.9%	0.0126	0.0282	na
22	65.6%	0.0294	0.0154	na
23	24.1%	0.0205	0.0646	na

na: no analysis/measurement

Example 30. Expression of pansy F3'5'H #40 gene and iris DFR gene and suppression of rose endogenous DFR gene in WKS77

Plasmid pSPB919 was transferred into the dark red-purple rose variety "WKS77", and 50 transformants were obtained. Accumulation of delphinidin was confirmed in 21 of the 23 pigment-analyzed plants. The delphinidin content was 81% at maximum (average: 19%). The flower color was altered from RHS Color Chart 57a (Red-Purple group) to 77b (Purple group).

Table 34

Plant No.	Del (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)
1	26.0%	1.2028	3.4033	0.0117
2	41.5%	0.6473	0.9093	0.0048
3	80.8%	0.2210	0.0526	na
4	68.0%	0.1865	0.0878	na
5	68.5%	0.2090	0.0951	0.0010
6	1.5%	0.0119	0.7731	0.0051
7	1.5%	0.0114	0.7304	0.0041
8	0.2%	0.0069	2.9266	0.0063
9	0.2%	0.0017	1.0791	0.0062
10	0.0%	0.0000	0.5013	0.0043
11	0.1%	0.0028	2.3418	0.0110
12	0.4%	0.0091	2.4603	0.0126
13	0.2%	0.0040	1.7766	0.0096
14	0.3%	0.0026	0.9046	0.0052
15	0.0%	0.0000	1.6063	0.0100
16	22.2%	0.3279	1.1392	0.0049
17	24.0%	0.2638	0.8288	0.0052
18	1.4%	0.0240	1.6777	0.0118
19	1.1%	0.0186	1.6352	0.0101
20	26.7%	0.2645	0.7230	0.0037
21	22.7%	0.2200	0.7460	0.0046
22	40.1%	0.8929	1.3374	0.0071

na: no analysis/measurement

Example 31. Expression of pansy F3'5'H #40 gene and *Nierembergia* DFR gene and suppression of rose endogenous DFR gene in WKS77

Plasmid pSPB920 was transferred into the dark red-purple rose variety "WKS77", and 30 transformants were obtained. Accumulation of delphinidin was confirmed in 26 of the 27 pigment-analyzed plants. The delphinidin content was 98% at maximum (average: 60%). The flower color was altered from RHS Color Chart 57a (Red-Purple group) to 77b (Purple group).

Table 35

Plant No.	Del (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)
1	93.9%	0.1679	0.0110	0.0000
2	97.6%	0.2311	0.0058	na
3	96.3%	0.1684	0.0065	na
4	97.1%	0.1012	0.0017	na
5	9.6%	0.0946	0.7810	0.1104
6	21.9%	0.1462	0.5166	0.0034
7	12.7%	0.1097	0.7495	0.0049
8	97.9%	0.1942	0.0042	na
9	98.1%	0.1228	0.0024	na
10	3.2%	0.0360	1.0689	0.0035
11	3.1%	0.0267	0.9587	0.0032
12	4.8%	0.1138	2.2562	0.0049
13	6.2%	0.1066	1.5999	0.0080
14	96.5%	0.3541	0.0132	na
15	2.1%	0.0173	0.7852	0.0068
16	94.7%	0.2898	0.0160	0.0000
17	96.7%	0.0819	0.0020	0.0000
18	95.8%	0.6969	0.0309	na
19	96.4%	0.4868	0.0181	na
20	64.3%	0.3092	0.1724	na
21	26.9%	0.2740	0.7431	0.0025
22	19.9%	0.3760	1.5028	0.0071
23	88.2%	0.0316	0.0042	na
24	94.2%	0.0259	0.0016	na
25	90.4%	0.0481	0.0051	na

na: no analysis/measurement

Example 32. Expression of pansy F3'5'H #40 gene and petunia DFR gene and suppression of rose endogenous DFR gene in WKS77

Plasmid pSPB921 was transferred into the dark red-purple rose variety "WKS77", and 15 transformants were obtained. Accumulation of delphinidin was confirmed in 12 of the 13 pigment-analyzed plants. The delphinidin content was 98% at maximum (average: 60%). The flower color was altered from RHS Color Chart 57a (Red-Purple group) to 72b (Red-Purple group).

Table 36

Plant No.	Del (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)
1	90.0%	0.0549	0.0061	na
2	38.4%	0.3397	0.5402	0.0041
3	56.9%	0.7834	0.5824	0.0099
4	58.5%	0.0196	0.0139	na
5	90.3%	0.1336	0.0144	na
6	90.9%	0.1251	0.0126	na
7	86.7%	0.1771	0.0274	na
8	91.6%	0.0113	0.0010	na
9	97.5%	0.0864	0.0022	na
10	9.5%	0.2687	2.6591	0.0000
11	8.8%	0.1421	1.4598	0.0071
12	0.4%	0.0060	1.3554	0.0053

na: no analysis/measurement

Example 33. Inheritance of traits to progeny

Cross-breeding was carried out in the same manner as Example 28, using a transformant (LA/919-4-10) obtained by transfer of pSPB919 into the pale violet rose variety "Lavande" as the pollen parent and the non-recombinant rose variety "Black Baccara" as the maternal parent. Fruit was collected on the 100th day after pollination. Seed production was accomplished by first peeling the fruit, harvesting the achene, peeling the achene, and then removing the germ and embedding it on moistened filter paper in a dish. The water used for seed production was sterilized water containing 1 ml/l PPM™ (Plant Preservative Mixture, Plant Cell Technology, Inc.) and 50 mg/l kanamycin, and seedlings were raised by potting only the normally budded plants.

Accumulation of delphinidin was confirmed in all 18 of the pigment-analyzed transformant progeny. The delphinidin content was 99.8% at maximum (average: 98.7%).

Table 37

Plant No.	Del (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)
1	97.8%	0.6633	0.0142	0.0009
2	99.0%	0.9002	0.0096	na
3	98.5%	0.5385	0.0080	na
4	99.5%	2.0561	0.0087	0.0016
5	99.8%	1.6556	0.0034	na
6	96.6%	0.5601	0.0200	na
7	99.0%	0.6148	0.0063	na
8	98.9%	1.6867	0.0193	na
9	95.0%	0.5740	0.0304	na
10	96.9%	0.1152	0.0036	na
11	99.3%	0.0683	0.0005	na
12	99.6%	0.1248	0.0005	na
13	99.5%	0.3574	0.0010	0.0000
14	99.6%	0.5500	0.0021	na
15	99.6%	1.2322	0.0049	na
16	99.7%	1.4384	0.0042	na
17	99.8%	0.5117	0.0010	na
18	98.3%	0.8073	0.0140	na

na: no analysis/measurement

Example 34. Expression of pansy F3'5'H #40 gene and suppression of rose endogenous F3'H gene in WKS77

Plasmid pSPB1106 (Fig. 10) was transferred into the dark red-purple rose variety "WKS77", and 40 transformants were obtained. Accumulation of delphinidin was confirmed in all 26 of the pigment-analyzed plants. The delphinidin content was 80.0% at maximum (average: 30.5%). The flower color underwent a major alteration from RHS Color Chart 57a (Red-Purple group) to 83d (Violet group).

Table 38

Plant No.	Del (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	68.7%	0.5497	0.2275	0.0241	na	na	na
2	78.8%	0.3449	0.0830	0.0096	na	na	na
3	80.0%	0.6949	0.1604	0.0144	na	na	na
4	71.2%	0.4377	0.1563	0.0214	na	na	na
5	72.7%	0.5260	0.1715	0.0266	0.3812	0.2275	1.7669
6	70.7%	0.3829	0.1449	0.0146	na	na	na
7	10.3%	0.0358	0.3031	0.0071	na	na	na
8	15.6%	0.1847	0.9530	0.0444	na	na	na
9	4.8%	0.0739	1.4586	0.0149	na	na	na
10	1.1%	0.0114	1.0411	0.0144	na	na	na
11	54.0%	1.3206	1.1166	0.0092	na	na	na
12	57.8%	0.8842	0.6410	0.0056	na	na	na
13	0.9%	0.0242	2.5500	0.0168	na	na	na
14	23.0%	0.2087	0.6909	0.0062	na	na	na
15	12.7%	0.1645	1.1271	0.0058	na	na	na
16	26.4%	0.5275	1.4645	0.0132	na	na	na
17	18.7%	0.3555	1.5310	0.0109	na	na	na
18	24.2%	0.4388	1.3687	0.0072	na	na	na
19	64.7%	0.4029	0.1945	0.0249	0.6368	0.3949	2.0567
20	0.1%	0.0021	1.8646	0.0077	na	na	na
21	0.0%	0.0000	0.9708	0.0062	na	na	na
22	0.1%	0.0022	2.6049	0.0127	na	na	na
23	0.4%	0.0066	1.8002	0.0066	na	na	na
24	0.5%	0.0079	1.4670	0.0056	0.0000	1.3096	0.2414
25	17.3%	0.1000	0.4671	0.0099	na	na	na
26	18.3%	0.1232	0.5418	0.0052	na	na	na

na: no analysis/measurement

Example 35. Expression of pansy F3'5'H #40 gene and suppression of rose endogenous F3'H gene in Lavande

Plasmid pSPB1106 was transferred into the pale violet rose variety "Lavande", and 40 transformants were obtained. Accumulation of delphinidin was confirmed in 23 of the 25 pigment-analyzed plants. The delphinidin content was 98.3% at maximum (average: 46.9%).

Table 39

Plant No.	Del (%)	Del (mg/g)	Cya (mg/g)	Pel (mg/g)	M (mg/g)	Q (mg/g)	K (mg/g)
1	76.8%	0.0732	0.0188	0.0032	0.5705	0.1595	0.3073
2	80.1%	0.1441	0.0296	0.0061	0.5298	0.1881	4.3294
3	3.7%	0.0086	0.2174	0.0027	na	na	na
4	4.4%	0.0079	0.1691	0.0034	na	na	na
5	8.8%	0.0158	0.1557	0.0070	na	na	na
6	39.0%	0.0212	0.0128	0.0204	0.0000	0.0363	1.3107
7	44.4%	0.0089	0.0027	0.0084	0.0756	0.0573	1.3689
8	40.4%	0.0165	0.0071	0.0172	0.0365	0.0592	2.5211
9	42.0%	0.0087	0.0036	0.0084	0.0752	0.0596	1.2661
10	13.5%	0.0153	0.0939	0.0040	0.1288	1.0594	0.5440
11	81.6%	0.2252	0.0447	0.0061	0.3947	0.1401	0.3947
12	78.8%	0.1022	0.0239	0.0036	0.6700	0.2137	0.5847
13	81.7%	0.2125	0.0438	0.0036	1.3616	0.4621	0.7478
14	80.9%	0.1829	0.0388	0.0044	0.4100	0.2405	0.0567
15	70.9%	0.0664	0.0204	0.0069	0.4230	0.1221	0.1788
16	0.0%	0.0000	0.0844	0.0000	na	na	na
17	98.0%	0.2363	0.0048	0.0000	0.0000	1.0613	0.2698
18	98.3%	0.1398	0.0025	0.0000	0.0479	0.7060	0.1299
19	4.2%	0.0078	0.1724	0.0040	0.0000	0.8627	0.2075
20	0.0%	0.0000	0.1696	0.0043	na	na	na
21	60.0%	0.0333	0.0115	0.0107	0.0000	0.0740	1.8678
22	14.3%	0.0091	0.0454	0.0088	0.1096	0.5305	0.6453
23	15.1%	0.0082	0.0408	0.0053	na	na	na
24	17.6%	0.0082	0.0324	0.0059	na	na	na
25	24.4%	0.0147	0.0375	0.0080	0.0000	0.2147	0.9765

na: no analysis/measurement

These results demonstrate that the transferred exogenous gene was inherited and expressed by the progeny, and that the trait of delphinidin production which is not found in ordinary rose petals was successfully inherited by the rose progeny. Thus, this gene can be used for cross-breeding cultivation of roses with altered colors to create roses with new colors including blue and purple.

Industrial Applicability

By artificially suppressing function of the endogenous metabolic pathway such as, for example, expression of dihydroflavonol reductase, in rose, and

expressing the gene coding for pansy flavonoid 3',5'-hydroxylase and a gene coding for dihydroflavonol reductase from species other than rose, it is possible to create blue to violet roses. These genes are inherited by subsequent generations, and the blue rose trait can be utilized for cross-breeding.

SEQUENCE LISTING

<110>International Flower Developments Proprietary Limited

<120>Process for production of rose with altered color

<130>P835

<160>21

<210>1

<211>1662

<212>DNA

<213>Pansy

<220>

<223>Nucleotide sequence encoding pansy #18 F3'5'H

<400>1

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gaattcggca cgagagccaa t atg gca att cca gtc act gac ctt gct gtc      51
                        Met Ala Ile Pro Val Thr Asp Leu Ala Val
                          1               5                  10
gcg gtt atc ctt ttc ttg atc act cgc ttc cta gtt cgt tct ctt ttc      99
Ala Val Ile Leu Phe Leu Ile Thr Arg Phe Leu Val Arg Ser Leu Phe
                 15                  20                  25
aag aaa cca acc gga ccg ctc ccg ccg ggt cct tca ggc tgg ccc ttg     147
Lys Lys Pro Thr Gly Pro Leu Pro Pro Gly Pro Ser Gly Trp Pro Leu
             30                  35                  40
gtg ggc gcg ctc cct ctc cta ggc gcc atg cct cac gtc aca cta gcc     195
Val Gly Ala Leu Pro Leu Leu Gly Ala Met Pro His Val Thr Leu Ala
         45                  50                  55
aac ctc gct aaa aaa tac ggt ccg atc atg tac cta aaa atg ggc acg     243
Asn Leu Ala Lys Lys Tyr Gly Pro Ile Met Tyr Leu Lys Met Gly Thr
     60                  65                  70
tgc gac atg gtg gtc gcg tcc act ccc gac tcg gct cga gcc ttc ctc     291
Cys Asp Met Val Val Ala Ser Thr Pro Asp Ser Ala Arg Ala Phe Leu
 75                  80                  85                  90
aaa acc cta gac ctc aac ttc tcc gac cgc ccg ccc aac gcc ggc gcc     339
Lys Thr Leu Asp Leu Asn Phe Ser Asp Arg Pro Pro Asn Ala Gly Ala
                 95                 100                 105
acc cat ttg gcg tac ggc gcg cag gac ttg gtc ttc gcg aag tac ggt     387
Thr His Leu Ala Tyr Gly Ala Gln Asp Leu Val Phe Ala Lys Tyr Gly
             110                 115                 120
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cca agg tgg aag acc cta aga aaa ttg agc aac ctc cac atg cta ggc      435
Pro Arg Trp Lys Thr Leu Arg Lys Leu Ser Asn Leu His Met Leu Gly
        125                 130                 135
ggg aag gcg ctg gac gat tgg gct cac gtg agg gct aac gag cta ggc      483
Gly Lys Ala Leu Asp Asp Trp Ala His Val Arg Ala Asn Glu Leu Gly
    140                 145                 150
cac atg ctt aac gcc atg tgc gag gcg agc cgg tgc gga gag ccc gtg      531
His Met Leu Asn Ala Met Cys Glu Ala Ser Arg Cys Gly Glu Pro Val
155                 160                 165                 170
gtg ctg gcc gag atg ctc acg tac gcc atg gcc aac atg atc ggt caa      579
Val Leu Ala Glu Met Leu Thr Tyr Ala Met Ala Asn Met Ile Gly Gln
                175                 180                 185
gtg ata ctg agt cgg cgc gtg ttc gtc acc aaa ggg aca gag tcg aac      627
Val Ile Leu Ser Arg Arg Val Phe Val Thr Lys Gly Thr Glu Ser Asn
            190                 195                 200
gag ttc aaa gat atg gtg gtc gag ttg atg act tcc gcg ggg tat ttc      675
Glu Phe Lys Asp Met Val Val Glu Leu Met Thr Ser Ala Gly Tyr Phe
        205                 210                 215
aac att ggt gac ttc ata ccg tcg att gct tgg atg gat ttg caa ggg      723
Asn Ile Gly Asp Phe Ile Pro Ser Ile Ala Trp Met Asp Leu Gln Gly
    220                 225                 230
atc gag cga ggg atg aag aaa ttg cac acg aaa ttc gat gtt ttg ttg      771
Ile Glu Arg Gly Met Lys Lys Leu His Thr Lys Phe Asp Val Leu Leu
235                 240                 245                 250
acg aag atg atg aag gag cac aga gcg acg agt cat gag cgc gaa ggg      819
Thr Lys Met Met Lys Glu His Arg Ala Thr Ser His Glu Arg Glu Gly
                255                 260                 265
aaa tcg gat ttc ctc gac gtc ctc ttg gaa gaa tgc gag aat aca aat      867
Lys Ser Asp Phe Leu Asp Val Leu Leu Glu Glu Cys Glu Asn Thr Asn
            270                 275                 280
ggc gag aag ctt aat gtt acc aac gtc aaa gct gtc ctc ttg aac tta      915
Gly Glu Lys Leu Asn Val Thr Asn Val Lys Ala Val Leu Leu Asn Leu
        285                 290                 295
ttc acg gcg ggt acg gac aca tct tca agc ata atc gaa tgg gcg tta      963
Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Ile Ile Glu Trp Ala Leu
    300                 305                 310
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acc gaa atg atg aag aat ccg acg atc tta aaa aag acc caa gaa gag      1011
Thr Glu Met Met Lys Asn Pro Thr Ile Leu Lys Lys Thr Gln Glu Glu
315                 320                 325                 330
atg gat cga gtc atc ggt cgc gat cgg aga ttg ctc gaa tcc gac gtt      1059
Met Asp Arg Val Ile Gly Arg Asp Arg Arg Leu Leu Glu Ser Asp Val
                335                 340                 345
tcg aaa ctc ccg tat tta caa gcc ata gcg aaa gaa aca tat cgt aaa      1107
Ser Lys Leu Pro Tyr Leu Gln Ala Ile Ala Lys Glu Thr Tyr Arg Lys
            350                 355                 360
cac cca tcg aca cct cta aac ctg ccg agg att gcg atc caa gca tgt      1155
His Pro Ser Thr Pro Leu Asn Leu Pro Arg Ile Ala Ile Gln Ala Cys
        365                 370                 375
gaa gtt gat ggc tac tac atc ccc aaa gac acg agg ctt agc gtc aac      1203
Glu Val Asp Gly Tyr Tyr Ile Pro Lys Asp Thr Arg Leu Ser Val Asn
    380                 385                 390
att tgg gcg atc ggt cgg gac cca agt gtt tgg gag aat cca tcg gag      1251
Ile Trp Ala Ile Gly Arg Asp Pro Ser Val Trp Glu Asn Pro Ser Glu
395                 400                 405                 410
ttc tcg cct gaa aga ttc ttg tct gag gag aat ggg aag atc agt cca      1299
Phe Ser Pro Glu Arg Phe Leu Ser Glu Glu Asn Gly Lys Ile Ser Pro
                415                 420                 425
ggc ggg aat gat ttt gag ctg att ccg ttt gga gca ggg agg aga att      1347
Gly Gly Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile
            430                 435                 440
tgt gct ggg aca agg atg gga atg gtc ctt gta agt tat att ttg ggc      1395
Cys Ala Gly Thr Arg Met Gly Met Val Leu Val Ser Tyr Ile Leu Gly
        445                 450                 455
act ttg gtc cat tct ttt gat tgg aaa tta cca aat ggg gtc agt gag      1443
Thr Leu Val His Ser Phe Asp Trp Lys Leu Pro Asn Gly Val Ser Glu
    460                 465                 470
att aac atg gat gag agt ttt ggg ctt gcg ttg caa aag gcc gtg cct      1491
Ile Asn Met Asp Glu Ser Phe Gly Leu Ala Leu Gln Lys Ala Val Pro
475                 480                 485                 490
ctc tcg gct acg gtc agt cca cga ttg gcc cca agc gcg tac gtt ata      1539
Leu Ser Ala Thr Val Ser Pro Arg Leu Ala Pro Ser Ala Tyr Val Ile
                495                 500                 505
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tgagctgatg ggctgggcct gagcccaaac atattgggtg tgttttatct gtaattttta 1599
atattataaa gttcgtaatt ttgtatttat ggttaattat gagttaaaaa aaaaaaaaaa 1659
aaa 1662

<210>2
<211>506
<212>PRT
<213>Pansy
<220>
<223>Amino acid sequence of pansy #18 F3'5'H
<400>2

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Met Ala Ile Pro Val Thr Asp Leu Ala Val Ala Val Ile Leu Phe Leu
 1               5                  10                  15
Ile Thr Arg Phe Leu Val Arg Ser Leu Phe Lys Lys Pro Thr Gly Pro
            20                  25                  30
Leu Pro Pro Gly Pro Ser Gly Trp Pro Leu Val Gly Ala Leu Pro Leu
        35                  40                  45
Leu Gly Ala Met Pro His Val Thr Leu Ala Asn Leu Ala Lys Lys Tyr
    50                  55                  60
Gly Pro Ile Met Tyr Leu Lys Met Gly Thr Cys Asp Met Val Val Ala
65                  70                  75                  80
Ser Thr Pro Asp Ser Ala Arg Ala Phe Leu Lys Thr Leu Asp Leu Asn
                85                  90                  95
Phe Ser Asp Arg Pro Pro Asn Ala Gly Ala Thr His Leu Ala Tyr Gly
            100                 105                 110
Ala Gln Asp Leu Val Phe Ala Lys Tyr Gly Pro Arg Trp Lys Thr Leu
        115                 120                 125
Arg Lys Leu Ser Asn Leu His Met Leu Gly Gly Lys Ala Leu Asp Asp
    130                 135                 140
Trp Ala His Val Arg Ala Asn Glu Leu Gly His Met Leu Asn Ala Met
145                 150                 155                 160
Cys Glu Ala Ser Arg Cys Gly Glu Pro Val Val Leu Ala Glu Met Leu
                165                 170                 175
Thr Tyr Ala Met Ala Asn Met Ile Gly Gln Val Ile Leu Ser Arg Arg
            180                 185                 190
Val Phe Val Thr Lys Gly Thr Glu Ser Asn Glu Phe Lys Asp Met Val
        195                 200                 205
```

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

Pro Arg Leu Ala Pro Ser Ala Tyr Val Ile
500 505

<210>3
<211>1795
<212>DNA
<213>Pansy
<220>
<223>Nucleotide sequence encoding pansy #40 F3'5'H
<400>3

gaattcggca cgaggacaac atg gca att cta gtc acc gac ttc gtt gtc 50
Met Ala Ile Leu Val Thr Asp Phe Val Val
1 5 10

gcg gct ata att ttc ttg atc act cgg ttc tta gtt cgt tct ctt ttc 98
Ala Ala Ile Ile Phe Leu Ile Thr Arg Phe Leu Val Arg Ser Leu Phe
15 20 25

aag aaa cca acc cga ccg ctc ccc ccg ggt cct ctc ggt tgg ccc ttg 146
Lys Lys Pro Thr Arg Pro Leu Pro Pro Gly Pro Leu Gly Trp Pro Leu
30 35 40

gtg ggc gcc ctc cct ctc cta ggc gcc atg cct cac gtc gca cta gcc 194
Val Gly Ala Leu Pro Leu Leu Gly Ala Met Pro His Val Ala Leu Ala
45 50 55

aaa ctc gct aag aag tat ggt ccg atc atg cac cta aaa atg ggc acg 242
Lys Leu Ala Lys Lys Tyr Gly Pro Ile Met His Leu Lys Met Gly Thr
60 65 70

tgc gac atg gtg gtc gcg tcc acc ccc gag tcg gct cga gcc ttc ctc 290
Cys Asp Met Val Val Ala Ser Thr Pro Glu Ser Ala Arg Ala Phe Leu
75 80 85 90

aaa acg cta gac ctc aac ttc tcc aac cgn cca ccc aac gcg ggc gca 338
Lys Thr Leu Asp Leu Asn Phe Ser Asn Arg Pro Pro Asn Ala Gly Ala
95 100 105

tcc cac cta gcg tac ggc gcg cag gac tta gtc ttc gcc aag tac ggt 386
Ser His Leu Ala Tyr Gly Ala Gln Asp Leu Val Phe Ala Lys Tyr Gly
110 115 120

ccg agg tgg aag act tta aga aaa ttg agc aac ctc cac atg cta ggc 434
Pro Arg Trp Lys Thr Leu Arg Lys Leu Ser Asn Leu His Met Leu Gly
125 130 135

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ggg aag gcg ttg gat gat tgg gca aat gtg agg gtc acc gag cta ggc      482
Gly Lys Ala Leu Asp Asp Trp Ala Asn Val Arg Val Thr Glu Leu Gly
    140                 145                 150
cac atg ctt aaa gcc atg tgc gag gcg agc cgg tgc ggg gag ccc gtg      530
His Met Leu Lys Ala Met Cys Glu Ala Ser Arg Cys Gly Glu Pro Val
155                 160                 165                 170
gtg ctg gcc gag atg ctc acg tac gcc atg gcg aac atg atc ggt caa      578
Val Leu Ala Glu Met Leu Thr Tyr Ala Met Ala Asn Met Ile Gly Gln
                175                 180                 180
gtg ata ctc agc cgg cgc gtg ttc gtg acc aaa ggg acc gag tct aac      626
Val Ile Leu Ser Arg Arg Val Phe Val Thr Lys Gly Thr Glu Ser Asn
            185                 190                 195
gag ttc aaa gac atg gtg gtc gag ttg atg acg tcc gcc ggg tac ttc      674
Glu Phe Lys Asp Met Val Val Glu Leu Met Thr Ser Ala Gly Tyr Phe
        200                 205                 210
aac atc ggt gac ttc ata ccc tcg atc gct tgg atg gat ttg caa ggg      722
Asn Ile Gly Asp Phe Ile Pro Ser Ile Ala Trp Met Asp Leu Gln Gly
    215                 220                 225
atc gag cga ggg atg aag aag ctg cac acg aag ttt gat gtg tta ttg      770
Ile Glu Arg Gly Met Lys Lys Leu His Thr Lys Phe Asp Val Leu Leu
230                 235                 240                 245
acg aag atg gtg aag gag cat aga gcg acg agt cat gag cgc aaa ggg      818
Thr Lys Met Val Lys Glu His Arg Ala Thr Ser His Glu Arg Lys Gly
                250                 255                 260
aag gca gat ttc ctc gac gtt ctc ttg gaa gaa tgc gac aat aca aat      866
Lys Ala Asp Phe Leu Asp Val Leu Leu Glu Glu Cys Asp Asn Thr Asn
            265                 270                 275
ggg gag aag ctt agt att acc aat atc aaa gct gtc ctt ttg aat cta      914
Gly Glu Lys Leu Ser Ile Thr Asn Ile Lys Ala Val Leu Leu Asn Leu
        280                 285                 290
ttc acg gcg ggc acg gac aca tct tcg agc ata atc gaa tgg gcg tta      962
Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Ile Ile Glu Trp Ala Leu
    295                 300                 305
acg gag atg atc aag aat ccg acg atc tta aaa aag gcg caa gag gag     1010
Thr Glu Met Ile Lys Asn Pro Thr Ile Leu Lys Lys Ala Gln Glu Glu
310                 315                 320                 325
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atg gat cga gtc atc ggt cgt gat cgg agg ctg ctc gaa tcg gac ata     1058
Met Asp Arg Val Ile Gly Arg Asp Arg Arg Leu Leu Glu Ser Asp Ile
                330                 335                 340
tcg agc ctc ccg tac cta caa gcc att gct aaa gaa acg tat cgc aaa     1106
Ser Ser Leu Pro Tyr Leu Gln Ala Ile Ala Lys Glu Thr Tyr Arg Lys
            345                 350                 355
cac ccg tcg acg cct ctc aac ttg ccg agg att gcg atc caa gca tgt     1154
His Pro Ser Thr Pro Leu Asn Leu Pro Arg Ile Ala Ile Gln Ala Cys
        360                 365                 370
gaa gtt gat ggc tac tac atc cct aag gac gcg agg ctt agc gtg aac     1202
Glu Val Asp Gly Tyr Tyr Ile Pro Lys Asp Ala Arg Leu Ser Val Asn
    375                 380                 385
att tgg gcg atc ggt cgg gac ccg aat gtt tgg gag aat ccg ttg gag     1250
Ile Trp Ala Ile Gly Arg Asp Pro Asn Val Trp Glu Asn Pro Leu Glu
390                 395                 400                 405
ttc ttg ccg gaa aga ttc ttg tct gaa gag aat ggg aag atc aat ccc     1298
Phe Leu Pro Glu Arg Phe Leu Ser Glu Glu Asn Gly Lys Ile Asn Pro
                410                 415                 420
ggt ggg aat gat ttt aag ctg att ccg ttt gga gcc ggg agg aga att     1346
Gly Gly Asn Asp Phe Lys Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile
            425                 430                 435
tgt gcg ggg aca agg atg gga atg gtc ctt gta agt tat att ttg ggc     1394
Cys Ala Gly Thr Arg Met Gly Met Val Leu Val Ser Tyr Ile Leu Gly
        440                 445                 450
act ttg gtc cat tct ttt gat tgg aaa tta cca aat ggt gtc gct gag     1442
Thr Leu Val His Ser Phe Asp Trp Lys Leu Pro Asn Gly Val Ala Glu
    455                 460                 465
ctt aat atg gat gaa agt ttt ggg ctt gca ttg caa aag gcc gtg ccg     1490
Leu Asn Met Asp Glu Ser Phe Gly Leu Ala Leu Gln Lys Ala Val Pro
470                 475                 480                 485
ctc tcg gcc ttg gtc agc cca cgg ttg gcc tca aac ccg tac gca acc     1538
Leu Ser Ala Leu Val Ser Pro Arg Leu Ala Ser Asn Pro Tyr Ala Thr
                490                 495                 500
tgagctaatg ggctgggcct agttttgtgg gccctaattt agagactttt gtgttttaag   1598
gtgtgtactt tattaattgg gtgcttaaat gtgtgtttta atttgtattt atggttaatt   1658
atgactttat tgtataatta tttatttttc ccttctgggt attttatcca tttaattttt   1718
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cttcagaatt atgatcatag ttatcagaat aaaattgaaa ataatgaatc ggaaaaaaaa 1778
aaaaaaaaaa aaaaaaa 1795

<210>4
<211>501
<212>PRT
<213>Pansy
<220>
<223>Amino acid sequence of pansy #40 F3'5'H
<400>4

Met Ala Ile Leu Val Thr Asp Phe Val Val Ala Ala Ile Ile Phe Leu
1 5 10 15
Ile Thr Arg Phe Leu Val Arg Ser Leu Phe Lys Lys Pro Thr Arg Pro
20 25 30
Leu Pro Pro Gly Pro Leu Gly Trp Pro Leu Val Gly Ala Leu Pro Leu
35 40 45
Leu Gly Ala Met Pro His Val Ala Leu Ala Lys Leu Ala Lys Lys Tyr
50 55 60
Gly Pro Ile Met His Leu Lys Met Gly Thr Cys Asp Met Val Val Ala
65 70 75 80
Ser Thr Pro Glu Ser Ala Arg Ala Phe Leu Lys Thr Leu Asp Leu Asn
85 90 95
Phe Ser Asn Arg Pro Pro Asn Ala Gly Ala Ser His Leu Ala Tyr Gly
100 105 110
Ala Gln Asp Leu Val Phe Ala Lys Tyr Gly Pro Arg Trp Lys Thr Leu
115 120 125
Arg Lys Leu Ser Asn Leu His Met Leu Gly Gly Lys Ala Leu Asp Asp
130 135 140
Trp Ala Asn Val Arg Val Thr Glu Leu Gly His Met Leu Lys Ala Met
145 150 155 160
Cys Glu Ala Ser Arg Cys Gly Glu Pro Val Val Leu Ala Glu Met Leu
165 170 175
Thr Tyr Ala Met Ala Asn Met Ile Gly Gln Val Ile Leu Ser Arg Arg
180 180 185
Val Phe Val Thr Lys Gly Thr Glu Ser Asn Glu Phe Lys Asp Met Val
190 195 200
Val Glu Leu Met Thr Ser Ala Gly Tyr Phe Asn Ile Gly Asp Phe Ile

205 210 215

Pro Ser Ile Ala Trp Met Asp Leu Gln Gly Ile Glu Arg Gly Met Lys
220 225 230 235

Lys Leu His Thr Lys Phe Asp Val Leu Leu Thr Lys Met Val Lys Glu
240 245 250

His Arg Ala Thr Ser His Glu Arg Lys Gly Lys Ala Asp Phe Leu Asp
255 260 265

Val Leu Leu Glu Glu Cys Asp Asn Thr Asn Gly Glu Lys Leu Ser Ile
270 275 280

Thr Asn Ile Lys Ala Val Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp
285 290 295

Thr Ser Ser Ser Ile Ile Glu Trp Ala Leu Thr Glu Met Ile Lys Asn
300 305 310 315

Pro Thr Ile Leu Lys Lys Ala Gln Glu Glu Met Asp Arg Val Ile Gly
320 325 330

Arg Asp Arg Arg Leu Leu Glu Ser Asp Ile Ser Ser Leu Pro Tyr Leu
335 340 345

Gln Ala Ile Ala Lys Glu Thr Tyr Arg Lys His Pro Ser Thr Pro Leu
350 355 360

Asn Leu Pro Arg Ile Ala Ile Gln Ala Cys Glu Val Asp Gly Tyr Tyr
365 370 375

Ile Pro Lys Asp Ala Arg Leu Ser Val Asn Ile Trp Ala Ile Gly Arg
380 385 390 395

Asp Pro Asn Val Trp Glu Asn Pro Leu Glu Phe Leu Pro Glu Arg Phe
400 405 410

Leu Ser Glu Glu Asn Gly Lys Ile Asn Pro Gly Gly Asn Asp Phe Lys
415 420 425

Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Thr Arg Met
430 435 440

Gly Met Val Leu Val Ser Tyr Ile Leu Gly Thr Leu Val His Ser Phe
445 450 455

Asp Trp Lys Leu Pro Asn Gly Val Ala Glu Leu Asn Met Asp Glu Ser
460 465 470 475

Phe Gly Leu Ala Leu Gln Lys Ala Val Pro Leu Ser Ala Leu Val Ser
480 485 490

Pro Arg Leu Ala Ser Asn Pro Tyr Ala Thr

495 500

<210>5

<211>1474

<212>DNA

<213>Rose

<220>

<223>Nucleotide sequence encoding rose chalcone synthase

<400>5

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gctaccgtcc tggccatcgg gacagcaact cctcccaact gtattgacca gagcacatac 120

cccgactact acttccgtat cactaagagc gagcacaagg ctgagctcaa ggagaaattc 180

cagcgcatgt gtgacaaatc tatgatcaag aagcgctaca tgtacttgac cgaagaaatt 240

cttaaggaga atcctagtat gtgtgagtac atggcccctt cacttgatgc aagacaagat 300

atggtggttg ttgaaattcc aaagcttgga aaagaggctg ccactaaggc tattaaggaa 360

tggggtcagc ccaagtccaa aatcacccac ttggtctttt gtaccactag tggcgtcgac 420

atgccccggg ccgattacca gctcactaag ctcttaggcc tccgcccgtc cgtgaagcgt 480

ctcatgatgt accaacaagg gtgtttcgcc ggaggcacgg tgctccggtt ggctaaggac 540

ttggccgaga acaacaaggg tgcacgtgtt cttgttgttt gctcagagat cactgccgtg 600

actttccgtg ggcctagcga cacccatctc gatagtcttg tgggccaagc cttgttcggt 660

gatggtgctg cggccattat tgttggggcc gacccattgc ccgaggttga gaagccttcg 720

ttcgagttgg tctcggcagc ccaaactatc cttcctgaca gtgacggagc catcgacggg 780

catcttcgtg aagttgggct cacatttcac ctcctcaaag atgttcccgg gctgatttca 840

aagaacatcg agaagagcct caacgaggcc ttcaaacctt tgaacatcac agactggaac 900

tcacttttct ggattgcaca cccgggtggc cctgcaattt tagaccaagt agaggctaaa 960

ttgggcctga agcccgaaaa gttagaagcc acaaggcata tattatccga gtacggcaat 1020

atgtctagtg cttgtgtgtt gtttattttg gacgaggtgc ggagaaagtc tgcagctaat 1080

gggcacaaga ccactggaga aggcctggag tggggtgtcc tatttggttt tgggccaggg 1140

ctcaccgtcg agaccgtcgt gcttcacagt gtggctgctt aaacttgaag gcatctgggt 1200

tcacttgagt gatctgctcc tggatttgtt cttatatatg tatcgtttcc actctacttt 1260

ccttgttaga tttccttttt tggatttatt tttctggtga atttagcaat atatgtaatg 1320

atgaataata ttattccaca aatttcatac gagcaaaagt tcctgcaata atttagttag 1380

aagttgactt tccggaagat ttagagcggg gaatatatct cccactagct gaaagattat 1440

ccggggatag agtacgttca aaaaaaaaaa aaaa 1474

<210>6

<211>420

<212>DNA

<213>Rose
<220>
<223>Nucleotide sequence encoding part of rose anthocyanidin synthase
<400>6
gaagaaggga ggctggagaa ggaggtcggt ggactcgaag aactcgtcct gcaaatgaaa 60
atcaactact acccaaaatg ccctcagccg gaacttgccc tcggcgtgga agcccacacc 120
gacataagtg cactcacctt catcctccac aacatggttc ccggcctgca gctcttctac 180
ggcggcaaat gggtgacagc gaaatgcgtg cccaactcca tcgtcatgca catcggcgac 240
aacttggaga ttctgagcaa cggcaagtac aagagcattt ttcacagggg ggattgtcaa 300
caagggagaa ggtgaggttc tcgttggcgg ttttcttgta gccacccagg aggaggtcat 360
tctcaagccg ttgcgacgac tgtctcgagg aggaaccgcg tcttccaccc gacttttcgg 420
<210>7
<211>1808
<212>DNA
<213>Torenia
<220>
<223>Nucleotide sequence encoding Torenia anthocyanin acyl transferase
<400>7
cttcaaagcc aaaaagaaac aattaatca atg gct gtt gaa gcc ccc aaa aca 53
Met Ala Val Glu Ala Pro Lys Thr
1 5
ata tgt gca gtc ctc gaa aac tct ctt att aca cca caa agt acc gat 101
Ile Cys Ala Val Leu Glu Asn Ser Leu Ile Thr Pro Gln Ser Thr Asp
10 15 20
aca gaa caa act ctt tca ctc aca ttc ttt gac atc aaa tgg gtt cat 149
Thr Glu Gln Thr Leu Ser Leu Thr Phe Phe Asp Ile Lys Trp Val His
25 30 35 40
ttt cat cca atg caa tgc ctt gtg ttg tac aac ttc cca tgt tct aag 197
Phe His Pro Met Gln Cys Leu Val Leu Tyr Asn Phe Pro Cys Ser Lys
45 50 55
tca cat ttt ctc gaa gcc aca gtt ccg agc ttc aaa tca tca ctc tcc 245
Ser His Phe Leu Glu Ala Thr Val Pro Ser Phe Lys Ser Ser Leu Ser
60 65 70
aaa act ctc aga cac tat ctt cca tta tca gga aac tta tac tat cca 293
Lys Thr Leu Arg His Tyr Leu Pro Leu Ser Gly Asn Leu Tyr Tyr Pro
75 80 85

```
aac ccg acc cat gac atg gat gat gat gaa tcg aac atg ccc gag atc      341
Asn Pro Thr His Asp Met Asp Asp Asp Glu Ser Asn Met Pro Glu Ile
     90                  95                 100
cgt tat aaa cct ggc gac tcg gtt tct cta acc gtt gca gag tac ttc      389
Arg Tyr Lys Pro Gly Asp Ser Val Ser Leu Thr Val Ala Glu Tyr Phe
105                 110                 115                 120
tcc ggt cat gaa gac aat acg act act gaa gaa tac ttc aat tac ctc      437
Ser Gly His Glu Asp Asn Thr Thr Thr Glu Glu Tyr Phe Asn Tyr Leu
                125                 130                 135
act gga aat ttc cag aga gat tgc gat caa ttc tat gat ctc tta ccc      485
Thr Gly Asn Phe Gln Arg Asp Cys Asp Gln Phe Tyr Asp Leu Leu Pro
            140                 145                 150
gat ttt cga gac ccg gaa acc gaa tcc aat tgc aca gta atc cca ctt      533
Asp Phe Arg Asp Pro Glu Thr Glu Ser Asn Cys Thr Val Ile Pro Leu
        155                 160                 165
ata gca gtt caa atc aca ctc ttt cca ggt gct ggg ata tgt ctg ggg      581
Ile Ala Val Gln Ile Thr Leu Phe Pro Gly Ala Gly Ile Cys Leu Gly
    170                 175                 180
gtc atc aac agt cac gta gtt ggc gat gcg agt tcc ata gtg gga ttc      629
Val Ile Asn Ser His Val Val Gly Asp Ala Ser Ser Ile Val Gly Phe
185                 190                 195                 200
atc aaa gct tgg agt aaa gtt gca atg tat gaa gac gat gaa gag att      677
Ile Lys Ala Trp Ser Lys Val Ala Met Tyr Glu Asp Asp Glu Glu Ile
                205                 210                 215
cta gct aac aac aat ttg att cca tct tat gac aga tca gtc gtg aaa      725
Leu Ala Asn Asn Asn Leu Ile Pro Ser Tyr Asp Arg Ser Val Val Lys
            220                 225                 230
gat cca aaa ggg atc aaa tct ttg ctc tgg aac aag atg aag aac gtg      773
Asp Pro Lys Gly Ile Lys Ser Leu Leu Trp Asn Lys Met Lys Asn Val
        235                 240                 245
aaa tat caa ccc caa ccc gca aaa cat ctc cca aca aac aag gtc cga      821
Lys Tyr Gln Pro Gln Pro Ala Lys His Leu Pro Thr Asn Lys Val Arg
    250                 255                 260
gcc aca tac acc ttg aga aag aac gat atc gag agg ctg aaa acc cga      869
Ala Thr Tyr Thr Leu Arg Lys Asn Asp Ile Glu Arg Leu Lys Thr Arg
265                 270                 275                 280
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atc cga tcc aag aaa cca ggc aca acc tgc tta tca tct ttc aca atc 917
Ile Arg Ser Lys Lys Pro Gly Thr Thr Cys Leu Ser Ser Phe Thr Ile
285 290 295
gca aca gcc tat gct tgg aca tgc ctt gca aaa tct gca gca gaa gct 965
Ala Thr Ala Tyr Ala Trp Thr Cys Leu Ala Lys Ser Ala Ala Glu Ala
300 305 310
gaa gaa caa gta gtc caa gac agt gac gac gag cac ttg ctc atg ccc 1013
Glu Glu Gln Val Val Gln Asp Ser Asp Asp Glu His Leu Leu Met Pro
315 320 325
gtt gat ttg aga cca aga ata gat cct cca tta cca cct tct tac ttt 1061
Val Asp Leu Arg Pro Arg Ile Asp Pro Pro Leu Pro Pro Ser Tyr Phe
330 335 340
gga aac tgc gtt ctt cca tct ttt gcg aaa acg acg cat ggg ctt ttg 1109
Gly Asn Cys Val Leu Pro Ser Phe Ala Lys Thr Thr His Gly Leu Leu
345 350 355 360
aaa gga gag tta ggg ctt ttt aat gca gtg gaa gtg att agt gat gtc 1157
Lys Gly Glu Leu Gly Leu Phe Asn Ala Val Glu Val Ile Ser Asp Val
365 370 375
att acc ggt atc gtt agc aag aaa tat gac ttg ttc aaa gac tta gac 1205
Ile Thr Gly Ile Val Ser Lys Lys Tyr Asp Leu Phe Lys Asp Leu Asp
380 385 390
aga caa ggt gag att ttt cgt gcc ttg ttc gga aaa cga gtg ttg gcg 1253
Arg Gln Gly Glu Ile Phe Arg Ala Leu Phe Gly Lys Arg Val Leu Ala
395 400 405
atc atg ggt tcg cct aag ttc gat ctc tac gaa gtt gat ttc ggg tgg 1301
Ile Met Gly Ser Pro Lys Phe Asp Leu Tyr Glu Val Asp Phe Gly Trp
410 415 420
ggt aag ccg aag aag att gaa cct gtg tcc att gat aga gag agg acg 1349
Gly Lys Pro Lys Lys Ile Glu Pro Val Ser Ile Asp Arg Glu Arg Thr
425 430 435 440
act atg tgg att agc aag tct ggc gag ttt gag ggt gga ttg gag att 1397
Thr Met Trp Ile Ser Lys Ser Gly Glu Phe Glu Gly Gly Leu Glu Ile
445 450 455
ggt ttt tct ttc aat aag aag aaa atg gat gct ttt ggc gag tgt ttt 1445
Gly Phe Ser Phe Asn Lys Lys Lys Met Asp Ala Phe Gly Glu Cys Phe
460 465 470

aac agc ggt ttg aag gat att taatttaaaa aattgtttag ctttgatgca 1496
Asn Ser Gly Leu Lys Asp Ile
475

tgcgttttat atatgttgtg aaataatgtg gtgtgcaata actagagtaa ctttaggtta 1556
ataaattcgg tttttctgtt aaatctggat gattcgtgca agcaaactgt cgatgcgttg 1616
gatggatgtc gggtggtgtg gagattgttg aagaaggaaa tggatgcttt ttttatggtg 1676
gtttgaagga tttgaatgtg tagattattg gtttattgag gttgtttata tttgtgtatg 1736
ttgtttatgc atgaaaaata tttagatccc aacattttat gtatgacgtg gtttaatatt 1796
tcgatttcga tc 1808

<210>8
<211>479
<212>PRT
<213>Torenia
<220>
<223>Amino acid sequence of Torenia anthocyanin acyl transferase
<400>8

Met Ala Val Glu Ala Pro Lys Thr Ile Cys Ala Val Leu Glu Asn Ser
1 5 10 15
Leu Ile Thr Pro Gln Ser Thr Asp Thr Glu Gln Thr Leu Ser Leu Thr
20 25 30
Phe Phe Asp Ile Lys Trp Val His Phe His Pro Met Gln Cys Leu Val
35 40 45
Leu Tyr Asn Phe Pro Cys Ser Lys Ser His Phe Leu Glu Ala Thr Val
50 55 60
Pro Ser Phe Lys Ser Ser Leu Ser Lys Thr Leu Arg His Tyr Leu Pro
65 70 75 80
Leu Ser Gly Asn Leu Tyr Tyr Pro Asn Pro Thr His Asp Met Asp Asp
85 90 95
Asp Glu Ser Asn Met Pro Glu Ile Arg Tyr Lys Pro Gly Asp Ser Val
100 105 110
Ser Leu Thr Val Ala Glu Tyr Phe Ser Gly His Glu Asp Asn Thr Thr
115 120 125
Thr Glu Glu Tyr Phe Asn Tyr Leu Thr Gly Asn Phe Gln Arg Asp Cys
130 135 140
Asp Gln Phe Tyr Asp Leu Leu Pro Asp Phe Arg Asp Pro Glu Thr Glu
145 150 155 160

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

Glu Phe Glu Gly Gly Leu Glu Ile Gly Phe Ser Phe Asn Lys Lys Lys
450 455 460
Met Asp Ala Phe Gly Glu Cys Phe Asn Ser Gly Leu Lys Asp Ile
465 470 475

<210>9
<211>1252
<212>DNA
<213>Iris
<220>
<223>Nucleotide sequence encoding Iris dihydrofravonol reductase
<400>9

aaacaatata tcgag atg atg agc ccc gtt gtc gtg acc gga gcg agc ggc 51
Met Met Ser Pro Val Val Val Thr Gly Ala Ser Gly
1 5 10

tac gtc ggt tca tgg ctt gtt atg aag ctc ctt cgc gac ggc tac gcc 99
Tyr Val Gly Ser Trp Leu Val Met Lys Leu Leu Arg Asp Gly Tyr Ala
15 20 25

gtt cga gcc act gtc aga gac cca acc aat gtg gag aag acg aag ccg 147
Val Arg Ala Thr Val Arg Asp Pro Thr Asn Val Glu Lys Thr Lys Pro
30 35 40

ctg ttg gac ctc ccc gga gct gac gcg ctg ctc acc atc tgg aag gca 195
Leu Leu Asp Leu Pro Gly Ala Asp Ala Leu Leu Thr Ile Trp Lys Ala
45 50 55 60

gac ctc ggc cag gac gga agc ttc gac aag gcg gtc gca gga tgc acc 243
Asp Leu Gly Gln Asp Gly Ser Phe Asp Lys Ala Val Ala Gly Cys Thr
65 70 75

gcg gtc ttc cac gtc gcc acg ccc atg gat ttc gag tcc aag gac cca 291
Ala Val Phe His Val Ala Thr Pro Met Asp Phe Glu Ser Lys Asp Pro
80 85 90

gaa aac gag gtg atc aag ccg acc ata aat ggc gtt tta agt atc atg 339
Glu Asn Glu Val Ile Lys Pro Thr Ile Asn Gly Val Leu Ser Ile Met
95 100 105

agg tcc tgt aag aag gcc gga acg gtc aaa cgc gtc gtc ttc act tca 387
Arg Ser Cys Lys Lys Ala Gly Thr Val Lys Arg Val Val Phe Thr Ser
110 115 120

tcc gcc ggg acg gtg gac gtg aaa gaa cat cag cag acg gag tac gac 435

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Ser Ala Gly Thr Val Asp Val Lys Glu His Gln Gln Thr Glu Tyr Asp
125                 130                 135                 140
gag agc tcg tgg agc gac gtc gac ttc tgc aga cgt gtc aag atg aca      483
Glu Ser Ser Trp Ser Asp Val Asp Phe Cys Arg Arg Val Lys Met Thr
                145                 150                 155
ggc tgg atg tat ttt gtg tcg aag act ctg gcc gag aga gca gcc tgg      531
Gly Trp Met Tyr Phe Val Ser Lys Thr Leu Ala Glu Arg Ala Ala Trp
            160                 165                 170
gaa ttt gca aga gag aat ggc ata gac ttc ata agc atc atc ccc acg      579
Glu Phe Ala Arg Glu Asn Gly Ile Asp Phe Ile Ser Ile Ile Pro Thr
        175                 180                 185
cta gtc gtc ggt cct ttc atc acc aca act atg cca ccc agc atg gtg      627
Leu Val Val Gly Pro Phe Ile Thr Thr Thr Met Pro Pro Ser Met Val
    190                 195                 200
act gcg cta tca ttc atg aca gga aac gaa gca cac tat cac ata atc      675
Thr Ala Leu Ser Phe Met Thr Gly Asn Glu Ala His Tyr His Ile Ile
205                 210                 215                 220
aag cac gcg cag ctc gtc cac ctt gac gac ctg tgc gct gcc cac att      723
Lys His Ala Gln Leu Val His Leu Asp Asp Leu Cys Ala Ala His Ile
                225                 230                 235
tac ctc ctg aat cgc ccc gaa gcg aac ggg agg tac ata tgc tca tcg      771
Tyr Leu Leu Asn Arg Pro Glu Ala Asn Gly Arg Tyr Ile Cys Ser Ser
            240                 245                 250
cac gaa gcc acc atc cac gac ctg gcg agg atg gtc agg gag agg cac      819
His Glu Ala Thr Ile His Asp Leu Ala Arg Met Val Arg Glu Arg His
        255                 260                 265
cct tgg tgc ggc tcc ata ccc gaa aag ttc gac ggc atc gag aag gac      867
Pro Trp Cys Gly Ser Ile Pro Glu Lys Phe Asp Gly Ile Glu Lys Asp
    270                 275                 280
gtc aga acc gtg cac ttc tct tcc aag agg ctt ttg gac ctc ggg ttc      915
Val Arg Thr Val His Phe Ser Ser Lys Arg Leu Leu Asp Leu Gly Phe
285                 290                 295                 300
gag ttc aag tac acg gtg gaa gaa atg ttc gac gaa gcg ata cgg tcg      963
Glu Phe Lys Tyr Thr Val Glu Glu Met Phe Asp Glu Ala Ile Arg Ser
                305                 310                 315
tgc gtc gag aag aag ctc ata ccc ctc cct gag aat ggc aac gtg gac     1011
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Cys Val Glu Lys Lys Leu Ile Pro Leu Pro Glu Asn Gly Asn Val Asp
320 325 330

gca gct gcc ggg gct aaa gac atg gtt cat gga gca gag gaa cat gcc 1059
Ala Ala Ala Gly Ala Lys Asp Met Val His Gly Ala Glu Glu His Ala
335 340 345

cga att gct atg gaa cta gaa cca aaa aaa aag gtc aag tgaaatgtga 1108
Arg Ile Ala Met Glu Leu Glu Pro Lys Lys Lys Val Lys
350 355 360

agatacaaca ttttatgcgt atggacatta caatcttaga tgttcaaggt ttcaaattgt 1168

atcttaagtg tatgatttat gttgacactc ggaagtttca ttgaaattaa taaaaaggga 1228

tttgctcaaa aaaaaaaaaa aaaa 1252

<210>10

<211>361

<212>PRT

<213>Iris

<220>

<223>Amino acid sequence encoding Iris dihydrofravonol reductase

<400>10

Met Met Ser Pro Val Val Val Thr Gly Ala Ser Gly Tyr Val Gly Ser
1 5 10 15

Trp Leu Val Met Lys Leu Leu Arg Asp Gly Tyr Ala Val Arg Ala Thr
20 25 30

Val Arg Asp Pro Thr Asn Val Glu Lys Thr Lys Pro Leu Leu Asp Leu
35 40 45

Pro Gly Ala Asp Ala Leu Leu Thr Ile Trp Lys Ala Asp Leu Gly Gln
50 55 60

Asp Gly Ser Phe Asp Lys Ala Val Ala Gly Cys Thr Ala Val Phe His
65 70 75 80

Val Ala Thr Pro Met Asp Phe Glu Ser Lys Asp Pro Glu Asn Glu Val
85 90 95

Ile Lys Pro Thr Ile Asn Gly Val Leu Ser Ile Met Arg Ser Cys Lys
100 105 110

Lys Ala Gly Thr Val Lys Arg Val Val Phe Thr Ser Ser Ala Gly Thr
115 120 125

Val Asp Val Lys Glu His Gln Gln Thr Glu Tyr Asp Glu Ser Ser Trp
130 135 140

Ser Asp Val Asp Phe Cys Arg Arg Val Lys Met Thr Gly Trp Met Tyr
145 150 155 160
Phe Val Ser Lys Thr Leu Ala Glu Arg Ala Ala Trp Glu Phe Ala Arg
165 170 175
Glu Asn Gly Ile Asp Phe Ile Ser Ile Ile Pro Thr Leu Val Val Gly
180 185 190
Pro Phe Ile Thr Thr Thr Met Pro Pro Ser Met Val Thr Ala Leu Ser
195 200 205
Phe Met Thr Gly Asn Glu Ala His Tyr His Ile Ile Lys His Ala Gln
210 215 220
Leu Val His Leu Asp Asp Leu Cys Ala Ala His Ile Tyr Leu Leu Asn
225 230 235 240
Arg Pro Glu Ala Asn Gly Arg Tyr Ile Cys Ser Ser His Glu Ala Thr
245 250 255
Ile His Asp Leu Ala Arg Met Val Arg Glu Arg His Pro Trp Cys Gly
260 265 270
Ser Ile Pro Glu Lys Phe Asp Gly Ile Glu Lys Asp Val Arg Thr Val
275 280 285
His Phe Ser Ser Lys Arg Leu Leu Asp Leu Gly Phe Glu Phe Lys Tyr
290 295 300
Thr Val Glu Glu Met Phe Asp Glu Ala Ile Arg Ser Cys Val Glu Lys
305 310 315 320
Lys Leu Ile Pro Leu Pro Glu Asn Gly Asn Val Asp Ala Ala Ala Gly
325 330 335
Ala Lys Asp Met Val His Gly Ala Glu Glu His Ala Arg Ile Ala Met
340 345 350
Glu Leu Glu Pro Lys Lys Lys Val Lys
355 360

<210>11
<211>1297
<212>DNA
<213>Nierembergia hybrida
<220>
<223>Nucleotide sequence encoding Nierembergia hybrida dihydrofravonol reductase
<400>11

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attcatacta cattttcccg tccttaagta aattttattt ctgaaa atg gca agc        55
                                                    Met Ala Ser
                                                      1
gaa gca gtt cat gct agt ccg aca gtt tgt gtc acc gga gca gct gga       103
Glu Ala Val His Ala Ser Pro Thr Val Cys Val Thr Gly Ala Ala Gly
  5                  10                  15
ttc att ggc tct tgg ctt gtc atg aga ctc ctt gaa cgc ggt tat aat       151
Phe Ile Gly Ser Trp Leu Val Met Arg Leu Leu Glu Arg Gly Tyr Asn
 20                  25                  30                  35
gtt cat gct act gtt cgt gat cct gag aac aag aag aag gtg aaa cat       199
Val His Ala Thr Val Arg Asp Pro Glu Asn Lys Lys Lys Val Lys His
                 40                  45                  50
cta cag gaa ttg cca aaa gct gat acg aac tta acg ctg tgg aaa gcg       247
Leu Gln Glu Leu Pro Lys Ala Asp Thr Asn Leu Thr Leu Trp Lys Ala
             55                  60                  65
gac ttg gcg gta gaa gga agc ttt gat gaa gcc att aaa ggc tgt caa       295
Asp Leu Ala Val Glu Gly Ser Phe Asp Glu Ala Ile Lys Gly Cys Gln
         70                  75                  80
gga gta ttt cat gtg gcc act cct atg gat ttc gag tcc aag gac cct       343
Gly Val Phe His Val Ala Thr Pro Met Asp Phe Glu Ser Lys Asp Pro
     85                  90                  95
gag aat gaa gta atc aag cca aca gtc cag gga atg ttg agc atc ata       391
Glu Asn Glu Val Ile Lys Pro Thr Val Gln Gly Met Leu Ser Ile Ile
100                 105                 110                 115
gaa tca tgt gtt aaa gca aac aca gtg aag agg ttg gtt ttc act tcg       439
Glu Ser Cys Val Lys Ala Asn Thr Val Lys Arg Leu Val Phe Thr Ser
                120                 125                 130
tct gct gga act cta gat gtc caa gag caa caa aaa ctc ttc tac gat       487
Ser Ala Gly Thr Leu Asp Val Gln Glu Gln Gln Lys Leu Phe Tyr Asp
            135                 140                 145
gag acc agc tgg agc gac ttg gac ttc ata aat gcc aag aag atg aca       535
Glu Thr Ser Trp Ser Asp Leu Asp Phe Ile Asn Ala Lys Lys Met Thr
        150                 155                 160
gga tgg atg tac ttt gtt tca aag ata ctc gcg gag aag gct gca atg       583
Gly Trp Met Tyr Phe Val Ser Lys Ile Leu Ala Glu Lys Ala Ala Met
    165                 170                 175
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gaa gaa gct aaa aag aac aac att gat ttc att agc atc ata cca cca      631
Glu Glu Ala Lys Lys Asn Asn Ile Asp Phe Ile Ser Ile Ile Pro Pro
180                 185                 190                 195
ctg gtt gtt ggt cca ttc atc acc cct tcg ttc ccg cct agt tta atc      679
Leu Val Val Gly Pro Phe Ile Thr Pro Ser Phe Pro Pro Ser Leu Ile
                200                 205                 210
act gcc ctt tca cta att act ggg aat gaa gct cac tac tgc atc att      727
Thr Ala Leu Ser Leu Ile Thr Gly Asn Glu Ala His Tyr Cys Ile Ile
            215                 220                 225
aaa caa ggt caa tat gtg cat ttg gat gat ctt tgt gag gct tac ata      775
Lys Gln Gly Gln Tyr Val His Leu Asp Asp Leu Cys Glu Ala Tyr Ile
        230                 235                 240
ttc ttg tat gaa cac cct aaa gca gag gga agg ttc att tgc tcg tcc      823
Phe Leu Tyr Glu His Pro Lys Ala Glu Gly Arg Phe Ile Cys Ser Ser
    245                 250                 255
cat cat gct atc atc tat gat gta gct aag atg atc cga gaa aaa tgg      871
His His Ala Ile Ile Tyr Asp Val Ala Lys Met Ile Arg Glu Lys Trp
260                 265                 270                 275
cca gag tac tac gtt cct aca gag ttt aaa ggc atc gct aag gac cta      919
Pro Glu Tyr Tyr Val Pro Thr Glu Phe Lys Gly Ile Ala Lys Asp Leu
                280                 285                 290
cct gtg gtg gct ttt tcg tca aag aag ttg aca gat atg ggt ttt cag      967
Pro Val Val Ala Phe Ser Ser Lys Lys Leu Thr Asp Met Gly Phe Gln
            295                 300                 305
ttc aag tac act ttg gag gat atg tat aaa ggg gcc att gag act tgt     1015
Phe Lys Tyr Thr Leu Glu Asp Met Tyr Lys Gly Ala Ile Glu Thr Cys
        310                 315                 320
cga cag aag cag ttg ctt ccc ttt tct acc aat agg cct tcg gaa aat     1063
Arg Gln Lys Gln Leu Leu Pro Phe Ser Thr Asn Arg Pro Ser Glu Asn
    325                 330                 335
gga ctt gac aaa gaa gcc att tcc att tct tct gaa aac ttt gca agt     1111
Gly Leu Asp Lys Glu Ala Ile Ser Ile Ser Ser Glu Asn Phe Ala Ser
340                 345                 350                 355
gga aaa gag aat gca cca gtt gca aat cac aaa gta aag tta aca agt     1159
Gly Lys Glu Asn Ala Pro Val Ala Asn His Lys Val Lys Leu Thr Ser
                360                 365                 370
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gtt gaa att tagaactgca atctttcaaa tgtaaaagag gcaagcttgc ctatcaacat 1218
Val Glu Ile
ctttgcttct aagttgtcat ctatttgttt ctttaatgct aaagcagtaa aaggttcaat 1278
gaaaaaaaaa aaaaaaaaa 1297

<210>12
<211>374
<212>PRT
<213>Nierembergia hybrida
<220>
<223>Amino acid sequence of Nierembergia hybrida dihydrofravonol reductase
<400>12

Met Ala Ser Glu Ala Val His Ala Ser Pro Thr Val Cys Val Thr Gly
1 5 10 15
Ala Ala Gly Phe Ile Gly Ser Trp Leu Val Met Arg Leu Leu Glu Arg
20 25 30
Gly Tyr Asn Val His Ala Thr Val Arg Asp Pro Glu Asn Lys Lys Lys
35 40 45
Val Lys His Leu Gln Glu Leu Pro Lys Ala Asp Thr Asn Leu Thr Leu
50 55 60
Trp Lys Ala Asp Leu Ala Val Glu Gly Ser Phe Asp Glu Ala Ile Lys
65 70 75 80
Gly Cys Gln Gly Val Phe His Val Ala Thr Pro Met Asp Phe Glu Ser
85 90 95
Lys Asp Pro Glu Asn Glu Val Ile Lys Pro Thr Val Gln Gly Met Leu
100 105 110
Ser Ile Ile Glu Ser Cys Val Lys Ala Asn Thr Val Lys Arg Leu Val
115 120 125
Phe Thr Ser Ser Ala Gly Thr Leu Asp Val Gln Glu Gln Gln Lys Leu
130 135 140
Phe Tyr Asp Glu Thr Ser Trp Ser Asp Leu Asp Phe Ile Asn Ala Lys
145 150 155 160
Lys Met Thr Gly Trp Met Tyr Phe Val Ser Lys Ile Leu Ala Glu Lys
165 170 175
Ala Ala Met Glu Glu Ala Lys Lys Asn Asn Ile Asp Phe Ile Ser Ile
180 185 190
Ile Pro Pro Leu Val Val Gly Pro Phe Ile Thr Pro Ser Phe Pro Pro

195 200 205

Ser Leu Ile Thr Ala Leu Ser Leu Ile Thr Gly Asn Glu Ala His Tyr
210 215 220

Cys Ile Ile Lys Gln Gly Gln Tyr Val His Leu Asp Asp Leu Cys Glu
225 230 235 240

Ala Tyr Ile Phe Leu Tyr Glu His Pro Lys Ala Glu Gly Arg Phe Ile
245 250 255

Cys Ser Ser His His Ala Ile Ile Tyr Asp Val Ala Lys Met Ile Arg
260 265 270

Glu Lys Trp Pro Glu Tyr Tyr Val Pro Thr Glu Phe Lys Gly Ile Ala
275 280 285

Lys Asp Leu Pro Val Val Ala Phe Ser Ser Lys Lys Leu Thr Asp Met
290 295 300

Gly Phe Gln Phe Lys Tyr Thr Leu Glu Asp Met Tyr Lys Gly Ala Ile
305 310 315 320

Glu Thr Cys Arg Gln Lys Gln Leu Leu Pro Phe Ser Thr Asn Arg Pro
325 330 335

Ser Glu Asn Gly Leu Asp Lys Glu Ala Ile Ser Ile Ser Ser Glu Asn
340 345 350

Phe Ala Ser Gly Lys Glu Asn Ala Pro Val Ala Asn His Lys Val Lys
355 360 365

Leu Thr Ser Val Glu Ile
370

<210>13
<211>20
<212>DNA
<213>Artificial Sequence
<220>
<221>
<222>
<223>Primer DFR-2F
<400>13
caagcaatgg catcggaatc 20
<210>14
<211>22
<212>DNA

<213>Artificial Sequence
<220>
<221>
<222>
<223>Primer DFR-2B
<400>14
tttccagtga gtggcgaaag tc 22
<210>15
<211>20
<212>DNA
<213>Artificial Sequence
<220>
<221>
<222>
<223>Primer ANS-2F
<400>15
tggactcgaa gaactcgtcc 20
<210>16
<211>19
<212>DNA
<213>Artificial Sequence
<220>
<221>
<222>
<223>Primer ANS-2B
<400>16
cctcaccttc tcccttgtt 19
<210>17
<211>17
<212>DNA
<213>Artificial Sequence
<220>
<221>
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<223>ATC Primer
<400>17

gayttyggit ggggiaa 17

<210>18

<211>23

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Origo dT Primer

<400>18

ttttttttt ttttttctc gag 23

<210>19

<211>26

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer RDF310

<400>19

ccctcgagcc cttgatggcc tcgtcg 26

<210>20

<211>26

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer RDF830

<400>20

gggtcgacgc ggccctctgc tttcgg 26

<210>21

<211>2934

<212>DNA

<213>Rose

<220>

<223>Nuceotide sequence of rose chalcone synthase promotor

<400>21

aagcttcagc aagagttgaa gaaataggga cagagccatc catgtgcttt gatgaatctg 60
atgggataca aaatgtgaaa gattcacttg ctgatttatc cagaatttct tcatatagtg 120
aggagaatgt tgaaagatct aatgatgagc actctgttaa actagacgga attcatgtgc 180
agcacgagtg tcatgagggc agtgaagaag acaaacctga tggtaagagc ggtgagaatg 240
cagttgatct ggctaatcat ggcatggctc gaactgattt ttgtcagata acagaagaga 300
ttgagaatgg agtagtcatc actgagatga gcaacattgc caaccctgat aaaactgata 360
ttccaaacgg ggtgcctcaa aatgagactg atgatggatt taataacact caggatgatg 420
ctaatacaaa ggaagtgaca gaagagaatt ctgacagacg tgcgaaggaa gtgacagaag 480
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What is claimed is:

1. A method for producing a rose characterized by artificially suppressing the rose endogenous metabolic pathway and expressing the pansy gene coding for flavonoid 3',5'-hydroxylase.

2. A method for producing a rose according to claim 1, characterized by artificially suppressing the rose endogenous metabolic pathway, and expressing the pansy gene coding for flavonoid 3',5'-hydroxylase and the gene coding for dihydroflavonol reductase.

3. A method for producing a rose according to claim 2, characterized by artificially suppressing expression of rose endogenous dihydroflavonol reductase, and expressing the pansy gene coding for flavonoid 3',5'-hydroxylase and the gene coding for dihydroflavonol reductase derived from a plant other than rose.

4. A method for producing a rose according to claim 1, characterized by artificially suppressing expression of rose endogenous flavonoid 3'-hydroxylase and expressing the pansy gene coding for flavonoid 3',5'-hydroxylase.

5. A rose obtained by the production method according to any one of claims 1 to 4, or a progeny or tissue thereof having the same properties as the rose.

6. A rose obtained by the production method according to any one of claims 1 to 4, or a progeny or tissue thereof having the same properties as the rose, wherein the petal color of the rose is violet, blue-violet or blue.

7. A rose according to claim 6, or a progeny or tissue thereof having the same properties as the rose, wherein the petal color of the rose belongs to the "Violet group", "Violet-Blue" group or "Blue group" according to the Royal Horticultural Society Colour Chart (RHSCC).

8. A rose according to claim 7, or a progeny or tissue thereof having the same properties as the rose,

wherein the petal color of the rose belongs to "Violet group" 85a or 85b according to the Royal Horticultural Society Colour Chart (RHSCC).