Phosphinothricin (PTC, 2-amino-4-methylphosphinobutyric acid) is an inhibitor of glutamine synthetase. PTC is a "structural unit" of the antibiotic phosphinothricyl-alanyl-alanine. This tripeptide (PTT) is active against Gram-positive and Gram-negative bacteria as well as against the fungus Botrytis cinerea (Bayer et al., Helv. Chim. Acta 55 (1972) 224). PTT is produced by the strain Streptomyces viridochromogenes Tü 494 (DSM 40736, DSM 4112).

German Patent 2,717,440 discloses that PTC acts as a total herbicide. The published PCT Application WO 86/02097 describes plants whose resistance to PTC is attributable to overproduction of glutamine synthetase. Overproduction of this type, for example resulting from gene amplification, entails the risks of instability. Hence, such an instability would be associated with a decrease in the overproduction of glutamine synthetase, and the competitive inhibitory action of PTC would reappear.

In contrast, the invention, which is defined in the patent claims, relates to a PTC resistance gene and to its use for the production of PTC-resistant plants. In addition, this gene can also be used as a resistance marker. The gene is also suitable for the selective N-acetylation of the L-form of racemic PTC.

The PTC resistance gene according to the invention can be obtained by cutting, with BamHI, the total DNA from Streptomyces viridochromogenes DSM 4112 which has been selected for PTT resistance, by cloning a fragment 4.0 kb in size, and by selection for PTT resistance. The resistance (sic) map (Figure 1) details the characteristics of this 4.0 kb fragment in more detail.

Cloning experiments on sections of this 4 kb fragment were carried out to localize the position of the coding

region more accurately. It emerged from this that the resistance gene is located on the 1.6 kb SstII-SstI fragment (positions 0.55 to 2.15 in Fig. 1). Digestion with BglII resulted in the fragment which is 0.8 kb in size and which, after incorporation into a plasmid and transformation of S. lividans, confers PTT resistance. Thus resistance is caused by N-acetylation of PCT.

Maxam and Gilbert sequencing of the 0.8 kb fragment reveals DNA sequence I (Annex). The position of the resistance gene can be determined from the open reading frame of this sequence (from position 258). The end of the gene is located at the penultimate nucleotide shown (position 806), i.e. the last nucleotide (position 807) is the first of the stop codon.

The Shine-Dalgarno sequence in DNA sequence I is emphasized by underlining, as is the GTG acting as start codon. Thus, the top line depicts the definitive reading frame.

DNA sequence II shows the restriction sites within the sequenced gene. Enzymes which cut the sequence more than six times are not indicated.

The antibiotic PTT is taken up by bacteria and broken down to PTC. The latter also inhibits glutamine synthetase in bacteria, so that the bacteria die of a lack of glutamine. Hence, PTT-producing bacteria ought to have a mechanism which protects them from the action of PTT, that is to say either prevents reuptake of the PTT which has been produced or permits a modification of the breakdown product PTC. However, surprisingly, the PTT producer S. viridochromogenes DSM 4112 is sensitive to its own antibiotic. Unexpectedly, it proved possible, however, by selection for PTT resistance to find, at the surprisingly high rate of 10^{-5}, selectants which are resistant to PTT and, moreover, suppress the background

growth of adjacent colonies.

A gene bank was set up from the DNA of these selectants by isolating the DNA and cleaving it with BamHI and ligating it into a Streptomycetes vector. The ligation mixture was transformed into the commercially available strain S. lividans TK 23, resulting in about 5000 to 10000 transformants having an insert of about 1 to 5 kb per 1 µg of ligation mixture. Among the transformants there were PTT-resistant S. lividans strains. It was possible, by isolation of the plasmid and retransformation into S. lividans, to show that the resistance is plasmid-coded. The gene responsible for the resistance is located on a 4 kb BamHI fragment (Figure 1). The coding region is located on the 0.8 kb BGlII fragment. The BamHI fragment contains no cleavage sites for the enzymes ClaI, EcoRI, EcoRV, HindIII, HpaI, KpnI, PvuI, PvuII and XhoI.

Comparison with the restriction map of a resistance gene, which has not been characterized in detail, for S. hygroscopicus FERM BP-130/ATCC 21705 (European Patent Application with the publication no. 0,173,327, Figure 7) shows that the resistance gene according to the invention differs from the known gene, which was found during the search for PTT biosynthesis genes.

It was possible to show, by incubation of cell extracts from S. viridochromogenes DSM 4112 and S. lividans TK 23 on the one hand, and the PTT-resistant S. viridochromogenes selectant and a plasmid-carrying S. lividans transformant, on the other hand, with PTC and acetyl-coenzyme A, that the latter cells have acetylating activity. Chromatography tests show that the acetylation takes place on the amino group.

Since PTT resistance has also been found in E. coli, and thus the resistance mechanism also functions in Gram-negative bacteria, it is possible to rule out resistance

based on transport phenomena. Thus, after coupling to plant promoters and using suitable vectors, the resistant gene according to the invention can be transformed into plants, and in this way PTC-resistance plants can be produced.

The N-acetylation of PTC can also be used for racemate resolution of synthetic D,L-PTC since selective acetylation of only the L-form takes place.

Thus the invention also relates to the use of the resistance gene for the selective N-acetylation of the L-form of racemic PTC.

The PTC acetyltransferase coded for by the resistance gene according to the invention can thus be used to separate racemic PTC, as can be obtained, for example, by the method of German Patent 2,717,440, into the optical antipodes by exposing the racemate to the acetylating action of this enzyme, since there is selective attack on the L-form while the D-form remains unchanged. The mixture thus obtained can then be fractionated in a manner known per se on the basis of the differences in properties.

The contacting of N-acyl-D,L-amino acids with acylases, which are immobilised on carriers where appropriate, with selective liberation of the L-amino acid, which can be extracted with water-immiscible solvents from the mixture with the N-acyl-D-amino acid after acidification, has been disclosed (British Patent 1,369,462). A corresponding fractionation of N-acyl-D,L-PTC is disclosed, for example, in German Offenlegungsschrift 2,939,269 or US Patent 4,226,941.

The D-PCT which remains according to the invention can be racemized in known manner (European Patent Application with the publication no. (EP-A) 0,137,371, example 8),

and then returned to the process.

It is possible, but not necessary, to isolate the enzyme, this also being intended to mean, here and hereinafter, always the enzymatically active part. If the enzyme is isolated, it can be used in the free form or the form immobilised on a carrier. Examples of suitable carriers are described in EP-A 0,141,223. However, it is expedient not to isolate the enzyme but to use any desired PTC-resistant cells which express the enzyme according to the invention. Thus, it is possible and expedient to use the PTT-resistant selectants of S. viridochromogenes DSM 4112. Moreover, it is possible and advantageous to use any desired cell which has been transformed with the gene according to the invention and which is able to express PTC acetyltransferase. In this connection, the gene according to the invention, this also being intended to mean active parts thereof, can be introduced into the host cell in plasmid-integrated form or by using other customary methods of gene manipulation, for example by transfection. For example, incorporation into a E. coli expression plasmid and transformation of E. coli with such a plasmid is expedient, for example by the methods known from EP-A 0,163,249 and 0,171,024.

For the N-acetylation, according to the invention, of L-PTC in the racemate the cells which express PTC acetyltransferase can be used in the free or immobilised form, with the customary methods of immobilisation being used (for example German Offenlegungsschrift 3,237,341 and literature cited therein).

The enzymatic acetylation, according to the invention, of L-PTC is carried out in the manner customary for enzymatic reactions, with the conditions of the method being governed by the characteristics of the organism used. In principle, methods suitable for this are the same as for the abovementioned selective deacylation method.

The invention is illustrated in detail in the examples which follow. Unless otherwise stated, parts and percentage data relate to weight.

Example 1: PTT-resistant selectants

The strain S. viridochromogenes DSM 4112 was cultured on minimal medium (Hopwood et al., Genetic Manipulation of Streptomyces, A Laboratory Manual, The John Innes Foundation, Norwich, England (1985), page 233) and increasing concentrations of PTT were added. At a concentration of 100 µg/ml one resistant colony was found per 10^5 colonies, approximately.

Example 2: Preparation of the vector

The plasmid pSVH1 (European Patent 0,070,522) is cut with BglII, and the fragment about 7.1 kb in size is isolated and ligated with the 1.1 kb BclI fragment having thiostreptone resistance (European Patent Application with the publication number 0,158,201). The plasmid pEB2 which is 8.15 kb in size is obtained (Figure 2).

Example 3: Isolation of the resistance gene

The total DNA is isolated from the selectants obtained in example 1, and it is cleaved with BamHI. The plasmid pEB2 is likewise opened with BamHI, and the two mixtures are combined and ligated. The ligation mixture is transformed into S. lividans TK 23 (obtainable from the John Innes Foundation), with 5000 to 10000 transformants having an insert of about 1 - 5 kb being obtained per 1 µg of ligation mixture. Selection for PTT resistance produces two resistant S. lividans colonies. The plasmid which has been taken up is isolated from the latter and is cut with BamHI. A 4 kb BamHI fragment which carries the gene responsible for resistance is found. This

plasmid was called pPR1 (Figure 3).

Retransformation into S. lividans TK 23 shows that the PTT resistance is plasmid-coded, since the transformants grow on minimal medium containing 100 µg/ml PTT.

Example 4: Demonstration of the inactivation of PTC by N-acetylation

The following strains were examined to demonstrate the acetylating activity of the cloned fragment: S. viridochromogenes DSM 40736, S. viridochromogenes (PTT-resistant mutant), S. lividans TK23 and S. lividans TK 23 (pPR1).

This entails the strains being inoculated into lysis medium A (European Patent Application with the publication number 0,158,872, page 6) and incubated at 30°C in an orbital shaker for 2 days. After harvesting, 1 mg of mycelium is disrupted with ultrasound in a suitable buffer (for example RS buffer: C. J. Thompson et al., J. Bacteriol. 151 (1982), 678-685). The procedure for a typical experiment to measure PTC breakdown is as follows:

100 µl of PTC solution (250 µg/ml) and 50 µl of acetyl-CoA (4 mg/ml) are added to 250 µl of crude extract, and the mixture is incubated at 30°C for 2 hours. The amounts of PTC which are still present after this time are measured by HPLC. The results of this are as follows:

Strain	unreacted PTC introduced PTC
S. lividans TK23	100%
S. viridochromogenes (DSM 40736)	72%
S. viridochromogenes Selectant	7%
S. lividans TK23 (pPR1)	31%

A comparison with reference substances on thin-layer chromatography (no stain with ninhydrin) demonstrates that N-acetylation of the PTC has taken place.

DNA sequence I

```
  IleTrpSerAspValLeuGlyAlaGlyProValLeuProGlyAspAspPhePheSerLeuGlyGlyThrSerIle
 AspLeuGluArgArgProGlyGlyArgSerGlyAlaAlaArgGlyArgLeuLeuLeuProArgArgHisLeuHis
ArgSerGlyAlaThrSerTrpGlyProValArgCysCysProGlyThrThrSerSerProSerAlaAlaProPro
AGATCTGGAGCGACGTCCTGGGGGCCGGTCCGGTGCTGCCCGGGGACGACTTCTTCTCCCTCGGCGGCACCTCCA 75
TCTAGACCTCGCTGCAGGACCCCCGGCCAGGCCACGACGGGCCCCTGCTGAAGAAGAGGGAGCCGCCGTGGAGGT
SerArgSerArgArgGlyProProArgAspProAlaAlaArgProArgSerArgArgGlyArgArgCysArgTrp
  AspProAlaValAspGlnProGlyThrArgHisGlnGlyProValValGluGluGlyGluAlaAlaGlyGlyAsp
 IleGlnLeuSerThrArgProAlaProGlyThrSerGlyProSerSerLysLysGluArgProProValGluMet

  SerAlaLeuArgValValSerArgIleArgLysGluLeuGlyValProLeuArgLeuAlaValIlePheGluThr
 LeuGlyValAlaGlyGlyLeuAlaHisProGlnGlyThrArgArgAlaThrProAlaArgArgAspLeuArgAsp
SerArgArgCysGlyTrpSerArgAlaSerAlaArgAsnSerAlaCysHisSerGlySerProOP SerSerArg
TCTCGGCGTTGCGGGTGGTCTCGCGCATCCGCAAGGAACTCGGCGTGCCACTCCGGCTCGCCGTGATCTTCGAGA 150
AGAGCCGCAACGCCCACCAGAGCGCGTAGGCGTTCCTTGAGCCGCACGGTGAGGCCGAGCGGCACTAGAAGCTCT
ArgProThrAlaProProArgAlaCysGlyCysProValArgArgAlaValGlyAlaArgArgSerArgArgSer
  ArgArgGlnProHisAspArgAlaAspAlaLeuPheGluAlaHisTrpGluProGluGlyHisAspGluLeuArg
 GluAlaAsnArgThrThrGluArgMetArgLeuSerSerProThrGlySerArgSerAlaThrIleLysSerVal

  ProSerLeuGluAlaValAlaGluSerValLeuArgGluLeuLysGlyThrAM OC ArgGlyAlaArgHisPro
 AlaValProGlySerGlyGlyArgIleArgThrProArgThrGluGlyAspValValLysArgCysProProPro
ArgArgProTrpLysArgTrpProAsnProTyrSerAlaAsnOP ArgGlyArgSerLysGluValProAlaThr
CGCCGTCCCTGGAAGCGGTGGCCGAATCCGTACTCCGCGAACTGAAGGGGACGTAGTAAAGAGGTGCCCGCCACC 225
GCGGCAGGGACCTTCGCCACCGGCTTAGGCATGAGGCGCTTGACTTCCCCTGCATCATTTCTCCACGGGCGGTGG
AlaThrGlyProLeuProProArgIleArgValGlyArgValSerProSerThrThrPheLeuHisGlyGlyGly
  ArgGlyGlnPheArgHisGlyPheGlyTyrGluAlaPheGlnLeuProArgLeuLeuSerThrGlyAlaValArg
 GlyAspArgSerAlaThrAlaSerAspThrSerArgSerSerPheProValTyrTyrLeuProAlaArgTrpGly

  LeuSerGlnAsnThrGluGlyArgProHisValSerProGluArgArgProValGluIleArgProAlaThrAla
 AlaPheAlaGluHisArgArgLysThrThrArgGluProArgThrThrProGlyArgAspProSerArgHisArg
ArgPheArgArgThrProLysGluAspHisThrOP AlaGlnAsnAspAlaArgSerArgSerValProProPro
CGCTTTCGCAGAACACCGAAGGAAGACCACACGTGAGCCCAGAACGACGCCCGGTCGAGATCCGTCCCGCCACCG 300
GCGAAAGCGTCTTGTGGCTTCCTTCTGGTGTGCACTCGGGTCTTGCTGCGGGCCAGCTCTAGGCAGGGCGGTGGC
AlaLysAlaSerCysArgLeuPheValValArgSerGlyLeuValValGlyProArgSerGlyAspArgTrpArg
  LysArgLeuValGlyPheSerSerTrpValHisAlaTrpPheSerAlaArgAspLeuAspThrGlyGlyGlyGly
 SerGluCysPheValSerProLeuGlyCysThrLeuGlySerArgArgGlyThrSerIleArgGlyAlaValAla

  AlaAspMetAlaAlaValCysAspIleValAsnHisTyrIleGluThrSerThrValAsnPheArgThrGluPro
 ArgArgHisGlyGlyGlyLeuArgHisArgGlnSerLeuHisArgAspGluHisGlyGlnLeuProTyrGlyAla
ProProThrTrpArgArgSerAlaThrSerSerIleThrThrSerArgArgAlaArgSerThrSerValArgSer
CCGCCGACATGGCGGCGGTCTGCGACATCGTCAATCACTACATCGAGACGAGCACGGTCAACTTCCGTACGGAGC 375
GGCGGCTGTACCGCCGCCAGACGCTGTAGCAGTTAGTGATGTAGCTCTGCTCGTGCCAGTTGAAGGCATGCCTCG
ArgArgCysProProProArgArgCysArgOP AspSerCysArgSerSerCysProOP SerGlyTyrProAla
  GlyValHisArgArgAspAlaValAspAspIleValValAspLeuArgAlaArgAspValGluThrArgLeuArg
 AlaSerMetAlaAlaThrGlnSerMetThrLeuOP AM MetSerValLeuValThrLeuLysArgValSerGly

  GlnThrProGlnGluTrpIleAspAspLeuGluArgLeuGlnAspArgTyrProTrpLeuValAlaGluValGlu
 AlaAspSerAlaGlyValAspArgArgProGlyAlaProProGlyProLeuProLeuAlaArgArgArgGlyGly
ArgArgLeuArgArgSerGlySerThrThrTrpSerAlaSerArgThrAlaThrProGlySerSerProArgTrp
CGCAGACTCCGCAGGAGTGGATCGACGACCTGGAGCGCCTCCAGGACCGCTACCCCTGGCTCGTCGCCGAGGTGG 450
GCGTCTGAGGCGTCCTCACCTAGCTGCTGGACCTCGCGGAGGTCCTGGCGATGGGGACCGAGCAGCGGCTCCACC
AlaSerGluAlaProThrSerArgArgGlyProAlaGlyGlyProGlySerGlyArgAlaArgArgArgProPro
  LeuSerArgLeuLeuProAspValValGlnLeuAlaGluLeuValAlaValGlyProGluAspGlyLeuHisLeu
 CysValGlyCysSerHisIleSerSerArgSerArgArgTrpSerArgAM GlyGlnSerThrAlaSerThrSer
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DNA sequence I (continued)

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  GlyValValAlaGlyIleAlaTyrAlaGlyProTrpLysAlaArgAsnAlaTyrAspTrpThrValGluSerThr
 GlyArgArgArgArgHisArgLeuArgArgProLeuGluGlyProGlnArgLeuArgLeuAspArgArgValAsp
ArgAlaSerSerProAlaSerProThrProAlaProGlyArgProAlaThrProThrThrGlyProSerSerArg
AGGGCGTCGTCGCCGGCATCGCCTACGCCGGCCCCTGGAAGGCCCGCAACGCCTACGACTGGACCGTCGAGTCGA 525
TCCCGCAGCAGCGGCCGTAGCGGATGCGGCCGGGGACCTTCCGGGCGTTGCGGATGCTGACCTGGCAGCTCAGCT
ProArgArgArgArgCysArgArgArgArgGlyArgSerProGlyCysArgArgArgSerSerArgArgThrSer
  AlaAspAspGlyAlaAspGlyValGlyAlaGlyProLeuGlyAlaValGlyValValProGlyAspLeuArgArg
 ProThrThrAlaProMetAlaAM AlaProGlyGlnPheAlaArgLeuAlaAM SerGlnValThrSerAspVal

  ValTyrValSerHisArgHisGlnArgLeuGlyLeuGlySerThrLeuTyrThrHisLeuLeuLysSerMetGlu
 GlyValArgLeuProProAlaProAlaAlaArgThrGlyLeuHisProLeuHisProProAlaGluValHisGly
ArgCysThrSerProThrGlyThrSerGlySerAspTrpAlaProProSerThrProThrCysOP SerProTrp
CGGTGTACGTCTCCCACCGGCACCAGCGGCTCGGACTGGGCTCCACCCTCTACACCCACCTGCTGAAGTCCATGG 600
GCCACATGCAGAGGGTGGCCGTGGTCGCCGAGCCTGACCCGAGGTGGGAGATGTGGGTGGACGACTTCAGGTACC
ProThrArgArgGlyGlyAlaGlyAlaAlaArgValProSerTrpGlyArgCysGlyGlyAlaSerThrTrpPro
  HisValAspGlyValProValLeuProGluSerGlnAlaGlyGlyGluValGlyValGlnGlnLeuGlyHisLeu
 ThrTyrThrGluTrpArgCysTrpArgSerProSerProGluValArgAM ValTrpArgSerPheAspMetSer

  AlaGlnGlyPheLysSerValValAlaValIleGlyLeuProAsnAspProSerValArgLeuHisGluAlaLeu
 GlyProGlyLeuGlnGluArgGlyArgArgHisArgThrAlaGlnArgProGluArgAlaProAlaArgGlyAla
ArgProArgAlaSerArgAlaTrpSerProSerSerAspCysProThrThrArgAlaCysAlaCysThrArgArg
AGGCCCAGGGCTTCAAGAGCGTGGTCGCCGTCATCGGACTGCCCAACGACCCGAGCGTGCGCCTGCACGAGGCGC 675
TCCGGGTCCCGAAGTTCTCGCACCAGCGGCAGTAGCCTGACGGGTTGCTGGGCTCGCACGCGGACGTGCTCCGCG
ProGlyProSerOP SerArgProArgArgOP ArgValAlaTrpArgGlySerArgAlaGlyAlaArgProAla
  GlyLeuAlaGluLeuAlaHisAspGlyAspAspSerGlnGlyValValArgAlaHisAlaGlnValLeuArgGlu
 AlaTrpProLysLeuLeuThrThrAlaThrMetProSerGlyLeuSerGlyLeuThrArgArgCysSerAlaSer

  GlyTyrThrAlaArgGlyThrLeuArgAlaAlaGlyTyrLysHisGlyGlyTrpHisAspValGlyPheTrpGln
 ArgIleHisArgAlaArgAspAlaAlaGlySerArgLeuGlnAlaArgGlyLeuAlaArgArgGlyValLeuAla
SerAspThrProArgAlaGlyArgCysGlyGlnProAlaThrSerThrGlyAlaGlyThrThrTrpGlySerGly
TCGGATACACCGCGCGCGGGACGCTGCGGGCAGCCGGCTACAAGCACGGGGGCTGGCACGACGTGGGGTTCTGGC 750
AGCCTATGTGGCGCGCGCCCTGCGACGCCCGTCGGCCGATGTTCGTGCCCCCGACCGTGCTGCACCCCAAGACCG
ArgIleCysArgAlaArgSerAlaAlaProLeuArgSerCysAlaArgProSerAlaArgArgProThrArgAla
  SerValGlyArgAlaProArgGlnProCysGlyAlaValLeuValProAlaProValValHisProGluProLeu
 ProTyrValAlaArgProValSerArgAlaAlaProAM LeuCysProProGlnCysSerThrProAsnGlnCys

  ArgAspPheGluLeuProAlaProProArgProValArgProValThrGlnIle
 AlaArgLeuArgAlaAlaGlyProAlaProProArgProAlaArgHisThrAsp
SerAlaThrSerSerCysArgProArgProAlaProSerGlyProSerHisArgSer
AGCGCGACTTCGAGCTGCCGGCCCCGCCCCGCCCCGTCCGGCCCGTCACACAGATCT 807
TCGCGCTGAAGCTCGACGGCCGGGGCGGGGCGGGGCAGGCCGGGCAGTGTGTCTAGA
AlaArgSerArgAlaAlaProGlyAlaGlyGlyArgGlyAlaArgOP ValSerArg
  AlaValGluLeuGlnArgGlyArgGlyAlaGlyAspProGlyAspCysLeuAsp
 ArgSerLysSerSerGlyAlaGlyGlyArgGlyThrArgGlyThrValCysIle
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DNA sequence II

```
   1  AGATCTGGAGCGACGTCCTGGGGGCCGGTCCGGTGCTGCCCGGGGACGACTTCTTCTCCC
      TCTAGACCTCGCTGCAGGACCCCCGGCCAGGCCACGACGGGCCCCTGCTGAAGAAGAGGG
      ^^  ^    ^^  ^       ^^      ^  ^^          ^     ^

      1 BGLII XHOII, 2 DPNI SAU3A, 5 GSUI, 12 AATII ACYI, 13 MAEII
      , 17 APYI ECORII, 26 RSRII, 27 AVAII, 35 BBVI, 39 AVAI NCII
      SMAI, 40 NCII, 52 MBOII, 59 MNLI,

  61  TCGGCGGCACCTCCATCTCGGCGTTGCGGGTGGTCTCGCGCATCCGCAAGGAACTCGGCG
      AGCCGCCGTGGAGGTAGAGCCGCAACGCCCACCAGAGCGCGTAGGCGTTCCTTGAGCCGC
           ^  ^                    ^  ^^

      66 HGICI, 70 MNLI, 97 FNUDII, 100 SFANI, 101 FOKI,

 121  TGCCACTCCGGCTCGCCGTGATCTTCGAGACGCCGTCCCTGGAAGCGGTGGCCGAATCCG
      ACGGTGAGGCCGAGCGGCACTAGAAGCTCTGCGGCAGGGACCTTCGCCACCGGCTTAGGC
       ^          ^ ^     ^       ^       ^   ^   ^

      122 BGLI, 140 DPNI SAU3A, 142 MBOII, 149 ACYI HGAI TTH111I,
      158 APYI ECORII, 159 CFRI GDIII, 174 HINFI, 180 RSAI,

 181  TACTCCGCGAACTGAAGGGGACGTAGTAAAGAGGTGCCCGCCACCCGCTTTCGCAGAACA
      ATGAGGCGCTTGACTTCCCCTGCATCATTTCTCCACGGGCGGTGGGCGAAAGCGTCTTGT
           ^          ^       ^ ^^

      185 FNUDII, 201 MAEII, 211 MNLI, 213 HGICI, 214 SDUI,

 241  CCGAAGGAAGACCACACGTGAGCCCAGAACGACGCCCGGTCGAGATCCGTCCCGCCACCG
      GGCTTCCTTCTGGTGTGCACTCGGGTCTTGCTGCGGGCCAGCTCTAGGCAGGGCGGTGGC
           ^     ^^^  ^         ^   ^      ^^

      247 MBOII, 254 AFLIII, 255 PMACI, 256 MAEII, 260 HGIJII SDUI
      , 271 ACYI HGAI, 275 NCII, 283 XHOII, 284 BINI DPNI SAU3A,

 301  CCGCCGACATGGCGGCGGTCTGCGACATCGTCAATCACTACATCGAGACGAGCACGGTCA
      GGCGGCTGTACCGCCGCCAGACGCTGTAGCAGTTAGTGATGTAGCTCTGCTCGTGCCAGT
        ^  ^^                ^                          ^     ^

      303 BGLI, 308 NLAIII, 324 TTH111I, 350 HGIAI SDUI, 357 HINCI
      I,

 361  ACTTCCGTACGGAGCCGCAGACTCCGCAGGAGTGGATCGACGACCTGGAGCGCCTCCAGG
      TGAAGGCATGCCTCGGCGTCTGAGGCGTCCTCACCTAGCTGCTGGACCTCGCGGAGGTCC
           ^          ^                ^^      ^^   ^  ^^ ^  ^

      367 RSAI, 380 HINFI, 394 BINI, 395 DPNI SAU3A, 404 APYI ECOR
      II, 405 GSUI, 409 HAEII, 413 MNLI, 414 GSUI, 416 APYI ECORII
      , 419 AVAII,

 421  ACCGCTACCCCTGGCTCGTCGCCGAGGTGGAGGGCGTCGTCGCCGGCATCGCCTACGCCG
      TGGCGATGGGGACCGAGCAGCGGCTCCACCTCCCGCAGCAGCGGCCGTAGCGGATGCGGC
           ^          ^   ^ ^^      ^   ^          ^

      430 APYI ECORII, 444 MNLI, 450 MNLI, 453 ACYI, 454 HGAI, 462
       NAEI, 466 SFANI, 477 NAEI,

 481  GCCCCTGGAAGGCCCGCAACGCCTACGACTGGACCGTCGAGTCGACGGTGTACGTCTCCC
      CGGGGACCTTCCGGGCGTTGCGGATGCTGACCTGGCAGCTCAGCTGCCACATGCAGAGGG
         ^                    ^       ^ ^       ^ ^

      484 APYI ECORII, 511 AVAII, 519 HINFI, 521 ACCI HINCII SALI,
       530 RSAI, 532 MAEII,
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DNA sequence II (continued)

```
541  ACCGGCACCAGCGGCTCGGACTGGGCTCCACCCTCTACACCCACCTGCTGAAGTCC
     TGGCCGTGGTCGCCGAGCCTGACCCGAGGTGGGAGATGTGGGTGGACGACTTCAGGT
        ^   ^           ^       ^   ^   ^          ^^

     544 HGICI, 549 NSPBII, 563 HGIJII SDUI, 572 MNLI, 578 TAQII,
      583 BSPMI, 595 NCOI STYI, 596 NLAIII, 600 MNLI,

601  AGGCCCAGGGCTTCAAGAGCGTGGTCGCCGTCATCGGACTGCCCAACGACCCGAGCGTGC
     TCCGGGTCCCGAAGTTCTCGCACCAGCGGCAGTAGCCTGACGGGTTGCTGGGCTCGCACG
        ^                                                 ^

     605 APYI ECORII, 650 AVAI,

661  GCCTGCACGAGGCGCTCGGATACACCGCGCGCGGGACGCTGCGGGCAGCCGGCTACAAGC
     CGGACGTGCTCCGCGAGCCTATGTGGCGCGCGCCCTGCGACGCCCGTCGGCCGATGTTCG
           ^ ^             ^^^ ^   ^  ^     ^  ^      ^

     669 MNLI, 671 HAEII, 686 FNUDII, 687 BSSHII, 688 FNUDII, 690
      FNUDII, 695 HGAI, 698 BBVI, 705 BBVI, 708 NAEI, 716 TTH111I
     I,

721  ACGGGGGCTGGCACGACGTGGGGTTCTGGCAGCGCGACTTCGAGCTGCCGGCCCCGCCCC
     TGCCCCCGACCGTGCTGCACCCCAAGACCGTCGCGCTGAAGCTCGACGGCCGGGGCGGGG
              ^   ^.          ^   ^       ^^  ^

     732 DRAIII, 736 MAEII, 749 BBVI, 753 FNUDII, 763 ALUI, 764 B
     BVI, 767 NAEI,

781  GCCCCGTCCGGCCCGTCACACAGATCT
     CGGGGCAGGCCGGGCAGTGTGTCTAGA
                 ^     ^^

     795 MAEIII, 802 BGLII XHOII, 803 DPNI SAU3A,
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Patent claims for BE, CH, DE, FR, GB, IT, LI, LU, NL, SE

1. A phosphinothricin (PTC) resistance gene which can be obtained by cutting, with BamHI, the total DNA from Streptomyces viridochromogenes DSM 4112 which has been selected for phosphinothricyl-alanyl-alanine (PTT) resistance, by cloning a fragment 4.0 kb in size, and by selection for PTT resistance.

2. The gene as claimed in claim 1, which has the restriction map shown in Figure 1.

3. The gene as claimed in claim 1 and 2, which has the DNA sequence I (annex), position 258-806.

4. The use of the gene as claimed in claims 1 to 3 for the production of PTC-resistant plants.

5. The use of the gene as claimed in claims 1 to 3 as PTT resistance marker in bacteria.

6. The use of the gene as claimed in claims 1 to 3 as PTC resistance marker in plant cells.

7. The use of the gene as claimed in claims 1 to 3 for the selective N-acetylation of the L-form of racemic PTC.

8. PTC-resistant plants which have a gene as claimed in any of claims 1 to 3.