PATENT COURT
THE THIRD DEPARTMENT
DECISION

Case No.: 2001Heo1006 Final Rejection (Patent)

Plaintiff: Institut National De La Recherche Agronomique
Counsel for the Plaintiff: Seungho KIM,
Jinhee KIM, Patent Attorney
Younghee KIM, Patent Attorney

Defendant: Commissioner of the Korean Intellectual Property Office ("KIPO")
KIPO Litigator: Heesoo KIM

Closure of Hearing: April 11, 2002

Order

1. The Plaintiff's claim is dismissed.
2. The trial costs shall be borne by the Plaintiff.

Tenor of Claim

The decision by the Intellectual Property Tribunal ("IPT") in Case No. 99Won1918 issued on December 30, 2000 shall be cancelled.

Reasoning

1. Background facts

According to Exhibit Nos. K1, K26, and E1 to E3, the following facts are acknowledged.

A. The patent application of the present case ("Subject Application")

1) Title: DNA sequence imparting cytoplasmic male sterility, mitochondrial genome, nuclear genome, mitochondria and plant containing said sequence, and process for the preparation of hybrids

2) Application Date/Application No.: March 22, 1993 / 1993-700857
Priority Date: September 21, 1990 / French Patent Application No. 90-11670

3) Applicant: Plaintiff

4) Claims (as amended on June 30, 1999)

1. An Ogura sterility DNA sequence which comprises:
   a) a DNA sequence bounded by the nucleotides numbered 928 and 2273 in FIG. 1, or
   b) a sequence having at least 90% homology with said sequence, wherein said sequence confers cytoplasmic male sterility on a plant when it is present in the mitochondrial genome of said plant.

2. The DNA sequence according to claim 1, which comprises a DNA sequence bounded by the nucleotides numbered 928 and 1569 in FIG. 1 or a sequence having at least 90% homology with said sequence, wherein said sequence is transcribed to RNA in the mitochondria of a male sterile plant.

3. A recombinant plant mitochondrial genome which contains an Ogura sterility DNA sequence which consists
   a) of a sequence bounded by the nucleotides numbered 928 and

1569 in FIG. 1, or

b) of a sequence having at least 90% homology with said sequence mentioned in a), and confers cytoplasmic male sterility on a plant when it is present in the cytoplasm of said plant.

4. The recombinant plant mitochondrial genome according to claim 3, containing an Ogura sterility DNA sequence which comprises a sequence bounded by the nucleotides numbered 928 and 1569 in FIG. 1 or a sequence having at least 90% homology with said sequence.

5. The mitochondrial genome according to claim 3 or 4, wherein, in the recombinant genome, the Raphanus sequences of two formylmethionine transfer RNA genes used for translation initiation and a Cox1 gene coding for subunit No. 1 of cytochrome oxidase have been substituted with the corresponding Brassica sequences.

6. ~ 7.7. (Deleted)

8. The mitochondrial genome according to claim 5, wherein said genome contains a sequence which gives a 2.5-kb fragment after NcoI digestion, gives a 6.8-kb fragment after NruI digestion and a 4.4-kb fragment after SalI digestion.

9. ~ 10. (Deleted)

11. A mitochondrion comprising the genome according to claim 3 or 4.

12. ~ 27. (Deleted)

28. A nucleic acid probe comprising a first sequence of at least 10 bases of a sequence bounded by the nucleotides numbered 928 and 1569 shown in FIG. 1, said second sequence conferring

cytoplasmic male sterility character, labelled by a radioactive or non-radioactive means.

29. ~ 32. (Deleted)

33. A mitochondrion comprising the genome according to claim 5.

34. A mitochondrion comprising the genome according to claim 8.

35. ~ 38. (Deleted)

B. Procedural history

1) Final rejection

KIPO issued a final rejection in the Subject Application on February 27, 1999 on the grounds that the specification fails to meet the description requirements because a broad limitation "having at least ~ homology" is used to describe the claimed invention, rendering its constitution unclear.

2) Plaintiff's petition before the IPT (Case No. 99 Won 1918)
   a) IPT decision: Dismissal of petition (December 30, 2000)
   b) Gist of the grounds of the IPT decision
   A claim directed to a gene should in principle be defined by a nucleotide sequence. In the Subject Application, while claims 1 to 4 (hereinafter, "Claims 1 to 4 Invention") use limitations such as "a sequence having at least 90% homology with a DNA sequence bounded by the nucleotides numbered 928 and 2273 or 928 and 1569 in FIG. 1" to define the subject gene, the basis for limiting the degree of homology as such cannot be found anywhere in the specification. Moreover, the detailed description of the invention, unlike the claims, recites "a DNA sequence having at least 50% homology."

Thus, the claims of the Subject Application are not clearly described or supported by the detailed description of the invention. Accordingly, the Subject Application fails to meet the requirements prescribed by Article 42(4) of the Korean Patent Act, and therefore, the final rejection issued in the Subject Application is proper.

2. Appeal Grounds Submitted by the Plaintiff

A. Claims 1 to 4 are not unclear given that they are limited to DNA sequences having the function of "conferring male sterility" in addition to having at least 90% homology with a specific reference sequence.

B. In DNA-related inventions, due to the characteristics of "codon degeneracy" in DNA and "flexibility in amino acid substitution," sequences that are homologous to a DNA specified with its sequence and retain the same function as the original DNA should also be included in the scope of the invention in order to effectively protect inventors. Therefore, it is inevitable that claims be drafted using the expression "having at least ~% homology with a nucleic acid sequence···" in such a case. Regarding Claim 1 of the Subject Application, for example, a person having ordinary skill in the art ("PHOSITA") could easily understand that the phrase "a sequence having at least 90% homology to a sequence bounded by nucleotides numbered 928 and 2273 (1346 bp) in FIG. 1" denotes "a sequence which is identical to the specified sequence in at least 1211 out of 1346 nucleotides (i.e., 90%)." Further, since a change in sequence can occur by mutation, etc. at any position among the 1346 nucleotides, it would be impossible to describe in the detailed description of the invention the specific parts where a sequence change may occur by conducting experiments with respect to every possible sequence change.

C. The U.S. and Japanese counterpart applications to the Subject Application were granted as patents with claims defined by the expression “a DNA sequence shown in FIG. 1 or a DNA sequence encoding a protein translation product identical to that encoded by the DNA sequence shown in FIG. 1,” which are broader than the claims of the Subject Application reciting “a sequence having at least 90% homology.” In view of the above, the Subject Application should also be granted a patent.

3. Determination regarding the propriety of the IPT decision

A. Whether Claims 1 to 4 of the Subject Application fail to meet the description requirements

1) Article 42(4) of the Korean Patent Act prescribes that claims shall be supported by the detailed description of the invention, describe the claimed invention clearly and concisely, and be described only with indispensable elements of the claimed invention. Thus, expressions rendering the constitution of the claimed invention unclear cannot be used in the claims (see Supreme Court Decision No. 97 Hu 1337 rendered on October 2, 1998). In gene-related inventions, which are characterized by having the potential to produce a protein with a different functional profile by a single point mutation in the DNA sequence, genes should be specified with their nucleotide sequence and, in principle, using vague expressions in a claim such as “a nucleotide sequence having ~% homology” with a certain reference sequence is not allowed. However, in a case where a DNA sequence having a new utility has been discovered, if the detailed description of invention provides the concrete bases for determining what degree of homology with the specific DNA sequence is required for the variant to have the same function as the original sequence, claims with a broader scope that use the expression “a nucleotide sequence having ~% homology” with a specific sequence cannot be said to be unclear.

2) Claims 1 to 4 are directed to Ogura sterility DNA sequences which comprise a DNA sequence bounded by the nucleotides numbered 928 and 2273 (1346 bp) or 928 and 1569 (642 bp) in FIG. 1 and confer cytoplasmic male sterility on a plant, as well as "a sequence having at least 90% homology" with the above sequences, and recombinant plant mitochondrial genomes containing such sequences. Although it could be known that "a sequence having at least 90% homology" means that the sequence is identical to the above specified sequence in at least 90% of the nucleotides out of 1346 (or 642) bp, it is unclear as to which specific nucleotides should be identical or what are the grounds for limiting the degree of homology to 90%. Accordingly, the claims of the Subject Application can be deemed to be clearly described only when the grounds for limiting the degree of homology to 90% are presented, for example, by illustrating different variants having the same function as the original sequence while satisfying the homology degree. However, Exhibit No. E3 mentioned above merely establishes the fact that the detailed description of the invention of the Subject Application describes the following: "the present invention relates to a DNA sequence, which we shall refer to as Ogura sterility DNA sequence, characterized in that: a) it is carried by a DNA sequence bounded by nucleotides numbered 928 and 2273 in FIG. 1, or b) it possesses an at least 50% homology with the said sequence mentioned in a), and confers, when it is present in the mitochondrial genome of a plant, a cytoplasmic male sterility on the said plant. In particular, the subject of the present invention is an Ogura sterility DNA sequence, characterized in that: c) it is carried by the sequence bounded by nucleotides numbered 928 and 1569 in FIG. 1, or d) it possesses an at least 50% homology with the said sequence mentioned in c), and in that it is transcribed to RNA in the mitochondria of male-sterile plants."; "a cytoplasm containing a DNA sequence possessing an at least 50% homology with the sequence bounded by nucleotides numbered 928 and 2273 in FIG. 1, or a cytoplasm containing a DNA sequence possessing an at least 50%

homology with the sequence bounded by nucleotides numbered 928 and 1569 in FIG. 1, and transcribed to RNA, conferring the CMS character"; "the invention relates to a recombinant plant nuclear or mitochondrial genome, characterized in that it contains an Ogura sterility DNA sequence: a) which is carried by a DNA sequence bounded by nucleotides numbered 928 and 2273 of the sequence shown in FIG. 1, or b) which possesses an at least 50% homology with the said sequence mentioned in a), and confers, when it is present in the cytoplasm of a plant, a cytoplasmic male sterility on the said plant. In particular, one of the subjects of the present invention is a recombinant plant nuclear or mitochondrial genome, characterized in that it contains an Ogura sterility DNA sequence, c) which is carried by a sequence bounded by the nucleotides numbered 928 and 1569 in FIG. 1, or d) which possesses an at least 50% homology with the said sequence mentioned in c), and confers, when it is present in the cytoplasm of a plant and is transcribed to RNA, a cytoplasmic male sterility on the said plant." The detailed description of the invention does not present any grounds for limiting the degree of homology to 90%, such as illustrative examples of variants having 90% or higher homology with the specified sequence while retaining the same function. Furthermore, nowhere in the detailed description of the invention can the description "at least 90% homology" can even be found. Therefore, Claims 1 to 4 of the Subject Application cannot be deemed to be clearly described, nor are they supported by the detailed description of the invention.

3) Determination regarding the Plaintiff's arguments

The Plaintiff argues that Claims 1 to 4 are not unclear because even when a DNA sequence has at least 90% homology with a DNA sequence bounded by the nucleotides numbered 928 and 2273 (1346 bp) or 928 and 1569 (642 bp) in FIG. 1, it is excluded from the claimed scope if it does not have the function of conferring male sterility, and "a sequence having at least 90% homology" indicates that at least 90% of the nucleotides, i.e., 1211 or 578 nucleotides out of 1346 or 642 nucleotides, respectively, are identical to those in the specified sequence, which could be clearly understood by PHOSITA. As discussed earlier, however, homologous nucleotide sequences encompass variants, fused genes, and the like, and there would be numerous sequence combinations exhibiting 90% homology with the above 1346 bp or 642 bp nucleotide sequences. Thus, it would be difficult for PHOSITA to clearly understand and reproduce the subject matter of Claims 1 to 4 in the absence of descriptions regarding the representative variants indicating which of the above combinations may result in male sterility. Therefore, the above Plaintiff's arguments have no merit.

Regarding, for example, "a sequence having at least 90% homology" to a sequence bounded by nucleotides numbered 928 and 2273 (1346 bp) in FIG. 1 in Claim 1, the Plaintiff argues that since a sequence change can occur by mutation, etc. at any position among the 1346 nucleotides, it would be unreasonable to require specific descriptions in the detailed description of the parts where a sequence change may occur by conducting experiments with respect to every possible sequence change. Although it is not required that the specification describe every working example of nucleotide sequences having at least 90% homology to the 1346 bp sequence while conferring male sterility, at least some representative examples of variants showing the critical significance of the claimed limitation of 90% homology should be described. Therefore, the Plaintiff's above arguments also have no merit.

The Plaintiff also argues that the Subject Application should be granted a patent as its U.S. and Japanese counterparts were granted as patents with claims broader than those of the Subject Application. However, whether or not a patent should be granted for a Korean patent application should not be influenced by the patent examination status in other countries. Moreover, even the U.S. and Japanese counterpart patents (Exhibit Nos. K7 and E4) show that they claim "a DNA sequence encoding a protein translation product identical to that encoded by the DNA sequence shown in FIG. 1" instead of "a sequence having at least 90% homology with said sequence." Thus, these counterpart patents claim a DNA sequence encoding only the same protein with the identical amino acid sequence, the scope of which is clear, unlike Claims 1 to 4 of the Subject Application. Therefore, the Plaintiff's above arguments also have no merit.

B. Sub-conclusion

Thus, Claims 1 to 4 of the Subject Application are not clearly described and are not supported by the detailed description of the invention. Accordingly, the Subject Application cannot be patented under Article 42(4) of the Korean Patent Act, and therefore, the IPT decision affirming the final rejection issued in the Subject Application is proper.

4. Conclusion

Therefore, since the Plaintiff's claim seeking cancellation of the IPT decision is without merit, the Court dismisses the claim and issues a decision as stated in the Order.

May 30, 2002

Presiding Judge	Chijoong KIM
Judge	Jeongyul CHOI
Judge	Youngsun CHO

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                                                                T
         N                                                      a
     B   l                 H      T                      C      q
     sDNSa         D       i      sPM                   Av      I
     asctI         d       n      pll                   li      I
     JaoyI         e       f      Eey                   uJ      -
     IIIII         I       I      III                   II      2
      ///                                               /
     CCATGGACAATAATCTTAGTCGGAGTCAAATTCCTTACCTTTCCACCCAAAGCTGAACAT
   1 ---------+---------+---------+---------+---------+---------+ 60
     GGTACCTGTTATTAGAATCAGCCTCAGTTTAAGGAATGGAAAGGTGGGTTTCGACTTGTA

                                       S                     B  N
                                   BB Na      B           E  p  l
        S                 M    A   asDlu    A sT          c  u  a
        p                 n    l   mtpa3    l ta          o  1  I
        i                 l    w   HYnIA    w Bq          3  0  I
        I                 I    I   IIIVI    I II          I  I  I
                                   / //        /
     ATCCGCACAGATATTCCATTTTTTTTATTGAGGATCCATTTTCGAACTGAACTACTCATG
  61 ---------+---------+---------+---------+---------+---------+ 120
     TAGGCGTGTCTATAAGGTAAAAAAAATAACTCCTAGGTAAAAGCTTGACTTGATGAGTAC

                                 T
                                 t
                                 h                    F
       B                         1       C   C        n         N
     D s        M               M1     BAvMNAvS    M  u         l
     d p        w               s1     bliahlif    n  4         a
     e C        o               eI     vuJeeuJe    l  H         I
     I I        I               II     IIIIIIII    I  I         V
                                          /// //
     CTTAGGCAAAACAAGCAAGGGAGTTGTTAATAAGGAGCTAGCTACAGTGCTGCGGAGGGT
 121 ---------+---------+---------+---------+---------+---------+ 180
     GAATCCGTTTTGTTCGTTCCCTCAACAATTATTCCTCGATCGATGTCACGACGCCTCCCA

     S                      F
     t               NC  S  n  C
     y         M     lvMNc  u Av       B
     S         s     aiscr  4 li       b
     J         e     IJpiF  H uJ       v
     I         I     VIIII  I II       I
     /                   /     /
     TCCGTGCTTATTAAGGAGCCGGGCAGCTACGCAACACTTCCTTGCAACTCATACCTACTA
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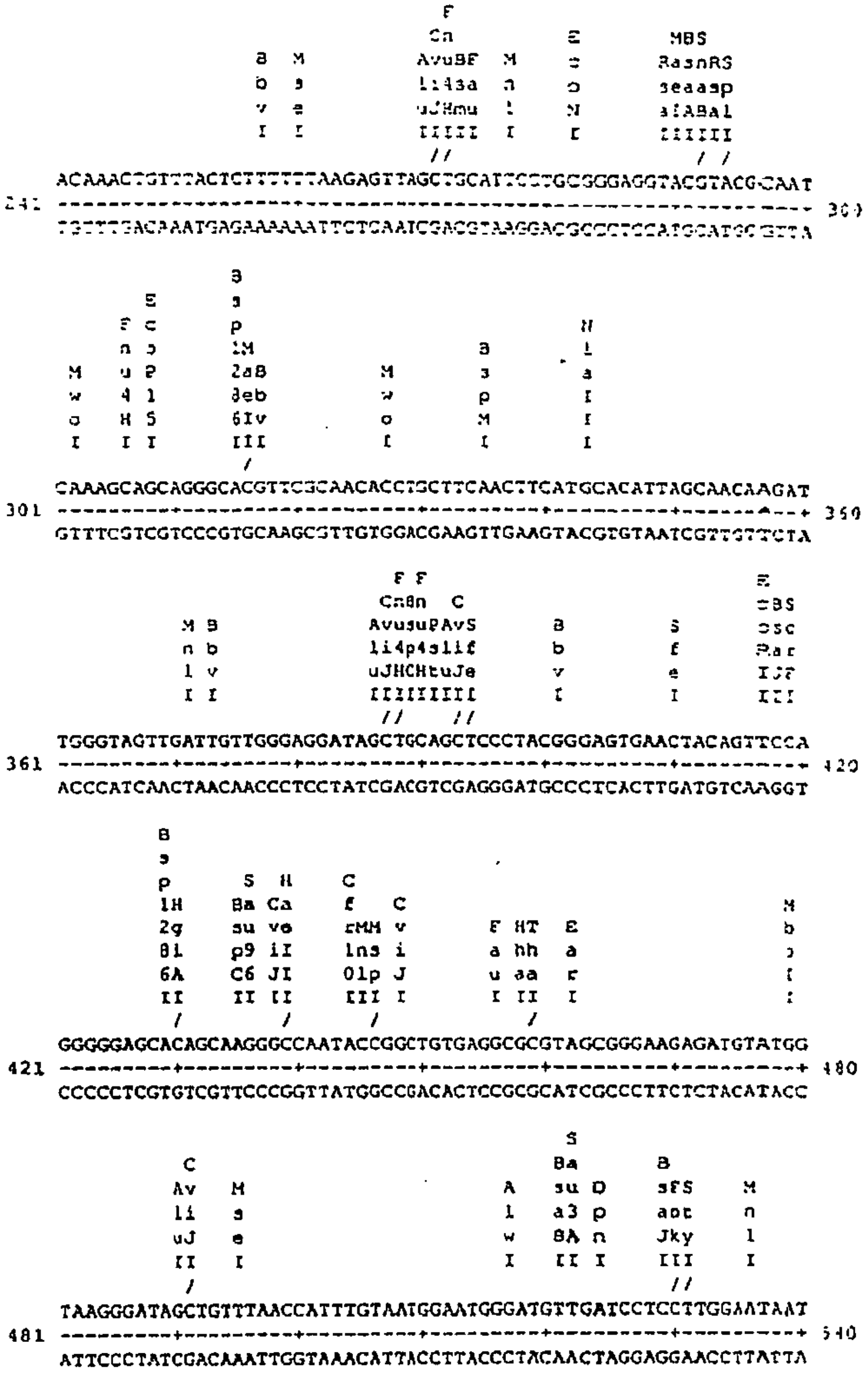
Fig. 1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301
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421
480
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TAAGGGATAGCTGTTTAACCATTTGTAATGGAATGGGATGTTGATCCTCCTTGGAATAAT
481
540
ATTCCCTATCGACAAATTGGTAAACATTACCTTACCCTACAACTAGGAGGAACCTTATTA

Fig. 1

```
                                                     F
    MBS                   M                          n
    asn    M      X       c3              T          uS
    eaa    m      m       cs              a          4p
    IAB    e      n       Ic              q          Hi
    III    I      I       II              I          II
      /
    ACGTATATAAGAAGATTTTCATTCCAGTTGGAAAGCAATCGAGAAAACGCCGCCCAAATA
541 ---------+---------+---------+---------+---------+---------- 600
    TGCATATATTCTTCTAAAAGTAAGGTCAACCTTTCGTTAGCTCTTTTGCGGCGGGTTTAT

             A
             fBM    C         HB                  a
             lsaP   v   P     is  NT   M        HBsM
             Iaem   i   l     np  ch   l        ssmc
             IAIl   J   e     fM  ua   y        paAr
             IIII   I   I     II  II   I        IIII
               //                  /              //
    CGCTTCGCCACGTGTAGCCCTGTATGGACTCGCGAAGCAGGTCTCCGGTCGGTGTCCAAG
601 ---------+---------+---------+---------+---------+---------+ 660
    GCGAAGCGGTGCACATCGGGACATACCTGAGCGCTTCGTCCAGAGGCCAGCCACAGGTTC

       S
       a                                             MBS
       u D      M                                    asnB
       3 p      n                                    eaab
       A n      l                                    IABv
       I I      I                                    IIII
                                                       /
    ATTTGATCTAACTATTGAGTGAGGACTACTTACCGATTGATAGAATAATACGTATATAAG
661 ---------+---------+---------+---------+---------+---------- 720
    TAAACTAGATTGATAACTCACTCCTGATGAATGGCTAACTATCTTATTATGCATATATTC

           F           S
          Cn   M       a                T            H         H
         Avu   b       u D      T       sM          Ha         i
         li4   o       3 p      a       ps          he         n
         uJH   I       A n      q       Ee          aI         f
         III   I       I I      I       II          II         I
         //
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721 ---------+---------+---------+---------+---------+---------+ 780
    TTCTTCGACGAAACACCTCACTAGAAAGAGCTTTACTTAATTCATTCCGCGATACAAGTC

                                                    E
      A    D                        C               c        9
    T l    r      MSM               v     M         o        sA
    f w    d      npa               i     w         5        av
    i N    I      lee               J     o         7        Ja
    I I    I      III               I     I         I        II
    ATTCTGAACCAAAGCACTAGTTGAGGTCTGAAGCCTTATGAGCAGAAGTAATAAATACCT
781 ---------+---------+---------+---------+---------+---------+ 840
    TAAGACTTGGTTTCGTGATCAACTCCAGACTTCGGAATACTCGTCTTCATTATTTATGGA
```

Fig. 1

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                                  H                N
                     M      T     i         C  B   l
        F   M  M     b      s     n         v  s   a
        a   n  n     o      p     c         i  p   I
        u   l  l     I      E     I         J  H   I
        I   I  I     I      I     I         I  I   I
     CGGGGAAGAAGCGGGGTAGAGGAATTGGTCAACTCATCAGGCTCATGACCTGAAGATTAC
841  ---------+---------+---------+---------+---------+---------+ 900
     GCCCCTTCTTCGCCCCATCTCCTTAACCAGTTGAGTAGTCCGAGTACTGGACTTCTAATG

               E
        M      c                                   S
        b      o   F   S     F                     f            T
        o      5   i   p     a                     a            a
        I      7   n   i     u                     N            q
        I      I   I   I     I                     I            I
     AGGTTCAAATCCTGTCCCCGCACCGTAGTTTCATTCTGCATCACTCTCCCTGTCGTTATC
901  ---------+---------+---------+---------+---------+---------+ 960
     TCCAAGTTTAGGACAGGGGCGTGGCATCAAAGTAAGACGTAGTGAGAGGGACAGCAATAG

                             H X       M TE
                        G  GCa m       aBsc      M
                        d EdveMa       ecpo      b S
                        i aiiIcI       Ie45      o p
                        I eIJIrI       If57      I i
                        I IIIIII       IIII      I I
                           / ///
     GACATCGCAAGGTTTTTGAAACGGCCGAAACGGGAAGTGACAATACCGCTTTTCTTCAGC
961  ---------+---------+---------+---------+---------+---------+ 1020
     CTGTAGCGTTCCAAAAACTTTGCCGGCTTTGCCCTTCACTGTTATGGCGAAAAGAAGTCG

                             B      T
                             sT     s
                             ta     p
                             Bq     E
                             II     I
                              /
     ATATAAATGCAATGATTACCTTTTTCGAAAAATTGTCCACTTTTTGTCATAATCTCACTC
1021 ---------+---------+---------+---------+---------+---------+ 1080
     TATATTTACGTTACTAATGGAAAAAGCTTTTTAACAGGTGAAAAACAGTATTAGAGTGAG

                                                            S H
                                               C            aCa
                                              Av            uve
                                              li            9iI
                                              uJ            6JI
                                              II            III
                                               /              /
     CTACTGAATGTAAAGTTAGTGTAATAAGTTTCTTTCTTTTAGCTTTTTTACTAATGGCCC
1081 ---------+---------+---------+---------+---------+---------+ 1140
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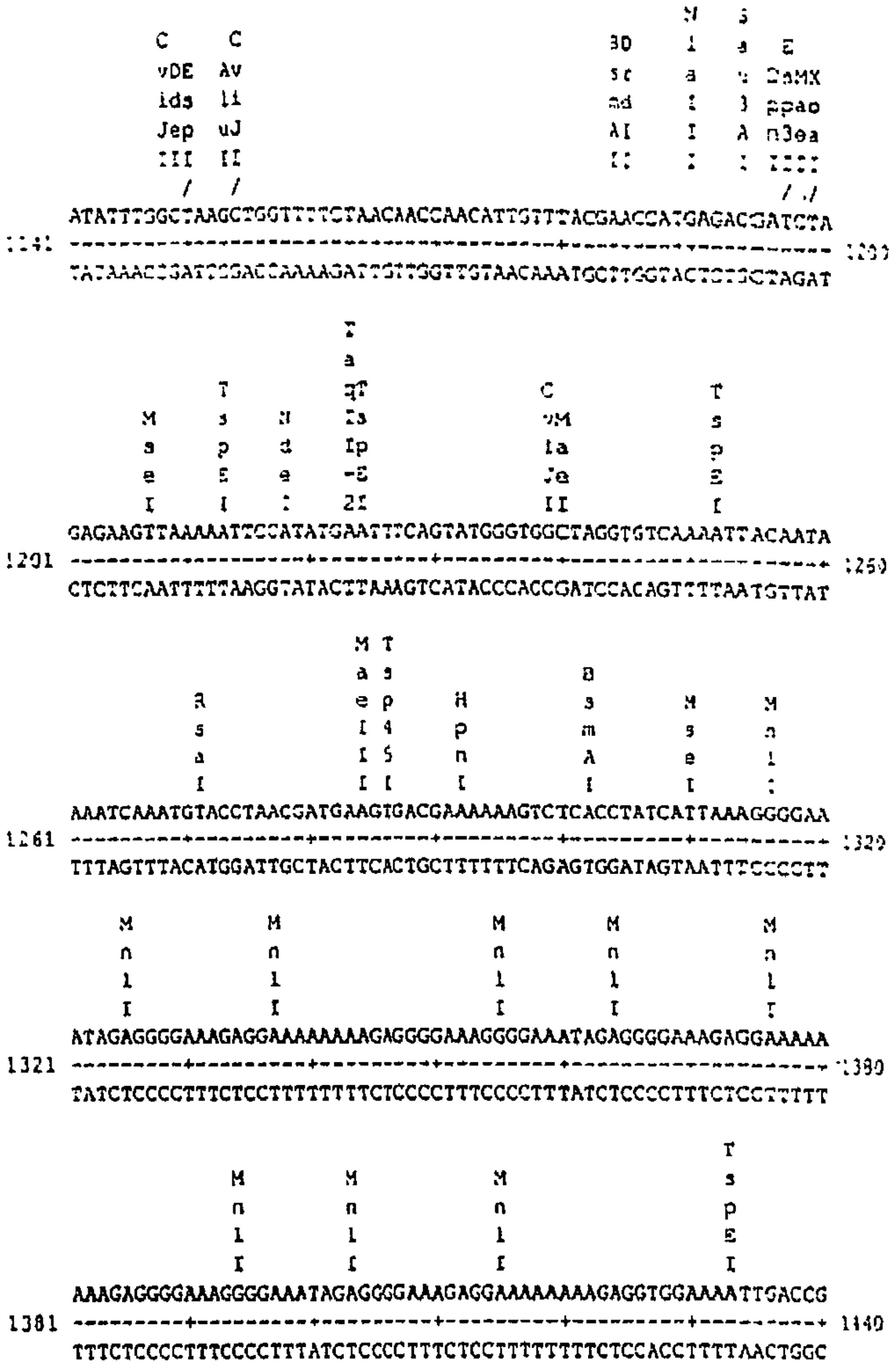
Fig. 1



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1261 ---------+---------+---------+---------+---------+---------+ 1320
     TTTAGTTTACATGGATTGCTACTTCACTGCTTTTTTCAGAGTGGATAGTAATTTCCCCTT

     ATAGAGGGGAAAGAGGAAAAAAAAGAGGGGAAAGGGGAAATAGAGGGGAAAGAGGAAAAA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     TATCTCCCCTTTCTCCTTTTTTTTCTCCCCTTTCCCCTTTATCTCCCCTTTCTCCTTTTT

     AAAGAGGGGAAAGGGGAAATAGAGGGGAAAGAGGAAAAAAAAGAGGTGGAAAATTGACCG
1381 ---------+---------+---------+---------+---------+---------+ 1440
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Fig. 1

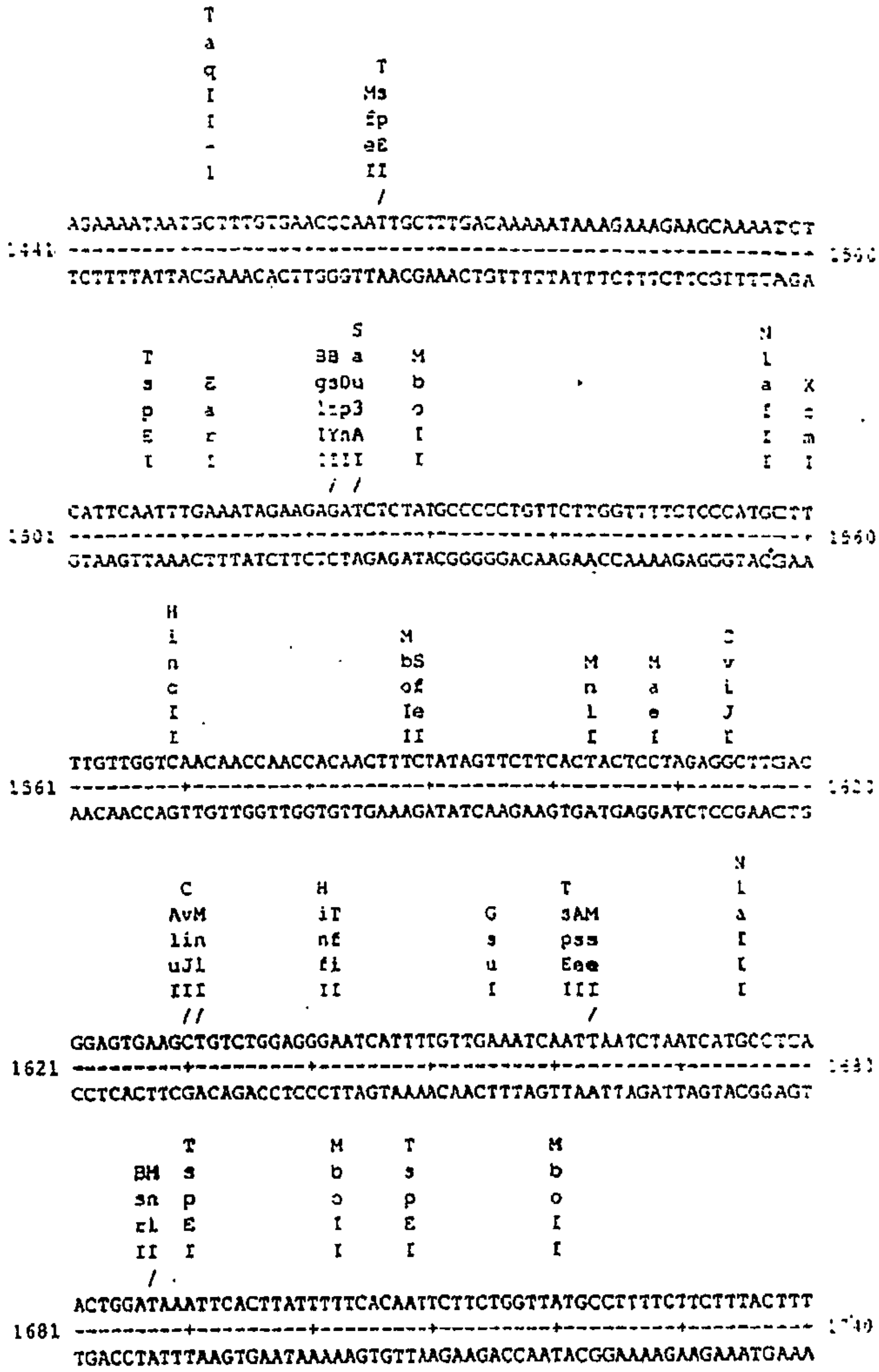

Fig. 1

```
                                                 E
                                          S      c
                                          a      o  E T
               N                    RS    u D    P Ac s
               d                    sc    3 p    1 lo p
               e                    aa    A n    5 wR E
               I                    II    I I    I II I
                                     /
     CTATATTTTCATATGCAATGATGGAGATGGAGTACTTGGGATCAGCAGAATTCTAAAACT
1741 ------------------------------------------------------------ 1800
     GATATAAAAGTATACGTTACTACCTCTACCTCATGAACCCTAGTCGTCTTAAGATTTTGA

                                                   E
                                                   c
                                           S       o  S
         ND               B  S     E   B   tM     AONPa       B
         lr             F sMNc     c   b   yb     v1lpu       s
         ad             o ascr     o   v   Lo     a0au9       t
         II             k JpiF     P   I   TI     I9IM6       X
         VI             I IIII     I   I   II     IIVII       I
                           ///                     / //
     ACGGAACCAACTGCTTTCACACCGGGGGAAGACCATCCAGAGCAAGGACCCCAACAGTTT
1801 ---------+---------+---------+---------+---------+---------+ 1860
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           S
        BB a      M                                             B
        gsDu      b                   B                M        s
        ltp3      o                   s                a        t
        IYnA      I                   r                e        B
        IIII      I                   I                I        I
         / /
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1861 ---------+---------+---------+---------+---------+---------+ 1920
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                            H   H                               S
             B             Ca   i                               a
     T       c             ve SAnT        M                     u
     a       e             iI acca        n                     3
     q       f             JI lcIq        l                     A
     I       I             II IIII        I                     I
     /                      /    /
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1921 ---------+---------+---------+---------+---------+---------+ 1980
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                               C
      D                      M vB
      p                      n is
      n                      l Jl
      I                      I II
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1981 ---------+---------+---------+---------+---------+---------+ 2040
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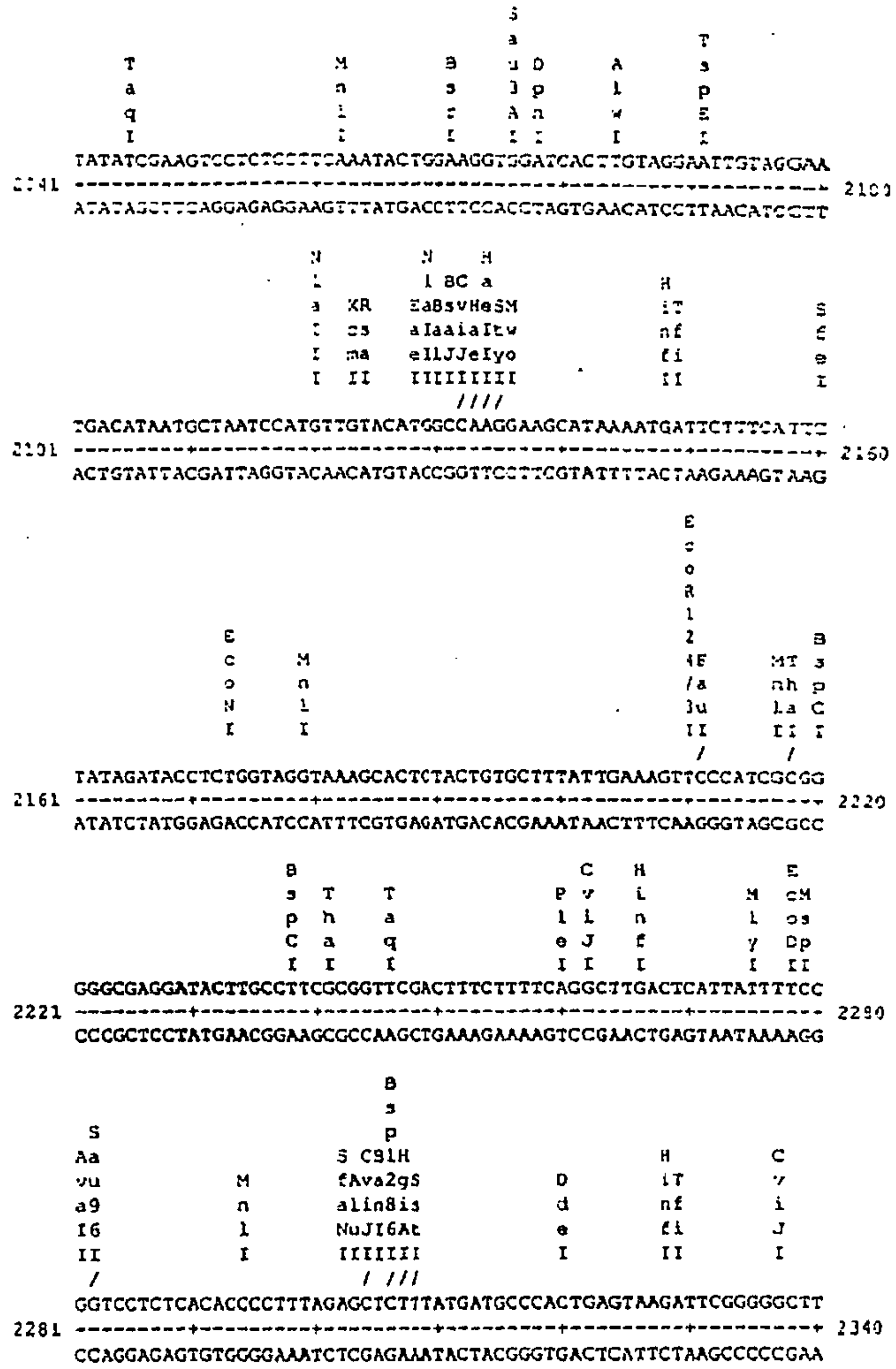
Fig. 1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RsaI
HinfI
TfiI
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EcoNI
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BspCI
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2161
2220
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BspCI
ThaI
TaqI
PleI
CviJI
HinfI
MlyI
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2221
2280
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MnlI
DdeI
HinfI
TfiI
CviJI
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2281
2340
CCAGGAGAGTGTGGGGAAATCTCGAGAAATACTACGGGTGACTCATTCTAAGCCCCCGAA

Fig. 1

```
                               N
        S     B   C          B sS   ENM         B         M
      MNc  H  s  Av     F    sDpaST slb         sT E      a   EM
      scr  h  p  li     a    asBcph pao         ma a      e   an
      piF  a  C  uJ     u    JaIIla 3II         Aq r      I   rl
      III  I  I  II     I    IIIIII IVI         II I      I   II
       //         /           / //   /                         /
     CCCGGCGCAGAAGCTCATTCTGAACCGCGGAACCTTCGTCTCTTCGACACAAACG TTTT
2341 -----------------------------+---------+---------+----- ---- 2400
     GGGCCGCGTCTTCGAGTAAGACTTGGCGCCTTGGAAGCAGAGAAGCTGTGTTTGC AAAA

                                S
             C     M      BBB N a
             v   M b  A   sasDlHu
             i   n o  l   amtpap3
             J   l I  u   BHYnIhA
             I   I I  I   IIIIVII
                            / / /
     ATGAAGAGGCTGATGGTGATGAGGATCC
2401 ---------------------------- 2428
     TACTTCTCCGACTACCACTACTCCTAGG
```

Restriction enzymes:

```
      AccI     AflIII       AluI       AlwI      AlwNI       AseI       AvaI      AvaII
      BalI      BamHI      BanII       BbvI      BbvII      BcefI      BglII     Bpu10I
      BsaI      BsaAI      BsaBI      BsaJI       BsiI       BsmI      BsmAI  Bsp1286I
     BspCI      BspHI      BspMI       BsrI      BstBI      BstXI      BstYI     Cfr10I
     CviJI       DdeI       DpnI      DrdII       DsaI       EaeI       EarI     Eco57I
     EcoBI      EcoDI      EcoNI   EcoO109I      EcoPI    EcoP15I      EcoRI     EcoRII
EcoR124/3I       EspI      Esp3I       FauI       FinI     Fnu4HI       FokI      GdiII
      GsuI       HaeI      HaeII     HaeIII      HgiAI       HhaI     HincII      HinfI
      HphI       MaeI      MaeII     MaeIII      MboII       McrI       MfeI       MlyI
      MmeI       MnlI       MseI       MspI       MwoI       NciI       NcoI       NdeI
      NheI     NlaIII      NlaIV       NruI     NspBII       PleI       PmlI      PpuMI
      PstI       RsaI      SacII       SalI     Sau96I     Sau3AI       ScaI      ScrFI
     SfaNI       SfeI      SnaBI       SpeI       SpiI       SplI       SstI       StyI
    StyLTI     StySJI       TaqI    TaqII-1    TaqII-2       TfiI       ThaI     Tsp45I
     TspEI    Tth111II       XbaI       XcmI     XmaIII       XmnI
```

Restriction enzymes:

```
    AatII      AflII       AgeI      AhaII       ApaI      ApaLI      AvrII       BanI
     BcgI       BclI       BglI      BspGI     BspMII     BssHII     BstEII     Bsu36I
    CfrAI       ClaI       DraI     DraIII       DrdI       EciI   Eco47III      EcoAI
  EcoDXXI      EcoEI      EcoKI   EcoR124I      EcoRV       FseI       FspI       HgaI
   HgiEII    HindIII    HinfIII       HpaI       KpnI       MluI       NaeI       NarI
     NotI       NsiI       NspI      PflMI      PshAI       PvuI      PvuII      RleAI
    RsrII       SfiI      SgrAI       SmaI       SnaI       SphI       SspI       StuI
   StySBI     StySPI     StySQI    Tth111I   Uba1105I   Uba1108I       XhoI
```

Fig. 1