CLAIMS

1. A method for introducing a foreign DNA molecule at a predefined site in a genome of a plant cell comprising the steps of

a. inducing a double stranded DNA break at said predefined site;

b. introducing said foreign DNA molecule in said plant cell; and

c. selecting a plant cell wherein said foreign DNA is introduced at said predefined site;

characterized in that said predefined site is a nucleotide sequence different from a recognition site for a natural occurring meganuclease, said predefined site being a nucleotide sequence commonly introduced as part of a transgene in a transgenic plant~~comprised within a DNA region encoding a phosphinotricin acetyltransferase as encoded by Streptomyces hygroscopicus (bar coding region)~~ and wherein~~that said~~ double stranded DNA break is induced by introduction of a non-naturally occurring single chain meganuclease or a pair of non-naturally occurring meganucleases which recognizes or recognize in concert said predefined site and induces or induce said double stranded break.

2. The method according to claim 1, wherein said predefined site is comprised within a DNA region encoding a phosphinotricin acetyltransferase as encoded by Streptomyces hygroscopicus (bar coding region).

3~~2~~. The method according to claim 1 or 2, wherein said predefined site comprises the nucleotide sequence of SEQ ID No. 1 or SEQ ID No. 2.

43. The method according to ~~claim 1 or~~ claim 2, wherein said bar coding region comprises the nucleotide sequence of SEQ ID No.: 3.

54. A method for introducing a foreign DNA molecule at a predefined site in a genome of a plant cell comprising the steps of

a. inducing a double stranded DNA break at said predefined site;

b. introducing said foreign DNA molecule in said plant cell; and

c. selecting a plant cell wherein said foreign DNA is introduced at said predefined site;

characterized in that said predefined site is a nucleotide sequence different from a recognition site for a naturally occurring meganuclease and comprises the nucleotide sequence of SEQ ID No. 1 or SEQ ID No. 2 and that said double stranded DNA break is induced by introduction of a non-naturally occurring single chain meganuclease or a pair of non-naturally occurring meganucleases which recognizes or recognize in concert said predefined site and induces or induce said double stranded break.

65. The method according to any one of claims 1 to 54, wherein said meganuclease or said pair of meganucleases is/are derived from I-CreI and wherein the following amino acids are present in meganuclease unit 1:

a. S at position 32;

b. Y at position 33;

c. E at position 38;

d. R at position 40;

e. K at position 66;

f. Q at position 80;

g. T at position 42;

h. R at position 77;

i. R at position 68;

j. R at position 70;

k. Q at position 44;

l. I at position 24;

m. S at position 26;

n. S at position 28;

o. R at position 30.

and wherein the following amino acids are present in meganuclease unit 2:

p. R at position 70;

q. T at position 44;

r. I at position 24;

s. S at position 26;

t. S at position 28;

u. N at position 30;

v. S at position 32;

w. R at position 33;

x. Q at position 38;

y. Q at position 80;

z. R at position 40;

aa. K at position 66;

bb. T at position 42;

cc. R at position 77;

dd. R at position 68.

76. The method according to any one of claims 1 to 65, wherein said pair of meganucleases obligatory forms heterodimers or wherein said meganuclease is a single chain meganuclease comprising two domains derived from I-CreI covalently connected by a linker.

87. The method according to any one of claims 1 to 76, wherein said pair of meganucleases comprises the amino acid sequence of SEQ ID No. 5 and SEQ ID No. 6, respectively, or said single chain meganuclease comprises the amino acid sequence of SEQ ID No. 18 from position 1 to 167 and from position 206 to 362.

98. The method according to any one of claims 1 to 87, wherein said pair of meganucleases is encoded by a nucleic acid comprising the nucleotide sequence of SEQ ID No. 4 from nucleotide position 2004 to nucleotide position 2525 or to 2522 and the nucleotide sequence of SEQ ID No. 4 from nucleotide position 4885 to nucleotide position 5405 or to 5403, or said single chain meganuclease is encoded by a nucleic acid molecule comprising the nucleotide sequence of SEQ ID No. 17 from nucleotide position 1267 to 1605 and from 1795 to 1956 and from 2071 to 2541, or said single chain meganuclease is encoded by a nucleic acid molecule comprising the nucleotide sequence of SEQ ID No. 17 from nucleotide position 1267 to 1605 and from 1795 to 2541.

109. The method according to any one of claims 1 to 98, wherein said meganuclease or said pair of meganucleases is encoded by a nucleic acid which has been codon-optimized for expression in said cell of said plant.

1110. The method according to any one of claims 1 to 109, wherein said foreign DNA is introduced by direct DNA transfer.

1211. The method according to any one of claims 1 to 1110, wherein said foreign DNA is introduced without any further DNA.

1312. The method according to any one of claims 1 to 1211, wherein said foreign DNA is comprised within a repair DNA, said repair DNA comprising at least one flanking nucleotide sequence homologous to the upstream or downstream sequence of the nucleotide sequence of SEQ ID No. 1.

1413. The method according to any one of claims 1 to 1312, wherein said meganuclease or said pair of meganucleases is expressed from a chimeric gene or a pair of chimeric genes, each comprising a plant expressible promoter operably linked to a coding region encoding said meganuclease or one of said pair of meganucleases, and further operationally linked to a DNA region involved in transcription termination and polyadenylation functional in a plant cell.

15~~14~~. The method according to claim 14~~13~~, wherein said chimeric gene is introduced transiently into said plant cell.

16~~15~~. The method according to claim 14, wherein said chimeric gene is introduced stably into said plant cell.

17~~16~~. The method according to any one of claims 1 to 16~~15~~, wherein said foreign DNA comprises a selectable marker gene.

18~~17~~. The method according to any one of claims 1 to 17~~16~~, wherein said foreign DNA comprises a plant expressible gene of interest.

19~~18~~. The method according to claim 18~~17~~, wherein said plant expressible gene of interest is selected from the group of a herbicide tolerance gene, an insect resistance gene, a disease resistance gene, an abiotic stress resistance gene, an enzyme involved in oil biosynthesis, carbohydrate biosynthesis, an enzyme involved in fiber strength or fiber length, an enzyme involved in biosynthesis of secondary metabolites.

20~~19~~. The method according to any one of the preceding claims wherein said plant cell is further regenerated into a plant.

21~~20~~. A plant cell wherein said foreign DNA has been introduced into said predefined site, obtained by the method according to any one of claims 1 to 20~~19~~.

2221. A plant wherein said foreign DNA has been introduced into said predefined site, obtained by the method according to claim 2019.

2322. A seed or propagating part of a plant comprising said foreign DNA integrated at said predefined site, from the plant of claim 2221.

2423. A method of growing a plant according to claim 2221, comprising the step of applying a chemical to said plant or substrate wherein said plant is grown.

2524. A process for producing a plant comprising foreign DNA integrated at the bar coding region, comprising the step of crossing a plant consisting essentially of the plant cells of claim 2120 with another plant or with itself and optionally harvesting seeds.

2625. A process of growing a plant in the field comprising the step of applying a chemical compound on a plant of claim 2221.

2726. A process of producing treated seed comprising the step applying a chemical compound on a seed of plant according to claim 2322.

2827. Use of a meganuclease or a pair of meganucleases as described in any one of claims 1 to 1615 to introduce a foreign DNA into the bar coding region.

2928. Use of a non-naturally occurring~~custom made~~ meganuclease to introduce a foreign DNA of interest at a predefined site in the genome of a plant cell~~.~~.

~~29. A method for introducing a foreign DNA molecule at a predefined site in a genome of a plant cell comprising the steps of~~

~~a. inducing a double stranded DNA break at said predefined site;~~

~~b. introducing said foreign DNA molecule in said plant cell; and~~

~~c. selecting a plant cell wherein said foreign DNA is introduced at said predefined site;~~

~~characterized in that said double stranded DNA break is induced by introduction of a non-naturally occurring single chain meganuclease or a pair of non-naturally occurring meganucleases which recognizes or recognize in concert said predefined site and induces or induce said double stranded break.~~

~~30. A method for introducing a foreign DNA molecule at a predefined site in a genome of a transgenic plant cell comprising the steps of~~

~~a. inducing a double stranded DNA break at said predefined site;~~

~~b. introducing said foreign DNA molecule in said plant cell; and~~

~~c. selecting a plant cell wherein said foreign DNA is introduced at said predefined site;~~

~~characterized in that~~ wherein said predefined site is a nucleotide sequence different from a recognition site for a natural occurring meganuclease~~,~~ and is~~said predefined site being~~ a nucleotide sequence commonly introduced as part of a transgene in a transgenic plant ~~and wherein double stranded DNA break is induced by introduction of a non-naturally occurring single chain meganuclease or a pair of non-naturally occurring meganucleases~~

~~which recognizes or recognize in concert said predefined site and induces or induce said double stranded break~~.