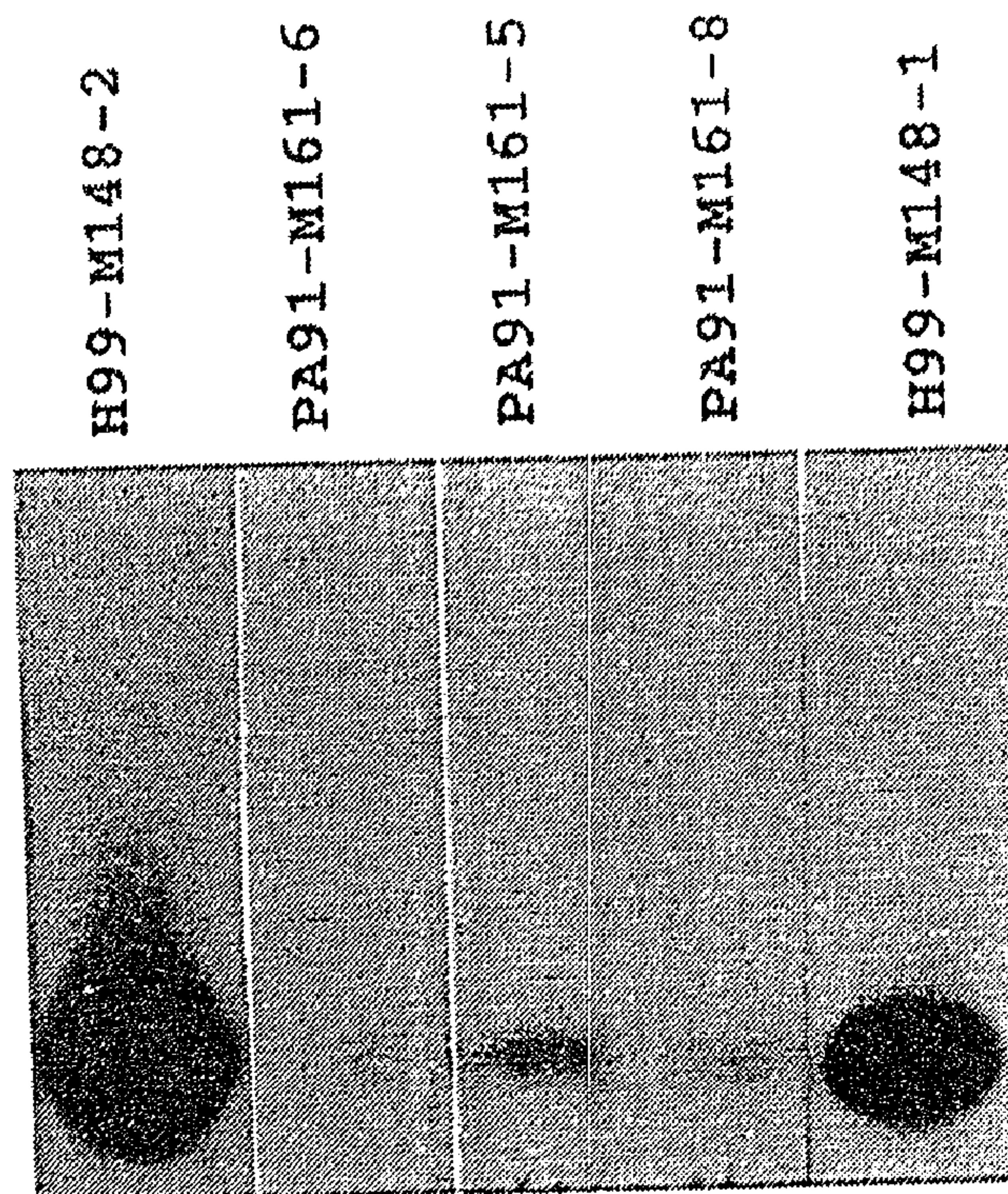




(86) Date de dépôt PCT/PCT Filing Date: 1991/11/21
(87) Date publication PCT/PCT Publication Date: 1992/06/11
(45) Date de délivrance/Issue Date: 2007/08/07
(85) Entrée phase nationale/National Entry: 1993/05/21
(86) N° demande PCT/PCT Application No.: EP 1991/002198
(87) N° publication PCT/PCT Publication No.: 1992/009696
(30) Priorités/Priorities: 1990/11/23 (EP90403332.1);
1991/07/08 (EP91401888.2)

(51) Cl.Int./Int.Cl. *C12N 15/87* (2006.01),
A01H 5/00 (2006.01), *C12N 15/82* (2006.01),
C12N 5/10 (2006.01)
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(54) Titre : PROCÉDE POUR LA TRANSFORMATION DE PLANTES MONOCOTYLEDONES
(54) Title: PROCESS FOR TRANSFORMING MONOCOTYLEDONOUS PLANTS



(57) Abrégé/Abstract:

Novel method of transforming monocotyledonous plants, particularly cereals, by wounding and/or degrading the cells of either intact tissue of the plant that is capable of forming compact embryogenic callus or the compact embryogenic callus itself.



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁵ : C12N 15/82, A01H 5/00 C12N 5/10		A1	(11) International Publication Number: WO 92/09696 (43) International Publication Date: 11 June 1992 (11.06.92)
(21) International Application Number: PCT/EP91/02198 (22) International Filing Date: 21 November 1991 (21.11.91) (30) Priority data: 90403332.1 23 November 1990 (23.11.90) GB 91401888.2 8 July 1991 (08.07.91) GB (71) Applicant (for all designated States except US): PLANT GENETIC SYSTEMS, N.V. [BE/BE]; Kolonel Bourgstraat 106, B-1040 Brussels (BE). (72) Inventors; and (75) Inventors/Applicants (for US only): D'HALLUIN, Kathleen [BE/BE]; Hooiland 48, B-9030 Mariakerke (BE). GÖBEL, Elke [DE/BE]; Jozef Kluyskensstraat 9, B-9000 Gent (BE). (74) Agents: GUTMANN, Ernest et al.; Ernest Gutmann-Yves Plasseraud S.A., 67 boulevard Haussmann, F-75008 Paris (FR).		(81) Designated States: AT (European patent), AU, BB, BE (European patent), BF (OAPI patent), BG, BJ (OAPI patent), BR, CA, CF (OAPI patent), CG (OAPI patent), CH (European patent), CI (OAPI patent), CM (OAPI patent), CS, DE (European patent), DK (European patent), ES (European patent), FI, FR (European patent), GA (OAPI patent), GB (European patent), GN (OAPI patent), GR (European patent), HU, IT (European patent), JP, KP, KR, LK, LU (European patent), MC, MG, ML (OAPI patent), MN, MR (OAPI patent), MW, NL (European patent), NO, RO, SD, SE (European patent), SN (OAPI patent), SU ⁺ , TD (OAPI patent), TG (OAPI patent), US. Published <i>With international search report.</i>	
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PROCESS FOR TRANSFORMING MONOCOTYLEDONOUS PLANTS

This invention relates to a rapid and efficient method for transforming monocotyledonous plants generally, especially gramineous plants, particularly corn and other major cereals. The invention particularly relates to the use of either intact tissue capable of forming compact embryogenic callus or compact embryogenic callus obtained from such tissue to obtain transgenic monocotyledonous plants.

This invention also relates to novel transgenic gramineous plants, particularly cereals, which can be obtained by the transformation method of this invention.

Background of the Invention

In recent years, there has been a tremendous expansion of the capabilities for the genetic engineering of plants. Many transgenic dicotyledonous plant species have been obtained. However, many species of plants, especially those belonging to the Monocotyledonae and particularly the Gramineae, including economically important species such as corn, wheat and rice, have proved to be very recalcitrant to stable genetic transformation.

Difficulties have been encountered in achieving both: a) integrative transformation of monocot plant cells with DNA (i.e., the stable insertion of DNA into the nuclear genome of the monocot plant cells) and b) regeneration from transformed cells of phenotypically normal monocot plants, such as phenotypically normal, fertile adult monocot plants. It has been suggested that such difficulties have been predominantly due to the nonavailability of monocot cells that are competent with respect to: 1) DNA uptake, 2) integrative

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transformation with the taken-up DNA, and 3) regeneration of phenotypically normal, monocot plants from the transformed cells (Potrykus (1990) Bio/Technology 9:535). In general, direct gene transfer into protoplasts (using polyethyleneglycol treatment and/or electroporation) has seemed to have the best potential for success. Protoplasts for use in such direct gene transfer methods have most often been obtained from embryogenic cell suspension cultures (Lazzeri and Lörz (1988) Advances in Cell Culture, Vol.6, Academic press, p. 291; Ozias-Akins and Lörz (1984) Trends in Biotechnology 2:119). However, the success of such methods has been limited due to the fact that regeneration of phenotypically normal plants from protoplasts has been difficult to achieve for most genotypes.

Recently, success has been reported in the transformation of, and regeneration of phenotypically normal plants from, certain lines of rice (Shimamoto et al (1989) Nature 338:274; Datta et al (1990) Bio/Technology 8:736; and Hayashimoto et al (1990) Plant Physiol. 93:857) and corn (Gordon-Kamm et al (1990) Bio/Technology 2:603; Fromm et al (1990) Bio/Technology 8:833; Gould et al (1991) Plant Physiology 95:426; and PCT publications W091/02071 and W089/12102). However, it is not clear from such reports that their processes of transformation and regeneration are applicable to monocots generally, particularly gramineous plants, quite particularly cereals.

Summary of the Invention

This invention provides a novel method for efficiently and reproducibly transforming the genome of a monocotyledonous plant, particularly a gramineous plant such as a major cereal (e.g., corn, wheat, rice,

rye, etc.)). This method comprises the transformation with DNA of cells of either: a) an intact tissue of the monocotyledonous plant, which tissue is capable of forming compact embryogenic callus or b) a compact embryogenic callus, particularly its embryogenic sectors, obtained from such intact tissue, such cells being competent with respect to: 1) uptake of the DNA, 2) integrative transformation of the plant genome, preferably its nuclear genome, with the DNA and 3) regeneration of the phenotypically normal plant (e.g., phenotypically normal, fertile adult plant) from the cells following the transformation of their genome. Such competent cells are preferably obtained by wounding and/or degrading the intact tissue or the compact embryogenic callus of the plant, for example by: a) cutting either the intact tissue and the cells thereof or the compact embryogenic callus and the cells thereof obtained from such intact tissue; and/or b) depending upon the nature of the intact tissue or the compact embryogenic callus, treating the intact tissue or the compact embryogenic callus with an enzyme to degrade the cell walls of the intact tissue or compact embryogenic callus.

According to one aspect of the present invention, there is provided a process for the stable integration of a DNA, said DNA comprising a gene that is functional in a cell of a corn, rice or wheat plant, into the nuclear genome of a corn, rice or wheat plant, said process comprising: a) obtaining a compact embryogenic callus or an immature embryo of said corn, rice or wheat plant; b) wounding said compact embryogenic callus and transferring said DNA into the nuclear genome of a cell in said compact embryogenic callus to generate a transformed cell; or degrading said immature embryo by treatment with an enzyme capable of degrading the

3a

cell walls of the cells of said immature embryo for a period of 1 to 10 minutes so as not to cause a complete disruption of the tissues and transferring said DNA into the nuclear genome of a cell in said immature embryo to generate a
5 transformed cell; and c) regenerating a transformed corn, rice or wheat plant from said transformed cell.

The resulting wounded and/or degraded, intact tissue or compact embryogenic callus, containing the competent cells of this invention, can be transformed,
10 preferably by direct gene transfer, such as by means of electroporation, with one or more DNA fragments (e.g., foreign DNA fragments), preferably linear DNA fragments. Preferably, at least one of the DNA fragments contains a gene which can serve as a selectable or a screenable marker,
15 preferably a selectable marker, for transformed plant cells. Such a marker DNA fragment can be located on the same DNA

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fragment or on a separate DNA fragment as another gene or other gene(s) of interest.

The transformed cells can be separated in a conventional manner from non-transformed cells by culturing on a selective medium, preferably for a prolonged time, and the transformed cells, thus selected, can be regenerated in a conventional manner into phenotypically normal plants (e.g., mature plants) which possess the gene(s) of interest stably integrated in their genomes, particularly their nuclear genomes.

This invention also provides: novel competent cells of monocot plants, especially gramineous plants, particularly cereal plants, the genomes of which have been stably transformed with one or more DNA fragments; cell cultures consisting of such transformed cells; phenotypically normal plants (e.g., phenotypically normal, fertile plants) regenerated from such transformed cells; and seeds of such transformed plants. Among such transformed cells, cell cultures, plants and seeds are those transformed with a DNA fragment containing a gene that encodes a protein capable of killing or disabling a plant cell in which the protein is expressed and that is under the control of the tapetum-specific PTA29 promoter whereby the plants are male sterile. The transformed gramineous plants of this invention, particularly transformed corn and rice, are characterized by their being from plant lines, from which it is practically impossible with conventional techniques to regenerate the transformed plants, as phenotypically normal plants, from transformed embryogenic suspension cultures or from transformed protoplasts, particularly where for every 10,000 untransformed protoplasts of such plant lines, no more than about 500, especially no more than about 100, particularly no more than about 10, quite

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particularly no more than about 1, phenotypically normal plant(s) can be regenerated.

Brief Description of the Drawings

Figure 1: NPTII gel assays of Example 2 of five corn transformants obtained by electroporation of immature zygotic embryos.

Figure 2: Southern blots of Example 2 of genomic DNA of one of the corn transformants of Example 1 (H99-M148-1), using the sequence listed as Seq. Id. 2 as a probe. Lengths of standard fragments are indicated. The origin is indicated by O.

Lanes: 1 : PstI digested DNA of phage lambda + HindIII digested pTDM1 (positive control - probe should hybridizes to 2824 bp pTDM1 fragment)
2 : BglII digested genomic DNA
3 : EcoRI digested genomic DNA
4 : EcoRV digested genomic DNA
5 : HindIII digested genomic DNA
6 : BamHI digested genomic DNA
7 : PvuI digested genomic DNA
8 : PvuII digested genomic DNA
9 : PstI digested genomic DNA
10: EcoRI digested plant genomic DNA of untransformed H99 plant (negative control)

Figure 3: NptII gel assays of Example 4 of seven transformants obtained by electroporation of compact embryogenic callus fragments derived from immature zygotic embryos.

Figure 4: Southern blots of Example 4 of genomic DNA of one of the corn transformants of Example 3

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(Pa91-M146-2) using the sequence listed as Seq. Id. 2 as a probe. Lengths of standard fragments are indicated. The origin is indicated by O.

Lanes: 1 : PstI digested DNA of phage lambda + HindIII digested pTTM1 (positive control - probe should hybridizes to 2824 bp pTTM1 fragment)
2 : BglII digested genomic DNA
3 : EcoRI digested genomic DNA
4 : EcoRV digested genomic DNA
5 : HindIII digested genomic DNA
6 : BamHI digested genomic DNA
7 : PvuI digested genomic DNA
8 : PvuII digested genomic DNA
9 : PstI digested genomic DNA
10 : EcoRI digested plant genomic DNA (negative control)

SEQUENCE LISTING

Seq. Id. No. 1 : sequence of pDE108
Seq. Id. No. 2 : sequence of probe used to detect chimaeric neo gene in Southern hybridizations
Seq. Id. No. 3 : sequence of a DNA fragment of plasmid pTTM8 used in the construction of plasmids pVE107 and pVE108 and comprising the promoter from the TA29 gene of tobacco and the barnase gene
Seq. Id. No. 4 : sequence of pDE110

Detailed Description of the Invention

In monocots, embryogenic callus can be of two distinct and well known types (see: Vasil (1988) Bio/Technology 6:397; Armstrong and Green (1988) Crop

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Sci. 28:363). One type of embryogenic callus can best be described as compact and/or nodular and can often be considered as organized. Such callus, termed herein "compact embryogenic callus", is used in accordance with this invention. The other and generally less frequently occurring type of embryogenic callus can best be described as soft, friable and highly embryogenic, and such callus, termed herein "friable embryogenic callus", generally grows faster than the compact embryogenic callus. From either type of callus, phenotypically normal plants can be regenerated, and in both types of callus, somatic embryos are present in different stages of development. The appearance and final morphology of the two types of callus can differ in different monocot species, particularly in different cereal species. Nevertheless, the two types of callus can be readily distinguished from one another by persons skilled in the art of forming and manipulating tissue cultures of different monocot species.

In corn, compact embryogenic callus and friable embryogenic callus are more familiarly known as type I callus and type II callus, respectively. Various distinguishing features in the structure and properties of type I and type II corn calli are described in publications, such as: Armstrong and Phillips (1988) Crop Sci. 28:363; Springer et al (1979) Protoplasma 101:269; Fransz (1988) "Cytodifferentiation during callus initiation and somatic embryogenesis in Zea mays L.", Ph.D. Thesis, University of Wageningen, The Netherlands; Ozias-Akins et al (1982) Protoplasma 110:95; Novak et al (1983) Maydica 28:381; Ho et al (1983) Protoplasma 118:169; Green et al (1975) Crop Sci. 15:417; Freeling et al (1976) Maydica 21:97; Lu et al (1982) Theor. Appl. Genet. 62:109; Vasil et al (1985) Protoplasma 127:1; Dunstan et al (1978)

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Protoplasma 97:251; Vasil et al (1982) Bot. Gaz. 143:454; Green (1983) In: Basic biology of new developments in biotechnology, Hollaender et al (eds) Plenum Press, New York, pp. 195-209; Vasil et al (1984) Am. J. Bot. 71:158; and Kamo et al (1985) Bot. Gaz. 146:327.

Type I corn callus is essentially white, pale white or yellowish and compact in appearance, often has a nodular surface, and represents the generation and propagation of an organized set of tissues which is reflected in its nodular appearance. It is characterized by a high degree of cellular association and differentiation and by various structures, such as roots, leafy structures and vascular elements. Somatic embryos can generally be recognized. The origin of regenerated shoots is not always obvious and can apparently occur by both somatic embryogenesis and organogenesis. During somatic embryo development, embryoids can fuse and give rise to hard, white callus or can develop into secondary somatic embryos.

Type II corn callus is essentially soft, friable, white or pale-yellow, somewhat transparent in appearance and highly embryogenic. It grows rapidly and contains no vascular elements. Type II callus differs from non-embryogenic friable callus in containing numerous smooth and globular embryoids that may possess a suspensor-like structure by which the embryoids are attached to the callus. The embryoids can develop into well-organized somatic embryos.

Approximately the same distinguishing features, that are found in the two types of corn calli, can be used to distinguish between the compact embryogenic callus and the friable embryogenic callus of other monocot species, particularly cereal species such as rice (Kyozuka et al (1988) Theor. Appl. Genet. 76:887),

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wheat (Redway et al (1990) Theor. Appl. Genet. 76:609; Redway et al (1990) Plant Cell Reports 8:714), and barley.

From monocotyledonous plants generally, the compact embryogenic callus of this invention can be obtained by in vitro culture of explant sources such as immature zygotic embryos, mature seeds, leaf bases, anthers, microspores, young inflorescences, etc. In corn, the type I callus is most efficiently generated from immature zygotic embryos. The compact embryogenic callus can be induced from the appropriate explants and maintained in culture according to well-established methods (see Hodges et al (1986) Bio/Technology 4:219). During maintenance of the callus culture, care has to be taken to select and subculture only the embryogenic sectors of the calli in which are the embryogenic cells. Such cells can generally be characterized as small, tightly packed, thin-walled, richly cytoplasmic, highly basophilic cells containing many small vacuoles, lipid droplets and starch grains (Vasil (1988) supra). The most convenient way to remove, from a plant, tissues that are known to be capable of forming the compact embryogenic callus is by means of dissection.

The competent cells of this invention can be obtained directly from a monocotyledonous plant by cutting from the plant, in a conventional manner, intact tissue that is capable of forming compact embryogenic callus. The cells of such wounded intact tissue can then be stably transformed. However, it is preferred that such wounded intact tissue be cut into smaller fragments to wound further such tissue and provide more competent cells for transformation. The average maximum dimension of the tissue fragments is preferably 0.1 to 5 mm long, particularly 1 to 2.5 mm long, more particularly 1.25 to 1.75 mm long. In this

respect, the wounded intact tissue of this invention can be any piece of tissue that is cut from the plant or any fragments thereof (e.g., cut pieces). Thus, the term "intact tissue" should be understood as referring to aggregates of monocot plant cells that are obtained from a naturally occurring plant part, without a tissue-culturing stage in between.

It is believed that the mechanical disruption or wounding of the intact tissue and its individual cells, by cutting the intact tissue from the plant and possibly further cutting it so as to disrupt or wound it further, is generally sufficient to generate the competent cells of this invention. In this regard, the terms "mechanical disruption" and "wounding" are intended to encompass the significant damaging of the cell wall of one or more cells of the intact tissue in order to expose the cell(s) and render the cell(s) open to insertion of a DNA fragment in accordance with this invention. Thus, "mechanical disruption" or "wounding" in accordance with this invention is not limited to cutting the cell wall but includes other methods of physically removing one or more portions of the cell wall or rendering the cell wall discontinuous in one or more places, such as by abrading, squeezing or striking the cell wall.

However, the mechanical disruption or wounding of the intact tissue in accordance with this invention can be supplemented or even replaced by a treatment of the intact tissue with an enzyme or enzyme mixture to degrade the plant cell walls, especially when the intact tissue is relatively large. The enzyme treatment can be carried out in a conventional manner. Preferably, the enzyme is applied to the intact tissue primarily to generate pores in its cell walls. It is therefore preferred that the enzyme treatment be

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relatively short (e.g., from 1 to 10 minutes depending upon the nature and the consistency of the intact tissue) so as not to cause a complete disruption of the tissue. Depending upon the type of plant, various enzymes or enzyme solutions can be used such as those listed by Powell and Chapman (1985) "Plant Cell Culture, A Practical Approach", R.A. Dixon ed., Chapter 3.

When the intact tissue, obtainable from the plant, is too small to be wounded (e.g., cut) or wounded intact tissue is too small to be further wounded (e.g., cut into smaller pieces), the enzyme treatment can be used to generate additional competent cells. Such an enzyme treatment can also be particularly useful, by itself, for forming competent cells of this invention in embryos, particularly in immature zygotic embryos isolated from developing seeds and in mature zygotic embryos isolated from mature (e.g., dry) seeds of, for example, corn. Embryos are generally not cut to remove them from seeds and generally cannot be cut into significantly smaller fragments without destroying their ability to generate compact embryogenic callus. Immature embryos are particularly important in corn as they are the only convenient and reliable source of compact embryogenic callus. In rice and other monocots, mature embryos can also be used. In this regard, for plants such as corn, it is preferred that the intact tissue (e.g., immature corn embryos) have a maximum length of about 0.5 to 2 mm, preferably 0.5 to 1.5 mm, even though smaller lengths of 0.5 to 1 mm can be used.

In accordance with this invention, the intact tissue is also preferably subjected to a period of, for example, about 15 minutes or more, preferably about 30 minutes to about 5 hours, particularly 2 to 3 hours, of preplasmolysis which involves placing the tissue in a

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conventional hypertonic solution, such as the electroporation buffer discussed below. The purpose of this preplasmolysis treatment is to separate at least partly, in the cells of the intact tissue, their protoplasts, preferably all or at least part of their cell membranes, from their cell walls. Such preplasmolysis is preferably carried out after any wounding of the intact tissue but before any enzyme treatment of the intact tissue. When the intact tissue has already been degraded by an enzyme treatment, it is preferred that any subsequent preplasmolysis be only for a brief period, and after the enzyme treatment of immature embryos of corn, as discussed above, it is preferred that such preplasmolysis not be carried out at all.

The competent cells of this invention can also be obtained by: culturing in vitro the intact tissue of this invention to produce compact embryogenic callus; and then cutting the callus into smaller fragments. The resulting callus fragments should comprise, wholly or at least in part, the embryogenic sectors or parts of the callus. The callus fragments also preferably have an average maximum length of 0.5 to 2.5 mm, particularly 1 to 2 mm, more particularly 1.25 to 1.75 mm, and preferably have a minimum length of about 0.1 mm. To obtain sufficient amounts of compact embryogenic callus, it is preferred to propagate the primary callus, as obtained from tissue explants, for at least one month and to subculture the embryogenic sectors of such primary callus at least once during this period. It is believed that the mechanical disruption or wounding of the embryogenic sectors of the compact embryogenic callus and their cells by, for example, cutting them is generally sufficient to generate the competent cells of this invention. However, the

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mechanical disruption of the callus may be supplemented or replaced by an enzyme treatment to degrade the callus cell walls, especially when the compact embryogenic callus fragments remain relatively large. This enzyme treatment can be carried out in a conventional manner. The enzyme treatment preferably serves primarily to generate pores in the cell walls of the cells of the callus fragments, and it is therefore recommended that the enzyme treatment be relatively short, preferably from 1 to 10 minutes depending upon the consistency of the callus fragments, so as not to cause a complete disruption of the tissues. Depending upon the monocot plant, various enzymes or enzyme solutions can be used such as those listed by Powell and Chapman (1985) supra. Preferably, the compact embryogenic callus fragments are also subjected to a period (e.g., 2 to 3 hours) of preplasmolysis, as discussed above.

The wounded and/or degraded, intact tissue or compact embryogenic callus fragments, particularly their embryogenic sectors, obtained as described above, are then brought into contact with one or more DNA fragments containing gene(s) of interest in order to transform their competent monocot plant cells of this invention. It is preferred that at least one of the genes of interest be adapted to serve as a selectable marker in the resulting transformed monocot plant cells. It is believed that direct gene transfer, particularly electroporation, provides optimal transformation efficiency. However, other known DNA transfer techniques can be used such as direct gene transfer using polyethyleneglycol, bombardment with DNA-coated microprojectiles (i.e., biolistic transformation using, for example, a particle gun), and Agrobacterium-mediated transformation.

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The compact embryogenic callus, used in carrying out the plant transformation method of this invention, can have certain characteristics of a friable embryogenic callus. In this regard, a compact embryogenic callus or a friable embryogenic callus can change or be caused to change into a type of callus that has some of the characteristics of compact embryogenic callus as well as some characteristics of friable embryogenic callus. As a result, such an intermediate type of callus and embryogenic portions thereof can sometimes be transformed in accordance with this invention. Indeed, somatic embryos that develop on such an intermediate type of callus, as well as on friable embryogenic callus, can be isolated and can be wounded and/or degraded and then transformed as described above. Thus, in carrying out the method of this invention, such somatic embryos obtained from an intermediate type callus or a friable embryogenic callus can be regarded as equivalent to immature or mature zygotic embryos obtained from developing or mature seeds, particularly when electroporation is used as the means for transforming cells of the somatic embryos.

In accordance with this invention, electroporation can be carried out in a conventional manner. In this regard, the wounded and/or degraded intact tissue or callus fragments, particularly meristematic or embryogenic sections thereof, quite particularly embryogenic sections thereof, can be transferred to a cuvette suitable for use in an electroporation apparatus (e.g., as described by Dekeyser et al (1990) The Plant Cell 2:591). Preferably, about 10 to 500 mg, particularly about 50 to 200 mg, most particularly about 100 to 150 mg, of intact tissue or callus fragments per 200 μ l of electroporation buffer are

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transferred to the cuvette. For cereals, such as corn, (where it is preferred to use intact enzyme-treated immature embryos), it is preferred that about 10 to 500 embryos, particularly about 50 to 150 embryos, more particularly about 75 to 125 embryos, in 200 μ l of electroporation buffer are transferred to the cuvette. The DNA is then added to the cuvette, and the electroporation is carried out. Preferably, the DNA is coincubated (e.g., for about 1 hour) with the intact tissue or callus fragments prior to electroporation. It is believed that best results can be obtained with linear, rather than circular, DNA of relatively small size, preferably smaller than about 20 kb, especially smaller than 15 kb, particularly smaller than 10 kb, quite particularly smaller than 6 kb (e.g., down to about 2-3 kb). In this regard, multiple linear DNA fragments of different composition can be used to transform the competent cells of this invention with multiple genes of interests. Preferably, about 5 to 30 μ g, particularly about 10-25 μ g, quite particularly about 20 μ g, of DNA is added to the cuvette containing the intact tissue or callus fragments. Particular electroporation conditions are not believed to be critical, and good results can be obtained, for example, with a discharge of one pulse with a field strength of 375 V/cm from a 900 μ F capacitor using an electroporation buffer containing 150 mM NaCl or 80 mM KCl (Dekeyser et al (1990) supra).

When the transformation (e.g., by electroporation) is completed, the intact tissue or callus fragments, containing the transformed monocot cells, are transferred to a suitable culture medium, preferably a selective medium when the transformed cells contain a selectable marker. This transfer should be as soon as possible after, preferably immediately after, the

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transformation event and especially within one to three days after the transformation event. Preferably, the intact tissue or callus fragments transformed with a selectable marker are cultured using conventional culture conditions and culture media (see, e.g., references in Vasil (1988) supra) supplemented with a selective agent. The selection of the selective agent will depend on the selectable marker used in the DNA fragments to transform the cells of the intact tissue or callus fragments, as discussed below. The concentration of the selective agent should provide a very high selective pressure on the transformed cells so that only stable transformants, in which the DNA fragments containing the selectable marker are integrated, preferably fully integrated, in the genome of the cells, survive and can be isolated. Although such transformed intact tissue or callus fragments can be cultured for a few days on non-selective medium, it is preferred that they be transferred to selective medium as soon as possible and maintained for a prolonged period (e.g., as long as six months), preferably at least one month, especially two to three months, to produce significant amounts of transformed morphogenic callus, such as transformed compact embryogenic callus, which can be used to regenerate a phenotypically normal plant. It is also preferred that the hypertonicity of the medium be maintained for a limited time (e.g., up to two to three weeks), for instance by supplementing the medium with mannitol.

In accordance with this invention, any DNA fragment can be integrated in the genome, particularly the nuclear genome, of a monocotyledonous plant. Generally, the DNA fragment contains a foreign or endogenous gene or other DNA sequence which is functional in the transformed plant cells and confers

an additional property to such cells and to plants regenerated from the cells. To this end, the DNA fragment preferably comprises one or more chimaeric genes which contain the following operably linked DNA sequences: 1) a promoter sequence capable of directing expression of a coding sequence in the plant cell (a "promoter"); 2) a sequence (a "coding sequence") coding for a protein with a specific activity within the plant cell (a "protein of interest"); and 3) suitable 3' transcription regulation signals. In order to obtain the required functionality of the protein, it may also be necessary that the protein be targeted to one or more particular compartments of the plant cell, such as the cytosol, mitochondria, chloroplasts or endoplasmatic reticulum. For targeting to the cytosol, the chimaeric gene, as described above, can be used as such. However for targeting to the other compartments, it is required that there be an additional sequence (a "targeting sequence") between the DNA fragments 1) and 2) of the chimaeric gene. If required, the chimaeric gene can also contain transcriptional and/or translational enhancers, and the codon usage of the DNA sequences can be optimized for expression in plant cells.

Chimaeric genes in accordance with this invention can be constructed according to well-established principles and techniques. In this regard, the various DNA sequences should be linked so that translation is initiated at the initiation codon of the coding sequence of the protein (or of the targeting sequence when it is present).

It is believed that the various constitutive and organ- and tissue-specific promoters that are presently used to direct expression of genes in transformed dicotyledonous plants will also be suitable for use in

transformed monocots of this invention. In this regard, particular plant cells can be transformed with a chimaeric gene comprising: a coding sequence encoding a protein of interest; and upstream (i.e., 5') thereof, either a foreign or an endogenous promoter suitable for expression of the coding sequence. Suitable foreign constitutive promoters include: the promoter of the Cauliflower Mosaic Virus ("CaMV") isolates CM1841 (Gardner et al (1981) Nucl. Acids. Res. 9:2871) and CabbB-S (Franck et al (1980) Cell, 21:285) (the "35S promoter") which directs constitutive expression of heterologous genes (Odell et al (1983) Nature 313:810); a related promoter (the "35S3 promoter") which can be isolated from the CaMV isolate CabbB-JI (Hull and Howell (1978) Virology 86:482) and which differs from the 35S promoter in its sequence (the sequence of the 35S3 promoter is disclosed in European patent publication ("EP") 359617) and in its greater activity in transgenic plants (Harpster et al (1988) Mol. Gen. Genet. 212:182); and the TR1' and the TR2' promoters which drive the expression of the 1' and 2' genes, respectively, of the T-DNA of Agrobacterium (Velten et al (1984) EMBO J. 3:2723) and are wound-induced promoters. Suitable organ-specific, tissue-specific and/or inducible foreign promoters are also known (see, e.g., references cited in Kuhlemeier et al (1987) Ann. Rev. Plant Physiol. 38:221) such as the promoters of the small subunit genes (such as the 1A gene) of 1,5-ribulose biphosphate carboxylase of Arabidopsis thaliana (the "ssu" promoter) which are light inducible promoters (Krebbers et al (1988) Plant Mol. Biol. 11:745) active only in photosynthetic tissue; the anther-specific promoters disclosed in EP 344029; and the seed-specific promoters of, for example, Arabidopsis thaliana (Krebbers et al (1988) Plant

200813

Physiol. 87:859). Promoters of particular usefulness for transforming monocots to render them male-sterile, as described in EP 344029, are the tapetum-specific promoters PTA29, PTA26 and PTA13, particularly PTA29, of EP 344029.

Likewise, it is believed that known 3' transcription regulation sequences and polyadenylation signals used in transformed dicotyledonous plants can be used in transformed monocots of this invention. Such 3' transcription regulation signals can be provided downstream (i.e. 3') of the coding sequence. In this regard, a particular plant cell can be transformed with a chimaeric gene containing either foreign or endogenous transcription termination and polyadenylation signals suitable for obtaining expression of the chimaeric gene. For example, the foreign 3' untranslated ends of genes, such as gene 7 (Velten and Schell (1985) Nucl. Acids Res. 13:6998), the octopine synthase gene (Gielen et al (1983) EMBO J. 3:835) and the nopaline synthase gene of the T-DNA region of Agrobacterium tumefaciens Ti-plasmid can be used.

For construction of a chimaeric gene which can be expressed in a transformed plant cell, preferably in its cytoplasm followed by translocation of its protein of interest to the cell's mitochondria, chloroplasts and/or lumen of the endoplasmatic reticulum, suitable targeting sequences are known. Selection of such targeting sequences is not believed to be critical, and a particular plant cell can be transformed with a chimaeric gene containing either a foreign or endogenous targeting sequence encoding a targeting peptide which will provide translocation of the expression product of the gene. By "targeting peptide" is meant a polypeptide fragment which is normally

203843

associated, in an eucaryotic cell, with a chloroplast or mitochondrial protein or subunit of the protein or with a protein translocated to the endoplasmatic reticulum and which is produced in a cell as part of precursor protein encoded by the nuclear DNA of the cell. The targeting peptide is responsible for the translocation process of the nuclear-encoded chloroplast or mitochondrial protein or subunit into the chloroplast or the mitochondria or the lumen of the endoplasmatic reticulum. During the translocation process, the targeting peptide is separated or proteolytically removed from the protein or subunit. A targeting sequence can be provided in the chimaeric gene to express a targeting peptide which can translocate an expressed protein of interest within a transformed plant cell as generally described in European patent applications ("EPA") 85402596.2 and 88402222.9. A suitable targeting peptide for transport into chloroplasts is the transit peptide of the small subunit of the enzyme 1,5-ribulose biphosphate carboxylase (Krebbers et al (1988) Plant Mol. Biol. 11:745; EPA 85402596.2), but other chloroplast transit peptides, such as those listed by Watson (1984) Nucl. Acids Res. 12:5145 and Von Heijne et al (1991) Plant Mol. Biol. Rep. 9:104, can also be used. Suitable mitochondrial targeting peptides are the mitochondrial transit peptides as described by Schatz (1987) Eur. J. Biochem. 165:1 and listed by Watson (1984) supra. Suitable targeting peptides that can translocate a protein of interest to the lumen of the endoplasmatic reticulum of a plant cell are, for instance, the signal peptides described by Von Heijne (1988) Biochem. Biophys. Acta 947:307 and listed by Watson (1984) supra.

205843

21

Coding sequences that can be used for the production of transgenic dicotyledonous plants are well known (see, for example, the coding sequences listed in Weising et al (1988) Annual Rev. Genet. 22:421), and it is believed that such coding sequences can be put to equally good use in transformed monocotyledonous plants in accordance with this invention. In this respect, the coding sequences can be either foreign or endogenous to the plants and can, for example, code for proteins which: are toxic to insect species, thus protecting the plants against insect attack (EP 193259, EP 305275 and EP 358557); protect the plants against stress conditions (EP 359617); confer on the plants a resistance or tolerance to specific herbicides (EP 242236); kill or disable plant cells in which the proteins are expressed so that, when the coding sequences are under the control of a male or female organ-specific promoter, the proteins can render the plants respectively male sterile (EP 344029) or female sterile (EP 412006); can be extracted from the plants or selected plant organs and optionally be further processed so that the plants can be used as sources of economically important peptides or proteins (EP 319353); or are enriched in nutritionally important amino acids so that transformed plants or their organs, in which the proteins are expressed, can be used as food with enhanced nutritional value for animals or humans (EP 318341).

Coding sequences of particular usefulness for transforming monocots to render them insect-resistant are the genes isolated from Bacillus thuringiensis ("Bt") strains and truncated portions thereof that code for insecticidal crystal proteins and their insecticidal polypeptide toxins (for a review, see: Höfte and Whiteley (1989) Microbiol. Rev. 53:242). The

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following Bt genes are believed to be particularly important for insect control in cereals (e.g., corn, rice, wheat and barley): the CryIAb gene (EP 193259) and CryIAC gene for control of Helicoverpa species (e.g., H. zea and H. armigera); the CryIAb gene and the CryIb gene (EP 358557) for control of Ostrinia species (e.g., O. nubilalis) in corn; the CryIAC gene for the control of Agrotis species in corn and wheat; and the CryID and CryIE genes (EP 358557) for the control of Spodoptera species (e.g., S. frugiperda) in corn. To achieve sufficient expression of such genes in tissues of transgenic plants, it is preferred that the genes be modified as described in PCT application PCT/EP 91/00733 (PCT publication WO 91/16432).

Selectable markers in accordance with this invention are chimaeric genes in which the coding sequences encode proteins which confer on the plant cells, in which they are expressed, resistance to a selectable agent such as an antibiotic and/or herbicide. Screenable markers in accordance with this invention are chimaeric genes in which the coding sequences encode proteins which confer on the plant cells, in which they are expressed, a different appearance, such as a different color, making plants transformed with the screenable marker separable manually. The selection of a selectable or screenable marker, preferably a selectable marker, for transforming a monocotyledonous plant in accordance with this invention is not believed to be critical, and it is believed that conventional selectable and screenable markers can be used (see, for example, the markers listed in Weising et al (1988) supra). Examples of suitable coding sequences for selectable markers are: the neo gene (Beck et al (1982) Gene 19:327) that codes for the enzyme neomycin phosphotransferase which

200849

23

confers resistance to the antibiotic kanamycin; the hyg gene (Gritz and Davies (1983) Gene 25:179) that codes for the enzyme hygromycin phosphotransferase which confers resistance to the antibiotic hygromycin; and the bar gene (EP 242236) that codes for phosphinothricin acetyl transferase which confers resistance to the herbicide phosphinothricin. In using a selectable marker gene coding for a protein that confers tolerance or resistance to a herbicide or other selective agent that acts on chloroplast metabolism, such as the bar gene, it is preferred that the marker gene be part of a chimaeric gene together with a chloroplast targeting sequence as described above. Examples of suitable coding sequences for screenable markers are the gus gene (Jefferson et al (1986) Proc. Natl. Acad. Sci. USA 6:3901) encoding beta-glucuronidase and the luciferase gene (Ow et al (1986) Science 234:856).

As discussed above, the selection pressure, provided by the presence of a selectable agent, should preferably be rather high during culturing of transformed plant cells of this invention containing selectable markers. For example, when the neo gene is used as a selectable marker, kanamycin should be used in concentrations of at least about 100-200 mg per liter, preferably at least about 200 mg per liter, in the culture medium. Such high selection pressure should also be maintained for a prolonged time, for example, two to four months. It is believed, however, that particular selection pressures and durations are not critical and that the choice of selection pressures and their durations can be made in a conventional manner. However when the bar gene is used as a selectable marker gene, phosphinothricin (PPT) is preferably used

2036843

in concentrations of 0.5 to 50, particularly 2 to 20, mg per liter of the culture medium.

Morphogenic sectors, preferably embryogenic sectors, of morphogenic callus, preferably compact embryogenic callus, produced in a culture of transformed cells of wounded and/or degraded intact tissue or wounded and/or degraded embryogenic sectors of compact embryogenic callus of this invention, can then be regenerated into phenotypically normal (e.g., mature and fertile) plants in a conventional manner (see, for example, references in Vasil (1988) supra and Lazzeri and Lörz (1988) supra). The regenerated plants, thus obtained, will be transgenic and will at least possess the selectable or screenable marker, preferably the selectable marker, stably integrated into their nuclear genome. The presence and expression of other genes of interest can then be evaluated in a conventional manner, such as by means of Southern blotting and/or by the polymerase chain reaction (Sambrook et al (1990) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory).

For the purposes of this invention, a phenotypically normal plant as produced by the transformation and regeneration procedures of this invention should be understood as at least one plant that does not differ substantially from an untransformed plant of the same line in any of its phenotypic characteristics except in those characteristics that are added or changed due to the expression of the DNA fragments introduced in the plant's genome during transformation. Of course, any procedure for transforming plants usually produces a number of transgenic plants that display a variety of phenotypes, only some of which are phenotypically normal as defined above.

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The method of this invention can be applied to all monocotyledonous plant species from which compact morphogenic callus, such as compact embryogenic callus, can be obtained during in vitro culture of explants derived from various explant sources such as immature and mature zygotic embryos, leaf bases, young inflorescences, etc. The method will be especially useful for the transformation of economically important gramineous crops, particularly the major cereals, such as corn, wheat, rice, oats, barley, sorghum, rye and millet. The resulting transgenic plants of this invention can be used to create, in a rapid and efficient manner, novel lines and/or cultivars of high agronomic value. In this regard, transgenic plants can be created in accordance with this invention that can be used as pollinator plants, for example, as female-sterile pollinator plants for the production of hybrid seed as disclosed in EP 412006 (which is incorporated herein by reference).

This invention provides a rapid, efficient and reproducible method for transforming monocotyledonous plants, using intact tissue or compact embryogenic callus to produce cultures of transformed morphogenic callus, preferably compact embryogenic callus. This is surprising as neither intact tissue nor compact embryogenic callus has generally been regarded as a suitable starting material for obtaining stable transformants (see Vasil (1990) Bio/Technology 8:797). The use of intact tissue or compact embryogenic callus in accordance with this invention is a distinct improvement on existing monocot transformation methods which have required the use of friable embryogenic callus, embryogenic cell suspension cultures and/or protoplasts that are competent for: 1) DNA uptake, 2) integrative transformation and 3) efficient and

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reproducible, monocotyledonous plant regeneration. Such requirements of competence have, up to now, limited stable transformations of monocots to plant lines with very specific tissue culture properties. In corn for example, only certain lines, such as the inbred line A188, have had the capacity to form enough type II callus (i.e., to form type II callus at frequencies higher than 10%, up to, for example, 80% or more), from which competent suspension cultures and/or protoplasts could be obtained at appreciable frequencies. However, all such corn lines have been of low agronomic value, so that transformations of economically valuable corn lines have only been possible by laborious breeding programs in which appropriate tissue culture properties have been transferred to the valuable corn lines from the transformable low value lines.

Because the method of this invention requires only a relatively short period of in vitro culture, the method is far less time and labor consuming than previous methods. The short tissue culture period also ensures that the occurrence of somaclonal variation is reduced.

The method of this invention provides novel, phenotypically normal (e.g., fertile), transgenic monocotyledonous plants, particularly gramineous plants, quite particularly cereals, most particularly corn and rice, which are transformed with at least one (e.g., foreign) gene of interest, stably integrated into their nuclear genome. The method is believed to be independent of the genotype of the plant, being transformed, and capable of transforming cells of any plant, from which compact embryogenic callus can be obtained from at least one of its tissues. This makes it possible to transform the majority of monocot species and a substantial number of lines within each

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species. Moreover, the capacity to form compact embryogenic tissue can be transferred, by means of classical breeding programs, from one line that possesses such capacity to another line that does not.

The novel transgenic monocot plants of this invention regenerated from transformed morphogenic callus, particularly transformed compact embryogenic callus, are characterized by the fact that from such monocots, using conventional culture conditions as described, for example, in Datta et al (1990) supra, Shimamoto et al (1989) supra, Hayashimoto et al (1990) supra, Gordon-Kamm et al (1990) supra, and Fromm et al (1990) supra, it is practically impossible to obtain embryogenic suspension cultures and/or protoplasts or it is practically impossible to obtain embryogenic suspension cultures and/or protoplasts which have sufficient capability of being stably transformed and then regenerated as phenotypically normal (e.g., fertile), transgenic plants. In regard to this second type of impossibility, it is not believed practical to obtain embryogenic suspension cultures or protoplasts of such monocots that: 1) have a high probability of being regenerable into phenotypically normal plants; 2) have a high probability of being competent with respect to DNA uptake and integrative transformation of the so taken-up DNA; and 3) when so transformed, have a high probability of being regenerable into phenotypically normal, transgenic plants.

In particular, this invention provides novel transgenic rice plants of rice lines, from which embryogenic suspension cultures (when obtainable) can generally be obtained, for example, according to the procedures described by Li et al (1990) Plant Mol. Biol. Report. 8:276, Datta et al (1990) Plant Sci.

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67:83, and Datta et al (1990) Plant Cell Rep. 9:253, and protoplasts (when obtainable) can generally be obtained from the embryogenic suspension cultures, for example, according to the procedures described by Li and Murai (1990) Plant Cell Rep. 9:216. However under conventional culture conditions as described, for example, in Shimamoto et al (1989) supra, Datta et al (1990) supra and Hayashimoto et al (1990) supra, it is practically impossible to regenerate phenotypically normal (e.g., fertile) plants from embryogenic suspension cultures or protoplasts of such rice lines.

This invention also provides novel transgenic corn plants of corn lines, from which embryogenic suspension cultures (when obtainable) can generally be obtained, for example, according to the procedures described by Shillito et al (1989) Bio/Technology 7:581, Prioli and Söndahl (1989) Bio/Technology 7:589, Gordon-Kamm et al (1990) supra, and Fromm et al (1990) supra, and protoplasts (when obtainable) can generally be obtained from such embryogenic suspension cultures, for example, according to the procedures described by Shillito et al (1989) supra and Prioli and Söndahl (1989) supra. However under conventional culture conditions as described, for example, by Shillito et al (1989) supra, Prioli and Söndahl (1989) supra, Gordon-Kamm et al (1990) supra and Fromm et al (1990) supra, it is practically impossible to regenerate phenotypically normal (e.g., fertile) plants from embryogenic suspension cultures or protoplasts of such corn lines. Furthermore, such corn lines have the capacity to form type I callus at high frequencies but do not possess the ability to form type II callus at frequencies higher than 10%, particularly at frequencies higher than 1%, quite particularly at frequencies higher than 0.1%, more quite particularly at frequencies higher than

208843

29

0.01. Type II corn callus is the only type of corn callus tissue, from which embryogenic suspension cultures and regenerable protoplasts can be suitably obtained that can be stably transformed, and thus, the inability to obtain type II callus for a particular corn line has meant, up to now, that one could not regenerate phenotypically normal (e.g., mature), transgenic corn plants from transformed callus of such corn line. The practical ability to obtain type II callus from a particular corn line can be assessed by the general procedures described by Gordon-Kamm et al (1990) supra and Fromm et al (1990) supra and the references mentioned therein. In making this assessment: callus cultures can be initiated from, for example, 1000 immature embryos of a corn line; the cultures can be maintained by subculturing every 3 weeks, and only those of the cultures that most resemble typical type II callus can be subcultured; and after 6 months, it can be determined at what frequencies a uniform type II callus is obtained.

More generally, to determine whether it is practical to obtain regenerable protoplasts from a specific line of a monocot species, the following well known procedures can be followed. In this regard, it is believed that regenerable protoplasts are most efficiently and reliably generated from embryogenic suspension cultures which, for any specific monocot, can be produced and maintained by conventional means. The extent and quality of an embryogenic suspension culture is generally dependent on its genotype, and it is generally only worthwhile to form protoplasts of a plant line, for transformation, if its embryogenic suspension culture is capable of plant regeneration. Embryogenic suspension cultures can generally be characterized as consisting of well dispersed, small

groups of richly cytoplasmic embryogenic cells, as being free of callus tissues or organized meristems, as having cell doubling times of 27-32 hours, and as being capable of forming somatic embryos and plants (Vasil (1988) Bio/Technology 6:397). It can be determined whether an embryogenic suspension culture of a particular line of a monocot species is suitable for plant regeneration by plating a large number (i.e., at least 100) of cell aggregates on a suitable regeneration medium and determining what proportion of the aggregates give rise to phenotypically normal, fertile plants. If normal fertile plants are obtained from 50% or more of the cell aggregates, it is generally considered worthwhile to proceed with protoplast generation. However, a specific monocot line can be considered as not being suitable for providing regenerable protoplasts suitable for plant transformation if, using conventional protoplast isolation, culture, and plant regeneration techniques: for every 10,000 protoplasts, no more than about 500, especially no more than about 100, particularly no more than about 10, quite particularly no more than about 1, phenotypically normal (e.g., fertile) plant(s) can be regenerated.

The Examples, which follow, illustrate this invention. Unless otherwise indicated, all experimental procedures for manipulating recombinant DNA were carried out by the standardized procedures described in Sambrook et al (1990) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory. Oligonucleotides were designed according to the general rules outlined by Kramer and Fritz (1968) Methods in Enzymology 154:350 and synthesized by the phosphoramidite method of Beaucage and Caruthers (1981) Tetrahedron Letters 22:1859 on an Applied Biosystems 380A DNA synthesizer

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(Applied Biosystems B.V., Maarssen, Netherlands). The following bacterial strains and plasmids, used in the Examples, are available from the Deutsche Sammlung für Mikroorganismen und Zellkulturen ("DSM"), Mascheroder Weg 1B, Braunschweig, Germany:

Bacterial strain	plasmid	DSM No	Date of Deposit
<u>E. coli</u> WK6	pMa5-8	DSM 4567	May 3, 1988
<u>E. coli</u> WK6	pMc5-8	DSM 4566	May 3, 1988

Example 1: Transformation of corn with a selectable marker gene by electroporation of DNA into zygotic immature embryos

Zygotic immature embryos of about 0.5 to 1 mm were isolated from developing seeds of two corn inbred lines, Pa91 and H99. The freshly isolated embryos were enzymatically treated for 1-2 minutes with an enzyme solution II (0.3% macerozyme (Kinki Yakult, Nishinomiya, Japan) in CPW salts (Powell & Chapman (1985) "Plant Cell Culture, A Practical Approach", R.A. Dixon ed., Chapter 3) with 10% mannitol and 5 mM 2-[N-Morpholino] ethane sulfonic acid (MES), pH 5.6). After 1-2 minutes incubation in this enzyme solution, the embryos were carefully washed with N6aph solution (macro- and micro-elements of N6 medium (Chu et al (1975) Sci. Sin. Peking 18:659) supplemented with 6mM asparagine, 12 mM proline, 1 mg/l thiamine-HCl, 0.5 mg/l nicotinic acid, 100 mg/l casein hydrolysate, 100 mg/l inositol, 30 g/l sucrose and 54 g/l mannitol). After washing, the embryos were incubated in the maize electroporation buffer, EPM-NaCl (150 mM NaCl, 5 mM CaCl₂, 10 mM HEPES (N-2-hydroxyethylpiperazine-N'-2-ethanesulfonic acid) and 0.425 M mannitol, pH 7.2).

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32

Approximately 100 embryos in 200 μ l EPM-NaCl were loaded in each cuvette. About 20 μ g of a plasmid DNA, pDE108 linearized with HindIII, were added per cuvette. pDE108 is a 5399 bp plasmid, the entire sequence of which is set forth in Seq. Id. No. 1 and which contains a chimaeric gene comprising the kanamycin resistance gene (neo) under the control of the 35S3 promoter (EP 359617).

After 1 hour DNA incubation with the explants, the cuvettes were transferred to an ice bath. After 10 minutes incubation on ice, the electroporation was carried out: one pulse with a field strength of 375 V/cm was discharged from a 900 μ F capacitor. The electroporation apparatus was as described by Dekeyser et al (1990) The Plant Cell 2:591. Immediately after electroporation, fresh liquid N6aph substrate was added to the explants in the cuvette, after which the explants were incubated for a further 10 minute period on ice.

Afterwards, the embryos were transferred to Mahl VII substrate (macro- and micro-elements and vitamins of N6 medium supplemented with 100 mg/l casein hydrolysate, 6 mM proline, 0.5 g/l MES, 1 mg/l 2,4-dichlorophenoxyacetic acid (2,4-D) and 2% sucrose solidified with 0.75 g/l $MgCl_2$ and 1.6 g/l Phytigel* (Sigma Chemical Company, St Louis, Mo. U.S.A.), pH 5.8) and supplemented with 0.2M mannitol. After 3 days for line H99 and 2 days for line Pa91, the embryos were transferred to the same substrate supplemented with 200 mg/l kanamycin. After approximately 14 days, the embryos were transferred to Mahl VII substrate without mannitol, supplemented with kanamycin. The embryos were further subcultured on this selective substrate for approximately 2 months with subculturing intervals of about 3 weeks. The induced embryogenic tissue was

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carefully isolated and transferred to MS medium (Murashige and Skoog (1962) *Physiol. Plant* 15:473) supplemented with 5 mg/l 6-benzylaminopurine for line H99 and 5 mg/l zeatin for line Pa91. The embryogenic tissue was maintained on this medium for approximately 14 days and subsequently transferred to MS medium without hormones and 6% sucrose for line H99 and 3% sucrose for line Pa91. Developing shoots were transferred to 1/2 MS medium with 1.5% sucrose for further development to normal plantlets. These plantlets were transferred to soil and cultivated in the greenhouse.

Example 2: Characterization of the transformed corn plants of Example 1

Seventeen plants from Example 1 were analysed for the presence of the chimaeric neo gene by means of the polymerase chain reaction (PCR). DNA was prepared according to the protocol described by Dellaporta et al (1983) *Plant Mol. Biol. Reporter* 1:19, adapted for application to tissue amounts of about 10 to 20 mg. For each plant, such an amount of tissue was macerated in extraction buffer in a microfuge tube. A 706 bp fragment, corresponding to part of the coding sequence of the neo gene, was amplified with the polymerase chain reaction according to the protocol described by Sambrook et al (1990) supra, using oligonucleotide probes complementary to the sequences of plasmid pDE108 from nucleotide 1384 to 1406 and 2089 to 2067 (numbering as in Seq. Id. No. 1). In total, 35 cycles with an annealing temperature of 50°C were carried out. The final DNA was analysed by electrophoresis on a 1.5% agarose gel. A 706 bp fragment could be identified in a total of 13 plants. One of the positive plants died at a later stage.

27620-9

34

Activity of the expression product of the neo gene (i.e., neomycin phosphotransferase II (NPTII)) was assayed in 9 of the plants as follows. Crude extracts were prepared by grinding plant tissue in extraction buffer (McDonnell et al (1987) Plant Molecular Biol. Reporter 5:380). The extracts were then subjected to non-denaturing polyacrylamide gel electrophoresis according to the procedure described by Reiss et al (1984) Gene 30:211. NPTII activity was then assayed by in situ phosphorylation of kanamycin using [γ - ^{32} P]ATP as a substrate (McDonnell et al (1987) supra). NPTII activity was found in 8 of the plants that were examined (Figure 1).

One of the plants (H99-M148-1), that was found to be positive on both the PCR and NPTII assay, was further analyzed by means of Southern hybridization. Genomic DNA was prepared from plant tissue according to the protocol described by Dellaporta et al (1983) supra supplemented by a treatment with RNase to remove remaining RNA. A non-transformed H99 plant was used as a control. Samples of the DNA were digested with one of the following restriction enzymes: BglII, EcoRI, EcoRV, HindIII, BamHI, PvuI, PvuII or PstI and subjected to horizontal agarose electrophoresis. Southern transfer to Hybond N+* (Amersham International PLC, Amersham, United Kingdom) membranes by means of the "alkali blotting of DNA" protocol and the subsequent hybridization were performed as recommended by the manufacturer (Amersham Hybond-N+* leaflet). Radioactive probes were prepared with the multi-prime DNA labelling kit (Amersham) according to the protocol supplied by the manufacturer which was derived from published procedures (Feinberg and Vogelstein (1983) Anal. Biochem. 132:6). As a probe, a 1184 bp EcoRI-HindIII fragment derived from another plasmid was used. The

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35

sequence of this plasmid is given in Seq. Id. No. 2. The banding patterns (e.g., see Figure 2) showed that at least the chimaeric neo gene was integrated into the plant genomic DNA.

Further analysis of this transformed plant (H99-m148-1) showed that it carries two almost intact copies of the plasmid pDE108 and part of a third rearranged copy. The two almost complete copies are apparently inserted in the plant genome in a head to tail concatamer configuration. However, some rearrangements must have occurred as an additional NcoI site and an additional BglII site were created, while the HindIII site (used for linearization of pDE108 prior to electroporation) at the junction of the two copies was lost. Sequencing of the junction of the two plasmid copies, as integrated in the plant genome, revealed that only the protruding 5' termini of the HindIII site are missing, thus creating a NcoI site as follows:

AGCCA	+	<u>AGCTTGGCG</u>	=	AGCCATGGCG
TCGGT <u>TCGA</u>		ACCGC		TCGGTACCGC

(the lost bases are underlined, and the created NcoI site at the junction is highlighted). Additional analysis showed that no or very few plasmid DNA sequences around the HindIII sites, flanking the plant genome, were lost. Although the other plants were not tested in this way, the PCR and NPTII assays showed that the chimaeric genes are present and expressed.

The mature transformed plants were fertile and phenotypically completely normal. The plant that was previously assayed by Southern hybridization was used as pollinator plant in three crossings with untransformed plants (two from corn inbred line H99 and one from corn inbred line Pa91). A total of 44 of the

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plants of the F1 progeny were assayed for NPTII activity as described above, and twenty of them were found to be positive. This does not differ significantly from the 1:1 ratio expected under normal Mendelian segregation assuming that the transformed pollinator plant had one active copy (or alternatively, multiple closely linked active copies) of the chimaeric neo gene ($\chi^2 = 0.36$).

Example 3 : Transformation of corn with a selectable marker gene by electroporation of DNA into type I callus derived from immature zygotic embryos

Immature zygotic embryos of about 0.5 to 1 mm in length were isolated from developing seeds of the corn inbred line Pa91 and cultured on Mah1 VII substrate with subsequent subculture intervals of about 14 days. Embryogenic tissue was carefully dissected out from developing type I callus. The embryogenic tissue in EPM (EPM-NaCl without NaCl) was then finely cut in fragments with a maximum length of about 1.5 mm. The resulting callus fragments were preplasmolysed for three hours in this buffer. After three hours, the callus fragments were transferred to EPM-NaCl. About 100-150 mg of callus fragments were transferred to 200 μ l EPM-NaCl per cuvette. 20 μ g DNA of plasmid pDE108 (Seq. Id. No. 1), linearized with HindIII, was added to each cuvette. The DNA was incubated with the callus fragments for one hour, after which the cuvettes were transferred to an ice bath.

After 10 minutes incubation on ice, the electroporation was carried out: one pulse with a field strength of 375 V/cm was discharged from a 900 μ F capacitor. The electroporation apparatus was as described by Dekeyser et al (1990) supra. Immediately after electroporation, fresh liquid N6aph substrate,

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supplemented with 6mM asparagine, 12 mM proline, 1 mg/l thiamine-HCl, 0.5 mg/l nicotinic acid, 100 mg/l casein hydrolysate, 100 mg/l inositol, 30 g/l sucrose and 54 g/l mannitol, was added to the callus fragments which were then further incubated for 10 minutes on ice.

After one day culture in liquid N6aph substrate supplemented with 1 mg/l 2,4-D, the callus fragments were transferred to Mahl VII substrate supplemented with 0.2M mannitol and 200 mg/l kanamycin. Fourteen days later, the callus fragments were subcultured on the same selective substrate but without mannitol and further cultured on this substrate for about 2 months with subculturing intervals of about 3 weeks. The embryogenic sectors of the resulting calli were isolated from the slimy tissue and transferred to MS substrate (Murashige and Skoog (1962) *Physiol. Plant* 15:473) with 3% sucrose and supplemented with 5 mg/l zeatin to germinate. Tissue was maintained on this medium for approximately 2 weeks and subsequently transferred to MS medium with 3% or 6% sucrose. Shoots that developed on this substrate were transferred to half-strength MS medium with 1.5% sucrose for further development to normal plantlets. These plantlets were transferred to soil and cultivated in the greenhouse.

Example 4: Characterization of the transformed corn plants of Example 3

Twenty nine plants from Example 3 were analysed for the presence of the chimaeric neo gene by means of the polymerase chain reaction. DNA was prepared according to Dellaporta et al (1983) *Plant Mol. Biol. Reporter* 1:19, adapted for application to tissue amounts of about 10 to 20 mg. For each plant, such an amount of tissue was macerated in extraction buffer in a microfuge tube. A 706 bp fragment, corresponding to

part of the coding sequence of the neo gene, was amplified with the polymerase chain reaction according to the protocol described by Sambrook et al (1990) supra, using oligonucleotide probes complementary to the sequences of plasmid pDE108 from nucleotide 1384 to 1406 and 2089 to 2067 (numbering as in Seq. Id. 1). In total, 35 cycles with an annealing temperature of 50C were carried out. The final DNA was analysed by electrophoresis on a 1.5% agarose gel. A 706 bp fragment could be identified in a total of 14 plants. One of the positive plants died at a later stage.

Activity of the NPTII expression product of the neo gene was assayed in 24 of the plants as follows. Crude extracts were prepared by grinding plant tissue in extraction buffer (McDonnell et al (1987) Plant Molecular Biol. Reporter 5:380). The extracts were then subjected to non-denaturing polyacrylamide gel electrophoresis according to the procedure described by Reiss et al (1984) Gene 30:211. NPTII activity was then assayed by in situ phosphorylation of kanamycin using [gamma-32P]ATP as a substrate (McDonnell et al, supra). NPTII activity was found in 14 of the plants that were examined (Figure 3). Two plants that were NPTII positive scored negative in a PCR assay.

Two of the plants (Pa91-M146-2 and Pa91-M149-1), that were found to be positive on both the PCR and NPTII assays, were further analyzed by means of Southern hybridization. Genomic DNA was prepared from plant tissue according to Dellaporta et al (1983) supra, supplemented by a treatment with RNase to remove remaining RNA. A non-transformed Pa91 plant was used as control. Samples of the DNA were digested with one of the following restriction enzymes: BglII, EcoRI, EcoRV, HindIII, BamHI, PvuI, PvuII or PstI and subjected to horizontal agarose electrophoresis. Southern transfer

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39

to Hybond N+ membranes by means of the "alkali blotting of DNA" protocol and the subsequent hybridization were performed as recommended by the manufacturer (Amersham). Radioactive probes were prepared with the multi-prime DNA labelling kit (Amersham) according to the protocol supplied by the manufacturer which was derived from published procedures (Feinberg and Vogelstein (1983) Anal. Biochem. 132:6). As a probe, a 1184 bp EcoRI-HindIII fragment derived from another plasmid was used. The sequence of this plasmid is given in Seq. Id. No. 2. The banding patterns (e.g., see Figure 4) showed that at least the chimaeric neo gene was integrated into the plant genomic DNA.

Further analysis of one of the transformed plants (Pa91-M146-2) showed that it carried two almost intact copies of the plasmid pDE108 in a head to tail configuration. The HindIII site (used for linearization of pDE108 prior to electroporation) at the junction of the two copies was lost. Sequencing of the junction of the two plasmid copies, as integrated in the plant genome, revealed that the protruding 5' termini of the HindIII site plus one base downstream of one of the HindIII sites are missing as follows:

AGCCA	+	<u>AGCTTGGCG</u>	=	AGCCAGGCG
TCGGT <u>TCGA</u>		<u>ACCGC</u>		TCGGTCCGC

(the lost bases are underlined). Additional analysis showed that no or very few plasmid DNA sequences around the HindIII sites, flanking the plant genome, were lost. Although the other plants were not tested in this way, the PCR and NPTII assays showed that the chimearic genes are present and expressed.

The adult plants were fertile and phenotypically completely normal. One of the plants, previously

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assayed by Southern hybridization, was used as a pollinator plant in a crossing with an untransformed plant from the corn inbred line H99. A total of 20 plants of the F1 progeny were assayed for NPTII activity as described above, and six of them were found to be positive. This does not differ significantly from the 1:1 ratio expected under normal Mendelian segregation assuming that the transformed pollinator plant had one active copy of the chimaeric neo gene ($\chi^2 = 3.2$).

Example 5: Transformation of corn with a male-sterility gene and a selectable marker by gene electroporation of DNA into zygotic immature embryos

Zygotic immature embryos of about 1 to 1.5 mm were isolated from developing seeds of corn inbred line H99. Freshly isolated embryos were enzymatically treated and washed as described in Example 1. After washing, the embryos were loaded in the maize electroporation buffer, EPM-KCl (80 mM KCl, 5 mM CaCl₂, 10 mM HEPES and 0.425 M mannitol, pH 7.2). Approximately 100 embryos in 200 μ l EPM-KCl were loaded in each cuvette. About 20 μ g of a plasmid DNA, pVE107 linearized with HindIII, were added per cuvette. pVE107 is a 6659 bp plasmid which is obtained by ligation of the 1287 bp EcoRV-EcoRI fragment of pTTM8 (EP 344029; Seq. Id. No. 3) to the large XbaI (filled-in with Klenow)-EcoRI fragment of plasmid pDE108 (Seq. Id. No. 1). pVE107 contains: a chimaeric gene comprising the kanamycin resistance gene (neo) under the control of the 35S3 promoter; and another chimaeric gene comprising the barnase gene (Hartley (1988) J. Mol. Biol. 202:913) under the control of the tapetum-specific promoter of the TA29 gene of Nicotiana tabacum (EP 344029).

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All vector constructions involving fragments of the barnase gene were carried out in E. coli strain WK6 containing the plasmid pMc5BS. pMc5BS contains the barstar gene (encoding an inhibitor of barnase) under the control of the tac promoter (De Boer et al (1983) Proc. Natl. Acad. Sci. USA 80:21). This plasmid is constructed by: cloning the EcoRI-HindIII fragment of plasmid pMT416 (see Hartley (1988) supra) into the EcoRI and HindIII sites of plasmid pMc5-8 (DSM 4566); and then deleting the sequence, starting with the initiation codon of the phoA signal sequence and ending with the last nucleotide before the translation initiation codon of the barstar coding region, by means of a looping-out mutagenesis procedure as generally described by Sollazo et al (1985) Gene 37:199.

After a 1 hour DNA incubation with the explants, the cuvettes were transferred to an ice bath. After 10 minutes incubation on ice, the electroporation was carried out as described in Example 1. Immediately after electroporation, fresh liquid N6aph substrate was added to the explants in the cuvette, after which the explants were incubated for a further 10 minute period on ice.

Afterwards, the embryos were transferred to Mahl VII substrate supplemented with 0.2 M mannitol and 200 mg/l kanamycin. After approximately 14 days, the embryos were transferred to Mahl VII substrate without mannitol but with the same selective agent, kanamycin. The embryos were further subcultured on this selective substrate for approximately 2 months, with subculturing intervals of about 3 to 4 weeks. The induced embryogenic tissue was carefully isolated and transferred to MS medium (Murashige and Skoog (1962) supra) supplemented with 5 mg/l 6-benzylaminopurine. The embryogenic tissue was maintained on this medium

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for approximately 14 days and subsequently transferred to MS medium without hormones and sucrose. Developing shoots were transferred to 1/2 MS medium with 1.5% sucrose for further development to normal plantlets. These plantlets were transferred to soil and cultivated in the greenhouse.

Example 6: Characterization of the transformed corn plants of Example 5

Seven plants from Example 5, designated RZM19-2, RZM19-3, RZM19-4, RZM19-5, RZM19-6, RZM19-7 and RZM19-8, were derived from the same embryogenic callus clump. They were subjected to extensive Southern analysis. In this regard, BamHI-NcoI digested genomic DNA of the plants was probed with pVE107 and with the small EcoRV-XbaI fragment of pTTM8 (containing PTA29-barnase; see Seq. Id. No. 3). In all plants, the strongest detected band was the expected 1400 bp fragment. However, the pattern found in these and other southern blots was very complex and indicated that transformation had resulted in many insertions of all or part of pVE107 into the plants' genomes. Some of the inserted copies of pVE107 were apparently incomplete and/or had undergone rearrangements. However, the same complex integration pattern was found in all seven plants. This could be explained by the fact that the seven transformants were all derived from one embryogenic callus clump.

The transformed plants were male sterile but otherwise phenotypically completely normal; female fertility, for instance, was normal. The spikelets of the male flowers were of about normal length but were very thin and appeared to be empty, and they never opened. A detailed analysis showed that the anthers were reduced to almost microscopic structures. This

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43

phenotype indicates not only that at least one copy of the barnase gene was expressed but also that it was selectively expressed in some or all of the tissues of the anthers.

Transformant RZM19-3 was pollinated with pollen from an untransformed H99 plant, and 53 progeny plantlets were recovered. Of these 53 plantlets, 32 (60%) scored positive in a NPTII assay, while 21 (40%) were NPTII negative. This proportion in the F1 progeny does not differ significantly from the 1:1 ratio expected under normal Mendelian segregation assuming that the transformed female parent had one active copy of the chimaeric neo gene ($\chi^2 = 2.28$). The NPTII negative progeny were male fertile, while the NPTII positive progeny were male sterile.

31 NPTII positive progeny plants were subjected to Southern analysis. 28 of these plants displayed the same integration pattern as that of the original transformant, RZM19-3, from which they were derived. 3 plants had a slightly altered pattern.

Example 7: Transformation of corn with a male-sterility gene and a herbicide resistance gene by electroporation of DNA into zygotic immature embryos

Zygotic embryos of corn inbred line H99 were isolated, enzymatically treated, washed, and loaded in electroporation buffer as described in Example 5. Approximately 100 embryos in 200 μ l EPM-KCl were loaded in each cuvette. About 20 μ g of a plasmid DNA, pVE108 linearized with HindIII, was added per cuvette. pVE108 is a 5620 bp plasmid which is obtained by ligation of the 1287 bp EcoRV-EcoRI fragment of pTTM8 (EP 344029; Seq. Id. No. 3) to the large EcoRI-StuI fragment of plasmid pDE110 (Seq Id. No. 4). pVE108 contains: a chimaeric gene comprising the bar gene (EP 242236),

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encoding phosphinothricin acetyl transferase (PAT) and conferring resistance to an herbicidal glutamine synthetase inhibitor such as phosphinothricin (PPT), under the control of the 35S3 promoter; and another chimaeric gene comprising the barnase gene (Hartley (1988) supra) under the control of the tapetum-specific promoter of the TA29 gene (EP 344029) of N. tabacum. All vector constructions involving DNA fragments comprising the barnase gene were carried out in E. coli strain WK6 containing the plasmid pMc5BS of Example 5.

After a 1 hour DNA incubation with the explants, the cuvettes were transferred to an ice bath. After 10 minutes incubation on ice, the electroporation was carried out as described in Example 1. Immediately after electroporation, fresh liquid N6aph substrate was added to the explants in the cuvette, after which the explants were incubated for a further 10 minute period on ice.

Afterwards, the embryos from one electroporation experiment were transferred to Mh1 VII substrate supplemented with 0.2 M mannitol and 2 mg/l PPT. After approximately 14 days, the embryos were transferred to Mh1 VII substrate (Mh1 VII substrate of Example 1 but without proline and casein hydrolysate) supplemented with 2 mg/l PPT but without mannitol. After approximately 4 weeks, the embryos were subcultured for another month on Mh1 VII substrate supplemented with 10 mg/l PPT. The induced embryogenic tissue was carefully isolated and transferred to MS medium supplemented with 5 mg/l 6-benzylaminopurine. The embryogenic tissue was maintained on this medium for approximately 14 days and subsequently transferred to MS medium without hormones and sucrose. Developing shoots were transferred to 1/2 MS medium with 1.5% sucrose for further development to normal plantlets. These plantlets survived an in vitro

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spraying with doses of BASTA^R (Hoechst AG, Frankfurt am Main, Germany) corresponding to 2 l/ha. These plantlets were then transferred to soil and cultivated in the greenhouse, and two of the transformed plantlets, designated RZM35-1 and RZM35-18, were further characterized (see Example 8).

The embryos from a second eletroporation experiment were transferred to Mh1 VII substrate supplemented with 2 mg/l PPT and 0.2 M mannitol. After about 14 days, the embryos were transferred to Mh1 VII substrate supplemented with 2 mg/l PPT but without mannitol. After approximately another three weeks, the embryos were transferred to Mh1 VII substrate supplemented with 10 mg/l PPT but without mannitol. After another three weeks, the induced embryogenic tissue was carefully isolated and transferred to MS medium supplemented with 2 mg/l PPT and 5 mg/l 6-benzylaminopurine. The embryogenic tissue was maintained on this medium for approximately 14 days and subsequently transferred to MS medium without hormones, sucrose or PPT. Developing shoots were transferred to 1/2 MS medium with 1.5% sucrose for further development to normal plantlets. The resulting plantlets were transferred to soil and cultivated in the greenhouse, and three of the transformed plantlets, designated RZM34-1, RZM34-12, and RZM34-14, were further characterized (see Example 8).

Example 8: Characterization of the transformed corn plants of Example 7

RZM34-1, RZM34-12, RZM34-14, RZM35-1, and RZM35-18 of Example 7 were grown in the greenhouse. Activity of the expression product of the bar gene in leaves of the plants was assayed as follows in a "PAT assay". 100 mg of leaf tissue from each plant, together with 50 mg of

2035843

46

acid-treated sea sand (Merck, Darmstadt, Germany) and 5 mg polyvinylpolypyrrolidone (PVPP), were ground in an Eppendorf tube with a glass rod in 50 μ l of extraction buffer (25 mM Tris-HCL pH 7.5, 1 mM Na₂-EDTA (ethylenediaminetetraacetic acid disodium salt), 0.15 mg/ml phenylmethylsulfonylfluoride (PMSF), 0.3 mg/ml dithiothreitol (DTT), and 0.3 mg/ml bovine serum albumin). The extract was centrifuged in a microfuge for 5 minutes at 16000 rpm. The supernatant was recovered and diluted ten times with TE 25/1 (25 mM Tris-HCL pH 7.5, 1 mM Na₂-EDTA. To twelve μ l of the diluted extract was then added: 1 μ l of 1 mM PPT in TE 25/1, 1 μ l of 2 mM AcetylCoenzyme A in TE 25/1, and 2 μ l of [¹⁴C]AcetylCoenzym A (60 mCi/mmol, 0.02 mCi/ml, [NEN Research Products, DUPONT, Wilmington, Delaware, USA). The reaction mixture was incubated for 30 minutes at 37°C and spotted on a aluminium sheet silicagel 60 t.l.c. plate with concentrating zone (Merck). Ascending chromatography was carried out in a 3 to 2 mixture of 1-propanol and NH₄OH (25% NH₃). ¹⁴C was visualized by overnight autoradiography (XAR-5 Kodak film).

The tolerance to the herbicide BASTA^R was tested by brushing a small area near the top of one leaf per plant with a 1% solution of the herbicide and observing the damage symptoms at and near the brushed sites. While RZM34-1, RZM35-1 and RZM35-18 showed no damage symptoms at all, RZM34-12 and RZM34-14 displayed slight browning and drying-out of the brushed site.

RZM34-1, RZM34-12, RZM34-14, RZM35-1 and RZM35-18 were also shown to be male sterile. The phenotype of each of these plants was identical to that described for the transformants of Example 5 which were analyzed in Example 6.

Southern analysis showed RZM35-1 and RZM35-18 to have an identical integration pattern, with only one

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47

copy of plasmid pVE108 being present in the genome of each. A small part of the plasmid DNA sequence adjacent to the HindIII site (used for linearization prior to electroporation) seemed to be absent in the integrated copy. Southern analysis of RZM34-1, RZM34-12 and RZM34-14 showed that each of these plants probably has two or three copies of part or all of pVE108 integrated into its genome. The copies are most likely not inserted in a concatemer configuration.

Transformants RZM35-1 and RZM34-1 were pollinated with pollen from an untransformed H99 plant and progeny plantlets were recovered. From the 35 plantlets recovered from RZM35-1, 16 (46%) scored positive in a PAT assay, while 19 (54%) were PAT negative. This proportion in the F1 progeny does not differ significantly from the 1:1 ratio expected under normal Mendelian segregation of one active copy of the chimaeric bar gene ($\chi^2 = 0.26$).

From the 34 plantlets recovered from RZM34-1, 19 (56%) scored positive in a PAT assay, while 15 (44%) were PAT negative. This proportion in the F1 progeny does not differ significantly from the 1:1 ratio expected under normal Mendelian segregation assuming that the transformed female parent had one active copy, or alternatively multiple active, but closely linked copies, of the chimaeric bar gene ($\chi^2 = 0.47$).

Example 9: Transformation of rice with a herbicide resistance gene by electroporation of DNA into compact embryogenic callus derived from dry seeds

Dehusked mature seeds of the rice cultivar Nipponbare were surfaced-sterilized, placed on solid 2N6 medium (N6 medium (Chu et al (1975) supra), supplemented with 0.5 mg/l nicotinic acid, 0.5 mg/l pyridoxine-HCl, 1.0 mg/l thiamine-HCl, 2.0 mg/l 2, 4-D,

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30 g/l sucrose, and 2.0 g/l Phytigel, pH 5.8), and cultured at 27°C in the dark. Callus developed from the scutella of the embryos within 3-4 weeks. Embryogenic portions of primary callus were transferred to N67 medium (N6 medium (Chu et al (1975) supra), supplemented with 0.5 mg/l nicotinic acid, 0.5 mg/l pyridoxine-HCl, 1.0 mg/l thiamine-HCl, 2.0 g/l casamino acids (vitamin assay, Difco), 1.0 mg/l 2,4-D, 0.5 mg/l 6-benzylaminopurine, 20 g/l sucrose, 30g/l sorbitol, and 2.0 g/l Phytigel, pH 5.8) for propagation into compact embryogenic callus.

Three to four weeks after subculture, the embryogenic callus was used for transformation experiments. The callus was cut into fragments with a maximum length of about 1.5 to 2 mm. The callus pieces were washed twice in EPM and then preplasmolyzed in this buffer for 30 minutes to 3 hours at room temperature (25°C). Then, the callus fragments were washed twice with EPM-KCl and transferred to electroporation cuvettes. Each cuvette was loaded with about 150 to 200 mg of callus fragments in 100 to 200 µl EPM-KCl. 10 to 20 µg of a plasmid DNA, either circular pDE110 or pDE110 linearized with HindIII or EcoRI, were added per cuvette. pDE110 is a 4883 bp plasmid, the entire sequence of which is set forth in Seq. Id. No. 4 and which contains a chimaeric gene comprising the bar gene under the control of the 35S3 promoter.

The DNA was incubated with the callus fragments for about 1 hour at room temperature. Electroporation was then carried out as described in Example 1. After electroporation, liquid N67 medium without casamino acids was added to the callus fragments. The callus fragments were then plated on solid N67 medium without casamino acids but supplemented with 5, 10 or 20 mg/l

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49

PPT and were cultured on this selective medium at 27°C under a light/dark regime of 16/8 hours for about 4 weeks. Developing PPT-resistant calli were isolated and subcultured for about two to three weeks onto fresh N67 medium without casamino acids but containing 5 mg/l PPT. Thereafter, selected PPT-resistant calli were transferred to plant regeneration medium N6M25 (N6 medium (Chu et al (1975) supra), supplemented with 0.5 mg/l nicotinic acid, 0.5 mg/l pyridoxine-HCl, 1.0 mg/l thiamine-HCl, 288 mg/l aspartic acid, 174 mg/l arginine, 7.0 mg/l glycine, 1.0 mg/l O-naphthalenacetic acid (NAA), 5.0 mg/l kinetin, 20 g/l sucrose and 2.0 g/l Phytigel, pH 5.8) supplemented with 5 mg/l PPT. Plantlets developed within approximately 1 month and were then transferred to hormone-free N6 medium (Chu et al (1975) supra), supplemented with 0.5 mg/l nicotinic acid, 0.5 mg/l pyridoxin-HCl, 1.0 mg/l thiamine-HCl, 1.0 g/l casamino acids, 20 g/l sucrose, and 2.0 g/l Phytogel, pH 5.8) on which they were kept for another 2 to 3 weeks, after which they were transferred to soil and cultivated in the greenhouse.

The compositions of the 2N6, N67, N6M25 and hormone-free N6 media, described above, were kindly provided by Japan Tobacco Inc., Plant Breeding and Genetics Research Laboratory, 700 Higashibara, Toyoda, Iwata, Shizuoka 438, Japan.

Example 10: Characterization of the transformed rice plants of Example 9

Two transformed rice plants of Example 9, obtained in different transformation experiments, were cultivated for four weeks in soil and were then sprayed with BASTA^R at a dosage corresponding to 2 l/ha. The two plants were BASTA^R resistant and survived the herbicide treatment whereas non-transformed control

plants turned brown and died within four days of herbicide spraying.

The two plants and four other in vitro plantlets, derived from two further transformation experiments of Example 9, were analyzed by means of a Southern hybridization in which plant genomic DNA, digested with PvuII, was probed with pDE110. This analysis showed that, in all analyzed plants, at least part of one copy of pDE110 was integrated in the rice genome. In five out of six plants, the 1.6 kb fragment corresponding to the pDE110 fragment containing most of the 35S-bar chimaeric gene could be unambiguously identified.

Example 11: Field tests with the transformed corn plants of Examples 2 and 4

The progeny of the corn transformant H99-M148-1 of Example 2 and of the corn transformant Pa91-M146-2 of Example 4 were tested under field conditions at the Plant Genetic Systems, N.V. experimental farm in Afsnee, Belgium. The field trial was authorized by the Belgian Ministry of Agriculture under registration number BIOT/91/M06. F1, F2, and F3 progeny were obtained from crosses as summarized in Table 1, below. In all cases one of the parents was assumed to be a heterozygote for the neo gene.

Up to 100 seeds of each seedlot were planted in 5 parallel rows, each with a length of 5 meters. Individual plants were 0.25 m apart, and the distance between rows was 1 m. 10 rows of experimental plants were alternated with 1 row of non-transformed H99 and 1 row of non-transformed Pa91 plants as controls. One plot consisted of F1 and F2 experimental plants with controls. Each of these plots was surrounded by i) a path with a width of 1 m and ii) 3 rows (1 m apart) of non-transformed corn plants (variety Sanora).

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Experimental plots were prepared, sowed and maintained according to the schedule in Table 2, below. For sowing, plant holes were made with a plant stick, and seeds were put in by hand to a depth of 4 to 5 cm.

The field trial was terminated by manual removal and subsequent steaming of all cobs of the experimental plants. The remainders of the plants were mechanically chopped with a mowing machine.

The following observations were made. At the 2-3 leaf stage, the total number of germinated seeds was counted for each seedlot. As can be seen from Table 3, below, the percentage of germination varied between 63% and 100% with the exception of seedlot P4482, from which only 42% of the seeds germinated. Germination of seedlots of untransformed H99 and Pa91 plants varied between 25% and 75%.

At the 3-4 leaf stage, the phenotype of the transgenic neo gene was assayed as follows. In each plant, an incision up to the midvein was made in two leaves with a small pair of scissors. The incisions were then brushed with a piece of cotton wool drenched in an aqueous suspension of 4% kanamycin and 0.2% SDS. Some plants were treated with a suspension of 5% kanamycin and 0.1% SDS. A plant was scored as sensitive and as lacking an active neo gene when the newly formed leaves were yellow. A plant was scored as resistant and as having an active neo gene when the newly formed leaves were normal and showed no bleaching. Discoloration of the newly formed leaves was assessed about 10 days after the brushing. 5-8% of the tested plants had an intermediate phenotype as they could not be unambiguously scored as sensitive or resistant. This was probably due to variations in environmental conditions and/or developmental stages of the tested

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plants and a less than optimal kanamycin (and/or SDS) concentration.

In later analyses, the intermediate phenotypes were pooled with the sensitive plants. The proportions of kanamycin resistant plants versus kanamycin sensitive plants (including intermediate phenotypes) for each crossing or self was determined by a chi-square goodness of fit test (Snedecor and Cochran (1967) 'Statistical Methods', the Iowa State University Press, Ames, Iowa, U.S.A.) under the assumption of a one locus Mendelian segregation of the neo gene. The results are summarized in Table 3, below.

From the data in Table 3, it can be concluded that the introduced neo gene remained stable over three generations regardless of whether the progeny was obtained through selfing, backcrossing, or outcrossing to an unrelated line. The pattern of segregation was consistent with each original transformant having had only one active copy or multiple closely linked active copies of the neo gene and with the neo gene trait having had a normal Mendelian one-locus inheritance.

In all cases, the experimental plants appeared to be morphologically completely normal when compared to untransformed control plants.

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53

Table 1

	Cross	Seedlot
F1	H99 x H99-M148-1	P3166
	Pa91 x H99-M148-1	P3169
	H99 x Pa91-M146-2	P3162
	Selfing of Pa91-M146-2	P3173 (1)
F2	P3169-024 x H99	P3651
	Selfing of P3166-002	P3989
	P3166-012 x H99	P3983
	P3166-018 x H99	P3982
	Selfing of P3173-003	P3996
	P3162-017 x H99	P4004
	P3162-008 x Pa91	P4008
F3	H99 x (P3166-005 x H99)-001	P4481
	H99 x (P3162-004 x H99)-011	P4483
	Selfing of (Selfing of P3166-001)-003	P4482
	Pa91 x (P3169-028 x Pa91)-004	P4310
	H99 x (P3169-036 x H99)-003	P4306

(1) not tested

Table 2

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Date	Activity	Quantity
March 29, 1991	lime treatment of soil	2000 kg/ha
May 23, 1991	NH ₄ NO ₃ treatment	740 kg/ha
May 23, 1991	superphosphate treatment	833 kg/ha
May 23, 1991	potassium sulphate	120 kg/ha
May 27, 1991	sowing of F1 and F2 seedlots	-
July 4, 1991	Herbicide treatment: Laddok paraffin oil	4 l/ha 105 l/ha
July 8, 1991	Sowing of F3 seedlots	-
July 26, 1991	Insecticide treatment: Pyrimor Ambush	0.265 kg/ha 0.133 l/ha
October 10, 1991	termination	-

Table 3

	Code	Emerg	%	T	R	I	S	ND	X'	Sign.
F1	P3169	16/20	5	16	5	6	4	1	1.67	n.s.
	P3166	79/100	4	79	36	0	35	8	0.01	n.s.
	P3162	86/100	4	84	47	1	31	3	2.85	n.s.
F2	P3651	65/100	4	62	26	11	16	9	0.02	n.s.
	P3989	91/100	4	83	66	1	10	5	4.71	p<0.05
	P3983	36/40	4	34	17	2	14	1	0.03	n.s.
	P3982	51/60	4	42	20	4	17	1	0.02	n.s.
	P3996	54/60	4	48	32	0	11	5	0.01	n.s.
	P4004	92/100	4	86	38	11	31	6	0.20	n.s.
	P4008	20/20	4	18	6	9	3	0	2.00	n.s.
F3	P4481	72/100	5	66	32	2	30	2	0	n.s.
	P4483	63/100	5	47	22	2	23	0	0.19	n.s.
	P4482	42/100	5	34	30	0	4	0	3.18	n.s.
	P4310	84/100	5	82	50	7	24	1	4.46	p<0.05
	P4306	85/100	5	79	39	1	39	0	0.01	n.s.

Code = seedlot (see Table 1); Emerg = number of seedlings per number of sowed seeds; % = percentage of kanamycin in solution used in brushing assay; T = total number of plants tested; R = number of kanamycin resistant plants; I = number of intermediate phenotypes; S = number of kanamycin sensitive plants; ND = number of tested plants that were not scored because seedlings were stopped in growth and died; X^2 = value of chi-square for segregation of R versus I+S (expected values in outcrossings are 50% R - 50% I+S; expected values in selfings are 75% R - 25% I+S under assumption of one locus segregation).

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SEQUENCE LISTING

1. General Information

- i) APPLICANT : PLANT GENETIC SYSTEM N.V.
- ii) TITLE OF INVENTION : Process for transforming monocotyledonous plants
- iii) NUMBER OF SEQUENCES : 4
- iv) CORRESPONDENCE ADDRESS :
 - A. ADDRESSEE : Plant Genetic Systems N.V.
 - B. STREET : Plateaustraat 22,
 - C. POSTAL CODE AND CITY : 9000 Ghent,
 - D. COUNTRY : Belgium
- v) COMPUTER READABLE FORM :
 - A. MEDIUM TYPE 5.25 inch, double sided, high density 1.2 Mb floppy disk
 - B. COMPUTER : IBM PC/AT
 - C. OPERATING SYSTEM : DOS version 3.3
 - D. SOFTWARE : WordPerfect
- vi) CURRENT APPLICATION DATA : Not Available
- (vii) PRIOR APPLICATION DATA :

European patent application 91401888.2 of July 8, 1991

European patent application 90403332.1 of November 23, 1990

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2. Information for SEQ. ID. NO. 1

i) Sequence characteristics

- A. TYPE: nucleic acid
- B. LENGTH: 5399 bp
- C. STRANDEDNESS: double stranded
- D. TOPOLOGY: circular

ii) MOLECULAR TYPE: pDE108 : plasmid DNA replicable in E. coli

ix) Features:

- 1 - 451 : pUC18 derived sequence
- 452 - 1284: "35S3" promoter sequence derived from Cauliflower mosaic virus isolate CabbB-JI
- 1285 - 2100: coding sequence of neomycin phosphotransferase gene
- 2101 - 3160: 3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA octopine synthase gene
- 3161-5399: pUC18 derived sequence

Other information: plasmid is replicable in E. coli,
confers ampicillin resistance to the bacterium

xi) Sequence description

TCGCGCGTTT	CGGTGATGAC	GGTGAAAACC	TCTGACACAT	GCAGCTCCCG	50
GAGACGGTCA	CAGCTTGTCT	GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCG	100
TCAGGGCGCG	TCAGCGGGTG	TTGGCGGGTG	TCGGGGCTGG	CTTAACTATG	150
CGGCATCAGA	GCAGATTGTA	CTGAGAGTGC	ACCATATGCG	GTGTGAAATA	200
CCGCACAGAT	GCGTAAGGAG	AAAATACCGC	ATCAGGCGCC	ATTCGCCATT	250
CAGGCTGCGC	AACTGTTGGG	AAGGGCGATC	GGTGCGGGCC	TCTTCGCTAT	300
TACGCCAGCT	GGCGAAAGGG	GGATGTGCTG	CAAGGCGATT	AAGTTGGGTA	350
ACGCCAGGGT	TTTCCCAGTC	ACGACGTTGT	AAAACGACGG	CCAGTGAATT	400
CGAGCTCGGT	ACCCGGGGAT	CCTCTAGAGT	CGACCTGCAG	GCATGCAAGC	450
TCCTACGCAG	CAGGTCTCAT	CAAGACGATC	TACCCGAGTA	ACAATCTCCA	500
GGAGATCAAA	TACCTTCCCA	AGAAGGTAA	AGATGCAGTC	AAAAGATTCA	550
GGACTAATTG	CATCAAGAAC	ACAGAGAAAG	ACATATTTCT	CAAGATCAGA	600
AGTACTATTC	CAGTATGGAC	GATTCAAGGC	TTGCTTCATA	AACCAAGGCA	650
AGTAATAGAG	ATTGGAGTCT	CTAAAAAGGT	AGTTCCTACT	GAATCTAAGG	700
CCATGCATGG	AGTCTAAGAT	TCAAATCGAG	GATCTAACAG	AACTCGCCGT	750
GAAGACTGGC	GAACAGTTCA	TACAGAGTCT	TTTACGACTC	AATGACAAGA	800
AGAAAATCTT	CGTCAACATG	GTGGAGCAGC	ACACTCTGGT	CTACTCCAAA	850
AATGTCAAAG	ATACAGTCTC	AGAAGACCAA	AGGGCTATTG	AGACTTTTCA	900
ACAAAGGATA	ATTTCGGGAA	ACCTCCTCGG	ATTCCATTGC	CCAGCTATCT	950
GTCACTTCAT	CGAAAGGACA	GTAAGAAAGG	AAGGTGGCTC	CTACAAATGC	1000
CATCATTGCG	ATAAAGGAAA	GGCTATCATT	CAAGATGCCT	CTGCCGACAG	1050
TGGTCCCAAA	GATGGACCCC	CACCCACGAG	GAGCATCGTG	GAAAAAGAAG	1100
ACGTTCCAAC	CACGTCTTCA	AAGCAAGTGG	ATTGATGTGA	CATCTCCACT	1150
GACGTAAGGG	ATGACGCACA	ATCCCACTAT	CCTTCGCAAG	ACCCTTCCTC	1200
TATATAAGGA	AGTTCATTTT	ATTTGGAGAG	GACACGCTGA	AATCACCAGT	1250
CTCTCTCTAT	AAATCTATCT	CTCTCTCTAT	AACCATGGAT	CCGGCCAAGC	1300
TAGCTTGGAT	TGAACAAGAT	GGATTGCACG	CAGGTTCTCC	GGCCGCTTGG	1350

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GTGGAGAGGC	TATTCGGCTA	TGACTGGGCA	CAACAGACAA	TCGGCTGCTC	1400
TGATGCCGCC	GTGTTCCGGC	TGTCAGCGCA	GGGGCGCCCG	GTTCTTTTGT	1450
TCAAGACCGA	CCTGTCCGGT	GCCCTGAATG	AACTGCAGGA	CGAGGCAGCG	1500
CGGCTATCGT	GGCTGGCCAC	GACGGGCGTT	CCTTGCGCAG	CTGTGCTCGA	1550
CGTTGTCACT	GAAGCGGGAA	GGGACTGGCT	GCTATTGGGC	GAAGTGCCGG	1600
GGCAGGATCT	CCTGTCATCT	CACCTTGCTC	CTGCCGAGAA	AGTATCCATC	1650
ATGGCTGATG	CAATGCGGCG	GCTGCATACG	CTTGATCCGG	CTACCTGCCC	1700
ATTCGACCAC	CAAGCGAAAC	ATCGCATCGA	GCGAGCACGT	ACTCGGATGG	1750
AAGCCGGTCT	TGTCGATCAG	GATGATCTGG	ACGAAGAGCA	TCAGGGGCTC	1800
GCGCCAGCCG	AACTGTTCCG	CAGGCTCAAG	GCGCGCATGC	CCGACGGCGA	1850
GGATCTCGTC	GTGACCCATG	GCGATGCCTG	CTTGCCGAAT	ATCATGGTGG	1900
AAAATGGCCG	CTTTTCTGGA	TTCATCGACT	GTGGCCGGCT	GGGTGTGGCG	1950
GACCGCTATC	AGGACATAGC	GTTGGCTACC	CGTGATATTG	CTGAAGAGCT	2000
TGGCGGCGAA	TGGGCTGACC	GCTTCCTCGT	GCTTTACGGT	ATCGCCGCTC	2050
CCGATTTCGA	GCGCATCGCC	TTCTATCGCC	TTCTTGACGA	GTTCTTCTGA	2100
GCGGGACTCT	GGGGTTCGAA	ATGACCGACC	AAGCGACGCC	CAACCTGCCA	2150
TCACGAGATT	TCGATTCCAC	CGCCGCCTTC	TATGAAAGGT	TGGGCTTCGG	2200
AATCGTTTTC	CGGGACGCCG	GCTGGATGAT	CCTCCAGCGC	GGGGATCTCA	2250
TGCTGGAGTT	CTTCGCCCAC	CCCCTGCTTT	AATGAGATAT	GCGAGACGCC	2300
TATGATCGCA	TGATATTTGC	TTTCAATTCT	GTTGTGCACG	TTGTAAAAAA	2350
CCTGAGCATG	TGTAGCTCAG	ATCCTTACCG	CCGGTTTCGG	TTCATTTCTAA	2400
TGAATATATC	ACCCGTTACT	ATCGTATTTT	TATGAATAAT	ATTCTCCGTT	2450
CAATTTACTG	ATTGTACCCT	ACTACTTATA	TGTACAATAT	TAAAATGAAA	2500
ACAATATATT	GTGCTGAATA	GGTTTATAGC	GACATCTATG	ATAGAGCGCC	2550
ACAATAACAA	ACAATTGCGT	TTTATTATTA	CAAATCCAAT	TTTAAAAAAA	2600
GCGGCAGAAC	CGGTCAAACC	TAAAAGACTG	ATTACATAAA	TCTTATTCAA	2650
ATTTCAAAAAG	GCCCCAGGGG	CTAGTATCTA	CGACACACCG	AGCGGCGAAC	2700
TAATAACGTT	CACTGAAGGG	AACTCCGGTT	CCCCGCCGGC	GCGCATGGGT	2750
GAGATTCCTT	GAAGTTGAGT	ATTGGCCGTC	CGCTCTACCG	AAAGTTACGG	2800
GCACCATTC	ACCCGGTCCA	GCACGGCGGC	CGGGTAACCG	ACTTGCTGCC	2850
CCGAGAATTA	TGCAGCATTT	TTTTGGTGTA	TGTGGGCCCC	AAATGAAGTG	2900
CAGGTCAAAC	CTTGACAGTG	ACGACAAATC	GTTGGGCGGG	TCCAGGGCGA	2950
ATTTTGCGAC	AACATGTCGA	GGCTCAGCAG	GGGCTCGATC	CCCTCGCGAG	3000
TTGGTTCAGC	TGCTGCCTGA	GGCTGGACGA	CCTCGCGGAG	TTCTACCGGC	3050
AGTGCAAATC	CGTCGGCATC	CAGGAAACCA	GCAGCGGCTA	TCCGCGCATC	3100
CATGCCCCCG	AACTGCAGGA	GTGGGGAGGC	ACGATGGCCG	CTTTGGTCTGA	3150
CCTGCAGCCA	AGCTTGGCGT	AATCATGGTC	ATAGCTGTTT	CCTGTGTGAA	3200
ATTGTTATCC	GCTCACAATT	CCACACAACA	TACGAGCCGG	AAGCATAAAG	3250
TGTAAAGCCT	GGGGTGCCTA	ATGAGTGAGC	TAACTCACAT	TAATTGCGTT	3300
GCGCTCACTG	CCCGCTTTCC	AGTCGGGAAA	CCTGTCTGTC	CAGCTGCATT	3350
AATGAATCGG	CCAACGCGCG	GGGAGAGGCG	GTTTGCGTAT	TGGGCGCTCT	3400
TCCGCTTCCT	CGCTCACTGA	CTCGCTGCGC	TCCGTCTGTC	GGCTGCGGCG	3450
AGCGGTATCA	GCTCACTCAA	AGGCGGTAAT	ACGGTTATCC	ACAGAATCAG	3500
GGGATAACGC	AGGAAAGAAC	ATGTGAGCAA	AAGGCCAGCA	AAAGGCCAGG	3550
AACCGTAAAA	AGGCCGCGTT	GCTGGCGTTT	TTCCATAGGC	TCCGCCCCCC	3600
TGACGAGCAT	CACAAAAATC	GACGCTCAAG	TCAGAGGTGG	CGAAACCCGA	3650
CAGGACTATA	AAGATACCAG	GCGTTTCCCC	CTGGAAGCTC	CCTCGTGCGC	3700
TCTCCTGTTT	CGACCCTGCC	GCTTACCGGA	TACCTGTCCG	CCTTTCTCCC	3750
TTCCGGGAAGC	GTGGCGCTTT	CTCAATGCTC	ACGCTGTAGG	TATCTCAGTT	3800
CGGTGTAGGT	CGTTCGCTCC	AAGCTGGGCT	GTGTGCACGA	ACCCCCCGTT	3850
CAGCCCGACC	GCTGCGCCTT	ATCCGGTAAC	TATCGTCTTG	AGTCCAACCC	3900
GGTAAGACAC	GACTTATCGC	CACTGGCAGC	AGCCACTGGT	AACAGGATTA	3950
GCAGAGCGAG	GTATGTAGGC	GGTGCTACAG	AGTTCTTGAA	GTGGTGGCCT	4000
AACTACGGCT	ACACTAGAAG	GACAGTATTT	GGTATCTGCG	CTCTGCTGAA	4050
GCCAGTTACC	TTCCGAAAAA	GAGTTGGTAG	CTCTTGATCC	GGCAAACAAA	4100

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CCACCGCTGG	TAGCGGTGGT	TTTTTTGTTT	GCAAGCAGCA	GATTACGCGC	4150
AGAAAAAAG	GATCTCAAGA	AGATCCTTTG	ATCTTTTCTA	CGGGGTCTGA	4200
CGCTCAGTGG	AACGAAAAC	CACGTTAAGG	GATTTTGGTC	ATGAGATTAT	4250
CAAAAAGGAT	CTTCACCTAG	ATCCTTTTAA	ATTAAAAATG	AAGTTTTAAA	4300
TCAATCTAAA	GTATATATGA	GTAAACTTGG	TCTGACAGTT	ACCAATGCTT	4350
AATCAGTGAG	GCACCTATCT	CAGCGATCTG	TCTATTTCGT	TCATCCATAG	4400
TTGCCTGACT	CCCCGTCGTG	TAGATAACTA	CGATACGGGA	GGGCTTACCA	4450
TCTGGCCCCA	GTGCTGCAAT	GATACCGCGA	GACCCACGCT	CACCGGCTCC	4500
AGATTTATCA	GCAATAAACC	AGCCAGCCGG	AAGGGCCGAG	CGCAGAAGTG	4550
GTCCTGCAAC	TTTATCCGCC	TCCATCCAGT	CTATTAATTG	TTGCCGGGAA	4600
GCTAGAGTAA	GTAGTTCGCC	AGTTAATAGT	TTGCGCAACG	TTGTTGCCAT	4650
TGCTACAGGC	ATCGTGGTGT	CACGCTCGTC	GTTTGGTATG	GCTTCATTCA	4700
GCTCCGGTTC	CCAACGATCA	AGGCGAGTTA	CATGATCCCC	CATGTTGTGC	4750
AAAAAAGCGG	TTAGCTCCTT	CGGTCCTCCG	ATCGTTGTCA	GAAGTAAGTT	4800
GGCCGCAGTG	TTATCACTCA	TGGTTATGGC	AGCACTGCAT	AATTCTCTTA	4850
CTGTCATGCC	ATCCGTAAGA	TGCTTTTCTG	TGACTGGTGA	GTACTCAACC	4900
AAGTCATTCT	GAGAATAGTG	TATGCGGCGA	CCGAGTTGCT	CTTGCCCCGC	4950
GTCAATACGG	GATAATACCG	CGCCACATAG	CAGAACTTTA	AAAGTGCTCA	5000
TCATTGGAAA	ACGTTCTTCG	GGGCGAAAAC	TCTCAAGGAT	CTTACCGCTG	5050
TTGAGATCCA	GTTCGATGTA	ACCCACTCGT	GCACCCAAC	GATCTTCAGC	5100
ATCTTTTACT	TTCACCAGCG	TTTCTGGGTG	AGCAAAAACA	GGAAGGCAAA	5150
ATGCCGCAAA	AAAGGGAATA	AGGGCGACAC	GGAAATGTTG	AATACTCATA	5200
CTCTTCCTTT	TTCAATATTA	TTGAAGCATT	TATCAGGGTT	ATTGTCTCAT	5250
GAGCGGATAC	ATATTTGAAT	GTATTTAGAA	AAATAAACAA	ATAGGGGTTC	5300
CGCGCACATT	TCCCCGAAAA	GTGCCACCTG	ACGTCTAAGA	AACCATTATT	5350
ATCATGACAT	TAACCTATAA	AAATAGGCGT	ATCACGAGGC	CCTTTCGTC	5399

20584360

3. Information for SEQ. ID. NO. 2

- i) Sequence characteristics
 - A. TYPE: nucleic acid
 - B. LENGTH: 1186 bp
 - C. STRANDEDNESS: double stranded
 - D. TOPOLOGY: linear
- ii) MOLECULAR TYPE: DNA used as probe for neo gene
- ix) Features:
 - 1 - 8 : sequence derived from tapetum specific promoter of Nicotiana tabacum
 - 9 - 790: coding sequence of neomycine phosphotransferase gene
 - 791 - end: 3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA gene 7

xi) Sequence description

AAGCTTGGAT	GGATTGCACG	CAGGTTCTCC	GGCCGCTTGG	GTGGAGAGGC	50
TATTCGGCTA	TGACTGGGCA	CAACAGACAA	TCGGCTGCTC	TGATGCCGCC	100
GTGTTCCGGC	TGTCAGCGCA	GGGGCGCCCG	GTTCTTTTGT	TCAAGACCGA	150
CCTGTCCGGT	GCCCTGAATG	AACTGCAGGA	CGAGGCAGCG	CGGCTATCGT	200
GGCTGGCCAC	GACGGGCGTT	CCTTGCGCAG	CTGTGCTCGA	CGTTGTCACT	250
GAAGCGGGAA	GGGACTGGCT	GCTATTGGGC	GAAGTGCCGG	GGCAGGATCT	300
CCTGTCATCT	CACCTTGCTC	CTGCCGAGAA	AGTATCCATC	ATGGCTGATG	350
CAATGCGGCG	GCTGCATACG	CTTGATCCGG	CTACCTGCCC	ATTCGACCAC	400
CAAGCGAAAC	ATCGCATCGA	GCGAGCACGT	ACTCGGATGG	AAGCCGGTCT	450
TGTTCGATCAG	GATGATCTGG	ACGAAGAGCA	TCAGGGGCTC	GCGCCAGCCG	500
AACTGTTCGC	CAGGCTCAAG	GCGCGCATGC	CCGACGGCGA	GGATCTCGTC	550
GTGACCCATG	GCGATGCCTG	CTTGCCGAAT	ATCATGGTGG	AAAATGGCCG	600
CTTTTCTGGA	TTCATCGACT	GTGGCCGGCT	GGGTGTGGCG	GACCGCTATC	650
AGGACATAGC	GTTGGCTACC	CGTGATATTG	CTGAAGAGCT	TGGCGGCGAA	700
TGGGCTGACC	GCTTCCTCGT	GCTTTACGGT	ATCGCCGCTC	CCGATTCGCA	750
GCGCATCGCC	TTCTATCGCC	TTCTTGACGA	GTTCTTCTGA	GCGGGACTCT	800
GGGGTTTCGAA	ATGACCGACC	AAGCGACGCC	CAACCTGCCA	TCACGAGATT	850
TCGATTCCAC	CGCCGCCTTC	TATGAAAGGT	TGGGCTTCGG	AATCGTTTTT	900
CGGGACGCCG	GCTGGATGAT	CCTCCAGCGC	GGGGATCTCA	TGCTGGAGTT	950
CTTCGCCCAC	CCCGATCCAT	GAGCTAAGCT	AGCTATATCA	TCAATTTATG	1000
TATTACACAT	AATATCGCAC	TCAGTCTTTC	ATCTACGGCA	ATGTACCAGC	1050
TGATATAATC	AGTTATTGAA	ATATTTCTGA	ATTTAAACTT	GCATCAATAA	1100
ATTTATGTTT	TTGCTTGGAC	TATAATACCT	GACTTGTTAT	TTTATCAATA	1150
AATATTTAAA	CTATATTTCT	TTCAAGATGG	GAATTC		1186

21,1843

4. Information for SEQ. ID. NO. 3

i) Sequence Characteristics

TYPE: nucleic acid

LENGTH: 1287 bp

STRANDEDNESS: double-stranded

TOPOLOGY: linear

ii) MOLECULAR TYPE: DNA comprising a chimaeric gene

ix) FEATURES:

1 - 545 : promoter from the TA29 gene from Nicotiana tabacum

546 - 881 : coding sequence of the barnase gene

882 - 3' regulatory sequence containing the polyadenylation site derived from the nopaline synthase gene from Agrobacterium T-DNA

xi) Sequence Description:

ATCTAGCTAA	GTATAACTGG	ATAATTTGCA	TTAACAGATT	GAATATAGTG	50
CCAAACAAGA	AGGGACAATT	GACTTGTCAC	TTTATGAAAG	ATGATTCAAA	100
CATGATTTTT	TATGTACTAA	TATATACATC	CTACTCGAAT	TAAAGCGACA	150
TAGGCTCGAA	GTATGCACAT	TTAGCAATGT	AAATTAAATC	AGTTTTTGAA	200
TCAAGCTAAA	AGCAGACTTG	CATAAGGTGG	GTGGCTGGAC	TAGAATAAAC	250
ATCTTCTCTA	GCACAGCTTC	ATAATGTAAT	TTCCATAACT	GAAATCAGGG	300
TGAGACAAAA	TTTTGGTACT	TTTTTCCTCAC	ACTAAGTCCA	TGTTTGCAAC	350
AAATTAATAC	ATGAAACCTT	AATGTTACCC	TCAGATTAGC	CTGCTACTCC	400
CCATTTTCCT	CGAAATGCTC	CAACAAAAGT	TAGTTTTGCA	AGTTGTTGTG	450
TATGTCTTGT	GCTCTATATA	TGCCCTTGTG	GTGCAAGTGT	AACAGTACAA	500
CATCATCACT	CAAATCAAAG	TTTTTACTTA	AAGAAATTAG	CTACCATGGT	550
ACCGGTTATC	AACACGTTTG	ACGGGGTTGC	GGATTATCTT	CAGACATATC	600
ATAAGCTACC	TGATAATTAC	ATTACAAAAT	CAGAAGCACA	AGCCCTCGGC	650
TGGGTGGCAT	CAAAAGGGAA	CCTTGCAGAC	GTCGCTCCGG	GGAAAAGCAT	700
CGGCGGAGAC	ATCTTCTCAA	ACAGGGAAGG	CAAACCTCCG	GGCAAAAGCG	750
GACGAACATG	GCGTGAAGCG	GATATTAAC	ATACATCAGG	CTTCAGAAAT	800
TCAGACCGGA	TTCTTTACTC	AAGCGACTGG	CTGATTTACA	AAACAACGGA	850
CCATTATCAG	ACCTTTACAA	AAATCAGATA	ACGAAAAAAA	CGGCTTCCTG	900
CGGAGGCCGT	TTTTTTCAGC	TTTACATAAA	GTGTGTAATA	AATTTTTCTT	950
CAAACCTCTGA	TCGGTCAATT	TCACTTCCG	GXXXXCTCTA	GAGGATCCGA	1000
AGCAGATCGT	TCAAACATTT	GGCAATAAAG	TTTCTTAAGA	TTGAATCCTG	1050
TTGCCGGTCT	TGCGATGATT	ATCATATAAT	TTCTGTTGAA	TTACGTTAAG	1100
CATGTAATAA	TTAACATGTA	ATGCATGACG	TTATTTATGA	GATGGGTTTT	1150
TATGATTAGA	GTCCCGCAAT	TATACATTTA	ATACGCGATA	GAAAACAAAA	1200
TATAGCGCGC	AAACTAGGAT	AAATTATCGC	GCGCGGTGTC	ATCTATGTTA	1250
CTAGATCGGG	AAGATCCCCG	GGTACCGAGC	TCGAATT		1287

5. Information for SEQ. ID. NO. 4

i) Sequence characteristics

- A. TYPE: nucleic acid
- B. LENGTH: 4883 bp
- C. STRANDEDNESS: double stranded
- D. TOPOLOGY: circular

ii) MOLECULAR TYPE: pDE110 : plasmid DNA replicable in E. coli

ix) Features:

- 1 - 395 : pUC18 derived sequence
- 396 - 1779: "35S3" promoter sequence derived from
Cauliflower mosaic virus isolate
CabbB-JI
- 1780 - 2331: coding sequence of phosphinotricin
acetyltransferase gene
- 2332 - 2619: 3' regulatory sequence containing the
polyadenylation site derived from
Agrobacterium T-DNA nopaline synthase
gene
- 2620 - 4883: pUC18 derived sequence

Other information: plasmid is replicable in E. coli,
confers ampicillin resistance to the bacterium

xi) Sequence description

TCGCGCGTTT	CGGTGATGAC	GGTGAAAACC	TCTGACACAT	GCAGCTCCCG	50
GAGACGGTCA	CAGCTTGTCT	GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCCG	100
TCAGGGCGCG	TCAGCGGGTG	TTGGCGGGTG	TCGGGGCTGG	CTTAACTATG	150
CGGCATCAGA	GCAGATTGTA	CTGAGAGTGC	ACCATATGCG	GTGTGAAATA	200
CCGCACAGAT	GCGTAAGGAG	AAAATACCGC	ATCAGGCGCC	ATTCGCCATT	250
CAGGCTGCGC	AACTGTTGGG	AAGGGCGATC	GGTGGGGGCC	TCTTCGCTAT	300
TACGCCAGCT	GGCGAAAGGG	GGATGTGCTG	CAAGGCGATT	AAGTTGGGTA	350
ACGCCAGGGT	TTTCCCAGTC	ACGACGTTGT	AAAACGACGG	CCAGTGAATT	400
CCAATCCCAC	CAAAACCTGA	ACCTAGCAGT	TCAGTTGCTC	CTCTCAGAGA	450
CGAATCGGGT	ATTCAACACC	CTCATAACCA	CTACTACGTC	GTGTATAACG	500
GACCTCATGC	CGGTATATAC	GATGACTGGG	GTTGTACAAA	GGCAGCAACA	550
AACGGTGTTT	CCGGAGTTGC	GCATAAGAAG	TTTGCCACTA	TTACAGAGGC	600
AAGAGCAGCA	GCTGACGCGT	ATACAACAAG	TCAGCAAACA	GATAGGTTGA	650
ACTTCATCCC	CAAAGGAGAA	GCTCAACTCA	AGCCCAAGAG	CTTTGCGAAG	700
GCCCTAACAA	GCCCACCAAA	GCAAAAAGCC	CACTGCTCAC	GCTAGGAACC	750
AAAAGGCCCA	GCAGTGATCC	AGCCCCAAAA	GAGATCTCCT	TTGCCCCGGA	800
GATTACAATG	GACGATTTC	TCTATCTTTA	CGATCTAGGA	AGGAAGTTTCG	850
AAGGTGAAGG	TGACGACACT	ATGTTACCA	CTGATAATGA	GAAGGTTAGC	900
CTCTTCAATT	TCAGAAAGAA	TGCTGACCCA	CAGATGGTTA	GAGAGGCCTA	950
CGCAGCAGGT	CTCATCAAGA	CGATCTACCC	GAGTAACAAT	CTCCAGGAGA	1000
TCAAATACCT	TCCCAAGAAG	GTTAAAGATG	CAGTCAAAAG	ATTCAGGACT	1050
AATTGCATCA	AGAACACAGA	GAAAGACATA	TTTCTCAAGA	TCAGAAGTAC	1100
TATTCCAGTA	TGGACGATTC	AAGGCTTGCT	TCATAAACCA	AGGCAAGTAA	1150
TAGAGATTGG	AGTCTCTAAA	AAGGTAGTTC	CTACTGAATC	TAAGGCCATG	1200
CATGGAGTCT	AAGATTCAAA	TCGAGGATCT	AACAGAACTC	GCCGTGAAGA	1250
CTGGCGAACA	GTTCATACAG	AGTCTTTTAC	GACTCAATGA	CAAGAAGAAA	1300

2000000

ATCTTCGTCA	ACATGGTGG	GCACGACACT	CTGGTCTACT	CCAAAAATGT	1350
CAAAGATACA	GTCTCAGAAG	ACCAAAGGGC	TATTGAGACT	TTTCAACAAA	1400
GGATAATTTTC	GGGAAACCTC	CTCGGATTCC	ATTGCCCAGC	TATCTGTCAC	1450
TTCATCGAAA	GGACAGTAGA	AAAGGAAGGT	GGCTCCTACA	AATGCCATCA	1500
TTGCGATAAA	GGAAAGGCTA	TCATTCAAGA	TGCCTCTGCC	GACAGTGGTC	1550
CCAAAGATGG	ACCCCCACCC	ACGAGGAGCA	TCGTGGAAAA	AGAAGACGTT	1600
CCAACCACGT	CTTCAAAGCA	AGTGGATTGA	TGTGACATCT	CCACTGACGT	1650
AAGGGATGAC	GCACAATCCC	ACTATCCTTC	GCAAGACCCT	TCCTCTATAT	1700
AAGGAAGTTC	ATTTCAATTG	GAGAGGACAC	GCTGAAATCA	CCAGTCTCTC	1750
TCTATAAATC	TATCTCTCTC	TCTATAACCA	TGGACCCAGA	ACGACGCCCG	1800
GCCGACATCC	GCCGTGCCAC	CGAGGCGGAC	ATGCCGGCGG	TCTGCACCAT	1850
CGTCAACCAC	TACATCGAGA	CAAGCACGGT	CAACTTCCGT	ACCGAGCCGC	1900
AGGAACCGCA	GGAGTGGACG	GACGACCTCG	TCCGTCTGCG	GGAGCGCTAT	1950
CCCTGGCTCG	TCGCCGAGGT	GGACGGCGAG	GTCCCGGCA	TCGCCTACGC	2000
GGGCCCCCTGG	AAGGCACGCA	ACGCCTACGA	CTGGACGGCC	GAGTCGACCG	2050
TGTACGTCTC	CCCCCGCCAC	CAGCGGACGG	GACTGGGCTC	CACGCTCTAC	2100
ACCCACCTGC	TGAAGTCCCT	GGAGGCACAG	GGCTTCAAGA	GCGTGGTTCG	2150
TGTCATCGGG	CTGCCCAACG	ACCCGAGCGT	GCGCATGCAC	GAGGCGCTCG	2200
GATATGCCCC	CCGCGGCATG	CTGCGGGCGG	CCGGCTTCAA	GCACGGGAAC	2250
TGGCATGACG	TGGGTTTCTG	GCAGCTGGAC	TTCAGCCTGC	CGGTACCGCC	2300
CCGTCCGGTC	CTGCCCGTCA	CCGAGATCTG	ATCTCACGCG	TCTAGGATCC	2350
GAAGCAGATC	GTTCAAACAT	TTGGCAATAA	AGTTTCTTAA	GATTGAATCC	2400
TGTTGCCGGT	CTTGCGATGA	TTATCATATA	ATTTCTGTTG	AATTACGTTA	2450
AGCATGTAAT	AATTAACATG	TAATGCATGA	CGTTATTTAT	GAGATGGGTT	2500
TTTATGATTA	GAGTCCCGCA	ATTATACATT	TAATACGCGA	TAGAAAACAA	2550
AATATAGCGC	GCAAACCTAGG	ATAAATTATC	GCGCGCGGTG	TCATCTATGT	2600
TACTAGATCG	GGAAGATCCT	CTAGAGTCGA	CCTGCAGGCA	TGCAAGCTTG	2650
GCGTAATCAT	GGTCATAGCT	GTTTCCTGTG	TGAAATTGTT	ATCCGCTCAC	2700
AATTCCACAC	AACATACGAG	CCGGAAGCAT	AAAGTGTAAG	GCCTGGGGTG	2750
CCTAATGAGT	GAGCTAACTC	ACATTAATTG	CGTTGCGCTC	ACTGCCCGCT	2800
TTCCAGTCGG	GAAACCTGTC	GTGCCAGCTG	CATTAATGAA	TCGGCCAACG	2850
CGCGGGGAGA	GGCGGTTTGC	GTATTGGGCG	CTCTTCCGCT	TCCTCGCTCA	2900
CTGACTCGCT	GCGCTCGGTC	GTTGCGCTGC	GGCGAGCGGT	ATCAGCTCAC	2950
TCAAAGGCGG	TAATACGGTT	ATCCACAGAA	TCAGGGGATA	ACGCAGGAAA	3000
GAACATGTGA	GCAAAGGCC	AGCAAAGGC	CAGGAACCGT	AAAAAGGCCG	3050
CGTTGCTGGC	GTTTTTCCAT	AGGCTCCGCC	CCCCTGACGA	GCATCACAAA	3100
AATCGACGCT	CAAGTCAGAG	GTGGCGAAAC	CCGACAGGAC	TATAAGATA	3150
CCAGGCGTTT	CCCCCTGGAA	GCTCCCTCGT	GCGCTCTCCT	GTTCCGACCC	3200
TGCCGCTTAC	CGGATACCTG	TCCGCCTTTC	TCCCTTCGGG	AAGCGTGGCG	3250
CTTTCCTCAAT	GCTCACGCTG	TAGGTATCTC	AGTTCGGTGT	AGGTCGTTTCG	3300
CTCCAAGCTG	GGCTGTGTGC	ACGAACCCCC	CGTTCAGCCC	GACCGCTGCG	3350
CCTTATCCGG	TAAGTATCGT	CTTGAGTCCA	ACCCGGTAAG	ACACGACTTA	3400
TCGCCACTGG	CAGCAGCCAC	TGGTAACAGG	ATTAGCAGAG	CGAGGTATGT	3450
AGGCGGTGCT	ACAGAGTTCT	TGAAGTGGTG	GCCTAACTAC	GGCTACACTA	3500
GAAGGACAGT	ATTTGGTATC	TGCGCTCTGC	TGAAGCCAGT	TACCTTCGGA	3550
AAAAGAGTTG	GTAGCTCTTG	ATCCGGCAAA	CAAACCACCG	CTGGTAGCGG	3600
TGGTTTTTTT	GTTTGCAAGC	AGCAGATTAC	GCGCAGAAAA	AAAGGATCTC	3650
AAGAAGATCC	TTTGATCTTT	TCTACGGGGT	CTGACGCTCA	GTGGAACGAA	3700
AACTCACGTT	AAGGGATTTT	GGTCATGAGA	TTATCAAAAA	GGATCTTCAC	3750
CTAGATCCTT	TTAAATTAAA	AATGAAGTTT	TAAATCAATC	TAAAGTATAT	3800
ATGAGTAAAC	TTGGTCTGAC	AGTTACCAAT	GCTTAATCAG	TGAGGCACCT	3850
ATCTCAGCGA	TCTGTCTATT	TCGTTCATCC	ATAGTTGCCT	GACTCCCCGT	3900
CGTGTAGATA	ACTACGATAC	GGGAGGGCTT	ACCATCTGGC	CCCAGTGCTG	3950
CAATGATACC	GCGAGACCCA	CGCTCACCGG	CTCCAGATTT	ATCAGCAATA	4000
AACCAGCCAG	CCGGAAGGGC	CGAGCGCAGA	AGTGGTCCTG	CAACTTTATC	4050

CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT 4100
CGCCAGTTAA TAGTTTGCGC AACGTTGTTG CCATTGCTAC AGGCATCGTG 4150
GTGTCACGCT CGTCGTTTGG TATGGCTTCA TTCAGCTCCG GTTCCCAACG 4200
ATCAAGGCGA GTTACATGAT CCCCCATGTT GTGCAAAAAA GCGGTTAGCT 4250
CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTTATCA 4300
CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT 4350
AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT 4400
AGTGTATGCG GCGACCGAGT TGCTCTTGCC CGGCGTCAAT ACGGGATAAT 4450
ACCGCGCCAC ATAGCAGAAC TTTAAAAGTG CTCATCATTG GAAAACGTTC 4500
TTCGGGGCGA AAACCTCTCA GGATCTTACC GCTGTTGAGA TCCAGTTCGA 4550
TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTCACC 4600
AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAGGG 4650
AATAAGGGCG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT 4700
ATTATTGAAG CATTTATCAG GGTATTGTC TCATGAGCGG ATACATATTT 4750
GAATGTATTT AGAAAAATAA ACAAATAGGG GTTCCGCGCA CATTTCCCCG 4800
AAAAGTGCCA CCTGACGTCT AAGAAACCAT TATTATCATG ACATTAACCT 4850
ATAAAAATAG GCGTATCACG AGGCCCTTTC GTC 4883

CLAIMS:

1. A process for the stable integration of a DNA, said DNA comprising a gene that is functional in a cell of a corn, rice or wheat plant, into the nuclear genome of a corn, rice or wheat plant, said process comprising:
 - a) obtaining a compact embryogenic callus or an immature embryo of said corn, rice or wheat plant;
 - b) wounding said compact embryogenic callus and transferring said DNA into the nuclear genome of a cell in said compact embryogenic callus to generate a transformed cell; or degrading said immature embryo by treatment with an enzyme capable of degrading the cell walls of the cells of said immature embryo for a period of 1 to 10 minutes so as not to cause a complete disruption of the tissues and transferring said DNA into the nuclear genome of a cell in said immature embryo to generate a transformed cell; and
 - c) regenerating a transformed corn, rice or wheat plant from said transformed cell.
2. The process of claim 1, wherein said immature embryo has a maximum length of 0.5 to 1.5 mm.
3. The process of claim 1, wherein said compact embryogenic callus is wounded prior to transferring said DNA or said immature embryo is degraded prior to transferring said DNA.
4. The process of claim 3, wherein said compact embryogenic callus is wounded by being cut into callus pieces.

5. The process of claim 4, wherein said callus pieces have a maximum length of 0.5 to 2.5 mm.

6. The process of claim 4, wherein said callus pieces have a maximum length of 1 to 2 mm.

5 7. The process of any one of claims 1 to 3, wherein said compact embryogenic callus or said immature embryo is treated with an enzyme for a period of 1 to 2 minutes.

8. The process of any one of claims 1 to 3 and 7, wherein said compact embryogenic callus or said immature
10 embryo is subjected to a period of plasmolysis prior to transferring said DNA.

9. The process of any one of claims 4 to 6 wherein said compact embryogenic callus pieces are subjected to a period of plasmolysis prior to transferring said DNA.

15 10. The process of any one of claims 1 to 9, wherein said DNA is transferred into the nuclear genome of a cell in said compact embryogenic callus or in said immature embryo by means of electroporation, direct gene transfer using polyethyleneglycol, microprojectile bombardment with DNA-
20 coated microprojectiles, or *Agrobacterium*-mediated DNA transfer.

11. The process of claim 10, wherein said DNA is transferred into the nuclear genome of a cell in said embryogenic callus or in said immature embryo by means of
25 electroporation.

12. The process of claim 1 or 2, wherein step (b) of said process is carried out by bombardment of said compact embryogenic callus with DNA-coated microprojectiles.

13. The process of any one of claims 1 to 12, wherein said gene comprises the DNA encoding barnase under the control of a stamen-specific promoter of the TA29 gene of tobacco with a sequence within the DNA of SEQ ID No. 3
5 between nucleotide 1 and 545.

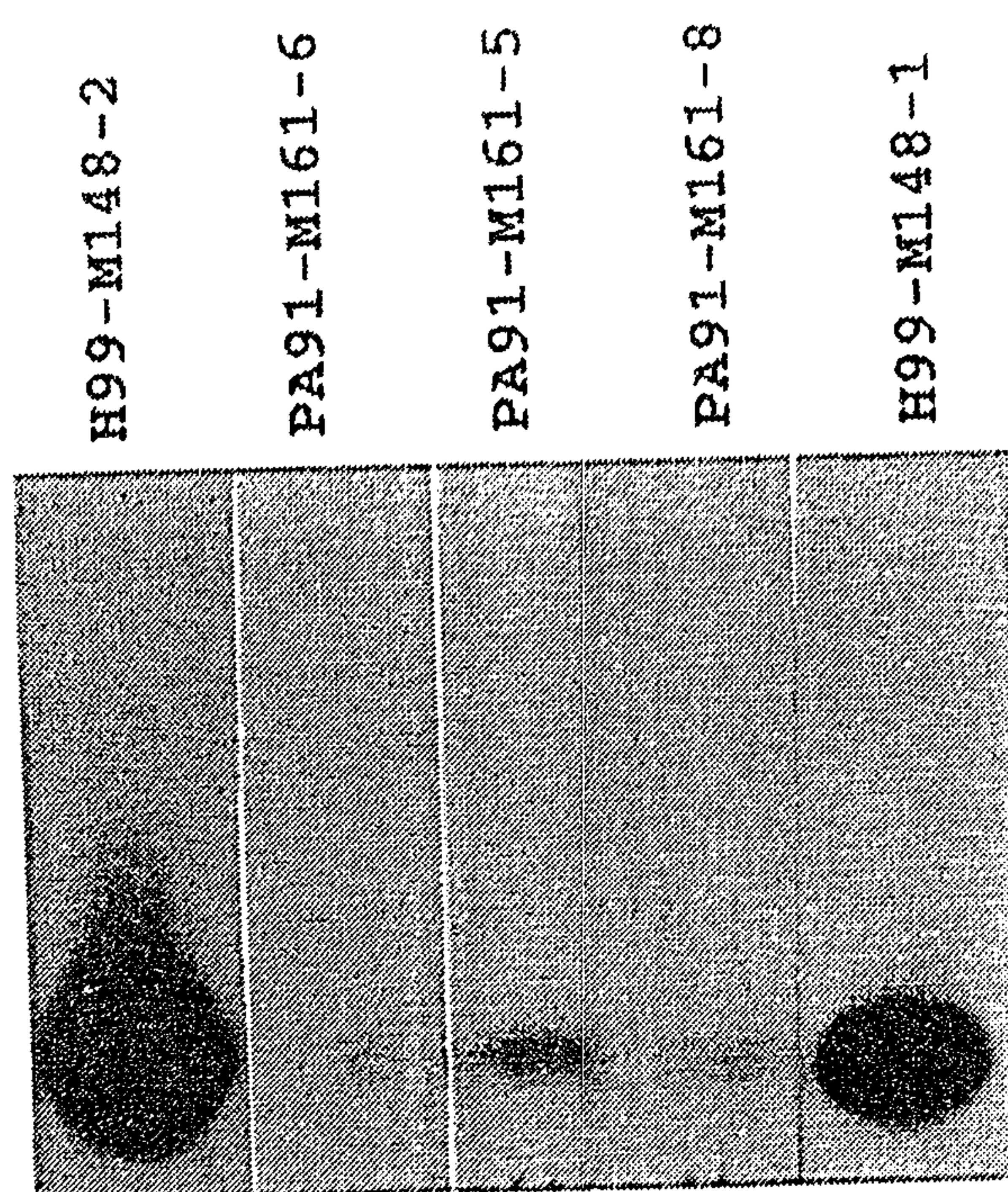
14. The process of any one of claims 1 to 12, wherein said gene comprises the DNA coding for a phosphinothricin acetyl transferase or a neomycin phosphotransferase.

FETHERSTONHAUGH & CO.
OTTAWA, CANADA

PATENT AGENTS

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FIG. 1

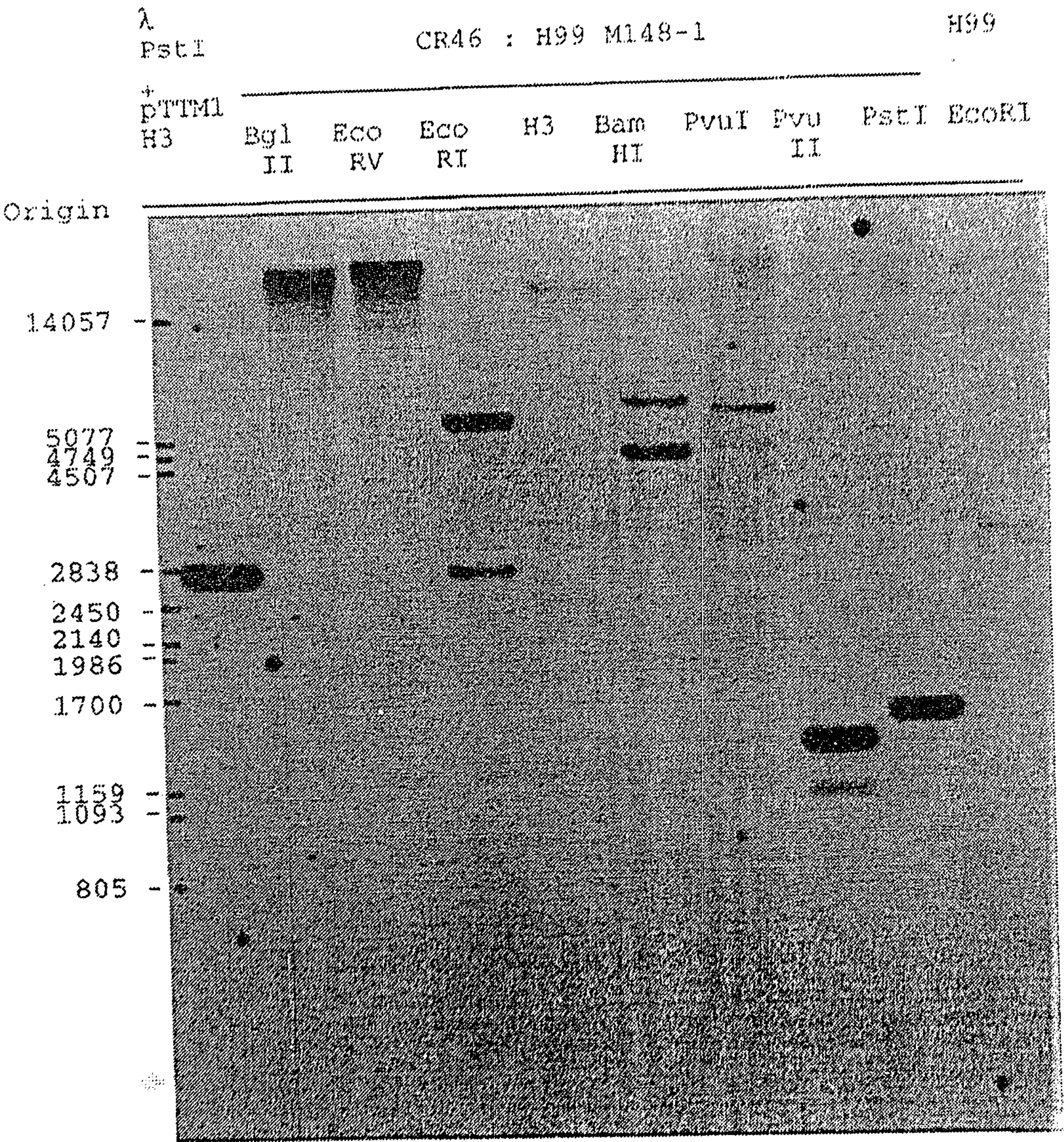


SUBSTITUTE SHEET

2673813

FIG. 2

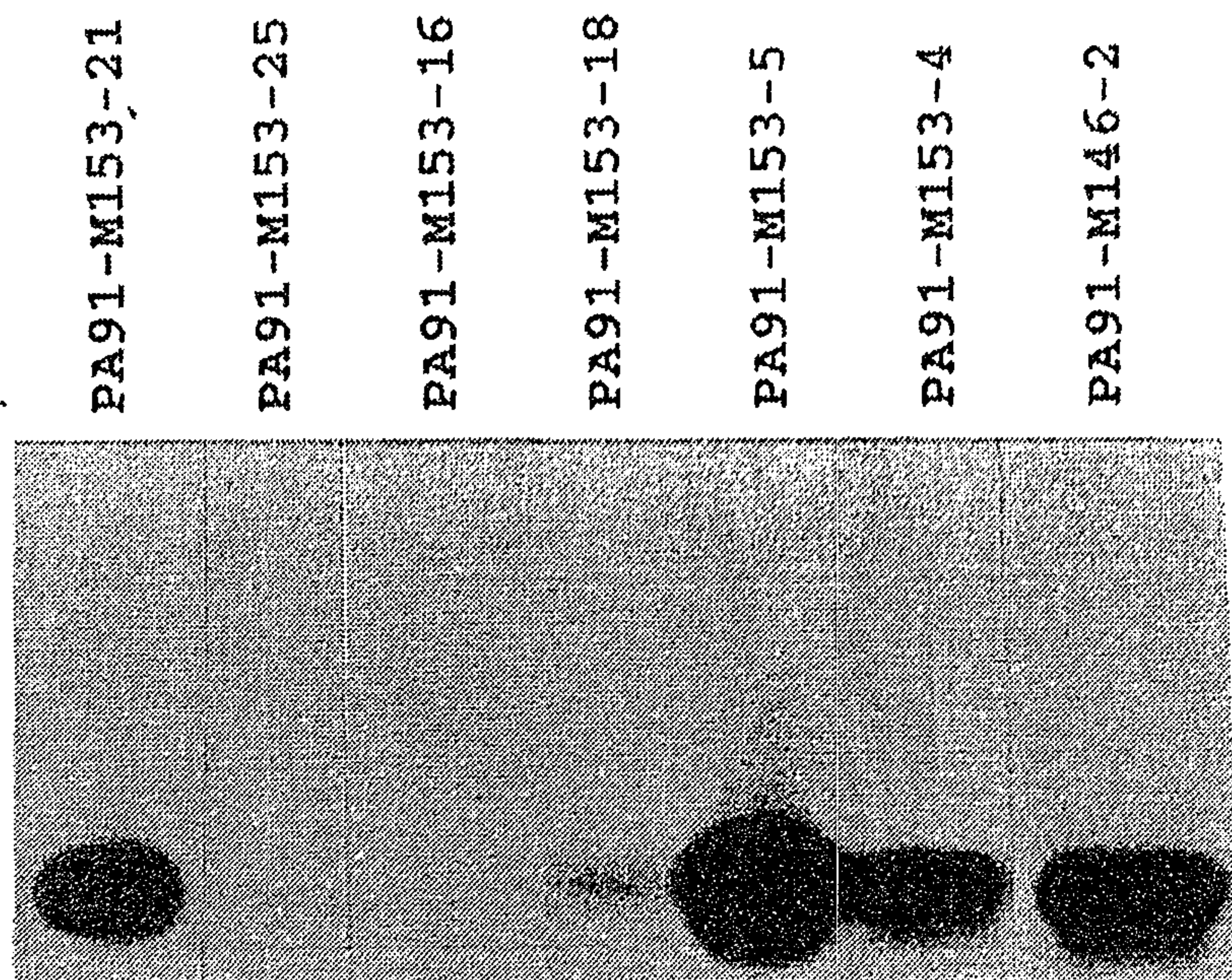
Blot : Corn 7 Probe pTTM1 E1-H3 for NPTII Exp : 48 hours



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2003342

FIG. 3

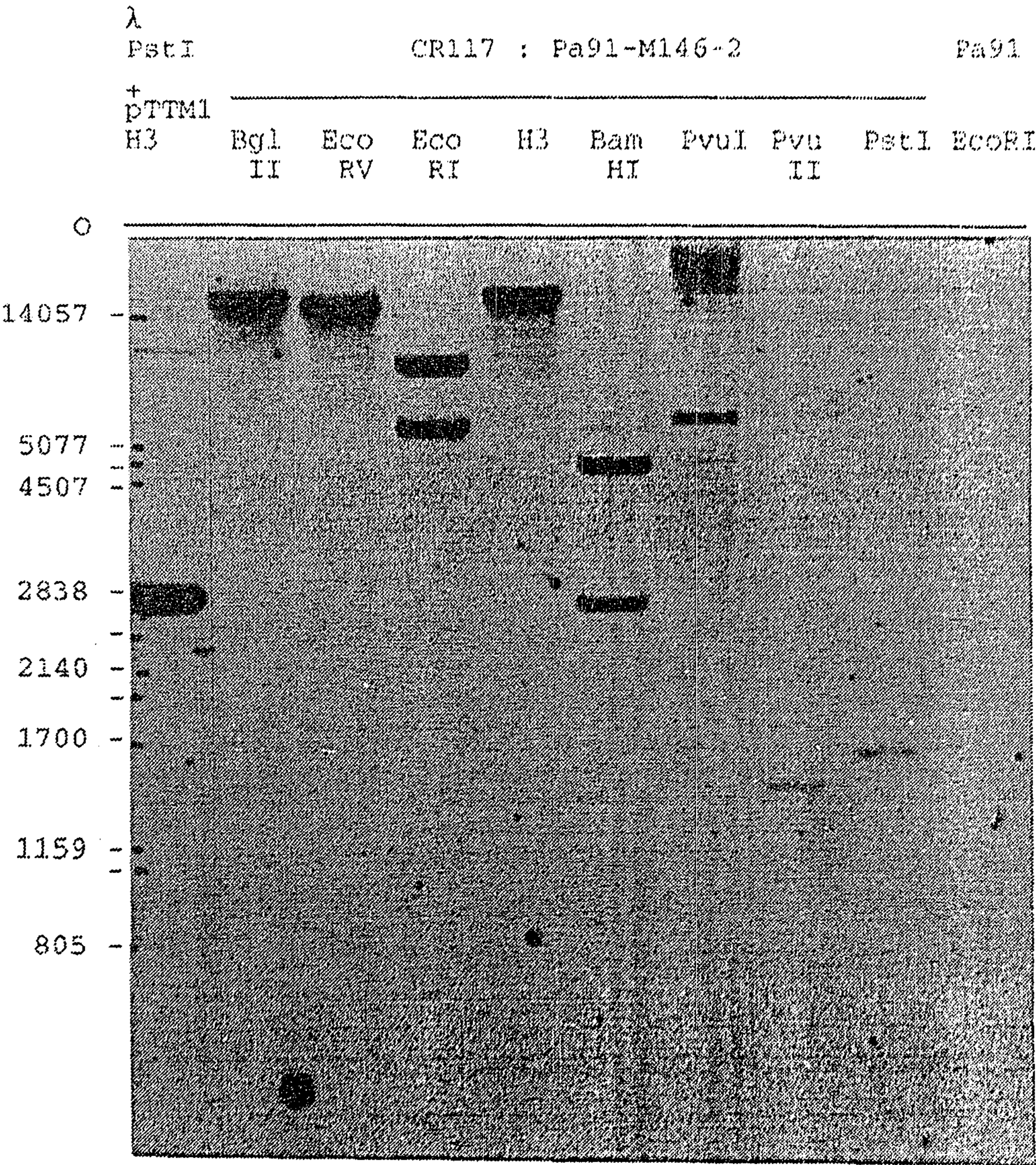


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FIG. 4

Blot : Corn 8 Probe pTTM1 E1-H3 for NPTII Exp : 48 hours



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