AUSTRALIA

PATENTS ACT 1952

B

APPLICATION BY ASSIGNEE OF INVENTOR

DECLARATION IN SUPPORT OF AN APPLICATION FOR A PATENT

NAME OF APPLICANT

In support of an application made by:

Rhone Merieux SA

TITLE

for a patent for an invention entitled:

Viral Vaccines

FULL NAME AND ADDRESS OF SIGNATORY

I, Guy Malher

of Rhone Merieux SA

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do solemnly and sincerely declare as follows:

1. I am authorised by the above mentioned applicant for the patent to make this declaration on its behalf.

FULL NAME AND ADDRESS OF INVENTOR(S)

2. The name and address of each actual inventor of the invention is as follows:

Louis Joseph Norman Ross of Institute for Animal Health Limited, Houghton Laboratory, Houghton, Huntingdon, Cambridgeshire PE17 2DA
~~Simon David Scott of Institute for Animal Health Limited, Houghton Laboratory, Houghton, Huntingdon, Cambridgeshire PE17 2DA~~
Matthew McKinley Binns of Institute for Animal Health Limited, ~~Houghton Laboratory, Houghton, Huntingdon, Cambridgeshire~~ PE17 2DA

SEE NOTES OVER

3. The facts upon which the applicant is entitled to make this application are as follows:

By Assignment and by virtue of employment by the applicant the actual inventors have transferred their rights in the said invention to the applicant

DELETE PARAGRAPHS 3 AND 4 FOR NON-CONVENTION APPLICATION

4. The basic application(s) as defined by Section 141 of the Act was (were) made as follows:

Country Great Britain on 13 September 1988

in the name(s) Rhone Merieux SA

and in on

in the name(s)

PLACE AND DATE OF SIGNING

5. The basic application(s) referred to in the preceding paragraph was (were) the first application(s) made in a Convention country in respect of the invention the subject of this application.

Declared at Lyon

this 21st day of March 1991.

Signed Guy MALHER

Position President

GRIFFITH HACK & CO

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A vaccine effective against Marek's disease virus (MDV) comprises an MDV attenuated by virtue of being TK- or a host expressing an MDV antigen, namely the respective MDV homologues of the HSV gB, gC, gD or gH glycoproteins (or antigenic parts thereof) or the respective MDV homologues of the HSV-1 immediate early genes IE-68 or IE-175. The host may be a herpes virus of turkeys (HVT), more particularly HVT in which the MDV antigen is inserted in the HVT homologue of the HSV gC gene, the ribonucleotide reductase (large subunit) gene or the thyamidine kinase (TK) gene.

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(54) Title: VIRAL VACCINES

(57) Abstract

A vaccine effective against Marek's disease virus (MDV) comprises (a) an MDV attenuated by virtue of being TK- or (b) a host expressing an MDV antigen, namely the respective MDV homologues of the HSV gB, gC, gD or gH glycoproteins (or antigenic parts thereof) or the respective MDV homologues of the HSV-1 immediate early genes IE-68 or IE-175. The host may be a herpes virus of turkeys (HVT), more particularly HVT in which the MDV antigen is inserted in the HVT homologue of the HSV gC gene, the ribonucleotide reductase (large subunit) gene or the thymidine kinase (TK) gene.

VIRAL VACCINES

The present invention relates to viral vaccines which may be used to provide immunity against disease and to nucleotide sequences for inclusion in the viruses of such vaccines.

Background and Description of prior art

Herpesviruses are large double stranded DNA viruses consisting of an icosahedral capsid surrounded by an envelope. The group has been classified as alpha, beta and gammaherpesviruses on the basis of genome structure and biological properties [Roizman, B et al (1981) Inter-virology 16, 201-217]. Avian herpes viruses include Marek's Disease Virus (MDV) (a gammaherpesvirus) which causes a lymphomatous disease of considerable economic importance in chickens [reviewed in Payne, L.N. (ed) Marek's Disease (1985), Martinus Nijhoff Publishing, Boston] and Infectious Laryngotracheitis Virus (ILTV) (an alphaherpesvirus) which causes an acute upper respiratory tract infection in chickens resulting in mortality and loss of egg production.

A recent unexpected finding in our laboratory is that there is sufficient amino acid homology between MDV, ILTV and mammalian herpesviruses, particularly varicella zoster (VZV) and Herpes Simplex Virus (HSV) to allow identification of numerous conserved genes. These include the MDV and Herpesvirus of

Turkeys (HVT) homologues of glycoproteins gB, gC and gH of HSV; the ILTV, MDV and HVT homologues of TK and ribonucleotide reductase genes and the ILTV homologue of gB and genes 34 and 35 of VZV [Buckmaster, A et al, (1988) J. gen. Virol, 69, 2033-2042].

Strains of MDV have been classified into three serotypes. Type 1 comprises pathogenic strains and their attenuated derivatives. Type 2 are a group of naturally-occurring non-pathogenic strains and type 3 is HVT. For more than a decade, vaccination with HVT has been remarkably effective in controlling Marek's disease. However, in recent years, new strains of MDV have been isolated which cause disease despite vaccination with HVT. Losses due to these 'very virulent' strains have occurred in parts of the U.S.A., Europe and the Middle East. Although the degree of protection can be improved by using a mixture of HVT, type 2 MDV and attenuated derivatives of very virulent strains for vaccination, the results have been erratic. These observations and the fact that there are MDV type-specific epitopes that are not shared by HVT or type 2 MDV have led us to the conclusion that improved vaccines might be constructed which are antigenically more related to MDV than existing vaccines. [Reviewed by Ross and Biggs in Goldman J.M. and Epstein M.A. (eds) Leukaemia and Lymphoma Research, Vaccine Intervention against Virus-Induced Tumour, p 13-31, Macmillan, 1986].

A number of herpesvirus antigens have been shown to confer protective immunity when expressed in a recombinant vaccinia virus. These include the gB gene of HSV [Cantin E.M. et al (1987) Proc. Natl. Acad. Sci. U.S.A. 84, 5908-5912], gD of HSV [Paoletti, E. et al (1984) Proc. Natl. Acad. Sci. U.S.A. 81, 193-197] and gp50 of pseudorabies virus (PRV), a homologue of HSV gD [Marchioli, C.C. et al (1987) J. Virol. 61, 3977-3981]. Because of the absolute requirement of gB for virus penetration and infectivity and because it is conserved among herpesviruses, gB and its homologues are important immunogens. Moreover, the presence of gB at the surface of infected cells has been shown to be an important target for humoral and cell-mediated immune responses [Blacklaws, B.A. et al J.gen. Virol. 68, 1103-1114 (1987); McLaughlin-Taylor, E. et al (1988) J. gen. Virol. 69, 1731-1734]. The recently described glycoprotein gH of HSV is also essential for infectivity and may also be an important immunogen [Desai, P.J. et al (1988) J. gen. Virol. 69, 1147-1156]. It has also been shown that gIII of pseudorabies virus (PRV), a homologue of gC, is a major target for neutralizing antibody and for cytotoxic T cells although it is a non-essential protein. Also of interest is the unexpected participation of immediate early proteins in T cell mediated cytotoxic reactions in cells infected with cytomegalovirus (CMV) [Kozinowski U.H. et al (1987) J. Virol. 61, 2054-2058]. Similar antigens could play an important role in the rejection of latently infected and transformed lymphocytes in Marek's

disease since immediate early RNA transcripts have been detected in lymphoblastoid cell lines established from Marek's disease tumours.

Although many recombinant vaccines have been constructed using the poxvirus vaccinia as a vector, there are also reports of the use of herpesviruses as vectors for the expression of foreign genes. Thus hepatitis antigen has been expressed in HSV [Shih, M.F. et al (1984) Proc. Natl. Acad. Sci. U.S.A. 81, 5867-5870] and human tissue plasminogen activator has been expressed in PRV [Thomsen, D.R. et al (1987) Gene 57, 261-265. In both cases, foreign genes were inserted in cloned fragments of non-essential herpes genes which were then introduced into the virus vector by homologous recombination. The hepatitis virus gene was fused to a herpesvirus promoter and the recombinant DNA was inserted within the TK gene of HSV. Homologous recombination following co-transfection of the recombinant DNA and wild-type HSV DNA resulted in TK- virus clones that expressed the hepatitis antigen.

In the case of PRV, the gX gene mapping in U_s was used as the site for insertion of the foreign gene. The strategy used involved insertion of the TK gene of HSV in the gX gene of a PRV mutant that had a defect in its TK gene resulting in a TK positive virus. The human tissue plasminogen activator gene was then inserted within a cloned fragement of HSV TK and the

recombinant was introduced into the PRV mutant by homologous recombination. TK- virus was selected which expressed the human gene (Thomsen et al as above). Similarly, VZV has been used as a vector [Lowe et al (1987) Proc. Natl. Acad. Sci. U.S.A. 84, 3896-3900]. Several herpesvirus genes have also been shown to be associated with virulence and to be non-essential for growth in vitro. These include the TK genes of HSV [Jamieson, A.T. et al (1974) J. gen. Virol. 24, 465-480; Field, H. and Wildy, P., (1987) J. Hygiene (Cambridge) 81, 267-277] and of PRV. Indeed it has long been known that PRV is readily attenuated by deletion of TK activity [Tatarov, G. (1968) Zentralbl. Vet. Med 15B, 848-853]. Furthermore, attenuation of the Bartha strain of PRV has been attributed to a defect in gI, a non-essential structural glycoprotein mapping in U_s [Mettenleiter, T. et al (1987) J. Virol. 61, 4030-4032].

Genes of HSV mapping in the internal repeat region (TRS) flanking the long unique sequence have also been associated with pathogenicity [Rosen, A. et al (1986) Virus Research 5, 157-175; Thompson, R.L. et al (1983) Virology 131, 180-192]. Several additional genes of HSV have been shown to be non-essential for growth in vitro although it is not known whether they are associated with virulence. These include UL24 (Sanders, P.G., (1982), J. gen. Virol. 63, 277-295, large subunit of ribonucleotide reductase (Goldstein D.J. and Weller, S.K. (1988) J. Virol. 62, 196-205), gC (Draper K.G. et al

(1984) J. Virol. 51, 578-585), dUTPase (Fisher, F.B. & Preston, V.G. (1986) Virology 148, 190-197), and U_L 55 and U_L 56 (MacLean, A.R. & Brown, S.M. (1987) J. gen. Virol. 68, 1339-1350). Moreover there is evidence that several genes of HSV mapping in Us are also non-essential for growth in vitro [Weber, P.C. et al (1987) Science 236, 576-579].

WO 88/07088 (published only on 22 September 1988) disclosed hybrid viral vectors based on HVT or MDV and including a gene of interest in a non-essential site, such as the TK region or the region encoding protein A. Protein A, in this context, appears to be the same as gC, disclosed by Velicer and Coussens.

Summary of the invention

One aspect of the present invention provides a nucleotide sequence substantially free of the sequences which would adjoin it in the wild-type virus associated with the sequence, the sequence being selected from the group consisting of:

(a) the MDV homologue of the HSV gB gene,

(b) the MDV homologue of the HSV gH gene,

(c) the TK gene of MDV,

(d) the MDV homologue of the immediate early gene IE-175 of HSV-1

(e) the MDV homologue of the immediate early gene IE-68 of HSV-I

(f) the MDV homologue of the HSV gD gene

and minor variations thereof.

In addition, the TK sequence of HVT, referred to hereinafter sometimes as sequence (x), and the MDV analogue of HSV gC, referred to hereinafter sometimes as sequence (y),and minor variations of either may be used as insertion sites for certain heterologous sequences or as deletion sites to obtain less virulent viruses but are not novel per se.

Each of sequences (a) to (f),.(x) and (y) may be associated with further elements such as suitable stop and start signals and other 5' and 3' non-coding sequences, including promoters, enabling expression of the sequence. Such further elements may be those associated with the sequence in its naturally-occurring state or may be heterologous to that sequence.

In particular the promoter may be one associated with one of the sequences (d) and (f) above.

The term "minor variations thereof" is intended to include changes in the nucleotide sequence which do not affect its essential nature, for example minor substitutions of

nucleotides for one another. In the case of sequences which are intended for insertion into a vector to encode an antigen, the "essential nature of the sequence refers to the protein or glycoprotein encoded. Conservative changes in the nucleotide sequence which give rise to the same antigen will clearly be included, as will changes which cause conservative alterations in the amino acid sequence which do not affect adversely the antigenic nature of the antigen, in particular, antigenic portions of the antigen sequences may be used alone, for example, the regions corresponding to nucleotides 816-863, 1377-1595, 1377-1630 or 1824-1985 of MDV gB, or nucleotides 483-633, 843-933 or 1203-1278 or MDV gC, and minor variations thereof. These sequences and the peptides encoded thereby form further aspects of the invention. In the case of a sequence which is an insertion site, it is necessary only that the sequence should be non-essential for the infectivity and replication of the virus and have sufficient homology with the defined sequence to enable recombination to occur. Thus an insertion of the nucleotide into the sequence could completely change the reading frame from then on in a downstream direction. In the case of an antigen-encoding sequence this would usually alter the amino acid sequence undesirably (depending on where the frameshift occurred), but in the case of an insertion site, the degree of homology would be almost the same, thereby allowing recombination to take place with almost the same ease.

Generally speaking, in an insertion site, if a nucleotide homology of at least 75% is present, the sequence is regarded as a "minor variation". Preferably, the sequence is at least 80, 85, 90, 95 or 99% homologous. It will be appreciated that such degrees of homology relate to substantially the entire portion of each sequence (a) to (f) and (x) defined above. Shorter sequences may be used as probes in the identification or isolation of such longer sequences,but in this case the degree of homology will in general need to be greater in order to ensure accurate hybridisation.

Thus, a further aspect of the invention provides sub-sequences of at least 13 nucleotides having at least 90% (preferably 95%, 99% or 100%) homology to at least one portion of any of the said sequences (a) to (f), (x) and (y) above.

In the above list, sequences (a), (b) and (d) to (f) are useful as antigen-expressing sequences and sequence (y) is useful as an insertion site for heterologous sequences. Sequence (c) is useful for deletion to provide TK$^-$ mutants.

The sequences may readily be isolated from naturally-occurring HVT and MDV viruses, using the sequence information given herein and standard techniques, for example involving the preparation of oligonucleotide probes and use thereof to hybridise to the naturally-occurring DNA.

The isolated polypeptides encoded by sequences (a), (b) and (f) above are novel and form a further aspect of the invention, together with minor variations thereof and any glycosylated forms thereof which result from expression of the said sequences in MDV-susceptible cells.

A second aspect of the invention provides MDV mutants which are insertional or deletional mutants in the TK gene.

The mutation may be in the coding or non-coding sequences of the region identified.

An MDV antigen-expressing gene may be isolated from a virulent strain of MDV and inserted into the TK region of a less virulent strain of MDV; this insertion would result in a novel "virus" if it did not result in a naturally-occurring virus.

Other heterologous antigen-encoding sequences may be included, as well as an MDV antigen-encoding sequence, for example.

The heterologous sequence may alternatively be one coding for an antigen associated with any one of the following diseases: avian encephalomyelitis (epidemic tremor), avian influenza (fowl plague), avian leukosis, avian paramyxoviruses other than Newcastle disease (PMV2 to PMV7), avian reovirus diseases (enteric disease, tenosynovitis), chicken anaemia (caused by

chicken anaemia agent), coccidiosis, egg drop syndrome (EDS76), fowl pox, infectious bronchitis, infectious bursal disease (Gumboro), inclusion body hepatitis (adenovirus), lymphoproliferative disease of turkeys, Newcastle disease, reticuloendotheliosis in chickens, reticuloendotheliosis in turkeys, rotavirus enteritis, turkey haemorrhagic enteritis and turkey rhinotracheitis. The sequence may alternatively encode paramyosin (a muscle protein common to all invertebrate parasites) or an antigenic part thereof, somatostatin or a growth-promoting part thereof or an immune regulator.

The vectors in accordance with the invention will then provide multivalent vaccine protection.

The mutant viruses are potentially useful in vaccines as attenuated viruses, without necessarily having a heterologous sequence inserted.

A convenient process for preparing the deletional or insertional mutants of the second aspect of the invention comprises simply introducing into a suitable cell, for example by co-transfection, a deletional or insertional mutant version of the TK region and either whole viral DNA or a whole virus (for example the wild-type virus). The naked DNA of such viruses has been found to be infectious, provided that it has not been sheared. A calcium phosphate precipitate of the DNA is generally advantageous. Suitable cells include chicken embryo

fibroblasts, chicken kidney cells and duck embryo fibroblasts, all preferably grown in sub-confluent monolayers in Petri dishes. The transfected DNA and the whole viral DNA will then recombine with one another in the infected cells by homologous recombination and the desired recombinants can be screened for, for example by the detection of hybridisation to suitable probes or by an immunoassay using suitable antibodies to the gene product of the region in question.

For homologous recombination to take place, the viral DNA must replicate. At present, no cell-free replication system for MDV is known. However, if such a system becomes available, then the process of the invention could be operated therein. The environment in which the replication and recombination occur is not critical.

Regions (a), (b) and (d) to (f), which were identified above as being responsible for encoding immunologically useful viral antigens, can be inserted into suitable vectors, for example into HVT or other vectors such as fowlpox-virus, bacteria or fungi. In the case of viral vectors, especially herpesvirus vectors and poxvirus vectors, such insertion can be achieved by recombination between the antigen-encoding sequence, flanked by suitable non-essential sequences, and the vector's genome in a suitable host cell as described above. When HVT is the vector, the promoter will usually be an HVT or MDV vector. When fowlpox-virus or other virus is the vector, the promoter will

usually be a promoter which is endogenous to the vector. In the case of bacteria and fungi, the antigen-encoding sequence may be inserted using known or yet-to-be-discovered techniques of DNA manipulation. A non-pathogenic strain of Salmonella may be used as such a host. The heterologous sequence may be inserted into the host's genome or be carried on an independently-replicating plasmid. A promoter which is endogenous to the host will usually be used to control expression of the heterologous (viral antigen-encoding) sequence.

The flanking sequences which are used may comprise all, virtually all or less of the region into which the heterologous sequence is to be inserted. If all the region is employed, then the sequence of that region will clearly still be present in the resulting virus, but the function of that region will have been deleted. If less than the whole region is used as flanking sequences, then the result will be a structural as well as functional deletion. Either approach may be used.

Thus, three strategies can be envisaged for the construction of improved Marek's disease vaccines: (1) Construction of recombinant HVT that express selected MDV genes; (2) Construction of deletional or insertional mutants of highly virulent strains of MDV, which are attenuated and hence suitable for use in vaccines; (3) Construction of recombinant viruses that express MDV proteins in other vectors such as fowl pox virus.

To prepare a vaccine in which HVT or MDV is the virus or vector, the virus is grown in suitable cells such as chick embryo fibroblasts in a standard culture medium which as 199 medium (Wellcome or Flow Laboratories) for 3 to 4 days at about 37oC. The cells are harvested by trypsinisation and suspended in medium containing 10% dimethyl sulphoxide and 4% calf serum before storage in liquid nitrogen in sealed ampoules.

For vaccination, typically, day-old chicks are injected intramuscularly with about 1,000 plaque-forming units. Immunity follows within a few days.

It should be noted that MDV and HVT are cell-associated viruses and are infectious only when present in cells. Thus, a vaccine based on such viruses will always include suitable infected cells.

The vaccines of the invention may be used to protect any fowl susceptible to MDV, including commercially-reared poultry such as chickens, turkeys, ducks and quail.

Preferred aspects of the invention will now be described by way of example and with reference to the accompanying drawings, in which:

Figure 1 is a map of the MDV genome showing in part the BamH1 site distribution and the location of the gB and TK genes;

Figure 2 (on 18 sheets) shows the nucleotide sequence of the gB gene of the RB1B strain of MDV, with the numbering referring to the MDV nucleotides, the sequence of part of the HVT gB gene shown under the line, homologies indicated by vertical bars, and amino acid differences between MDV gB and HVT gB shown above the line;

Figure 3 is a map of the HVT genome showing the positions of the gH (hatched), TK (solid black) and major capsid protein (MCP, dotted) genes, with HindIII sites shown as "H";

Figure 4 (on 8 sheets) shows the nucleotide sequence of most of the HVT gH gene, with the corresponding amino acid sequence shown above the line;

Figure 5 (on 10 sheets) shows the nucleotide sequence of the HVT TK gene, with the numbering referring to the HVT nucleotides, the sequence of part of the MDV TK gene shown under the line, homologies indicated by vertical bars and amino acid differences between MDV TK and HVT TK shown above the line;

Figure 6 (on 6 sheets) shows the nucleotide sequence of the gC gene of the RBIB strain of MDV, with corresponding amino acids shown above the line;

Figure 7 shows part of the nucleotide sequence of the HVT homologue of the VZV62/HSV-1 IE 175 gene with corresponding amino acids shown above the line;

Figure 8 shows part of the nucleotide sequence of the HVT ribonucleotide reductase (large subunit) gene with corresponding amino acids shown above the line;

Figure 9 (on 2 sheets) shows part of the nucleotide sequence of the MDV ribonucleotide reductase (large subunit) gene with corresponding amino acids shown above the line;

Figure 10 shows part of the nucleotide sequence of the MDV ribonucleotide reductase (small subunit) gene with corresponding amino acids shown above the line;

Figure 11 shows part of the nucleotide sequence of the MDV homologue of the HSV-1 IE-175 gene with corresponding amino acids shown above the line;

Figure 12 shows part of the MDV homologue of the HSV-1 IE-68 gene with corresponding amino acids shown above the line;

Figure 13 is a schematic representation of homologous recombination at a non-essential region of a viral genome and a homologous region of DNA cloned within a plasmid vector;

Figure 14 (on 27 sheets) supplements Figures 4 and 5, and shows the nucleotide and predicted amino acid sequences from the region containing the MDV and HVT TK and gH and flanking genes. The bracketed MDV amino acid sequences are those potentially encoded by this region of nucleotide sequence if the upstream ATG triplet were the true gene initiation site. Asterisks denote stop codons. Spaces have been inserted into the sequences in order to optimize alignments. Colons between the MDV and HVT DNA sequences indicate nucleotides conserved between the two viruses. MDV amino acids are only shown in positions where they differ from that in HVT; and

Figure 15 shows the partial nucleotide sequence of the MDV homologue of HSVgD, the predicted amino acids being shown above the MDV nucleotide sequence and residues in bold type being conserved between the MDV and HSV-1 gD regions.

EXAMPLES: General Approaches

Selected short sequences of the avian herpesviruses cloned in the bacteriophage vector M13 were used as probes to identify longer fragments that might contain the entire genes of interest. This was achieved by Southern blot hybridization of restriction fragments. Full details are given below.

Virus Strains. The 'highly oncogenic' strain RB1B of MDV [Schat, K.A. et al (1982) Avian Pathol. 11, 593-605] was

obtained from Professor B. Calnek, Cornell University, Ithaca, U.S.A. The virus received has been plaque purified in chicken kidney vells in tissue culture. It was passaged twice in SPF RIR chickens and 4 times in chick embryo fibroblasts (CEF). Its 'highly oncogenic' nature was demonstrated by a high incidence of gross tumours when inoculated in genetically resistant N-line chickens.

The FC126 strain of HVT [Witter, R.L. et al (1970) Am. J. Vet. Res. 31, 525-538], obtained from the Wellcome Research Laboratories, Beckenham, Kent, had been passaged 14 times in CEF. It was subsequently grown in duck embryo fibroblasts (DEF) and CEF in our laboratory. It was then plaque-purified and grown further in CEF. Viral DNA used for cloning in the present work was extracted from virus that had been passed 29 times since the original isolation.

Tissue culture. CEF were grown in roller bottles in 199 medium (Wellcome), supplemented with penicillin, streptomycin, Fungizone (Regd. T.M.) and calf serum as described previously [Ross, L.J.N. et al (1975) J. gen. Virol. 28, 37-47].

CKC were grown in 10 cm Petri dishes [Churchill, A.E. and Biggs P.M., (1967) Nature, 215, 528-530].

Isolation of MDV DNA. Cell associated RB1B was inoculated onto confluent monolayers of CEF in roller bottles at a multiplicity

of infection of approximately 0.001 plaque-forming units (pfu) per cell, and the cultures were incubated at 37°C. After 3 days, the medium was discarded and replaced with fresh 199 medium containing 2% calf serum. Cells were harvested for virus purification after 2 to 3 days when cytopathic effect was extensive. Virus was obtained by rate zonal centrifugation of the cytoplasmic fraction of infected cells [Lee, Y.S. et al (1980) J. gen. Virol. 51, 245-253]. Viral DNA was extracted by treating purified virus with sarcosyl, proteinase K and Tris buffer pH 9 overnight at 37°C and purified by rate zonal centrifugation in glycerol gradients as described previously (Lee et al, 1980). High molecular weight viral DNA was precipitated with ethanol and resuspended in 10 mM Tris pH 7.5 im 1mM EDTA (TE).

Cloning of MDV DNA. One μg of MDV DNA was cut with the restriction enzyme BamH1 and ligated to BamH1-cut, dephosphorylated pUC13 DNA (Pharmacia). Competent E.coli strain TG1 cells were transformed according to standard procedures [Hanahan, D. (1983) J. Mol. Biol. 166, 557-580] and were grown in the presence of ampicillin and X-gal. White colonies were picked and tested for the presence or MDV inserts by hybridization to nick-translated MDV DNA [Grunstein M. and Hogness, D.S. (1975) Proc. Natl. Acad. Sci. U.S.A. 72, 3961]. Positive colonies were cultured in small volume and plasmid DNA isolated by the procedure of Holmes, D.S. and Quigley, M.

[(1981) Anal. Biochem. 114, 193-297]. The size of the inserts was determined by electrophoresis of BamH1 digests of the recombinant DNA in agarose gels. Plasmids containing MDV inserts ranging from less than 1 to 18 Kbp were obtained.

Random sequencing of viral DNA. Sonicated fragments of viral DNA were cloned into SmaI-cut, dephosphorylated M13.mp10 (Amersham International PLC) and plaques containing MDV inserts were identified by hybridization to MDV DNA. The sequence was determined by the dideoxy method [Sanger, F. et al (1977) Proc. Natl. Acad. Sci. U.S.A. 74, 5463-5467] using ^{35}S dATP).

The same procedure was used to sequence cloned fragments of MDV DNA except that plaques were identified by hybridization to labelled insert so as to avoid colonies containing pUC13 fragments.

EXAMPLE 1: gB gene of MDV

An M13 clone of HVT homologous to the gB gene of VZV and HSV hybridized to BamH1 fragment I3 of MDV (see Figure 1). Sequencing of this fragment obtained from a BamH1 library of the RB1B strain of MDV showed that two thirds of the gene, starting with the NH_2 terminus, was contained within I3. The remainder of the gene was identified in the adjacent

restriction fragment K3. Figure 1 shows the map position of the gene which is 2.6Kbp long. Its mRNA has been estimated to be approximately 2.8 Kb. The translated protein is 865 amino acids long (Figure 2). This includes approximately 20 amino acids which may be part of a signal sequence domain. The primary translated sequence of MDV gB has a few features in common with gB of other herpes viruses such as the alignment of cysteine residues and the presence of hydrophobic sequences which are presumably capable of spanning a lipid bilayer [Pellet, P.E. et al (1985), J. Virol. 53, 243-253]. However, MDV gB has only 48% amino acid similarity with gB of HSV and has many unique features such as the insertion of 23 amino acids (residues 1851-1920, Figure 2) and the presence of extra sites with glycosylation potential. Comparison of the sequence of MDV gB with limited sequence data (702 bases) available for HVT gB (Figure 2) has shown 76.9% nucleic acid similarity and 87.1% amino acid similarity between these two glycoproteins. Amino acid substitutions in HVT gB compared to MDV gB were particularly marked in a region (residues 1323 - 1433) equivalent to a domain of HSV gB associated with virus neutralization [Pellet P.E. et al (1985) as above]. Amino acid substitutions between MDV and HVT gB were also noted in other regions of unknown function.

EXAMPLE 2: gH gene of HVT and gH gene of MDV

An M13 clone of HVT containing sequences homologous to HSV gH was isolated during our earlier work on gene identification and mapping (Buckmaster et al (1988) as above). This clone, when used as a probe, hybridized to a 6Kbp HindIII fragment of HVT (Figure 3). Sequencing revealed that this fragment contained approximately one quarter of the gH gene including the carboxy terminus. The adjacent HindIII fragment (3.2 Kbp) containing the remainder of the gH gene was identified by hybridization using a cloned HpaI fragment of HVT which overlapped the HindIII site. Figure 4 shows the sequence of the coding region of the gH gene of HVT (2.3 Kbp) and flanking sequences. The % amino acid identity between the gH gene of HVT and its homologue in HSV1, VZV and EBV was only 20, 24 and 20 respectively (estimated from maximised amino acid overlaps of 630, 644 and 153 respectively).

EXAMPLE 3: TK gene of HVT and TK gene of MDV

The whole coding region of the TK gene of HVT (1053 bp) was contained within the 3.2 Kbp HindIII fragment described above (Figure 3). The sequence of the entire gene and flanking regions is shown in Figure 5. Similarly the whole of the MDV TK gene is contained within the 3.6 Kbp BamH1 K2 fragment of MDV (Figure 1). The complete sequence of MDV TK gene is shown in Figure 14. Comparison of the MDV and HVT TK sequences shows

that the two genes have 60% amino acid identity. By contrast, the % amino acid identities between the TK gene of HVT and the TK genes of HSV 1, VZV and EBV are only 30, 27 and 24 respectively (estimated from amino acid overlaps of 320, 332 and 193 respectively). The predicted amino acid sequences of HVT and MDV TK show characteristic ATP and/or CTP binding site motifs described for a number of virus and eukaryotic proteins that are associated with phosphorylation (Gentry, G.A. (1985) Proc. Natl. Acad. Sci. U.S.A. 82, 6815-6819). These conserved sequences are examples of useful sites for insertion and expression of foreign genes and for producing TK- deletion mutants.

EXAMPLE 4: A antigen gene of MDV (gP57-65) (gC homologue)

The A antigen gene is of interest in vaccine development both as an immunogen (it encodes a major glycopolypeptide product) and also because we have identified it as the homologue of HSV gC, a potential non-essential region. The A antigen gene was mapped within the BamH1 B fragment of MDV (Isfort et al 1987), and the nucleotide sequence determined for the GA strain of MDV (Coussens and Velicer, Abstract OP18.51, VII International Congress of Virology, 9-14 August, (1987) Edmonton, Canada; J. Virol. 62, 2373-2379). During the random sequencing studies described earlier (Buckmaster et al 1988), we identified an M13 clone (No. 130) which came from the A antigen gene. This clone was then used to identify a 2.3 Kbp EcoR1/PvuII fragment from

the RB1B strain of MDV containing the A antigen. This fragment was cloned into a SmaI/EcoR1 cleaved pUC13 vector by standard protocols. One plasmid (pMB419) was sequenced by the M13 dideoxynucleotide method. The sequence of the MDV RB1B A antigen and the predicted amino acid sequence of the protein are presented in Figure 6. The A antigen regions of MDV and HVT are non-essential genes and they can therefore be used as sites in MDV and HVT into which other genes can be inserted into the virus by homologous recombination. Several lines of evidence support this as outlined below.

1)During our study we isolated and sequenced another RB1B A antigen clone. This had one extra T residue in the string of T's 45 bases 3' to the A antigen ATG codon. This extra T would cause a frameshift which would make it impossible for the gene to encode functional A antigen. As it is probable that this gene was cloned from a replicating MDV, the results suggest that the A antigen is non-essential to the virus.

2)On conducting a similarity search it became clear that the MDV A antigen gene is the homologue of HSV gC and PRV gpIII glycoproteins. Both of these homologous genes are known to be non-essential [for the HSV homologue, see Rosenthal et al (1987) J. Virol. 61, 2438 - 2447].

3)Strains of MDV lacking A antigen as judged by agar gel diffusion tests [Churchill, A.E. et al (1969) J. gen. Virol. 4,

557-564] or producing low levels using the more sensitive 2D radio-immunoprecipitation (van Zaane, D. et al (1982) Virology 121, 133-146] have been reported.

Furthermore, in view of the fact that the A antigen is a major secreted glycoprotein, it may be a particularly suitable location for the presentation of foreign epitopes within the A antigen as soluble, secreted proteins. This may be achieved by cloning oligonucleotides encoding these epitopes in frame within the A antigen gene.

STRATEGIES FOR INTRODUCING GENES INTO HVT VECTORS

Two possibilities can be envisaged: 1) insertion into non-essential genes of the vector or 2) substitution of foreign gene for corresponding gene of the vector. This would be possible only in regions which already have substantial homology as may be the case between some genes of MDV and HVT.

EXAMPLE 5: Insertion into non-essential genes of HVT or MDV

(a)Insertion at the TK locus of the vector.

1) HVT or MDV may be used as vectors for insertion and expression of avian herpesvirus genes. In particular gB, gH or gC of RB1B MDV may be inserted into HVT. One may use the promoter associated with the inserted gene or use heterologous

promoters, including those of a different class of genes (for example the immediate early promoter to optimise expression of gB).

2) HVT or MDV may be used as general vectors for the insertion and expression of genes unrelated to avian herpes viruses and likely to require manipulation of promoters for optimal expression.

The procedure to be used for gene insertion is substantially as described previously for the insertion of hepatitis antigen in HSV [Shih et al, 1984 as above].

MDV and HVT DNA obtained as described above is infectious provided that precautions are taken not to shear the DNA during extraction. Calcium phosphate precipitates of viral DNA prepared as described by Stow and Wilkie [(1976) J. gen. Virol. 33, 477] were added to sub-confluent monolayers of CEF. After absorption for 1h at 37°C, culture medium was added and cultures were incubated for 1 or 2 days until confluent. Monolayers were then trypsinised, replated (1:1 or 1:2) in 199 medium (Wellcome) containing 2 to 4% calf serum and incubated at 37°C until plaques developed, usually after 4 to 5 days. Approximately 200 plaques may be obtained per μg of HVT DNA and approximately 50 per μg of MDV DNA.

For homologous recombination and isolation of recombinant virus, genes of interest are inserted within non-essential genes such as TK or gC and co-transfected with wild-type viral DNA at molar ratios ranging from 10:1 to 2:1 as described above. Alternatively, intact wild-type virus may be used for co-infection.

Restriction enzyme sites that could be used for the insertion of foreign antigens into the TK of HVT strain Fc-126 include: BanII, Bsp1286, DraIII, EcoRI, HincII, HpaI, NheI and NspbII.

RE sites that could be used to produce defined TK deletion mutants in MDV serotype I strain RB1B include; BalI, HaeII, NdeI and SphI as insertion sites for foreign DNA that would disrupt the TK gene, and double digests of combinations of these four restriction enzymes (EcoK could also be used) to remove a portion of the TK gene, thus inactivating it.

Some of these enzymes also have sites in the plasmid vector into which the virus DNA fragments are cloned. Thus in order to linearize the clone DNA without also cutting within the vector, partial digests may be carried out.

None of the above enzymes should cause any disruption to flanking genes, HSV-1 homologues of which are known to play an important role in virus multiplication.

Virus recombination may be detected by 'plaque lifts' which involve transfer of infected cells and released virus which have adhered to the agar overlay to nitrocellulose and hybridization of the denatured DNA released from the cells and virus to suitable probes as described by Villareal, L. et al (1977) Science 196, 183-185. Virus which hybridizes to the probe may be recovered from the monolayer.

A similar procedure may be used to isolate recombinant virus which expressed epitopes of interest. In this instance the nitrocellulose "plaque lifts" are treated with antibody and the presence of bound antibody revealed using a suitable detection system such as labelled protein A or phosphatase conjugated anti-globulin antibody.

The gene of interest with appropriate promoters is first inserted within the cloned TK gene. The recombinant DNA is then co-transfected with infectious DNA of the vector in chick embryo fibroblasts or chicken kidney cells and TK- virus may be selected by growth in medium containing acyclovir [Ross, N. (1985) as above] or FMAU [Schat, K.A. et al (1984) Antiviral Research 4, 159-270]. Alternatively, or in addition, plaques are screened for the presence of the gene of interest using 'plaque lifts' on nitrocellulose and hybridization to any relevant labelled probe. Plaques are also screened for expression of the epitopes of interest using monoclonal antibodies or antipeptide antibodies.

The main advantage of this strategy is that the selection procedure increases the chances of obtaining virus recombinants containing the gene of interest. It also offers the opportunity of using different promoters for optimum expression. Thus the use of an immediate early promoter may allow expression in latently infected cells.

(b)Insertion at other non-essential sites of the vector.

Since the A antigen (HVT and MDV homologues of HSV gC) is not essential for virus growth in vivo and in vitro (see section on gC above) it is a potentially useful site for the insertion and expression of foreign genes. Moreover, since it is one of the most abundant antigens and is excreted, it may be particularly useful for enhancing the immunogenic properties of foreign proteins. The isolation of virus recombinants at this locus may be achieved by first inserting at least part of the gene of interest in frame within the gC gene and then co-transfecting with infectious viral DNA. Screening of virus plaques with sequence specific probes or with specific antibody allows the isolation of recombinants.

An antigen-encoding sequence can also be inserted into the ribonucleotide reductase (large subunit) gene of HVT or of MDV - see Figures 8 and 9.

EXAMPLE 6: Substitution of MDV genes for their homologues in HVT

Substitution may be achieved by co-transfection of cloned MDV sequences and infectious HVT DNA as described in Example 5. Substitution of the gB and gC genes derived from the RBIB strain of MDV for their counterparts in HVT may be effected as may substitution of the gH gene of MDV, other glycoproteins and immediate early genes.

Recombinants expressing MDV sequences and epitopes may be detected using MDV-specific monoclonal antibodies or anti-peptide antibodies raised against unique MDV sequences as described above.

The advantage of this procedure is that it is relatively simple and does not require manipulation of promoters. However, it may be limited to genes which share substantial homology.

EXAMPLE 7: Strategies for obtaining TK- mutants of MDV

Deletion mutants. Deletions may be introduced within any suitable part of the gene, for example the domains of the gene that are required for nucleoside binding. This may be achieved by restriction enzyme double digestion, for example with HaeII and any of the following enzymes: BalI, NdeI, SphI or EcoK. Appropriate fragments are then religated, followed by co-transfection with infectious viral DNA or transfection into virally-infected cells. Reference may be made to Figures 7 and 8, and to the section above relating to insertion of heterologous sequences, in choosing restriction enzymes and so on. TK- virus may be selected in the presence of acyclovir [Ross, N. (1985) as above] or FMAU [Schat, K.A. et al (1984) as above]. Plaque-purified clones may then be tested for the absence of the deleted portion of the TK gene by hybridization.

The deletion mutants of MDV may be used themselves as attenuated viruses for vaccine preparation, or may have sequences for heterologous antigens inserted.

Insertional mutants. A functional ß-galactosidase gene under the control of a herpesvirus promoter or any other suitable sequence or a single base is first introduced in a domain of the TK gene which is essential for TK activity. The recombinant DNA is then co-transfected with infectious viral DNA or transfected into virally-infected cells to allow homologous

recombination to occur. Selection in the presence of acylovir or FMAU will yield TK- insertional mutants. If a ß-galactosidase gene is introduced, mutants can be detected by the production of blue plaques in the presence of X-gal.

The TK gene and surrounding sequences may be subcloned into another suitable vector if necessary.

EXAMPLE 8: Insertion of MDV RB1B gB gene into HVT

The HVT TK gene is cloned in the plasmid vector pUC13 to generate a plasmid, which is termed pTK1B. This plasmid is linearised with, for example, the restriction endonuclease Rsr II which cleaves the plasmid only within the TK gene (nucleotide position 197 in Figure 5, enzyme recognition sequence CGGACCG). The "sticky" ends thus generated can be end repaired by standard techniques (see "Molecular Cloning: a Laboratory Manual", ed. Maniatis T., Fritsch E.F., and Sambrook J. Cold Spring Harbor Laboratory 1982).

The RB1B gB was originally cloned on two plasmids which may be termed RB1B-BamH1-I_3 and RB1B-BamH1-K_3. (Note I_3 had lost one BamH1 site during cloning.) To generate a complete gB copy on one plasmid, both plasmids were cleaved with BamH1 and the fragments ligated. Recombinants containing the desired configuration were identified by restriction enzyme analysis of plasmid DNA's. However, as described above, the complete gB

sequence was subsequently obtained on an EcoRI/SalI fragment.

Further information regarding the sequence encoding MDV gB and its manipulation may be found in Ross et al J. gen. Virol (1989) 70 1789-1804.

The single recombinant plasmid of Ross et al is then cleaved with EcoRI and SalI, the ends are repaired and the plasmid is cloned into PTK1B prepared as above. Alternatively, the MDV gB open reading frame could be excised from plasmid MSB27 by digestion with HincII and NaeI and the products ligated to HVT TK plasmid pTK1B, cleaved partially with HpaI. Recombinant plasmids containing both TK and gB sequences could be identified by hybridisation and further characterised by Southern blotting. The recombinant plasmids are then introduced into cells containing HVT virus (viral DNA) and homologous recombination will introduce the gB gene into the TK gene. HVT viral recombinants can be selected with acyclovir or FMAU or alternatively detected with labelled gB probes.

EXAMPLE 9: RB1B gC (A antigen) gene into HVT

Blunt ended PTK1B is prepared as in Example 8. The RB1B gC is cleaved from the plasmid pMB419 (Example 4) with the restriction endonucleases EcoR1 and HindIII (site within the pUC13 polylinker). The sticky ends generated are again end-repaired by standard protocols. The end-repaired gC fragment is

then cloned into the linearized end-repaired pTK1B as in Example 8. (The cloning can be verified by analysis of the resulting clones with restriction enzymes, probing with radio-actively labelled fragments, or DNA sequencing, or any combination of these).

The resulting plasmid with the RB1B gC gene cloned into the HVT TK gene can then be introduced into the HVT genome by transfecting the plasmid into HVT-infected cells using calcium phosphate precipitation or electro-poration. Homologous recombination, involving cross-overs either side of the gC gene, between the HVT virus and the flanking sequences of the HVT TK plasmid will carry the RB1B gC gene into the HVT viral genome. Viral recombinants can be selected for (as they are TK^-) or identified (eg by probing) as described above.

In analogous ways, the sequence information given above and in the Figures can be used to design cloning strategies for the insertion of these genes and others into the non-essential genes of the HVT described here or to generating combinations of antigen genes in HVT.

EXAMPLE 10: MDV gD gene

Figure 15 shows part of the sequence of the MDV gD gene. The sequence was obtained by sequencing random fragments of the U_s

region MDV DNA and comparing the sequence to the sequence of known herpesvirus genes (see Buckmaster et al, loc. cit.). The sequence gave homology scores of 189 and 216 respectively with HSV gD and PRV gp50. The sequence information assists in the preparation of suitable probes to isolate and characterise the gene.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A nucleotide sequence substantially free of the sequences which would adjoin it in the wild-type virus associated with that sequence, the sequence being selected from the group consisting of:

(a) the MDV homologue of the HSV gB gene, or portions 816-863, 1377-1595, 1377-1630 or 1824-1985 of the said homologue,

(b) the MDV homologue of the HSV gH gene,

(c) the TK gene of MDV,

(d) the MDV homologue of the immediate early gene IE-175 of HSV-I,

(e) the MDV homologue of the immediate early gene IE-68 of HSV-I,

(f) the MDV homologue of the HSV gD gene, and portions 483-633, 843-933 or 1203-1278 of the MDV homologue of HSV gC

and minor variations thereof, as hereinbefore defined.

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2. A sequence according to Claim 1 comprising the coding portion of the said sequence and at least part of the 5' and/or 3' non-coding portions thereof.

3. A plasmid vector comprising a sequence according to Claim 1 or 2 (except sequence c) which is suitable for transfection of an MDV- or HVT-susceptible cell.

4. A hybrid viral vector comprising, as a heterologous insert, sequence (a), (b), (d), (e) or (f) of Claim 1 and suitable for transfection of an MDV or HVT-susceptible cell.

5. A viral vector according to Claim 4 wherein the sequence is inserted into a non-essential site of HVT.

6. A viral vector according to Claim 5 wherein the non-essential site is in the region homologous to the HSV gC gene or in the ribonucleotide reductase (large subunit) gene or the TK gene.

7. A peptide encoded by any one of sequences (a), (b) or (f) of Claim 1 or any of the said portions of sequence (a) or portions 483-633, 843-933 or 1203-1278 of the MDV homologue of HSV gC.

8. An MDV virus, mutated by virtue of being TK-.

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9. A vaccine comprising MDV-susceptible cells and a viral vector according to any one of Claims 4 to 6 or a mutant MDV virus according to Claim 8 such that the virus is attenuated, at least partially as a result of such mutation.

10. A method of vaccinating a fowl against a disease of that fowl comprising administering to the fowl a non-toxic immunity-conferring amount of vaccine according to Claim 9.

11. A fowl when vaccinated by a method according to Claim 10.

Dated this 7th day of May 1992

RHONE-MERIEUX S.A.
By their Patent Attorneys
GRIFFITH HACK & CO

AUSTRALIAN PATENT OFFICE

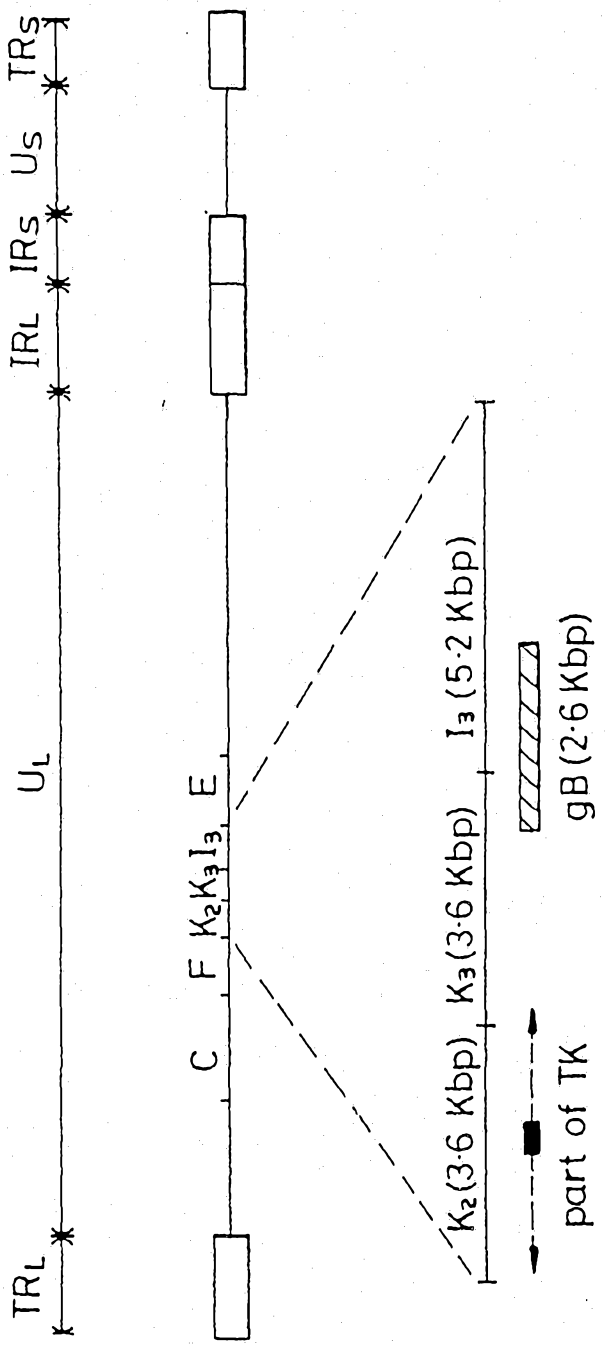
TRL
UL
IRL
IRS
US
TRS
C
F
K2
K3
I3
E
K2(3·6 Kbp)
K3(3·6 Kbp)
I3 (5·2 Kbp)
gB (2·6 Kbp)
part of TK
(400 bp)

Fig. 1

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FIG 2A

```
TCGAGCTCGCCGGGGATGTTTAGTCACGATAGACATCGGT
        10        20        30        40

TCGCCCAGCCGTCGAATACAGCATTATATTTTAGTGTTG
        50        60        70        80

AAAATGTAGGGCTGCTTCCTCACTTAAAGGAGGAAATGGCT
        90       100       110       120

CGATTCATGTTTCATAGCAGTAGAAAAACAGATTGGACCG
       130       140       150       160

TCAGTAAGTTTAGAGGGTTTTATGACTTTAGCACTATAGA
       170       180       190       200

TAATGTAACTGCGGCCCATCGCATGGCTTGGAAATATATC
       210       220       230       240

AAAGAACTGATTTTTGCAACAGCTTTATTTTCTTCTGTAT
       250       260       270       280

TTAAATGTGGCGAATTGCACATCTGTCGTGCCGACAGTTT
       290       300       310       320

GCAGATCAACAGCAATGGAGACTATGTATGGAAAAATGGA
       330       340       350       360
```

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FIG 2B

```
ATATATATAACATATGAAACCGAATATCCACTTATAATGA
      370        380        390        400

TTCTGGGGTCAGAATCAAGCACTTCAGAAACGCAAAATAT
      410        420        430        440

GACTGCAATTATTGATACAGATGTTTTTTCGTTGCTTTAT
      450        460        470        480

TCTATTTTGCAGTATATGGCCCCCGTTACGGCAGATCAGG
      490        500        510        520

TGCGAGTAGAACAGATTACCAACAGCCACGCCCCCATCTG
      530        540        550        560

ACCCGTCCAATATTCTTGTGTCCCTGCATTTTATCTCACA
      570        580        590        600

                                       M  H
CAATTTATGAACAGCATCATTAAGATCATCTCACTATGCA
      610        620        630        640

  Y  F  R  R  N  C  I  F  F  L  I  V  I
CTATTTTAGGCGGAATTGCATTTTTTTCCTTATAGTTATT
      650        660        670        680
```

FIG 2C

```
L  Y  G  T  N  S  S  P  S  T  Q  N  V  T
CTATATGGTACGAACTCATCTCCGAGTACCCAAAATGTGA
      690        700        710        720

   S  R  E  V  V  S  S  V  Q  L  S  E  E
CATCAAGAGAAGTTGTTTCGAGCGTCCAGTTGTCTGAGGA
      730        740        750        760

   E  S  T  F  Y  L  C  P  P  P  V  G  S
AGAGTCTACGTTTTATCTTTGTCCCCCACCAGTGGGTTCA
      770        780        790        800

 T  V  I  R  L  E  P  P  R  K  C  P  E  P
ACCGTGATCCGTCTAGAACCGCCGCGAAAATGTCCCGAAC
      810        820        830        840

   R  K  A  T  E  W  G  E  G  I  A  I  L
CTAGAAAAGCCACCGAGTGGGGTGAAGGAATCGCGATATTA
      850        860        870        880
```

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FIG 2D

```
        |-------------------------------------------
  F  K  E  N  I  S  P  Y  K  F  K  V  T
TTTAAAGAGAATATCAGTCCATATAAATTTAAAGTGACGC
        |||||||||||||| |||||||| ||||| || |
        GAGAATATCAGTCCGTATAAATTCAAAGTAACAC
        890       900       910       920

-----------------V-------------------------
L  Y  Y  K  N  I  I  Q  T  T  T  W  T  G
TTTATTATAAAAATATCATTCAGACGACGACATGGACGG
||||  |||||  ||   |  ||  ||  ||  |||||  |||||  |
TTTACTATAAGAACGTTATACAAACTACGACGTGGACTG
        930       940       950       960


-------------------------------------------
   T  T  Y  R  Q  I  T  N  R  Y  T  D  R
GGACGACATATAGACAGATCACTAATCGATATACAGATAG
|||||||  ||  ||||||||  |||||   |  ||||||||||
GGACGACGTACAGACAGATAACTAACAGGTATACAGATAG
        970       980       990       1000
```

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FIG 2E

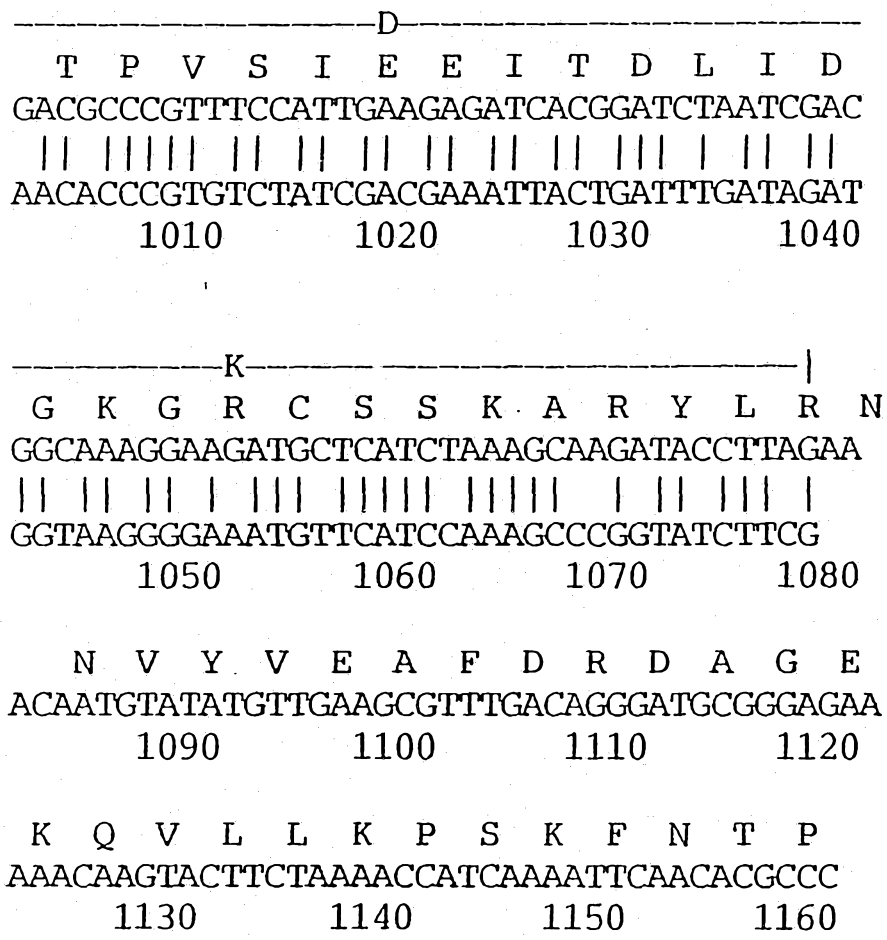

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FIG 2F

```
          |-------------------------------------
 E  S  R  A  W  H  T  T  N  E  T  Y  T  V
GAATCTAGGGCATGGCACACGACTAATGAGACGTATACCG
          ||||||||| |||||  || ||||||||  ||||
          GGCATGGCATACGACCAACGAGACGTACACCG
       1170       1180       1190       1200

--------------------V----------------------
   W  G  S  P  W  I  Y  R  T  G  T  S  V
TGTGGGGATCACCATGGATATATCGAACGGGAACCTCCGT
||||||||||  ||||||  |||||  |||||||  ||  |||||
TGTGGGGATCTCCATGGGTATATAGAACGGGCACGTCCGT
       1210       1220       1230       1240

-------------------------------------A-----
  N  C  I  V  E  E  M  D  A  R  S  V  F
CAATTGTATAGTAGAGGAAATGGATGCCCGCTCTGTGTTT
|||  ||  ||||||||  ||  |||||||||  |  ||  |  |||
CAACTGCATAGTAGAAGAGATGGATGCCAGATCAGCATTT
       1250       1260       1270       1280
```

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FIG 2G

```
--------T-----------------------------------------
 P  Y  S  Y  F  A  M  A  N  G  D  I  A  N
CCGTATTCATATTTTGCAATGGCCAATGGCGACATCGCGA
||  ||   |  ||  ||||||||||||||||||  ||  |||||  |
CCATACACGTACTTTGCAATGGCCAATGGAGATATCGCAA
      1290       1300       1310       1320

---M-------------------T--T-----T--D-------
   I  S  P  F  Y  G  L  S  P  P  E  A  A
ACATATCTCCATTTTATGGTCTATCCCCACCAGAGGCTGC
||||  |||||·||||||||||    |  |  |||  |  ||  ||  ||
ACATGTCTCCATTTTATGGAACAACTCCAACCGACGCGGC
      1330       1340       1350       1360

---------------S---------------R-----R-----
  A  E  P  M  G  Y  P  Q  D  N  F  K  Q
CGCAGAACCCATGGGATATCCCCAGGATAATTTCAAACAA
|||  ||  ||||||  |  |||||  ||  ||     ||||   |||
CGCGGAGCCCATGAGCTATCCGCAAGACCGATTCAGGCAA
      1370       1380       1390       1400
```

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FIG 2H

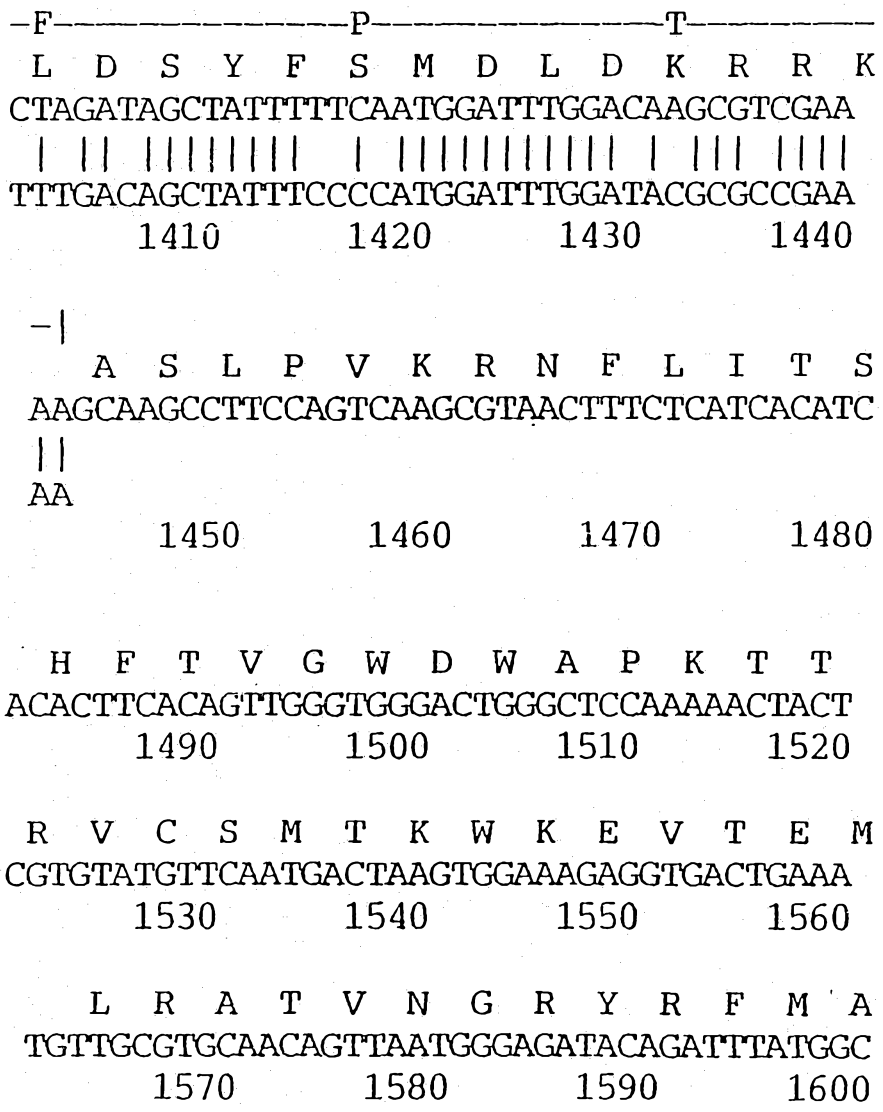

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FIG 2I

```
  R  E  L  S  A  T  F  I  S  N  T  T  E
CCGTGAACTTTCGGCAACGTTTATCAGTAATACGACTGAG
      1610       1620       1630       1640

  F  D  P  N  R  I  I  L  G  Q  C  I  K  R
TTTGATCCAAATCGCATCATATTAGGACAATGTATTAAAC
      1650       1660       1670       1680

     E  A  E  A  A  I  E  Q  I  F  R  T  K
 GCGAGGCAGAAGCAGCAATCGAGCAGATATTTAGGACAAA
      1690       1700       1710       1720

   Y  N  D  S  H  V  K  V  G  H  V  Q  Y
 ATATAATGACAGTCACGTCAAGGTTGGACATGTACAATA
      1730       1740       1750       1760

  F  L  A  L  G  G  F  I  V  A  Y  Q  P  V
TTTCTTGGCTCTCGGGGGATTTATTGTAGCATATCAGCCTG
      1770       1780       1790       1800

     L  S  K  S  L  A  H  M  Y  L  R  E  L
 TTCTATCCAAATCCCTGGCTCATATGTACCTCAGAGAATT
      1810       1820       1830       1840
```

SUBSTITUTE SHEET

FIG 2J

```
  M  R  D  N  R  T  D  E  M  L  D  L  V
GATGAGAGACAACAGGACCGATGAGATGCTCGACCTGGTA
      1850       1860       1870       1880

 N  N  K  H  A  I  Y  K  K  N  A  T  S  L
AACAATAAGCATGCAATTTATAAGAAAAATGCTACCTCAT
      1890       1900       1910       1920


    S  R  L  R  R  D  I  R  N  A  P  N  R
 TGTCACGATTGCGGCGAGATATTCGAAATGCACCAAATAG
       1930       1940       1950       1960
  K  I  T  L  D  D  T  T  A  I  K  S  T
AAAAATAACATTAGACGACACCACAGCTATTAAATCGACA
      1970       1980       1990       2000

 S  S  V  Q  F  A  M  L  Q  F  L  Y  D  H
TCGTCTGTTCAATTCGCCATGCTCCAATTTCTTTATGATC
      2010       2020       2030       2040

    I  Q  T  H  I  N  D  M  F  S  R  I  A
 ATATACAAACCCATATTAATGATATGTTTAGTAGGATTGC
       2050       2060       2070       2080
```

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FIG 2K

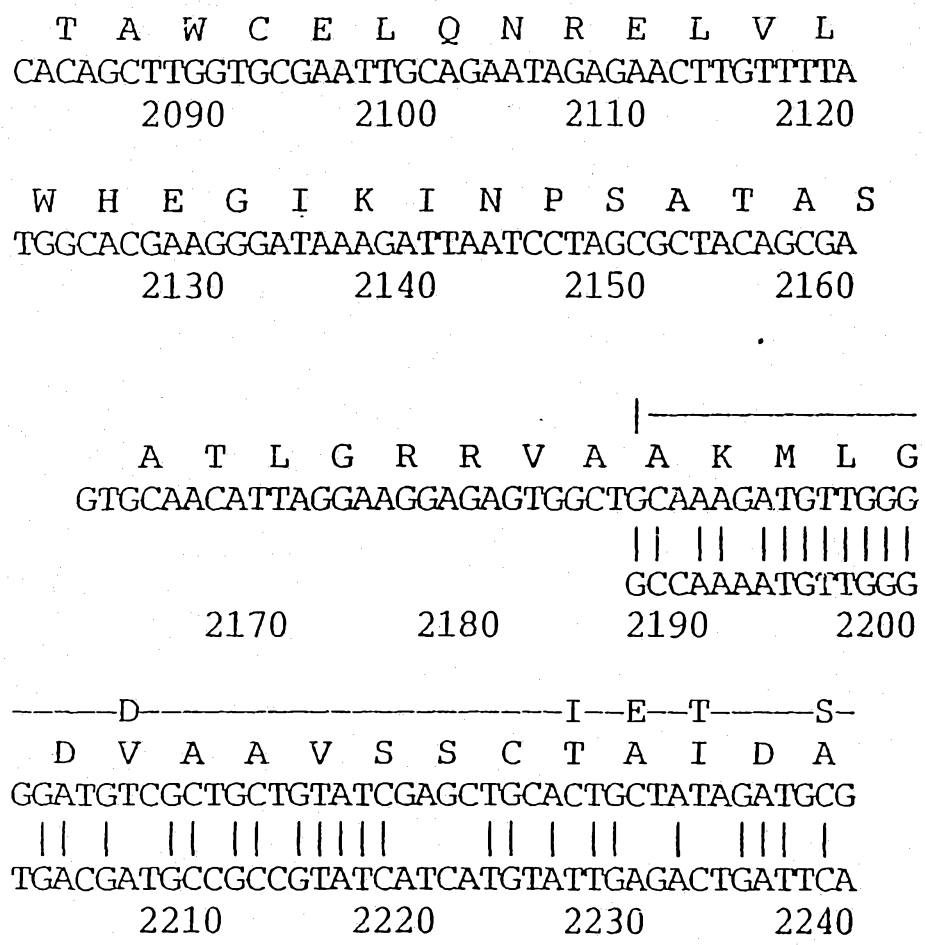

FIG 2L

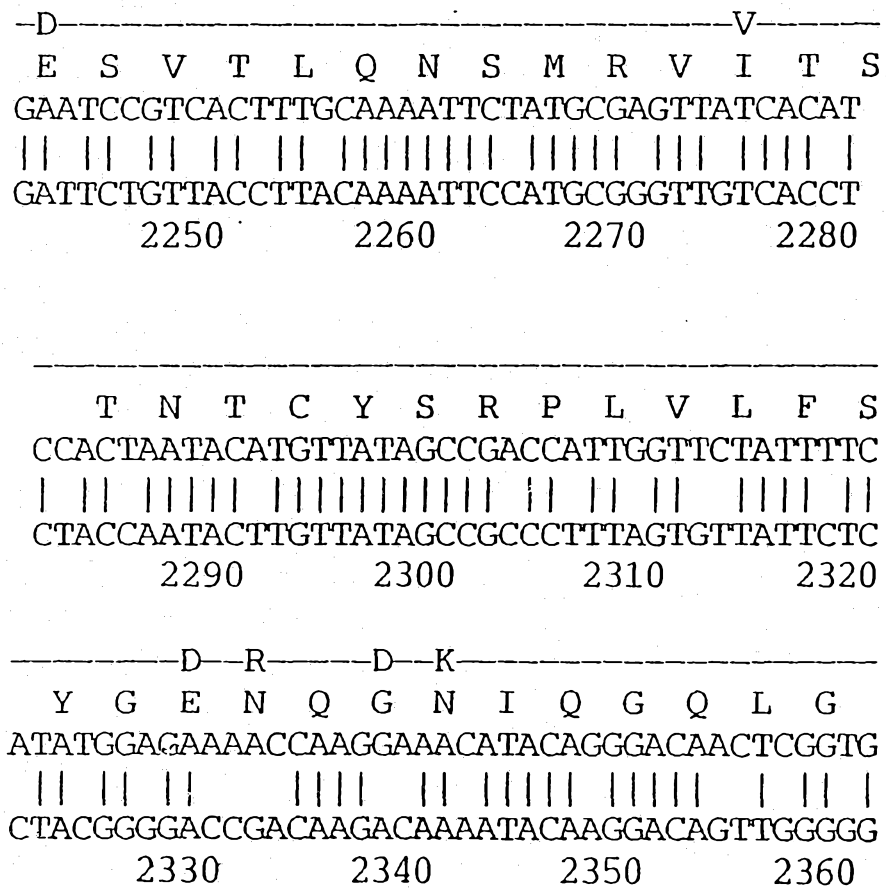

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FIG 2M

```
----------------I-----------------I------
E  N  N  E  L  L  P  T  L  E  A  V  E  P
AAAACAACGAGTTGCTTCCAACGCTAGAGGCTGTAGAGC
|||||||  ||  |||  |||||||  ||||||||  ||||||
AAAACAATGAATTGATTCCAACTCTAGAGGCCATAGAGC
     2370       2380       2390       2400

 ----------------------|
    C  S  A  N  H  R  R  Y  F  L  F  G  S
 CATGCTCGGCTAATCATCGTAGATATTTTCTGTTTGGATC
 ||||  |||||  ||||||||||||
 CATGTTCGGCCAATCATCGTAGA
       2410       2420       2430       2440

  G  Y  A  L  F  E  N  Y  N  F  V  K  M
CGGTTATGCTTTATTTGAAAACTATAATTTTGTTAAGATGG
      2450       2460       2470       2480

V  D  A  A  D  I  Q  I  A  S  T  F  V  E
TAGACGCTGCCGATATACAGATTGCTAGCACATTTGTCG
     2490       2500       2510       2520
```

4 FIG 2N

```
   L  N  L  T  L  L  E  D  R  E  I  L  P
AGCTTAATCTAACCCTGCTAGAAGATCGGGAAATTTTGCC
      2530       2540       2550       2560

  L  S  V  Y  T  K  E  E  L  R  D  V  G
TTTATCCGTTTACACAAAAGAAGAGTTGCGTGATGTTGGT
      2570       2580       2590       2600

 V  L  D  Y  A  E  V  A  R  R  N  Q  L  H
GTATTGGATTATGCAGAAGTAGCTCGCCGCAATCAACTAC
      2610       2620       2630       2640

   E  L  K  F  Y  D  I  N  K  V  I  E  V
ATGAACTTAAATTTTATGACATAAACAAAGTAATAGAAGT
      2650       2660       2670       2680

  D  T  N  Y  A  F  M  N  G  L  A  E  L
GGATACAAATTACGCGTTTATGAACGGTTTGGCCGAATTG
      2690       2700       2710       2720

 F  N  G  M  G  Q  V  G  Q  A  I  G  K  V
TTTAACGGTATGGGTCAGGTAGGGCAAGCTATAGGCAAAG
      2730       2740       2750       2760
```

FIG 2Ø

```
    V  V  G  A  A  G  A  I  V  S  T  I  S
TTGTAGTAGGGGCTGCCGGTGCAATCGTATCTACCATATC
      2770       2780       2790       2800

  G  V  S  A  F  M  S  I  P  L  G  L  S
TGGTGTCTCTGCTTTCATGTCAATCCCTTTGGGGCTTTCG
      2810       2820       2830       2840

 A  I  G  L  I  I  I  A  G  L  V  A  A  F
GCAATCGGTTTAATCATTATAGCAGGACTCGTGGCTGCAT
      2850       2860       2870       2880


    L  A  Y  R  Y  V  N  K  L  K  S  N  P
TTTTAGCATATCGTTATGTAAACAAGCTTAAAAGCAATCC
      2890       2900       2910       2920

  M  K  A  L  Y  P  M  T  T  E  V  L  K
AATGAAAGCCCTTTATCCTATGACAACAGAAGTGCTTAAG
      2930       2940       2950       2960

 A  Q  A  T  R  E  L  H  G  E  E  S  D  D
GCACAGGCAACGCGTGAGTTGCATGGCGAGGAATCAGATG
      2970       2980       2990       3000
```

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FIG 2P

```
    L  E  R  T  S  I  D  E  R  K  L  E  E
ATTTGGAACGAACATCTATTGATGAAAGAAAATTAGAAGA
      3010       3020       3030       3040

  A  R  E  M  I  K  Y  M  A  L  V  S  A
AGCTAGAGAAATGATAAAATATATGGCGTTAGTCTCCGCG
      3050       3060       3070       3080

 E  E  R  H  E  K  K  L  R  R  K  R  R  G
GAAGAACGCCACGAGAAAAAACTGCGGAGAAAGAGGCGAG
      3090       3100       3110       3120
    T  T  A  V  L  S  D  H  L  A  K  M  R
 GCACTACCGCCGTTCTATCGGACCACCTGGCAAAAATGAG
      3130       3140       3150       3160

  I  K  N  S  N  P  K  Y  D  K  L  P  T
GATTAAAAATAGTAACCCTAAATATGATAAGTTACCTACT
      3170       3180       3190       3200

 T  Y  S  D  S  E  D  D  A  V  *
ACATATTCAGACTCAGAAGATGATGCTGTGTAAGTGGGCA
      3210       3220       3230       3240

 CTATTATATTTGAACTGAATAAAACGCATAGAGCATGATA
      3250       3260       3270       3280
```

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FIG 2Q

TGGTTTACTCATTTATTGCGAGATATAAAGCATATTCAAT
3290 3300 3310 3320

ACGATATATTGCGAACGTGATGCTAAAAACATAGCTCCCT
3330 3340 3350 3360

GTATTATTGATGCGCCATCATTTGATTAATAAATACATCG
3370 3380 3390 3400

ACGCCGGCATCACTGGTGCGGTGTATACCAGCTACGGCGC
3410 3420 3430 3440

TAGCATTCATGGTATCCCGTGATTGCTCGATGCTTTCCTT
3450 3460 3470 3480

CTGAATTCCGTCGGAACGCTCCTGAGAGATGGTCGCAGTT
3490 3500 3510 3520

ATTGGTACATTTCGACCAGCCTCCGGATCTGAAACTGGCA
3530 3540 3550 3560

CAGGAATGCACCGTGGAATTGGTAGAAGTTTTTCCTTCCG
3570 3580 3590 3600

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FIG 2R

TGGAAGGCATAGGGCGTTCGACTCCCATGGGCCATGAAACTGTGGGATGT
3610 3620 3630 3640 3650

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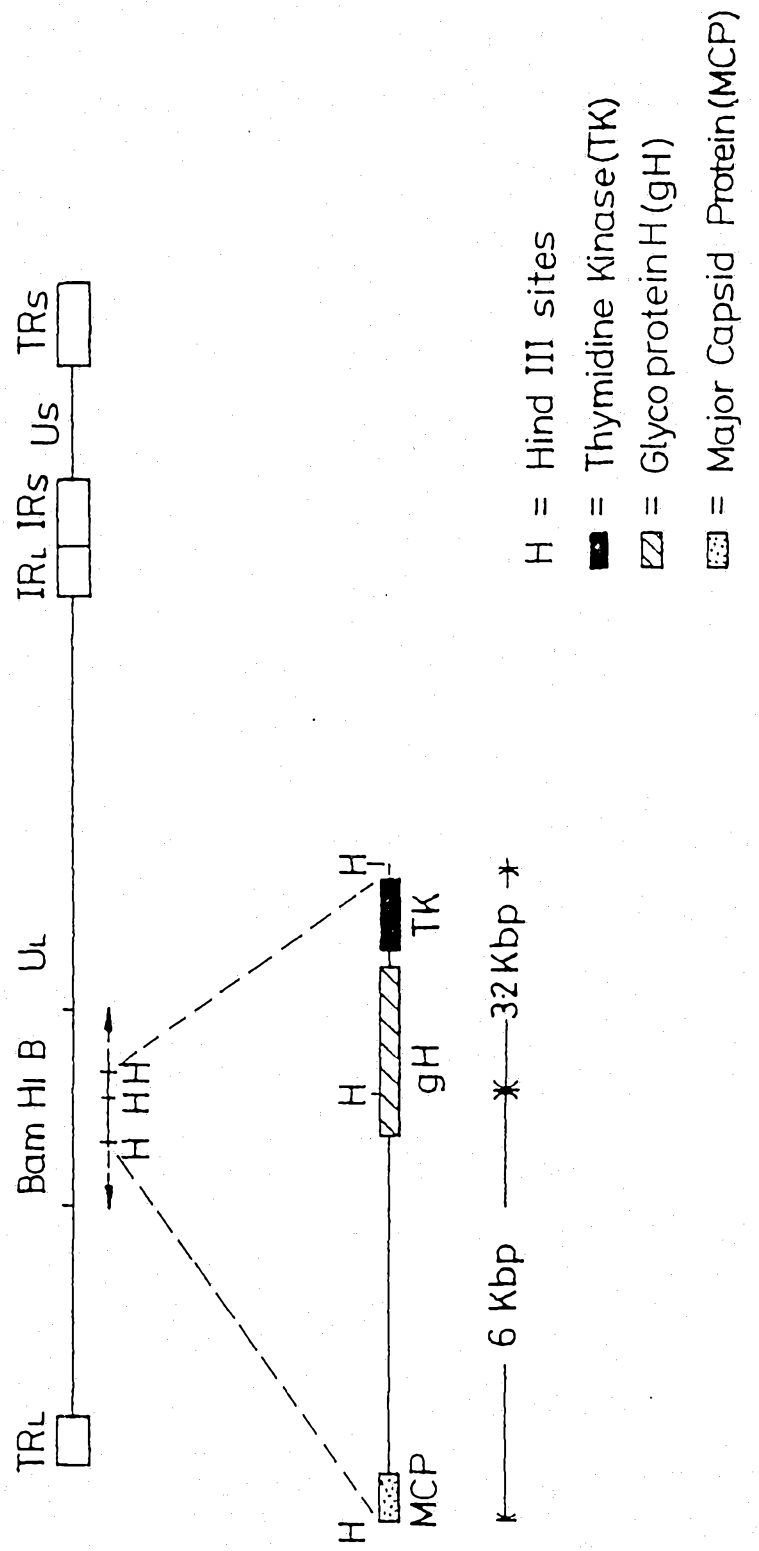
TRL
UL
IRL
IRS
US
TRS
Bam HI B
H HH
H
gH
TK
MCP
6 Kbp
3.2 Kbp
H = Hind III sites
= Thymidine Kinase (TK)
= Glyco protein H (gH)
= Major Capsid Protein (MCP)

Fig. 3

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FIG 4A

```
 TATTATTGGTCCATGCTAGAATAGTCATACGCTACGATCT
          10        20        30        40

GTTGCTATATATGACTATCGCCAAACTGTTAAACCCGCGA
          50        60        70        80

AGAATATATTTCATATAAACCTAAGGGCCCCTCAGTCTGA
          90       100       110       120

                                M  K  F  Y  C  L
 TTTTTTGTGAAAACGTGTATACCATGAAGTTTTACTGCCT
         130       140       150       160

  I  R  F  M  I  I  A  N  L  Y  S  S  Y
AATCCGTTTCATGATCATAGCGAATCTTTATTCATCTTAC
         170       180       190       200

 Q  I  S  L  P  G  T  Y  P  S  Q  I  L  L
CAAATATCGCTTCCAGGCACATATCCATCGCAAATATTGC
         210       220       230       240

    D  M  K  N  S  P  L  V  R  F  N  I  S
 TTGACATGAAGAACTCGCCGCTCGTACGCTTTAATATATC
         250       260       270       280
```

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FIG 4B

```
  T   R   D   Y   K   D   E   T   L   W   I   R   K
GACGCGTGATTATAAAGACGAGACACTCTGGATACGGAAA
        290         300         310         320

  N   S   T   F   V   Y   I   D   T   A   V   T   T   A
AATTCGACATTTGTTTATATCGATACGGCTGTGACGACAG
        330         340         350         360

    N   V   I   F   Y   L   P   I   G   Q   V   R   Q
 CGAACGTTATCTTTTATCTGCCGATCGGTCAGGTACGACA
        370         380         390         400

  M   V   F   F   K   R   P   I   S   R   L   L   T
AATGGTTTTTTTCAAGCGTCCAATATCCAGGCTACTAACG
        410         420         430         440

  S   N   N   L   V   K   F   I   N   T   G   S   Y   A
TCCAATAACCTGGTTAAATTTATT[illegible]ATACCGGTTCATACG
        450         460         470         480

    N   H   T   F   K   T   E   L   S   P   Y   L   S
 CCAATCATACATTCAAGACAGAACTTTCACCCTATTTGTC
        490         500         510         520
```

FIG 4C

```
  K   T   N   T   P   L   K   K   Y   E   I   V   V
GAAAACCAATACACCGTTGAAGAAATATGAAATTGTTGTC
        530         540         550         560

 D   Q   P   T   G   E   N   P   P   A   G   F   G   S
GATCAACCTACTGGAGAAAACCCTCCGGCAGGGTTCGGAA
        570         580         590         600

    L   K   P   A   D   F   L   N   P   G   Y   K   F
 GTTTAAAACCGGCAGACTTTCTCAACCCCGGATACAAGTT
        610         620         630         640

  V   L   T   S   E   L   V   G   A   Y   T   K   R
CGTTCTCACAAGCGAGTTGGTAGGAGCCTACACAAAACGA
        650         660         670         680

 S   C   F   V   D   P   M   D   S   L   V   P   I   D
TCTTGTTTTGTCGATCCGATGGATTCTCTCGTCCCGATAG
        690         700         710         720

    Y   D   H   V   R   T   I   I   F   G   S   A   G
 ATTATGATCATGTACGAACCATTATATTCGGATCTGCTGG
        730         740         750         760
```

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4

FIG 4D

```
  M   E   I   L   M   K   M   G   I   T   L   A   S
GATGGAGATTTTAATGAAGATGGGAATTACTTTGGCATCT
       770         780         790         800

  M   T   I   S   T   K   Y   N   P   P   I   E   L   I
ATGACCATTTCGACGAAATATAATCCTCCTATTGAACTGA
       810         820         830         840

    I   S   A   K   Y   R   N   L   S   L   L   W   P
 TAATATCTGCAAAGTACCGAAATTTATCACTGTTGTGGCC
       850         860         870         880

  P   R   Q   Q   Y   E   P   V   N   K   G   T   G
ACCCCGACAACAATATGAACCTGTAAATAAAGGGACTGGA
       890         900         910         920

  R   P   H   W   I   Y   L   L   G   V   Y   R   N   V
CGCCCCCATTGGATCTACCTATTAGGTGTGTATAGAAACG
       930         940         950         960

    S   D   S   E   R   D   S   Y   M   N   M   I   K
 TTTCGGACTCCGAGCGTGACTCATACATGAATATGATTAA
       970         980         990        1000
```

FIG 4E

```
  S   L   G   D   S   M   D   Y   H   F   L   I   S
GAGTCTGGGCGATTCTATGGATTATCACTTCCTAATTAGC
      1010        1020        1030        1040

  R   A   H   A   Q   M   L   I   L   A   A   E   D   R
AGAGCGCATGCCCAGATGCTGATACTGGCAGCAGAGGACC
      1050        1060        1070        1080

    L   V   D   E   M   H   S   F   R   N   V   I   A
 GGCTCGTGGATGAAATGCATAGTTTCAGGAACGTTATTGC
      1090        1100        1110        1120

  R   L   F   V   S   L   F   A   F   I   R   N   A
GCGTTTATTTGTATCGTTGTTCGCATTCATACGTAACGCA
      1130        1140        1150        1160

  F   Q   S   G   Y   T   S   L   N   D   I   I   E   I
TTTCAGTCTGGCTACACCTCTCTTAATGACATAATTGAAA
      1170        1180        1190        1200

    E   A   D   L   R   L   I   V   E   G   I   S   S
 TCGAAGCCGATTTGAGGTTAATTGTAGAAGGCATTTCTTC
      1210        1220        1230        1240
```

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FIG 4F

```
  A  A  F  R  K  D  A  S  T  H  F  L  I
TGCTGCATTTCGTAAAGACGCTAGTACACACTTTCTTATA
      1250       1260       1270       1280

 S  G  T  P  I  K  D  S  K  A  D  L  I  K
TCGGGAACGCCCATAAAAGATAGCAAAGCGGATTTAATTA
      1290       1300       1310       1320

    S  L  L  S  K  V  I  R  P  I  S  G  H
 AATCGTTGTTGTCTAAAGTCATTCGACCAATTTCCGGACA
      1330       1340       1350       1360

  T  R  P  L  S  A  I  Q  H  L  F  L  L
TACACGTCCCTTATCTGCGATACAACATCTATTCCTTTTG
      1370       1380       1390       1400

 R  S  A  Y  A  L  D  I  P  R  Q  N  G  S
AGATCCGCTTATGCATTGGATATACCCCGTCAAAACGGAT
      1410       1420       1430       1440

    L  S  E  Q  V  S  T  V  A  L  S  F  I
 CTTTGAGCGAACAGGTATCTACAGTGGCACTGTCGTTCAT
      1450       1460       1470       1480
```

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FIG 4G

```
  E  N  I  H  S  E  A  M  R  D  I  L  S.
TGAAAATATTCACAGCGAGGCCATGAGGGACATTCTGTCA
      1490       1500       1510       1520

 W  N  T  T  T  K  H  A  L  Y .Y  A  F  A
TGGAACACTACAACAAAGCATGCGTTGTATTATGCATTCG
      1530       1540       1550       1560

    S  I  L  Q  R  P  L  T  E  W  G  A  S
 CGAGTATTTTGCAACGGCCACTGACCGAATGGGGCGCCTC
      1570       1580       1590       1600

  R  N  A  R  R  A  I  L  L  A  S  S  M
AAGAAATGCACGGAGGGCAATACTATTAGCATCATCGATG
      1610       1620       1630       1640

 C  T  E  E  H  V  I  A  T  E  L  A  I  Q
TGTACAGAAGAGCATGTTATCGCAACTGAGTTGGCTATTC
      1650       1660       1670       1680

    E  L  Y  V  K  I  R  S  N  A  D  P  I
 AAGAACTGTATGTCAAAATCAGAAGTAATGCCGACCCAAT
      1690       1700       1710       1720
```

FIG 4H

```
  H   L   L   D   V   Y   T   P   C   L   S   S   L.
ACACCTTCTAGACGTATATACACCATGTCTTTCTTCACTA
      1730        1740        1750        1760

 R   L   D   L   S   E   H   H   R   I   Y   A   M   A
CGATTGGACCTTTCCGAACACCATCGGATATACGCAATGG
      1770        1780        1790        1800

    D   V   V   F   Y   P   D   I   Q   Q   Y   L   K
 CAGATGTAGTTTTCTATCCAGACATTCAGCAGTATTTGAA
       1810        1820        1830        1840

  K   K   S   H   E   G   N   M   K   E   D   D   L
AAAAAAATCCCATGAGGGTAATATGAAGGAAGATGATCTC
      1850        1860        1870        1880

 E   T   K   A   E   Y   I   L   T   K   L
GAAACAAAGGCGGAATACATCCTCACCAAGCTT
      1890        1900        1910
```

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FIG 5A

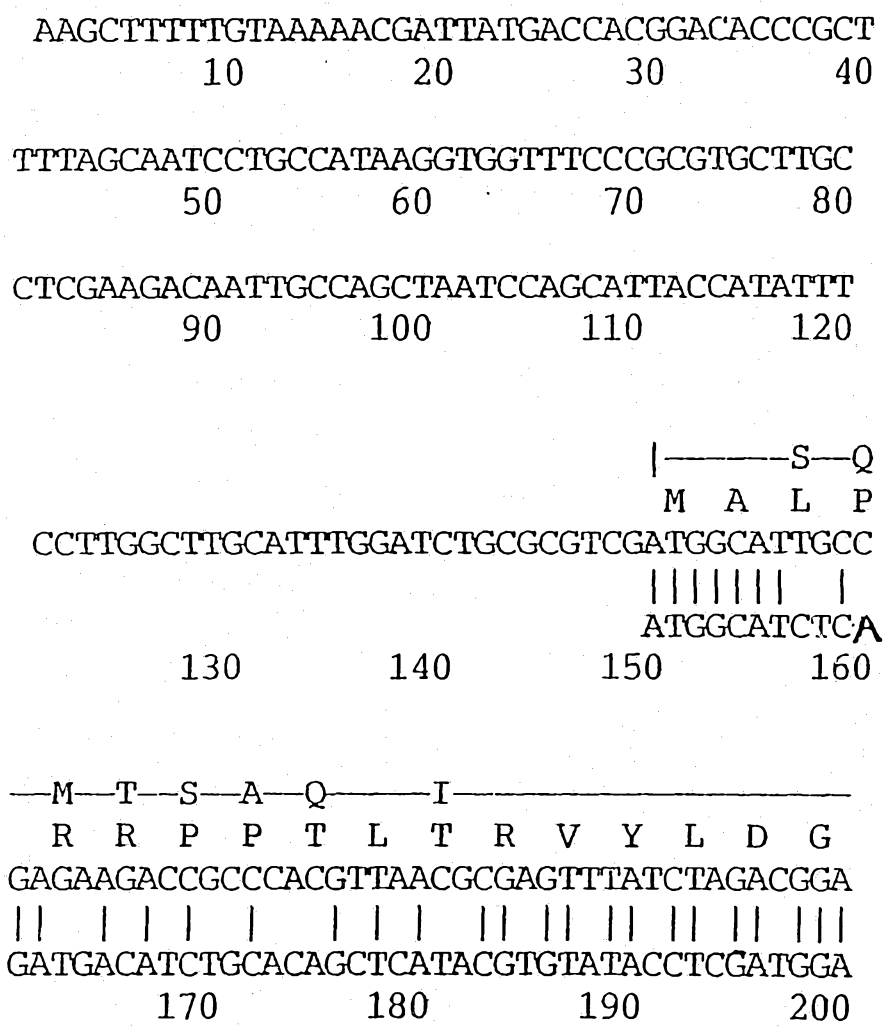

FIG 5B

```
-S--M--------------------M---------E--I--
 P  F  G  I  G  K  T  S  I  L  N  A  M  P
CCGTTTGGTATAGGCAAAACGTCTATACTAAACGCTATGC
 |  | |||||||| |||||||| ||  | || |  || |
TCAATGGGTATAGGTAAAACGTCAATGTTGAATGAGATAC
       210       220       230       240

---T-----L|
   D  H  T  P  D  G  A  P  I  L  K  V  Y
CCGACCACACGCCCGATGGGGCTCCTATATTGAAAGTGTA
|   ||
CGACGCATCTT
       250       260       270       280

  E  P  M  K  Y  W  R  C  Q  S  T  D  L
CGAACCAATGAAATATTGGAGATGCCAGTCTACCGATTTG
       290       300       310       320
```

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FIG 5C

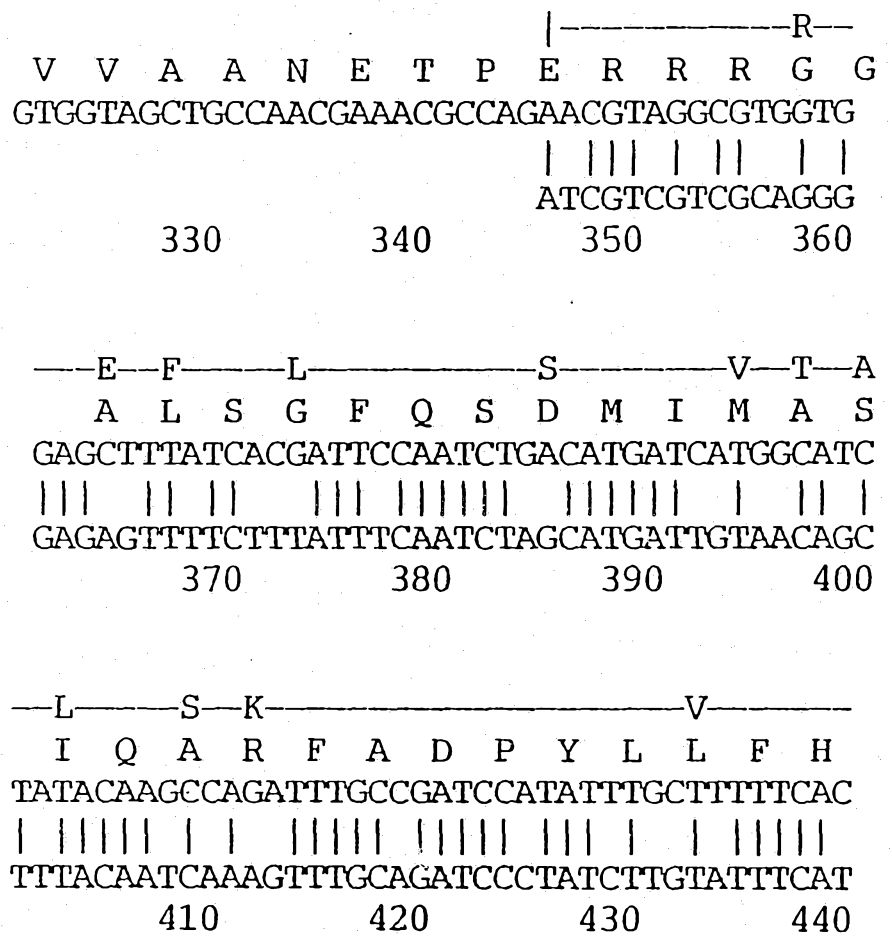

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FIG 5D

```
----------H--R--I--T--G--T--R
 E  R  L  S  S  K  C  R  G  K  I  E  I  C
GAACGGTTATCATCTAAATGTAGAGGAAAAATAGAAATAT
||  ||  |||||  ||  ||  |||     |  |  ||  ||  ||  |
GAGCGCTTATCGTCGAAGTGTCATCGCATAACAGGAACAC
        450        460        470        480

---G--N-----S--L--------I----------------
    D  T  P  A  I  I  L  M  L  D  R  H  P
GCGATACTCCAGCAATTATATTAATGCTGGATAGGCACCC
|  |   |  ||||  |  ||||||||||  ||  |||  |  ||  ||
GTGGCAATCCATCGCTTATATTAATTCTAGATCGACATCC
        490        500        510        520

--I--S-----T--V--------------A-----H----
  V  A  A  I  L  C  F  P  I  T  R  Y  L
TGTGGCGGCGATATTATGTTTCCCAATCACTCGCTATTTA
  |  |  ||  |   ||||||  ||  ||  ||||  |||||
CATATCCGCTACCGTATGTTTTCCCATTGCTCGACATTTA
        530        540        550        560
```

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FIG 5E

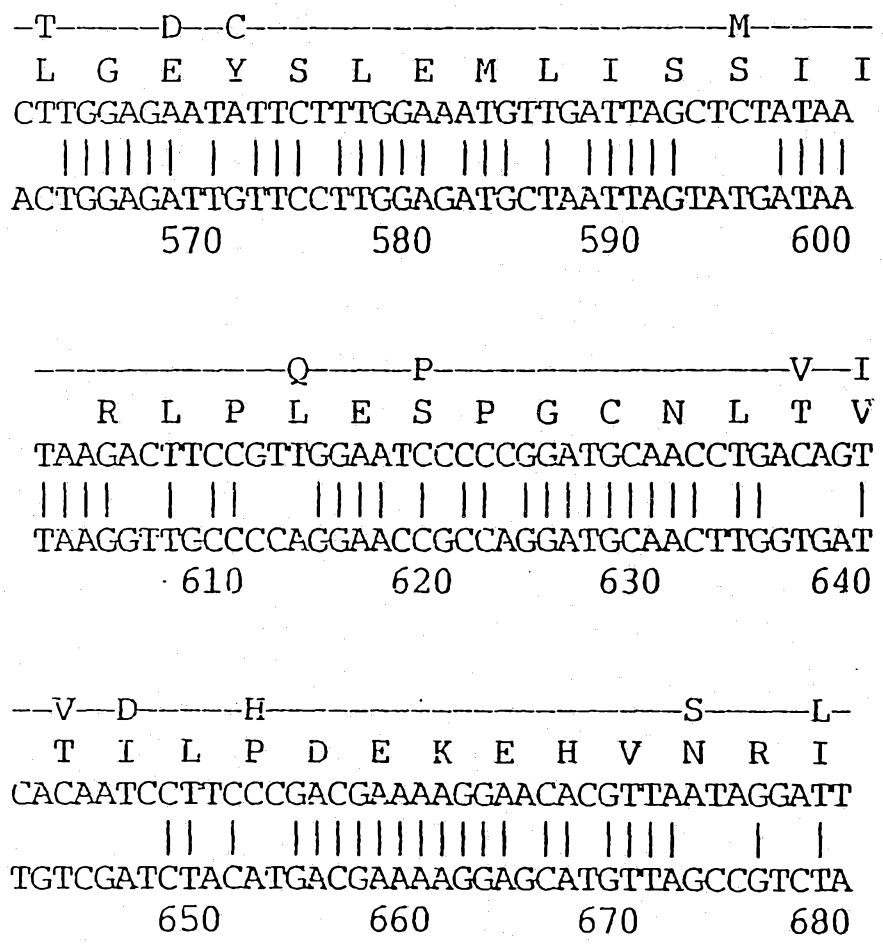

FIG 5F

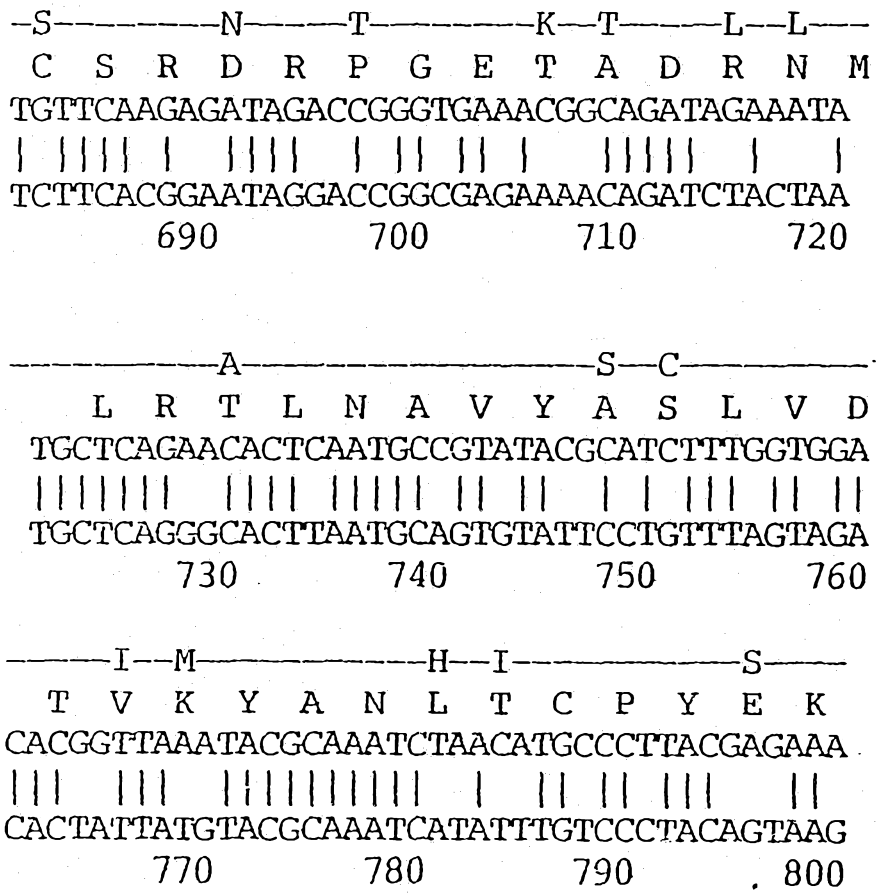

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FIG 5G

```
-D--E---------S----------D---------------D
 E  S  W  E  M  E  W  L  G  L  P  W  F  E
GAAAGCTGGGAAATGGAATGGTTGGGACTTCCCTGGTTTG
||    ||||||   ||||||||||  || || |||||||
GATGAATGGGAATCTGAATGGTTGGATCTACCATGGTTTG
       810        820        830        840

 ---T---------A--T--T---------N--E---------T
    E  S  L  L  E  E  F  I  S  R  P  R  P
 AAGAGTCATTACTTGAAGAATTCATCTCGCGCCCCCGCCC
 |    || ||       |   || ||       || ||  |
 ATACATCTTTGGCCACAACGTTTATAAACGAACCTCGTAC
       850        860        870        880

--...D--Y--R--G--S------V--S------H--H-----
  V  I  C  S  R  T  R  M  P  L  D  R  T
TGTTATTTGTTCGAGAACTCGAATGCCGCTGGACCGAACT
||    || |    | | | |  || |  |  |||  ||
TG...ATTATCGCGGTAGTAGGGTGTCATTACACCATACG
       890        900        910        920
```

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FIG 5H

```
——————————————————————R——————————|
 L  L  A  I  F  K  R  K  E  L  C  S  E  N
CTCCTGGCCATTTTTAAACGGAAAGAGCTGTGTAGCGAAA
||  | || || ||||| |||  |||  | |
CTTTTAGCGATATTTAAGCGGCGAGAATTATGT
       930       940       950       960

   G  E  L  L  T  Q  Y  S  W  I  L  W  G
 ATGGGGAGCTGTTAACTCAGTATTCTTGGATATTGTGGGG
       970       980       990      1000

  L  L  T  K  L  H  T  I  N  V  E  L  F
 ATTACTGACTAAACTACACACCATTAATGTCGAATTATTT
      1010      1020      1030      1040

                           |——V——E——L——L
 D  I  S  G  M  S  R  R  E  C  A  S  A  I
GACATTAGCGGTATGTCACGTCGAGAATGCGCCAGCGCTA
                           || |
                           TGTGTAGAACTGC
      1050      1060      1070      1080
```

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FIG 5I

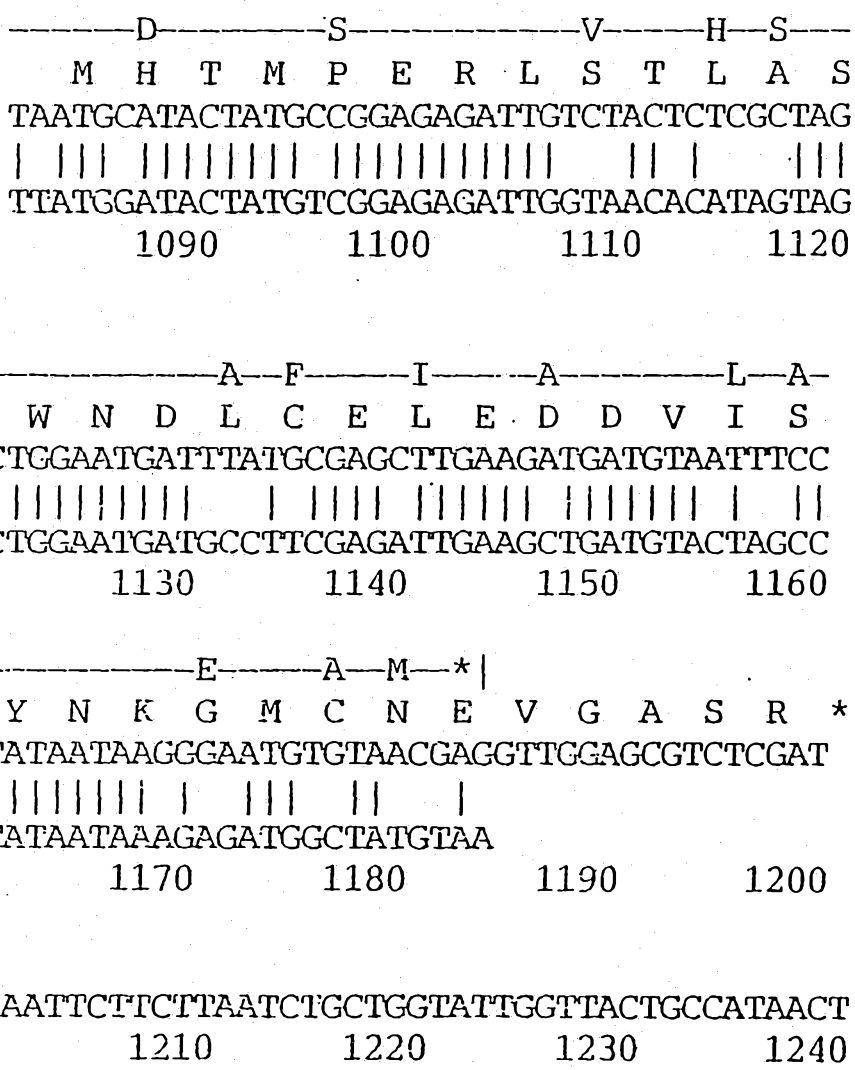

FIG 5J

TATTATTGGTCCATGCTAGAATAGTCATACGCTACGATCT
1250 1260 1270 1280

GTTGCTATATATGACTATCGCCAAACTGTTAAACCCGCGA
1290 1300 1310 1320

AGAATATATTTCATATAAACCTAAGGGCCCCTCAGTCTGA
1330 1340 1350 1360

TTTTTTGTGAAAACGTGTATACCA
1370 1380

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FIG 6A

```
      1 CAGCTGCCTATGTAGTGAAATCTATACTGGGATTT

ATCATAACTAGTTTACTTGTTTGTATATTAGTAGCGCTATCT

TGACCAAATCGTTGTTCACATCTTGGCCATATACGTATTGATC

    121 GTTGTTTCGAACCGCGAATAAAACTTTCATACATAC

TAAACGATGGAGTTGTGTTTTATGAGCGTTGAAAACAAAGGT

ACCATCGGTTTAAAACTAAGTTGCATATCGTAATCCACAAAA


    241 ATCATTTTATACATCATCCCGAAGAGACACCAAACG

                              M  L  T  P  R  V
TAACCCTCTACATATCTTCCCTCATGCTCACGCCGCGTGTGT

L  R  A  L  G  W  T  G  L  F  F  L  L  L  S
TACGAGCTTTGGGGTGGACTGGACTCTTTTTTTTGCTTTTAT

            P  S  N  V  L  G  A  S  L  S  R
    361 CTCCGAGCAACGTCCTAGGAGCCAGCCTTAGCCGG

 D  L  E  T  P  P  F  L  S  F  D  P  S
GATCTCGAAACACCCCCATTTCTATCCTTTGATCCATCCA
```

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FIG 6B

```
N  I  S  I  N  G  A  P  L  T  E  V  P  H  A  P
ACATTTCAATTAACGGCGCGCCTTTAACTGAGGTACCTCATGCAC

         S  T  E  S  V  S  T  N  S  E  S  T
  481 CTTCCACAGAAAGTGTGTCAACAAATTCGGAAAGTACC

 N  E  H  T  I  T  E  T  T  G  K  N  A  Y
AATGAACATACCATAACAGAAACGACGGGCAAGAACGCATACA

I  H  N  N  A  S  T  D  K  Q  N  A  N  D
TCCACAACAATGCGTCTACGGACAAGCAAAATGCGAACG

         T  H  K  T  P  N  I  L  C  D  T  E
  601 ACACTCATAAAACGCCCAATATACTCTGCGATACGGA

  E  V  F  V  F  L  N  E  T  G  R  F  V  C
AGAAGTTTTTGTTTTCCTTAACGAAACGGGAAGATTTGTTTGT

 T  L  K  V  D  P  P  S  D  S  E  W  S  N
ACTCTCAAAGTCGACCCCCCCTCGGATAGTGAATGGTCCA

         F  V  L  D  L  I  F  N  P  I  E  Y
  721 ACTTTGTTCTAGATCTGATCTTTAACCCAATTGAATA

  H  A  N  E  K  N  V  E  A  A  R  I  A  G
CCACGCCAACGAAAAGAATGTGGAAGCGGCGCGTATCGCTGGT
```

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FIG 6C

```
 L  Y  G  V  P  G  S  D  Y  A  Y  P  R  Q
CTCTATGGAGTCCCCGGATCAGACTATGCATACCCACGTC

        S  E  L  I  S  S  I  R  R  D  P
 841 AATCTGAATTAATTTCTTCGATTCGACGAGATCCCC

Q  G  T  F  W  T  S  P  S  P  H  G  N  K
AGGGCACATTTTGGACGAGCCCATCACCTCATGGAAACAA

  Y  F  I  W  I  N  K  T  T  N  T  M  G  V  E
GTACTTCATATGGATAAACAAAACAACCAATACGATGGGCGTGG

        I  R  N  V  D  Y  A  D  N  G  Y
 961 AAATTAGAAATGTAGATTATGCTGATAATGGCTAC

 M  Q  V  I  M  R  D  H  F  N  R  P  L
ATGCAAGTCATTATGCGTGACCATTTTAATCGGCCTTTAA
I  D  K  H  I  Y  I  R  V  C  Q  R  P  A  S  V

TAGATAAACATATTTACATACGTGTGTGTCAACGACCTGCATCAG

        D  V  L  A  P  P  V  L  S  G  E  N
1081 TGGATGTACTGGCCCCTCCAGTCCTCAGCGGAGAAAA

  Y  K  A  S  C  I  V  R  H  F  Y  P  P  G
TTACAAGGCATCTTGTATCGTTAGACACTTTTATCCCCCTGGA
```

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FIG 6D

```
 S  V  Y  V  S  W  R  Q  N  G  N  I  A  T
TCTGTCTATGTATCTTGGAGACAGAATGGAAACATTGCAA

          P  R  K  D  R  D  G  S  F  W  W  F
1201 CTCCTCGGAAAGATCGCGATGGAAGTTTTTGGTGGTT

 E  S  G  R  G  A  T  L  V  S  T  I  T  L
CGAATCTGGTAGAGGAGCTACGTTGGTTTCTACAATAACATTG

 G  N  S  G  I  D  F  P  P  K  I  S  C  L
GGAAATTCAGGAATTGATTTCCCCCCCAAAATATCTTGTC

          V  A  W  K  Q  G  D  M  I  S  T  T
1321 TGGTTGCCTGGAAGCAGGGTGATATGATCAGCACGAC

 N  A  T  A  I  P  T  V  Y  H  H  P  R  L
GAATGCCACAGCTATCCCGACGGTATATCATCATCCCCGTTTA

 S  L  A  F  K  D  G  Y  A  I  C  T  I  E
TCCCTGGCTTTTAAAGATGGGTATGCAATATGTACTATAG

          C  V  P  S  E  I  T  V  R  W  L  V
1441 AATGTGTCCCCTCTGAGATTACTGTACGGTGGTTAGT

 H  D  E  A  Q  P  N  T  T  Y  N  T  V  V
ACATGATGAAGCGCAGCCTAACACAACTTATAATACTGTGGTT
```

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FIG 6E

```
 T  G  L  C  R  T  I  D  R  H  R  N  L  L
ACAGGTCTCTGCCGGACCATCGATCGCCATAGAAATCTCC

          S  R  I  P  V  W  D  N  W  T  K  T
1561 TCAGCCGCATTCCAGTATGGGACAATTGGACGAAAAC

  K  Y  T  C  R  L  I  G  Y  P  F  D  E  D
AAAATATACGTGCAGACTCATAGGCTACCCCTTCGATGAAGAT

  K  F  Q  D  S  E  Y  Y  D  A  T  P  S  A
AAATTTCAAGATTCGGAATATTACGATGCAACTCCATCTG

          R  G  T  P  M  V  I  T  V  T  A  V
1681 CAAGAGGAACACCCATGGTTATTACGGTTACGGCAGT

  L  G  L  A  V  I  L  G  M  G  I  I  M  T
TTTGGGATTGGCTGTAATTTTAGGGATGGGGATAATCATGACT

  A  L  C  L  Y  N  S  T  R  K  N  I  R  L
GCCCTATGTTTATACAACTCCACACGAAAAAATATTCGAT

          *
1801 TATAATCTCATTGTTATGTAGTTGTGATTTATTAAAC

ATATTTTTTATAACTCTAGTATTCTCCGAGTACTTATATATT
```

FIG 6F

TATTTGTCAGACAATAATGCAATAGTGGAGAAACGTGAGG

1921 GGAGTCTGTAAACAGAATACGTATAATCATCTATTTG

AATAAAAGATTGTGGTATAAATGAAGATAGCGCAAGTCATTC

CAAGCTCTCCATTCTATTTAAACAATGTACAGTTTAAAGT

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FIG 7

HVT HOMOLOGUES OF VZV62/ HSV-1 IE 175

```
  S  N  V  V  R  Y  M  C  G  N  T  V  L
 TCGAATGTGGTGCGATACATGTGCGGGAACACGGTACTCC
         10        20        30        40

P  P  D  P  H  G  T  P  V  V  I  N  V  P
CCCCGGATCCCCATGGCACCCCCGTGGTGATCAACGTTCC
         50        60        70        80

  E  G  T  S  E  T  M  A  E  L  T  V  A
CGAGGGAACGTCCGAAACTATGGCGGAGCTTACTGTTGCT
         90        100       110       120

  H  V  G  R  K  S  I  G  W  P  T  S  E
 CACGTTGGGCGCAAGTCTATTGGGTGGCCGACCTCCGAGT
         130       140       150       160

W  H  S  A  T  I  L  Q  K  D  N  D  S  R  L  V  I  I  R
GGCATTCCGCTACAATCCTGCAGAAAGATAATGATAGTCGGCTGGTAATTATACGCC
        170       180       190       200       210
```

FIG 8

HVT HOMOLOGUE OF RIBONUCLEOTIDE REDUCTASE (LARGE SUBUNIT)

```
  Q  V  T  E  V  S  E  G  F  A  P  L  F
 CAAGTGACCGAGGTTAGCGAAGGATTTGCCCCTTTGTTCA
          10         20         30         40

S  N  M  F  S  K  V  T  S  A  G  E  L  L
GTAACATGTTCAGCAAGGTGACAAGTGCCGGGGAACTGCT
          50         60         70         80

  R  P  N  S  Q  L  M  R  E  L  R  Q  I
TAGACCCAACAGTCAATTAATGCGGGAGCTGAGACAAATA
          90         100        110        120

  Y  P  D  N
 TATCCCGATAAT
          130
```

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FIG 9A

MDV HOMOLOGUE OF RIBONUCLEOTIDE REDUCTASE (LARGE SUB-UNIT)

```
   G  I  M  E  G  S  D  V  P  T  E  K  S
 GGGGATAATGGAAGGAAGTGATGTACCGACGGAAAAATCT
         10         20         30         40

 H  S  G  R  E  R  N  R  S  M  G  I  G
CATTCTGGCCGAGAACGTAACAGATCGATGGGCATCGGCG
         50         60         70         80

V  Q  G  F  H  T  A  F  L  S  M  G  L  D
TGCAGGGCTTTCATACAGCTTTTCTATCTATGGGTCTTGA
         90        100        110        120

   L  C  D  E  R  A  R  S  L  N  K  L  I
 TTTATGCGATGAACGCGCTAGATCCCTCAACAAGCTAATT
        130        140        150        160

 F  E  F  M  L  L  E  A  M  T  V  S  C
TTTGAATTCATGTTATTGGAGGCGATGACAGTTAGTTGCG
        170        180        190        200

E  F  C  E  R  G  L  P  P  F  A  D  F  S
AATTCTGCGAACGAGGCCTGCCGCCGTTTGCTGATTTCTC
        210        220        230        240
```

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WO 90/02803

PCT/GB89/01076

FIG 9B

2

```
  N  S  Y  Y  A  R  G  R  L  H  F  D  G
TAACAGTTATTATGCACGAGGACGTCTGCATTTCGATGGG
        250        260        270        280

 W  A  N  V  E  L  A  A  V  E  E  W  N
TGGGCTAATGTAGAATTGGCTGCAGTGGAAGAGTGGAATA
        290        300        310        320
```

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FIG 10

MDV HOMOLOGUE OF RIBONUCLEOTIDE REDUCTASE (SMALL SUB-UNIT)

```
   L  D  V  E  A  I  L  C  Y  V  R  Y  S
TATTGGATGTTGAAGCAATATTATGTTACGTACGTTACAG
        10        20        30        40

  R  G  Q  T  T  E  R  I  D  M  P  P  I
CCGCGGACAGACTACTGAAAGAATAGATATGCCACCTATT
        50        60        70        80

 Y  N  E  P  K  P  T  A  D  F  P  H  A  L
TACAACGAACCTAAACCTACAGCTGATTTTCCGCATGCAC
        90       100       110       120

   T  A  S  N  N  T  N  F  F  E  R  R  N
TGACAGCTTCAAATAATACCAACTTCTTTGAGAGAAGAAA
       130       140       150       160

  T  A  Y  S  G  S  V  S  N  D  L  *
TACTGCATACTCTGGAAGCGTGTCAAACGATCTTTAA
       170       180       190
```


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FIG 11

MDV HOMOLOGUE OF HSV-1 IE-175

```
  P   I   P   V   Y   V   E   E   M   K   D   Y   A
 CCCATTCCCGTCTATGTAGAGGAAATGAAAGATTATGCCA
          10          20          30          40

K   Q   Y   D   A   L   V   N   S   L   F   H   K   S
AACAATACGACGCTCTCGTAAACTCTTTGTTTCACAAAAG
          50          60          70          80

  M   K   V   N   P   L   N   W   M   H   H   G   K
CATGAAAGTAAATCCTCTGAACTGGATGCACCACGGGAAG
          90         100         110         120

  L   S   T   A   D   A   A   L   N   H   I   Y   V
 CTGTCTACCGCCGATGCTGCCCTAAACCACATATATGTTC
          130         140         150         160

Q   K   F   Q   S   S   Y   D   S   P   G   A   A   V
AGAAATTCCAGAGTTCATACGATTCGCCCGGAGCGGCTGT
          170         180         190         200

  T   G   T   V   N
AACTGGCACAGTTAACA
          210
```

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FIG 12

MDV HOMOLOGUE OF HSV-1 IE-68

```
    S  D  Q  D  F  E  L  N  N  V  G  K  F
CGTCCGATCAAGACTTTGAACTTAATAATGTGGGCAAATT
        10        20        30        40

  C  P  L  P  W  K  P  D  V  A  R  L  C
TTGTCCTCTACCATGGAAACCCGATGTCGCTCGGTTATGT
        50        60        70        80

 A  D  T  N  K  L  F  R  C  F  I  R  C  R
GCGGATACAAACAAACTATTTCGATGTTTTATTCGATGTC
        90       100       110       120

    L  N  S  G  P  F  H  D  A  L  R  R  A
GACTAAATAGCGGTCCGTTCCACGATGCTCTTCGGAGAGC
       130       140       150       160

  L  F  D  I  H  M  I  G  R  M  G  Y  R  L  N
ACTATTCGATATTCATATGATTGGTCGAATGGGATATCGACTAAA
       170       180       190       200
```

Fig. 13

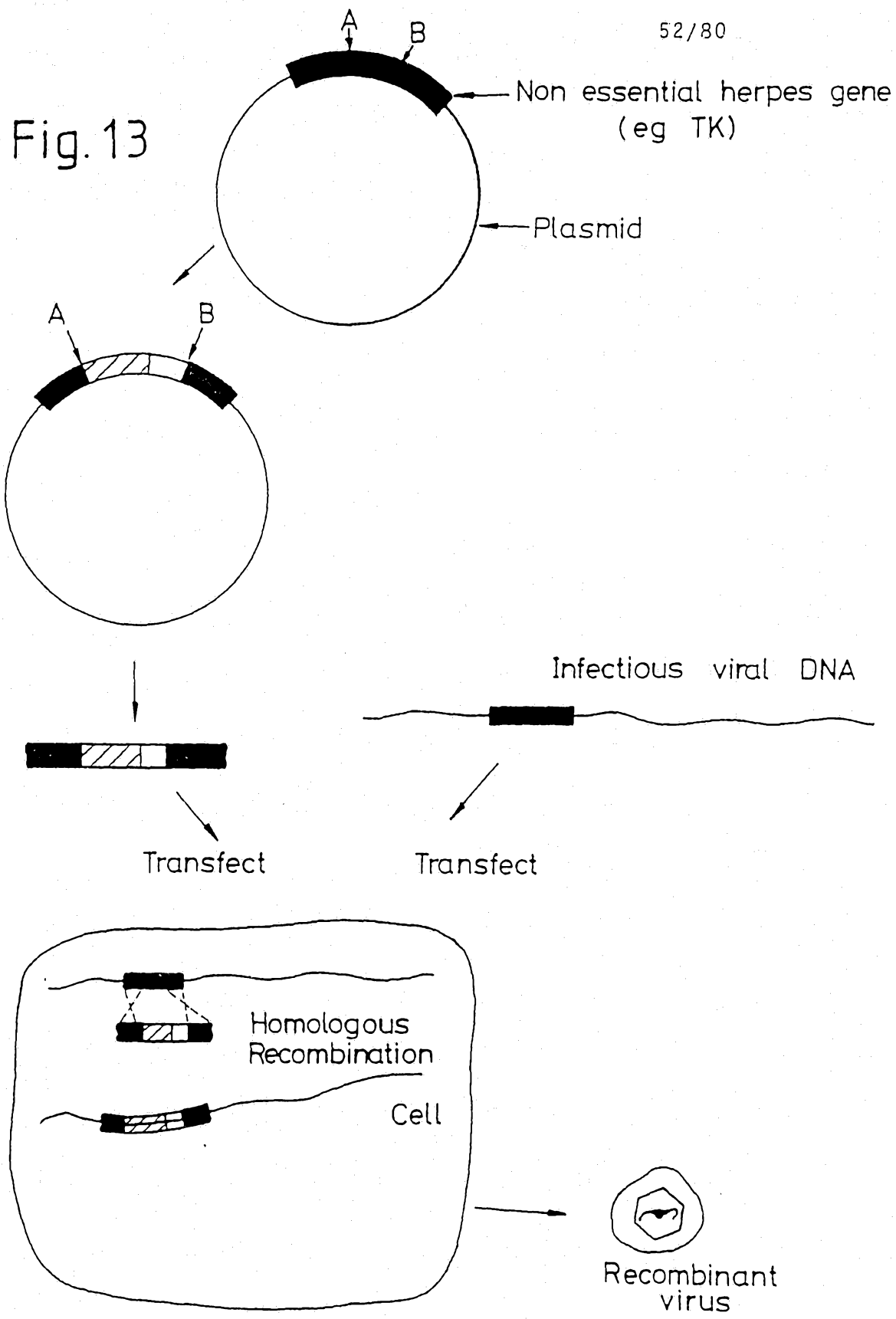
A
B
Non essential herpes gene
(eg TK)
Plasmid
A
B
Infectious viral DNA
Transfect
Transfect
Homologous
Recombination
Cell
Recombinant
virus

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FIG 14A

```
                10         20         30         40
MDV   AATGTCTTTTGAAGTCGAGCCCAATCGAAACCATATTTTTGTCTGCTA
        T  K  Q  L  R  A  W  D  F  G  Y  K  Q  R  S

      50         60         70         80         90
MDV   TCAGAACTAGCAAGTCTCGTTGACAGATGCTCCAAATAAGTG
      D  S  S  A  L  R  T  S  L  H  E  L  Y  T

               100        110        120        130
MDV    GGAACCGACTCAATCGCACTCATAAAGTTAGTGGGATGAGAAATATT
       P  V  S  E  I  A  S  M  F  N  T  P  H  S  I  N

      140        150        160        170        180
MDV   AGTCCCAGTTTTTGCATAGAATGCATATAAACAAAGAATCGCA
       T  G  T  K  A  Y  F  A  Y  L  C  L  I  A

               190        200        210        220
MDV    CATTCTAGAGAGGAATAATAACGGGTGCCTACATATAAACGTCCGCA
       C  E  L  S  S  Y  Y  R  T  G  V  Y  L  R  G  C

      230        240        250        260        270
MDV   TGATTGTAAAGATGTGATTGCCGTCACAATAAACGTTCGCGAC
       S  Q  L  S  T  I  A  T  V  I  F  T  R  S
```

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FIG 14B

```
                280        290        300        310
MDV    ATTCTTCCACCATGATAGTCTATTTTTCTGGCAACGCTGGGCTTGTC
        M  R  G  G  H  Y  D  I  K  R  A  V  S  P  K  D

       320        330        340        350        360
MDV    GGCAACCAGAGCATTTTGTAAAGTACGATACCACGTGCCGAAA
        V  A  L  A  N  Q  L  T  R  Y  W  T  G  F

                370        380        390        400
MDV    ACGACACCGGAGTTCACTACATTCCTATTTGCATAGACTAAGTTCAA
        V  V  G  S  N  V  V  N  R  N  A  Y  V  L  N  L

       410        420        430        440        450
MDV    GAGATCCACAGACAAATTAGAGTCGTATCTGAGCAAAGGATCA
        L  D  V  S  L  N  S  D  Y  R  L  L  P  D

                460        470        480        490
MDV    TTTTTCACGATTTGAATCTCACGGGCCGAAGTGATATTAACGTCTTC
        N  K  V  I  Q  I  E  R  A  S  T  I  N  V  D  E

       500        510        520        530        540
MDV    CTTGTGCTGTCCAGATTTTTCAACAGCACTAACGGCAATATCC
        K  H  Q  G  S  K  E  V  A  S  V  A  I  D
```

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FIG 14C

```
                550        560        570        580
MDV   ATTGCAGCGTCGGCAAGTTCTGCTGCAGCCGCTGCATGTTCCAGATC
       M  A  A  D  A  L  E  A  A  A  A  A  H  E  L  D

      590        600        610        620        630
MDV   CGCTAACGCTGTTGCGATATATTCAATTTTTTCTTCTATTGGT
       A  L  A  T  A  I  Y  E  I  K  E  E  I  P

                640        650        660        670
MDV   CGAAGTCTGCGGTCAATTTCTATTGCAATAGAGTCGGTATGACCATC
       R  L  R  R  D  I  E  I  A  I  S  D  T  H  G  D

      680        690        700        710        720
MDV   CAAATTATTTAATGCTGCAGTGGCGGCATTGTTTCGTGCAGTA
       L  N  N  L  A  A  T  A  A  N  N  R  A  T

                730        740        750        760
MDV   ATGATCGCAAGTTGTCGTTCCATATTGGCGCGGTTAGATGTAAATAC
       I  I  A  L  Q  R  E  M  N  A  R  N  S  T  F  V

      770        780        790        800        810
MDV   CGGTTCCTTCCAGAACTCGATGGGCCATGGGGGAGCTATAAAG
       P  E  K  W  F  E  I  P  W  P  P  A  I  F
```

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FIG 14D

```
            820        830        840        850
MDV   TTCTTCACATCGGCAGGGAACATTTCCATTCCATCGCCTGTCAATAT
       N  K  V  D  A  P  F  M  E  M  G  D  G  T  L  I

      860        870        880        890        900
MDV   TCTCGCGTCCCAAATAAAGTTTGCCATGATGGTGCTACTCGAT
       R  A  D  W  I  F  N  A  M

            910        920        930        940
MDV    ATAATCAGACAGAAGTTACAGGGAAACGCCACATGAGAAAATAATAC

      950        960        970        980        990
MDV   TACATTTAAACTACACAAGCTTATAAAAGTGTTACGGTCTCTG
                                      *  P  R  Q

           1000       1010       1020       1030
MDV    AACAAGACGGGCGATAATATTAGCCATGTTTCGCATAGCCGTACCT
        V  L  R  A  I  I  N  A  M  N  R  M  A  T  G

      1040       1050       1060       1070       1080
MDV   CCCGTTCTCTCCTGATTATTTGAAAATGATAAAGTAGCCGTTTT
       G  T  R  E  Q  N  N  S  F  S  L  T  A  T  K

           1090       1100       1110       1120
MDV    ATTACAAGCTATATGATTCCTCAAATCCGTTACGTTAGCAGACGCC
        N  C  A  I  H  N  R  L  D  T  V  N  A  S  A
```

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FIG 14E

```
      1130       1140       1150       1160       1170
MDV   TTTCCACTGCGTCGTTGTATATGTATCGTGTTTGTATTATGACG
      K  G  S  R  R  Q  I  H  I  T  N  T  N  H  R

            1180       1190       1200       1210
MDV    TTTTAAAATTTTATGAGTGTCAGTTATCCGTGCTTTATAGTCAGAC
         K  L  I  K  H  T  D  T  I  R  A  K  Y  D  S

      1220       1230       1240       1250       1260
MDV   GCGGTCGCCAATATAGAGCATAGTCTATGAAAATCAGTCACTAT
      A  T  A  L  I  S  C  L  R  H  F  D  T  V  I

            1270       1280       1290       1300
MDV    GTGCCTTTTCTTTAGGCACATCACATGTAGAACAGACAGTTTTCGT
         H  R  K  K  L  C  M  V  H  L  V  S  L  K  R

      1310       1320       1330       1340       1350
MDV   CTTGCTACAAATACTAACATTGGACAAATAACGATACAATCTGA
      R  A  V  F  V  L  M  P  C  I  V  I  C  D  S

            1360       1370       1380       1390
MDV    TCCTTGAGGCGCAATTTGCCCAATCAGAGATTTGGAATCCAATAAC
         G  Q  P  A  I  Q  G  I  L  S  K  S  D  L  L
```

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FIG 14F

```
     1400       1410       1420       1430       1440
MDV  TGCTTTATGCCGGTGAGTCTTTGTTCATGTTTACTGCGTGTCTT
     Q  K  I  G  T  L  R  Q  E  H  K  S  R  T  K

          1450       1460       1470       1480
MDV   CAGGTTACGAGAAAATTTGCAAGTTTTTAGTTCTAGAATGACGCAT
       L  N  R  S  F  K  C  T  K  L  E  L  I  V  C

     1490       1500       1510       1520       1530
MDV  ACTCCATCACAGCCTACTTCCCACAAATCACGAGGCAACTTAAA
     V  G  D  C  G  V  E  W  L  D  R  P  L  K  F

          1540       1550       1560       1570
MDV   CATGCAAATACAATCCGGTCTACGTCGTTCTAGGTTTACTTCGAAG
       M  C  I  C  D  P  R  R  R  E  L  N  V  E  F


     1580       1590       1600       1610       1620
MDV  ACCAATCGAAAATCCGTCAACTGTTTAAATACATCTAATACCAT
     V  L  R  F  D  T  L  Q  K  F  V  D  L  V  M
MDV  V  Q  S  G  L  C  M  A  E  A  Y -----R--------
HVT                                   L  K  K  Y
```

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FIG 14G

```
MDV     V  K  G  F  I  K  A  F  S  R  G  P  W  D  Y
MDV   GACCTTCCCAAAAATTTTGGCAAAGCTTCTCCCCGGCCAATCATAC
            1630       1640       1650       1660


MDV  V  Q  S  G  L  C  M  A  E  A  Y ----R-------
HVT                                  L  K  K  Y

HVT                                 AAGCTTTTTGTA
                                    ::::  ::::::
MDV  ACCTGAGATCCTAGACACATCGCTTCTGCATAAAGCCGTTTGTA
     1670       1680       1690       1700       1710


MDV   -------D-----C---------------A-----R--R--K--R--
HVT    F  R  N  H  G  R  V  G  A  K  L  L  G  A  M
HVT   AAAACGATTATGACCACGGACACCCGCTTTTAGCAATCCTGCCATA
      ::: ::::  ::::  :: ::::: ::   ::    ::      ::
MDV   AAAGCGATCGTGACATCGAACACCAGCCGCTAAACGTCGCTTTCTA
            1720       1730       1740       1750
```

FIG 14H

```
MDV   L   V   N   T   N   V   H   R   K   F   N   R   T   S   S
HVT
HVT   AGGTGGTT.........TCCCGCGTGCTTGCCTCGAAGACAAT
      ::    ::          : :::  ::            :   : :
MDV   AGGACATTCGTATTTACATGCCGTTTGAAATTTCGAGTGCTACT
      1760      1770      1780      1790      1800


MDV     V   Q   R   R   Y   R   K   L   V   N   K   E   G   M
HVT
HVT    TGCCAG.CTAATCCAGCATTACCATATTTCCTTGGCTTGCAT....
         :: : ::     : : ::    ::  : :::  ::  :::
MDV    AACCTGTCTGCGATATCTTTTGAGTACGTTCTTCTCTCCCATTGAA
            1810      1820      1830      1840


MDV    {M   S   E   P   Q   S   W   S   V}:-------S--Q--M--
HVT                                   M   A   L   P   R
HVT    ....TTGGATC.........TGCGCGTCGATGGCATTGCCGAGAA
          : ::: :          ::   ::   :::::::  : ::  :
MDV    CATGTCGGAGCCACAATCGTGGTCGGTAATGGCATCTCAGATGA
       1850      1860      1870      1880      1890
```

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FIG 14I

```
MDV    T--S--A--Q-----I----------------------S--M------
HVT    R  P  P  T  L  T  R  V  Y  L  D  G  P  F  G  I
HVT    GACCGCCCACGTTAACGCGAGTTTATCTAGACGGACCGTTTGGTAT
        : :  :   : : :  :: :: :: :: :: ::: :  : :::::
MDV    CATCTGCACAGCTCATACGTGTATACCTCGATGGATCAATGGGTAT
            1900       1910       1920       1930

MDV    ---------------M--------E--I-----T-----S--L--
HVT      G  K  T  S  I  L  N  A  M  P  D  H  T  P
HVT    AGGCAAAACGTCTATACTAAACGCTATGCCCGACCACACGCCCG
       ::: :::::::: ::  : :: :  :: ::     ::: :
MDV    AGGTAAAACGTCAATGTTGAATGAGATACCGACGCACTCTTTAA
       1940       1950       1960       1970       1980

MDV     M-----V-----V-----------F--------------------
HVT     D  G  A  P  I  L  K  V  Y  E  P  M  K  Y  W  R
HVT     ATGGGGCTCCTATATTGAAAGTGTACGAACCAATGAAATATTGGAG
          :: :  ::  :: : :: :: : :::::: :::::::: ::: :
MDV     TGGGAGTACCCGTACTAAAGGTTTTCGAACCTATGAAATACTGGCG
            1990       2000       2010       2020
```

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FIG 14J

```
MDV   --Y--Y--F---------------T--T--V-----D-----C--
HVT     C  Q  S  T  D  L  V  V  A  A  N  E  T  P
HVT   ATGCCAGTCTACCGATTTGGTGGTAGCTGCCAACGAAACGCCAG
        :   : : ::: ::::::::      : :  :: :: ::    :
MDV   GTATTATTTTACTGATTTGGTCACGACCGTAAATGATACATGTG
      2030      2040      2050      2060      2070

MDV   D----------R-----E--F-----L----------S------
HVT   E  R  R  R  G  G  A  L  S  G  F  Q  S  D  M  I
HVT   AACGTAGGCGTGGTGGAGCTTTATCACGATTCCAATCTGACATGAT
      : ::: : ::  : : ::  :: ::   ::: ::::::  ::::::
MDV   ATCGTCGTCGCAGGGGAGAGTTTTCTTTATTTCAATCTAGCATGAT
           2080      2090      2100      2110

MDV   --V--T--A--L-----S--K--------------------V--
HVT     M  A  S  I  Q  A  R  F  A  D  P  Y  L  L
HVT   CATGGCATCTATACAAGCCAGATTTGCCGATCCATATTTGCTTT
        :  :: :: ::::: : :  ::::: ::::: ::: :  : :
MDV   TGTAACAGCTTTACAATCAAAGTTTGCAGATCCCTATCTTGTAT
      2120      2130      2140      2150      2160
```

FIG 14K

```
MDV   ----------------------------H--R--I--T--G--T--R
HVT   F  H  E  R  L  S  S  K  C  R  G  K  I  E  I  C
HVT   TTCACGAACGGTTATCATCTAAATGTAGAGGAAAAATAGAAATATG
      :::: :: :: ::::: :: :: :::    : : :: :: :: :
MDV   TTCATGAGCGCTTATCGTCGAAGTGTCATCGCATAACAGGAACACG
           2170       2180       2190       2200

MDV   --G--N-----S--L---------I------------------I--
HVT     D  T  P  A  I  I  L  M  L  D  R  H  P  V
HVT   CGATACTCCAGCAATTATATTAATGCTGGATAGGCACCCTGTGG
       :  :  : : :  :::::::::: :: ::: : :: ::  :
MDV   TGGCAATCCATCGCTTATATTAATTCTAGATCGACATCCCATAT
      2210       2220       2230       2240       2250

MDV    S-----T--V---------------A-----H-----T-----D--C
HVT    A  A  I  L  C  F  P  I  T  R  Y  L  L  G  E  Y
HVT    CGGCGATATTATGTTTCCCAATCACTCGCTATTTACTTGGAGAATA
       : :: :   :::::: :: ::  ::::  :::::  :::::: :
MDV    CCGCTACCGTATGTTTTCCCATTGCTCGACATTTAACTGGAGATTG
           2260       2270       2280       2290
```

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FIG 14L

```
MDV   ------------------------M-------------------Q--
HVT     S   L   E   M   L   I   S   S   I   I   R   L   P   L
HVT   TTCTTTGGAAATGTTGATTAGCTCTATAATAAGACTTCCGTTGG
      ::: ::::: ::: : :::::     ::::::::  : ::   ::
MDV   TTCCTTGGAGATGCTAATTAGTATGATAATAAGGTTGCCCCAGG
      2300       2310       2320       2330       2340

MDV    ---P------------------V--I--V--D-----H----------
HVT    E   S   P   G   C   N   L   T   V   T   I   L   P   D   E   K
HVT    AATCCCCCGGATGCAACCTGACAGTCACAATCCTTCCCGACGAAAA
       :: : :: :::::::::: ::    :        :: :  ::::::::
MDV    AACCGCCAGGATGCAACTTGGTGATTGTCGATCTACATGACGAAAA
            2350       2360       2370       2380

MDV   ------------S-----L--S---------N-----T---------
HVT     E   H   V   N   R   I   C   S   R   D   R   P   G   E
HVT   GGAACACGTTAATAGGATTTGTTCAAGAGATAGACCGGGTGAAA
      ::: :: ::::    :  : : :::: :  ::::  : :: :: :
MDV   GGAGCATGTTAGCCGTCTATCTTCACGGAATAGGACCGGCGAGA
      2390       2400       2410       2420       2430
```

FIG 14M

```
MDV    K--T-----L--L----------A----------------S--C
HVT    T  A  D  R  N  M  L  R  T  L  N  A  V  Y  A  S
HVT    CGGCAGATAGAAATATGCTCAGAACACTCAATGCCGTATACGCATC
          :::::   :   :::::::::  :::: :::::  ::  ::   : :
MDV    AAACAGATCTACTAATGCTCAGGGCACTTAATGCAGTGTATTCCTG
             2440       2450       2460       2470

MDV    ---------------I--M----------H--I----------
HVT      L  V  D  T  V  K  Y  A  N  L  T  C  P  Y
HVT    TTTGGTGGACACGGTTAAATACGCAAATCTAACATGCCCTTACG
       :::  ::  :::::   :::   :::::::::   :   ::  ::  :::
MDV    TTTAGTAGACACTATTATGTACGCAAATCATATTTGTCCCTACA
       2480       2490       2500       2510       2520

MDV    S-----D--E---------S----------D---------------D
HVT    E  K  E  S  W  E  M  E  W  L  G  L  P  W  F  E
HVT    AGAAAGAAAGCTGGGAAATGGAATGGTTGGGACTTCCCTGGTTTGA
         ::  ::     ::::::   :::::::::  ::  ::  ::::::::
MDV    GTAAGGATGAATGGGAATCTGAATGGTTGGATCTACCATGGTTTGA
             2530       2540       2550       2560
```

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FIG 14N

```
MDV   --T---------A--T--T---------N--E---------T--...
HVT     E   S   L   L   E   E   F   I   S   R   P   R   P   V
HVT   AGAGTCATTACTTGAAGAATTCATCTCGCGCCCCCGCCCTGTTA
          :: ::       :   :: ::       :: ::  :::
MDV   TACATCTTTGGCCACAACGTTTATAAACGAACCTCGTACTG...
      2570       2580       2590       2600       2610

MDV   D--Y--R--G--S------V--S------H--H----------------
HVT   I   C   S   R   T   R   M   P   L   D   R   T   L   L   A   I
HVT   TTTGTTCGAGAACTCGAATGCCGCTGGACCGAACTCTCCTGGCCAT
       :: :     : : : :  :: :  :  :::  :: ::  : :: ::
MDV   ATTATCGCGGTAGTAGGGTGTCATTACACCATACGCTTTTAGCGAT
            2620       2630       2640       2650

MDV   ------------R------------A-----D-----S-----S--
HVT     F   K   R   K   E   L   C   S   E   N   G   E   L   L
HVT   TTTTAAACGGAAAGAGCTGTGTAGCGAAAATGGGGAGCTGTTAA
       ::::: :::  :::  : :::  :::: ::::      : : ::
MDV   ATTTAAGCGGCGAGAATTATGTGCCGAAGATGGTAGCTTATCAA
      2660       2670       2680       2690       2700
```

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FIG 14 (0)

```
MDV   ---T--H--A-------------------------M---------R--N
HVT   T  Q  Y  S  W  I  L  W  G  L  L  T  K  L  H  T
HVT   CTCAGTATTCTTGGATATTGTGGGGATTACTGACTAAACTACACAC
      :   : :: : :::::::::::::::::::: : :  ::::: :  :
MDV   CAACGCATGCATGGATATTGTGGGGATTATTAATGAAACTGCGGAA
            2710       2720       2730       2740

MDV   ---------------R------N------T------L------T--T--
HVT     I  N  V  E  L  F  D  I  S  G  M  S  R  R
HVT   CATTAATGTCGAATTATTTGACATTAGCGGTATGTCACGTCGAG
      :::::: ::::::  :::: : ::::  ::  ::::       :
MDV   CATTAACGTCGAACGATTTAATATTACTGGCCTGTCCACAACAA
      2750       2760       2770       2780       2790

MDV   K------V--E--S--F------D---------S------------V---
HVT   E  C  A  S  A  I  M  H  T  M  P  E  R  L  S  T
HVT   AATGCGCCAGCGCTATAATGCATACTATGCCGGAGAGATTGTCTAC
      : :  :       :  : ::: :::::::: ::::::::::   :
MDV   AGTGTGTAGAATCGTTCATGGATACTATGTCGGAGAGATTGGTAAC
            2800       2810       2820       2830
```

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FIG 14P

```
MDV   --H--M---------------A--F-----I-----A--------
HVT     L   A   S   W   N   D   L   C   E   L   E   D   D   V
HVT   TCTCGCTAGCTGGAATGATTTATGCGAGCTTGAAGATGATGTAA
        :     :::::::::::::    : :::: :::::: :::::::
MDV   ACATAGTAGCTGGAATGATGCCTTCGAGATTGAAGCTGATGTAC
      2840        2850        2860        2870        2880

MDV   L--A-----------E-----A--M--*
HVT   I   S   Y   N   K   G   M   C   N   E   V   G   A   S   R   *
HVT   TTTCCTATAATAAGGGAATGTGTAACGAGGTTGGAGCGTCTCGATA
      :   :::::::::: :   :::   ::    :          : :     ::
MDV   TAGCCTATAATAAAGAGATGGCTATGTAAAACTACCCATTCATATC
            2890        2900        2910        2920

HVT   ATTCTTCT.TAATCTGCTGGTATTGGTTACTGCCATAACTTATT
         ::::: ::::   ::: :       : ::    ::      : :
MDV   GCGCTTCTATAATTAGCTTGCCCACATCACAATGATGCGGCAAT
      2930        2940        2950        2960        2970

HVT   ATTGGTCCATGCTAGAATAGTCATACGCTACGATCTGTTGCTATAT
      ::::    ::  ::  :::::: ::  :       :  : : : :::
MDV   ATTGACTTATATTAAGATAGTAATTTGGCGTCCTTAGATCCAATAA
            2980        2990        3000        3010
```

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FIG 14Q

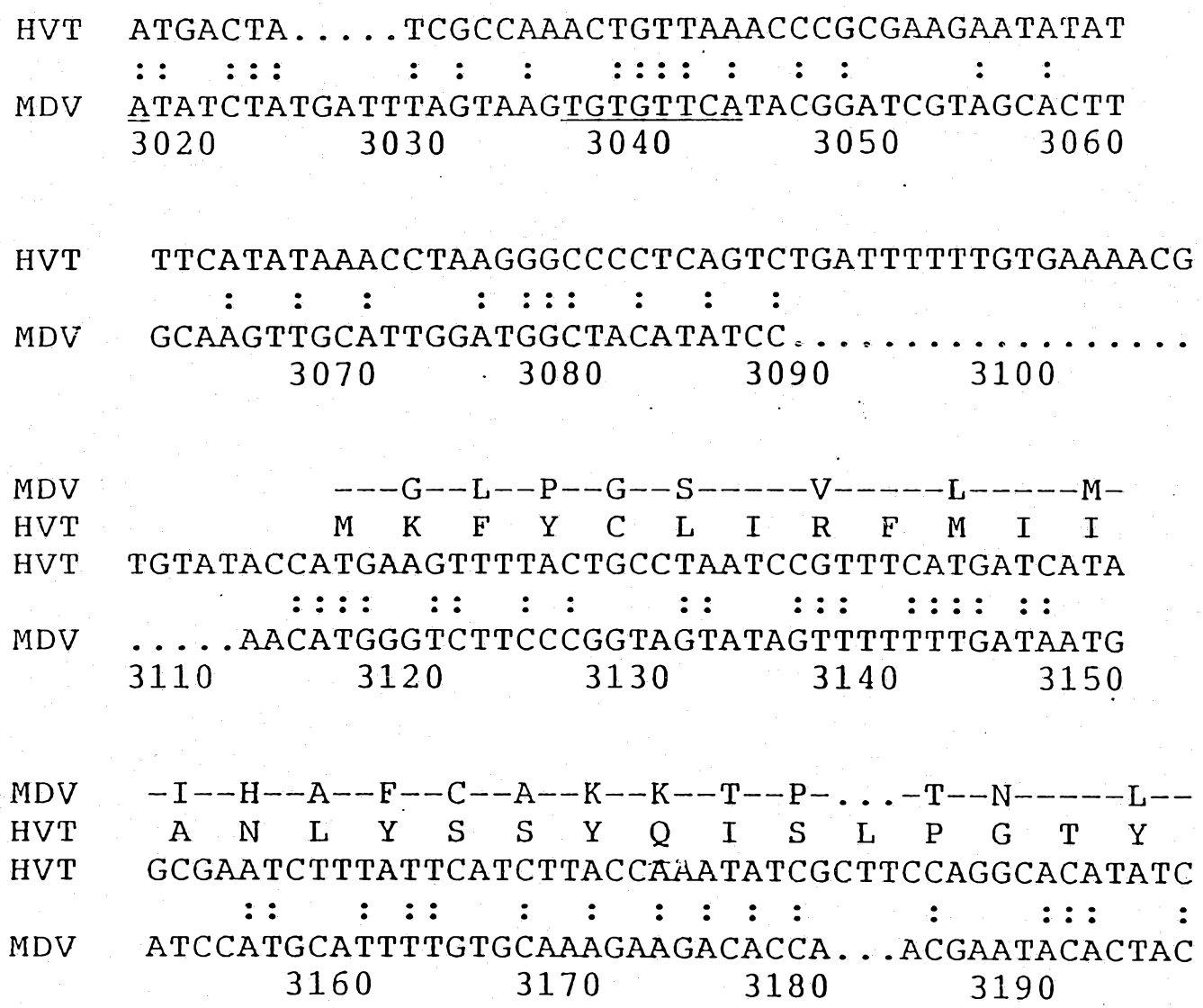

FIG 14R

```
MDV   ------L--L--S---------G--I--T--D--L-----S--L-
HVT   P  S  Q  I ... L  L  D  M  K  N  S  P  L  V
HVT   CATCGCAAATA...TTGCTTGACATGAAGAACTCGCCGCTCGTA
      :::::  : :    ::: : :  :: :   :   :::     :
MDV   CATCGTTATTGTCCTTGTTGGGAATTACAGATCTGCCTTCTCTG
      3200      3210      3220      3230      3240

MDV    ----L---------L--S--L-----G--S--A--N--N--Q--G--
HVT     R  F  N  I  S  T  R  D ..... Y  K  D  E  T
HVT    CGCTTTAATATATCGACGCGTGAT......TATAAAGACGAGACAC
       ::  : :::::  :   : :  :::          ::  :: :
MDV    CGACTGAATATTTTATCTCTCGATGGAAGCGCGAATAACCAAGGCT
            3250      3260      3270      3280

MDV   S-----V-----D-----T----------------G--A--S-
HVT   L  W  I  R  K  N  S  T  F  V  Y  I  D  T  A
HVT   TCTGGATACGGAAAAATTCGACATTTGTTTATATCGATACGGCT
       :::: ::::  : ::: : :::::::: ::::: :   :  :
MDV   CCTGGGTACGTGACAATACTACATTTGTGTATATTGGGGCATCC
      3290      3300      3310      3320      3330
```

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FIG 14S

```
MDV   -S--P--A--N--G-----L---------M-----T--S--H-----
HVT    V  T  T  A  N  V  I  F  Y  L  P  I  G  Q  V
HVT   GTGACGACAGCGAACGTTATCTTTTATCTGCCGATCGGTCAGGTAC
          :  ::       ::  : :::::: :::: :   :::: ::::
MDV   AGCCCAGCAAATGGTGTGTTGTTTTATATGCCAACAAGTCATGTAC
            3340       3350       3360       3370

MDV   Q---------T-----Y------------V-----K---------A-
HVT   R  Q  M  V  F  F  K  R  P  I  S  R  L  L  T
HVT   GACAAATGGTTTTTTTCAAGCGTCCAATATCCAGGCTACTAACG
       :::::::  ::: : ::: :: ::  ::::::  ::  :  ::
MDV   AACAAATGACTTTCTACAAACGGCCGGTATCCAAACTGTTGGCG
      3380       3390       3400       3410       3420

MDV   --------------I--------L------------------I-----
HVT    S  N  N  L  V  K  F  I  N  T  G  S  Y  A  N
HVT   TCCAATAACCTGGTTAAATTTATTAATACCGGTTCATACGCCAATC
      :::::::: ::  : :::::: : ::::: :: :: :::  :::::
MDV   TCCAATAATCTAATCAAATTTTTAAATACGGGGTCGTACATCAATC
            3430       3440       3450       3460
```

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FIG 14T

```
MDV   ---S-----M-----A--M--P---------R--R--N--V--Q-
HVT   H  T  F  K  T  E  L  S  P  Y  L  S  K  T  N
HVT   ATACATTCAAGACAGAACTTTCACCCTATTTGTCGAAAACCAAT
      :  : :::: ::: :   :  :::::::      ::     :
MDV   ACTCGTTCATGACGGCCATGCCACCCTACCGACGAAATGTGCAA
      3470       3480       3490       3500       3510

MDV    -I-----S--D--R--S--G--L--K--L-----D--K--E--D--
HVT      T  P  L  K  K  Y  E  I  V  V  D  Q  P  T  G
HVT    ACACCGTTGAAGAAATATGAAATTGTTGTCGATCAACCTACTGGAG
       :  :::  : :   :: ::   ::    : ::: :       :
MDV    ATTCCCTCGGACCGATCTGGTCTTAAATTAGATGACAAAGAGGATC
             3520       3530       3540       3560

MDV   P--L--D-
HVT   E  N  P  P  A  G  F  G  S  L  K  P  A  D  F
HVT   AAAACCCTCCGGCAGGGTTCGGAAGTTTAAAACCGGCAGACTTT
            :
MDV   CTCTAGAT
      3570       3580       3590       3600       3610
```

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FIG 14U

```
          L  N  P  G  Y  K  F  V  L  T  S  E  L  V  G
HVT   CTCAACCCCGGATACAAGTTCGTTCTCACAAGCGAGTTGGTAGGAG
            3620       3630       3640       3650

       A  Y  T  K  R  S  C  F  V  D  P  M  D  S  L
HVT   CCTACACAAAACGATCTTGTTTTGTCGATCCGATGGATTCTCTC
      3660       3670       3680       3690       3700

          V  P  I  D  Y  D  H  V  R  T  I  I  F  G  S
HVT   GTCCCGATAGATTATGATCATGTACGAACCATTATATTCGGATCTG
            3710       3720       3730       3740

       A  G  M  E  I  L  M  K  M  G  I  T  L  A  S
HVT   CTGGGATGGAGATTTTAATGAAGATGGGAATTACTTTGGCATCT
      3750       3760       3770       3780       3790

          M  T  I  S  T  K  Y  N  P  P  I  E  L  I  I
HVT   ATGACCATTTCGACGAAATATAATCCTCCTATTGAACTGATAATAT
            3800       3810       3820       3830

       S  A  K  Y  R  N  L  S  L  L  W  P  P  R  Q
HVT   CTGCAAAGTACCGAAATTTATCACTGTTGTGGCCACCCCGACAA
      3840       3850       3860       3870       3880
```

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FIG 14V

```
          Q   Y   E   P   V   N   K   G   T   G   R   P   H   W   I
HVT   CAATATGAACCTGTAAATAAAGGGACTGGACGCCCCCATTGGATCT
            3890        3900        3910        3920

        Y   L   L   G   V   Y   R   N   V   S   D   S   E   R   D
HVT   ACCTATTAGGTGTGTATAGAAACGTTTCGGACTCCGAGCGTGAC
      3930        3940        3950        3960        3970

          S   Y   M   N   M   I   K   S   L   G   D   S   M   D   Y
HVT   TCATACATGAATATGATTAAGAGTCTGGGCGATTCTATGGATTATC
            3980        3990        4000        4010

        H   F   L   I   S   R   A   H   A   Q   M   L   I   L   A
HVT   ACTTCCTAATTAGCAGAGCGCATGCCCAGATGCTGATACTGGCA
      4020        4030        4040        4050        4060

          A   E   D   R   L   V   D   E   M   H   S   F   R   N   V
HVT   GCAGAGGACCGGCTCGTGGATGAAATGCATAGTTTCAGGAACGTTA
            4070        4080        4090        4100

        I   A   R   L   F   V   S   L   F   A   F   I   R   N   A
HVT   TTGCGCGTTTATTTGTATCGTTGTTCGCATTCATACGTAACGCA
      4110        4120        4130        4140        4150
```

FIG 14W

```
          F   Q   S   G   Y   T   S   L   N   D   I   I   E   I   E
HVT   TTTCAGTCTGGCTACACCTCTCTTAATGACATAATTGAAATCGAAG
            4160        4170        4180        4190

        A   D   L   R   L   I   V   E   G   I   S   S   A   A   F
HVT   CCGATTTGAGGTTAATTGTAGAAGGCATTTCTTCTGCTGCATTT
      4200        4210        4220        4230        4240

          R   K   D   A   S   T   H   F   L   I   S   G   T   P   I
HVT   CGTAAAGACGCTAGTACACACTTTCTTATATCGGGAACGCCCATAA
            4250        4260        4270        4280

        K   D   S   K   A   D   L   I   K   S   L   L   S   K   V
HVT   AAGATAGCAAAGCGGATTTAATTAAATCGTTGTTGTCTAAAGTC
      4290        4300        4310        4320        4330

          I   R   P   I   S   G   H   T   R   P   L   S   A   I   Q
HVT   ATTCGACCAATTTCCGGACATACACGTCCCTTATCTGCGATACAAC
            4340        4350        4360        4370

        H   L   F   L   L   R   S   A   Y   A   L   D   I   P   R
HVT   ATCTATTCCTTTTGAGATCCGCTTATGCATTGGATATACCCCGT
      4380        4390        4406        4410        4420
```

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FIG 14X

```
          Q  N  G  S  L  S  E  Q  V  S  T  V  A  L  S
HVT   CAAAACGGATCTTTGAGCGAACAGGTATCTACAGTGGCACTGTCGT
            4430       4440       4450       4460

        F  I  E  N  I  H  S  E  A  M  R  D  I  L  S
HVT   TCATTGAAAATATTCACAGCGAGGCCATGAGGGACATTCTGTCA
      4470       4480       4490       4500       4510

          W  N  T  T  T  K  H  A  L  Y  Y  A  F  A  S
HVT   TGGAACACTACAACAAAGCATGCGTTGTATTATGCATTCGCGAGTA
            4520       4530       4540       4550

        I  L  Q  R  P  L  T  E  W  G  A  S  R  N  A
HVT   TTTTGCAACGGCCACTGACCGAATGGGGCGCCTCAAGAAATGCA
      4560       4570       4580       4590       4600

          R  R  A  I  L  L  A  S  S  M  C  T  E  E  H
HVT   CGGAGGGCAATACTATTAGCATCATCGATGTGTACAGAAGAGCATG
            4610       4620       4630       4640

        V  I  A  T  E  L  A  I  Q  E  L  Y  V  K  I
HVT   TTATCGCAACTGAGTTGGCTATTCAAGAACTGTATGTCAAAATC
      4650       4660       4670       4680       4690
```

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FIG 14Y

```
          R  S  N  A  D  P  I  H  L  L  D  V  Y  T  P
HVT   AGAAGTAATGCCGACCCAATACACCTTCTAGACGTATATACACCAT
          4700       4710       4720       4730

       C  L  S  S  L  R  L  D  L  S  E  H  H  R  I
HVT   GTCTTTCTTCACTACGATTGGACCTTTCCGAACACCATCGGATA
      4740       4750       4760       4770       4780

          Y  A  M  A  D  V  V  F  Y  P  D  I  Q  Q  Y
HVT   TACGCAATGGCAGATGTAGTTTTCTATCCAGACATTCAGCAGTATT
          4790       4800       4810       4820

       L  K  K  K  S  H  E  G  N  M  K  E  D  D  L
HVT   TGAAAAAAAAATCCCATGAGGGTAATATGAAGGAAGATGATCTC
      4830       4840       4850       4860       4870

          E  T  K  A  E  Y  I  L  T  K  L  R  S  P  L
HVT   GAAACAAAGGCGGAATACATCCTCACCAAGCTTAGGTCGCCGTTGA
          4880       4890       4900       4910

       I  R  T  L  S  A  Y  A  S  E  V  L  S  C  S
HVT   TCAGAACGCTGTCTGCCTATGCATCAGAAGTATTGTCCTGCTCC
      4920       4930       4940       4950       4960
```

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FIG 14Z

```
          D  Q  D  L  L  E  I  N  A  I  L  I  L  P  V
HVT   GACCAGGATCTATTAGAAATAAATGCTATTTTAATTCTGCCCGTTT
            4970       4980       4990       5000

       S  G  I  G  S  Y  V  V  S  R  R  A  G  M  Q
HVT   CCGGTATTGGGAGCTATGTAGTCTCTCGAAGGGCAGGAATGCAA
      5010       5020       5030       5040       5050

          G  I  V  Y  T  V  D  G  V  D  V  N  N  Q  L
HVT   GGCATTGTTTATACCGTAGACGGTGTTGATGTTAACAATCAGCTTT
            5060       5070       5080       5090

       F  I  T  Y  T  R  M  P  C  T  T  T  I  G  N
HVT   TTATAACATATACCAGGATGCCGTGCACTACAACGATAGGTAAC
      5100       5110       5120       5130       5140

          I  V  P  T  V  L  S  R  P  S  G  K  T  C  P
HVT   ATTGTTCCAACAGTATTGTCAAGACCCTCGGGAAAAACGTGTCCGT
            5150       5160       5170       5180

       Y  C  G  C  V  L  L  R  Y  S  A  D  G  N  I
HVT   ATTGCGGCTGTGTTTTGCTGCGATATTCCGCCGATGGAAATATC
      5190       5200       5210       5220       5230
```

FIG 14ZZ

```
          R  Y  S  I  Y  I  S  S
HVT   CGCTATTCTATTTACATTTCGTCCC
          5240      5250
```

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Fig15

```
  G  R  R  K  Y  D  A  L  V  A  -  F
GGGACGACGCAAATATGATGCTCTAGTAGCAT4GTTT


  V  L  G  R  A  C  G  R  P  I  Y  L  R
GTCTTGGGCAGAGCATGTGGGAGACCAATTTATTTACGT

  E  Y  A  N  C  S  T  N  E  P  F  G  T
GAATATGCCAACTGCTCTACTAATGAACCATTTGGAACT

  C  K  L  K  S  L  G  W  W  D  R  R  Y
TGTAAATTAAAGTCCCTAGGATGGTGGGATAGAAGATAT

  A  M  T  S  Y  I  D  R  D  E  L  K  L
GCAATGACGAGTTATATCGATCGAGATGAATTGAAATTG

  I  I  A  A  P  S  R  E  L  S  G  L  Y
ATTATTGCAGCACCCAGTCGTGAGCTAAGTGGATTATAT

  T  R  L  I  I  I  N  G  E  P  I  S  S
ACGCGTTTAATAATTATTAATGGAGAACCCATTTCGAGT

  D  I  L  L  T  V  K
GACATATTACTGACTGTTAAA
```