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Characterization of the gene and an antigenic determinant of equine herpesvirus type-1 glycoprotein 14 with homology to gB-equivalent glycoproteins of other herpesviruses

(Recombinant DNA; unusual signal sequence; hydropathic analysis; membrane-anchoring region; epitope)

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SUMMARY

The gene encoding glycoprotein 14 (gp14) of equine herpesvirus type 1 was sequenced. Nucleotide sequence analysis revealed a complete transcription unit composed of a CAT box, a TATA box, a ribosome-binding sequence, a polyadenylation signal and an open reading frame (ORF) of 2940 bp transcribed from left to right. The amino acid (aa) sequence deduced from this ORF corresponded to that of a protein with 979 aa and had the characteristic features of membrane gp including a 20-aa signal sequence at the N terminus, a 743-aa surface domain, a 40-aa membrane anchoring region, a 108-aa hydrophilic cytoplasmic domain at the C terminus and eleven potential sites for N-linked glycosylation. An unusual feature of this protein was an exceptionally long (66 aa) sequence, with a preponderance of hydrophilic residues, preceding the hydrophobic signal core. An antigenic determinant recognized by an anti-gp14 monoclonal antibody was present in the N terminus of the postulated surface domain. Comparison of gp14 with the gp of other herpesviruses indicated that gp14 was highly homologous to corresponding gp of pseudorabies (gII), bovine herpesvirus (gI), varicella-zoster virus (gII), as well as of herpes simplex virus, Epstein–Barr virus and human cytomegalovirus (gB).

INTRODUCTION

Equine herpesvirus type 1 (EHV-1), a member of the α-herpesvirus subfamily, is an infectious agent of horses causing acute upper respiratory tract infection, contagious viral abortion and neurological disease. The biological and biochemical properties of the EHV-1 closely parallel those of human herpes simplex virus. Thus, EHV-1 exhibits the typical characteristics of herpesviruses, including genomic isomerization, establishment of latent infections, induction of neurological disorder, generation of defective interfering particles, in vitro oncogenic transformation of cells, and α-β-γ gene regulation (O'Callaghan et al., 1981). EHV-1 has been utilized as a model system for studying the biological consequences of herpesvirus infection.

Glycoproteins (gp) are the principal immunogens of herpesvirus, stimulating both humoral and cellular immune response in the host. The well-characterized gp of HSV include gB, gC, gD, gE, gG, gH and gI. It has been demonstrated that gB and gD can elicit neutralizing antibodies from the infected host (Paoletti et al., 1984; Cantin et al., 1987). gC could stimulate class-I restricted CTL (Rosenthal et al., 1987; Glorioso et al., 1985) and gD could

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Abbreviations: aa, amino acid(s); βGal, β-galactosidase; BHV-1, bovine herpesvirus type 1; bp, base pair(s); CTL, cytotoxic T lymphocytes; EBV, Epstein–Barr virus; EHV-1, equine herpesvirus type 1; gB, glycoprotein B; gp, glycoprotein(s); *gp*, gene encoding gp; HCMV, human cytomegalovirus; HSV-1, herpes simplex virus type 1; kb, kilobase(s) or 1000 bp; nt, nucleotide(s); ORF, open reading frame; PRV, pseudorabies virus; Sig, signal sequence(s); VZV, varicella-zoster virus.

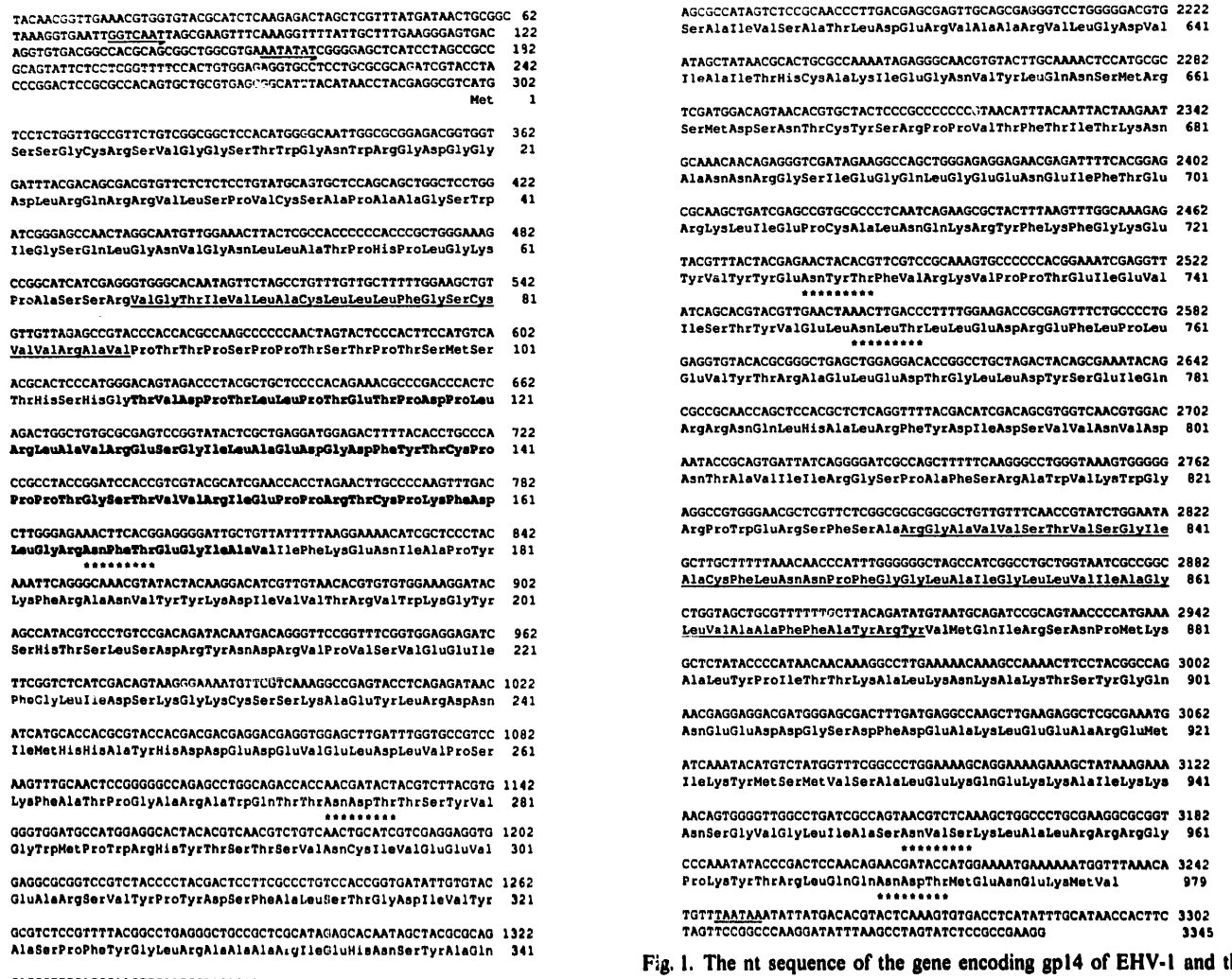

Fig. 1. The nt sequence of the gene encoding gp14 of EHV-1 and the deduced aa sequence. Arrows indicate the CAT box and the TATA box of the promoter, as well as the polyadenylation signal, AATAAA. The signal sequence at the N terminus and the membrane-spanning region at the C terminus are underlined. The predicted N-X-T/S consensus domains for N-linked glycosylation are marked with asterisks. Bold-face letters indicate the epitope recognized by an anti-gp14 monoclonal antibody. **Materials and methods:** Purified EHV-1 DNA (Kentucky strain) was supplied by Rhone-Merieux (Lyon, France). Anti-gp14 monoclonal antibody and phage λgt11 recombinant 4a1 expressing gp14 epitope were obtained as a gift from Dr. George Allen (University of Kentucky, Lexington, KY). Sequenase™ and T4 gene *32*-encoded protein were purchased from United States Biochemical Corp. and Boehringer-Mannheim, respectively. Allen and Yeargan (1987) reported that the *gp14* gene spans the junction between the *Bam*HI restriction fragments *a* and *i* of EHV-1 DNA. The identity of the EHV-1 genomic DNA from Rhone-Merieux and that in the present publication was confirmed by Southern-blot analysis with ^{32}P-labeled DNA fragments from λgt11 recombinant 4a1, following the procedure previously described (Guo et al., 1987). The EHV-1 DNA fragments *Bam*HI-*a* (about 21.3 kb) and *i* (about 7.1 kb) (Whalley et al., 1981) were isolated from EHV-1 genome by 0.8% agarose-gel electrophoresis. Plasmid pUC (*Bam*HI-*i*) was constructed by inserting the *Bam*HI-*i* fragment into plasmid pUC8 at the *Bam*HI site. The *Bam*HI-*a* fragment was digested with *Eco*RI and ligated into pUC8 digested with *Eco*RI + *Bam*HI. Since there are two *Eco*RI sites in the *Bam*HI-*a* fragment, only the two fragments at both ends could be ligated with the *Bam*HI + *Eco*RI linearized plasmid. Plasmid pUC (*Bam*HI-*a*-*Eco*RI) harboring a 10-kb insert was selected based on the

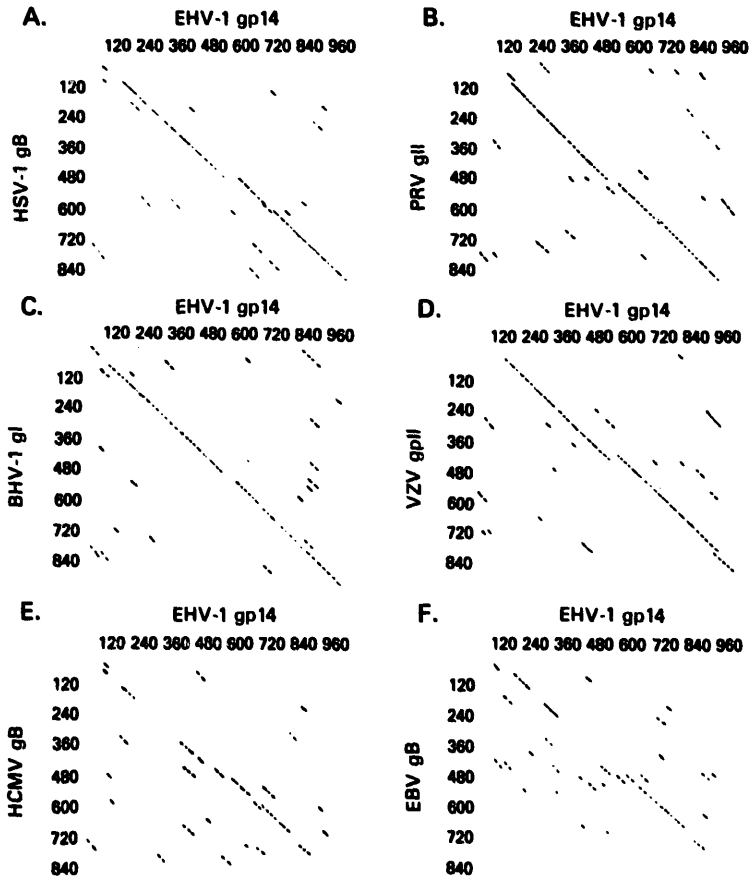

Fig. 2. Homology search of EHV-1 gp14 aa sequence vs. the gB-equivalent glycoproteins of other herpesvirus by DD-matrix with the subprogram of Forward Homology Search from the IBI/Pustell DNA and Protein Sequence Analysis System (IBM computer software, International Biotechnologies, Inc.). Numbers indicate aa residues. The parameters are: range = 10; scale = 0.90; hash level = 1; jump level = 2; step = 2; minimal value plotted = 30. For clarity, the lower-case letters in the original figures were replaced with the dashes (45° angle) when redrawn.

◀ size predicted from the restriction map (Whalley et al., 1981). To facilitate the DNA sequencing, different subclones from pUC (*Bam*HI-*a*-*Eco*RI) and pUC (*Bam*HI-*i*) were prepared. Nucleotide sequences from the subclones were transferred to the IBM computer files. Regions of sequence overlap were identified and the final sequence was assembled with the IBI/Pustell Sequence Analysis Program. The DNA was sequenced on both strands. Sequencing of the plasmid pUC (*Bam*HI-*a*-*Eco*RI) was started from the *Bam*HI site, since *gp14* spans the *Bam*HI junction (Allen and Yeargan, 1987). The orientation of the plasmid pUC (*Bam*HI-*i*) was determined by restriction enzyme digestion, the *Bam*HI end closer to the *Eco*RI site was demonstrated to be at the junction of *Bam*HI-*a* and *i*. Sequencing was started from this end. DNA sequencing was performed with Sequenase™ (Tabor and Richardson, 1987) by the dideoxy chain-termination method (Sanger et al., 1977), using double-stranded plasmid templates and the alkaline-denaturation method. The T4 gene *32*-encoded protein was utilized to improve sequencing efficiency. In most cases, M13 universal primers were utilized for sequences extending from the termini of each fragment in the subclones. Additional synthetic DNA primers were used to determine sequences further from the fragment termini: These primers were synthesized on a Biosearch 8700 or an Applied Biosystems 380B DNA synthesizer. The DNA fragment corresponding to the gp14 epitope contained in the λgt11 recombinant 4a1 was isolated from purified λgt11 DNA after *Eco*RI digestion, following the principle for purifying bacteriophage φ29 DNA (Guo et al., 1986). This fragment was cloned into the *Eco*RI site of pUC8. The nt sequencing was carried out as described above.

stimulate the class-II CTL (Zarling et al., 1986; Martin et al., 1987). gG is a target for antibody directed complement-dependent virus neutralization (Sullivan and Smith, 1988).

It has been demonstrated previously that gp13 of EHV-1 shows some homology to gC of HSV, gIII of PRV and gpV of VZV (Allen and Coogle, 1988; Guo et al., 1989), and that immunization of guinea pigs with recombinant vaccinia virus expressing the gp13-encoding gene protects the host against lethal challenge of EHV-1 (Guo et al., 1989). In this paper, I report the nt sequence of the gp14-encoding gene, compare its aa sequence with those of HSV gB (Bzick et al., 1984), PRV gII (Robbins et al., 1987), BHV-1 gI (Whitbeck et al., 1988), EBV gB (Pellett et al., 1985), VZV gII (Davidson et al., 1986) and HCMV gB (Cranage et al., 1986) and study an antigenic determinant of gp14. Our subsequent studies, truncation and expression of *gp14* in recombinant vaccinia virus and induction of protective immunity in immunized animals (Guo et al., 1990), further confirm that the reported ORF was indeed the gp14-coding sequence.

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EHV-1 gp14 137- F Y T C P P P T G S T V V R I E P P R T C P K F D L G R - N F T E G I A V -172
PRV gII    123- F Y V C P P P S G S T V V R L E P E Q A C P E Y S Q G R - N F T E G I A V -158
BHV-1 gI   125- F F V C P P P S G A T V V R L A P A R P C P E Y G L G R - N Y T E G I G V -160
VZV gpII    56- F Y V C P P P T G S T I V R L E P T R T C P D Y H L G K - N F T E G I A V - 91
HSV-1 gB   112- F Y V C P P P T G A T V V Q F E Q P R R C P T R P E G Q - N Y T E G I A V -147
HCMV gB     91- Y R V C S M A Q G T D L I R F E R N I I C T S M K P I N E D L D E G I M V -127
EBV gB      48- F R V C E L S S H G D L F R F S S D I Q C P S F G T - R E N H T E G L L M - 84
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Fig. 3. Sequence alignment of an epitope in gp14 of EHV-1 with the sequences in gB-equivalent gp of other herpesviruses. The identical aa are underlined. Two highly conserved Cys residues were marked with asterisks.

RESULTS AND DISCUSSION

(a) Nucleotide sequence analysis of the *gp14* gene

Analysis of the nt sequence revealed one ORF extending from nt 300 to 3239 (Fig. 1), reading from left-to-right on EHV-1 genome. The ATG start codon was contained in the *Bam*HI-*a*-*Eco*RI fragment, the stop codon TAA in the *Bam*HI-*i* fragment (Whalley et al., 1981; Allen and Yeargan, 1987). Putative transcriptional regulatory signals were found in the region 5′ to the ATG codon at nt 300. A TATA box having the sequence AATATAT (nt 154–160) and a potential CAT box, GGTCAATT (nt 75–82), were detected.

A scanning model has been proposed to explain the mechanism by which eukaryotic mRNAs initiate translation (Kozak, 1983; 1986). The cardinal rule of this model requires that ribosomes access initiation by first binding to the 5′ end, followed by linear scanning of the mRNA; commitment to initiation is usually at the first 5′-proximal AUG codon, although there are some exceptions (Kozak, 1986; Pelletier and Sonenberg, 1988). A purine at nt position −3 (upstream from the ATG codon) is essential for the initiation of translation and this translation is stimulated by C at nt positions −1 and −2 when the rest of the sequence is suboptimal (Kozak, 1986). The sequence context around the proposed start codon of gp14 was GTCATGT (nt 297–303) which qualified as a functional sequence context for translation initiation of eukaryotic mRNA. This sequence was identical to the corresponding sequence GAGATGT in the *gp13* gene (Allen and Coogle, 1988; Guo et al., 1989) in terms of the −3 and +4 position.

Out of 11 nt in the sequence, 5′–TCCTGCGCGCA–3′ (nt 221–231), 9 are complementary to the 18S ribosomal RNA sequence 3′–AGGAAGGCGT–5′ (Hagenbuchle et al., 1978). This sequence likely serves as the ribosome-binding site.

A polyadenylation signal, AATAAA (nt 3247–3252), was located 8 nt downstream from the stop codon TAA (nt 3237–3239).

(b) Analysis of the gp14 protein structure

The aa sequence predicted from the ORF codes for a 979-aa protein (about 108 kDa). Since gp14 is a membrane-

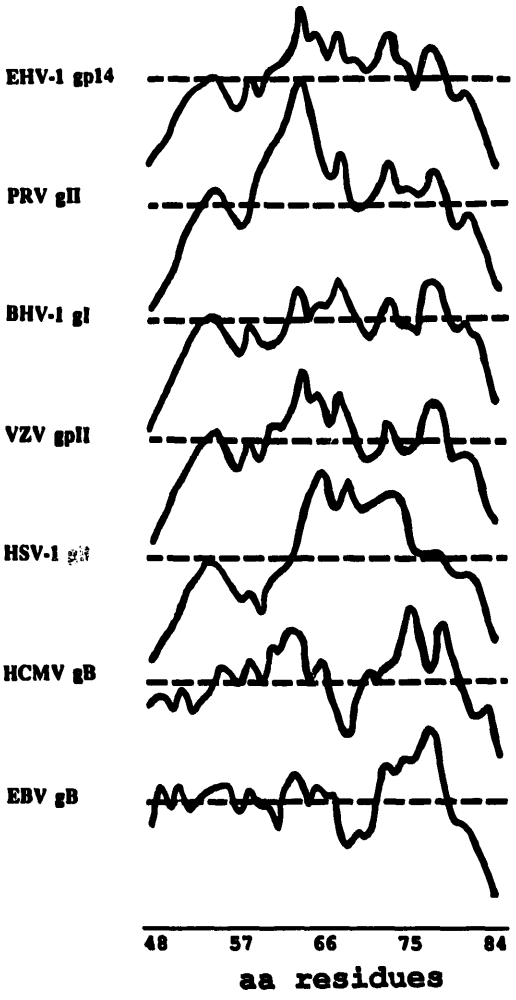

Fig. 4. Comparison of hydrophobic profiles of the epitopes shown in Fig. 3 (Kyte and Doolittle, 1982). Hydrophilic regions were plotted above the x axes (dashed lines). The scale has been compressed to allow multiple profiles on the panel and each profile is plotted one hydrophilicity unit below the previous one. Residue number represents the EBV gB epitope. For other aa see Fig. 3.

bound gp, it is predicted to possess a Sig and a membrane anchor region. Analysis of the aa sequence revealed a number of features common to membrane-bound gp.

(i) The signal sequence (Sig) domain

The region extending from aa 67–86 displayed hydrophobic character and is likely the Sig core (Fig. 1). Another common feature of Sig is that the hydrophobic sequence is preceded by a couple of positively charged aa (Perlman and Halvorson, 1983). However, in gp14 the hydrophobic Sig was preceded by an exceptionally long (66 aa) sequence with a preponderance of hydrophilic aa. This unusual feature has been detected in gII of PRV (Robbins et al., 1987) and gI of BHV-1 (Whitbeck et al., 1988) as well.

(ii) The membrane anchor region and the cytoplasmic domain

There was a hydrophobic peak extending from aa 831–871 (Fig. 1). The hydrophobic region consisting of 41 aa was assumed to be the transmembrane domain. The hydrophilic cytoplasmic domain was 108 aa in length (Fig. 1).

(iii) The predicted N-linked glycosylation sites

There were eleven N-X-T/S sites (where X can be any aa except proline) with potential for N-linked glycosylation (Montreuil, 1984). Interestingly, there were two sites in the cytoplasmic domain (Fig. 1). There was no direct evidence to prove that these sites are glycosylated.

(c) gp14 is homologous to gII of PRV, gI of BHV-1, gII of VZV, and gB of HSV, EBV and HCMV

A comparison of the aa sequence of EHV-1 gp14 with the gp of other herpesviruses revealed that gp14 is homologous to PRV gII (Robbins et al., 1987), BHV-1 gI (Whitbeck et al., 1988), VZV gII (Davidson and Scott, 1986), and gB of HSV-1 (Bzick et al., 1984), EBV (Pellett et al., 1985) and HCMV (Cranage et al., 1986) (Fig. 2).

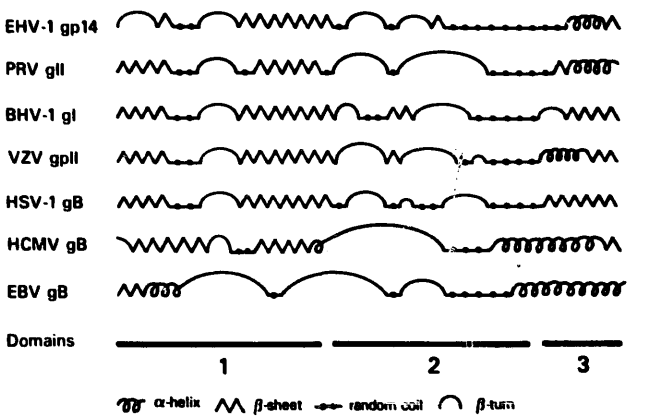

Fig. 5. Secondary structure prediction of the epitopes shown in Figs. 3 and 4. Except EBV, the structures of domains 1 and 3 are very similar in six herpesviruses. Domains 2, containing a preponderance of charged and polar aa (Fig. 4) predicted to be present on the surface of the protein, are more diverse.

(d) Analysis of an antigenic determinant recognized by an anti-gp14 monoclonal antibody

Antigenic determinants or epitopes are the portions on the surface of a protein that interact with the specific antibodies. They may be continuous (comprising a single segment of peptide chain) or discontinuous (comprising two or more chain segments brought together by the folding of the polypeptide chain) (Hopp, 1986; Westhof et al., 1984; Berzofsky et al., 1985).

The λgt11 expression system represents an ideal approach to identify the epitopes for specific monoclonal antibodies (Mehra et al., 1986). Bacteriophage λgt11 recombinant 4a1 expressing a gp14 epitope recognized by anti-gp14 monoclonal antibody 3F6 was constructed by Allen and Yeargan (1987). In their previous work, a library of the EHV-1 genome was constructed in the λgt11 expression vector. Recombinant bacteriophages expressing EHV-1 gp14 epitopes as fusion products with βGal were detected by immuno-screening with anti-gp14 monoclonal

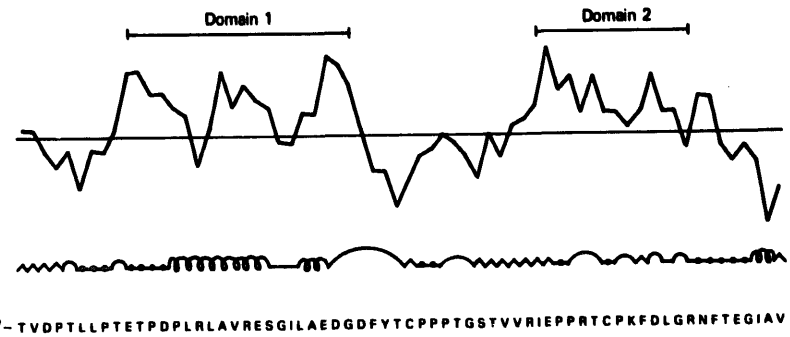

Fig. 6. Hydrophobic plot and secondary structure prediction of aa sequence coded by the EHV-1 DNA fragment in gt11 recombinant 4a1. Hydrophilic regions were plotted above the x-axes. See Fig. 5 for symbols.

antibodies, which was identified previously by Western-blot analysis and verified by immunoprecipitation with [^{3}H]glucosamine-labeled gp14. Phage λgt11 4a1 is one of the recombinant λ bacteriophages expressing gp14 epitopes that are recognized by the monoclonal antibody specific for gp14. The EHV-1 DNA fragment contained in this recombinant bacteriophage has been used as a hybridization probe for mapping the *gp14* gene (Allen and Yeargan, 1987). The viral DNA fragment from the λgt11 recombinant 4a1 was recloned and sequenced. Sequence comparison indicated that this fragment, coding for a 66-aa polypeptide (aa 107–172), originated from the N terminus of the deduced surface domain of gp14 (Fig. 1). Sequence alignment revealed that aa residues 137–172 were the best conserved regions among the gB glycoproteins of the EHV-1, PRV, BHV-1, VZV, HSV-1, HCMV and EBV viruses (Figs. 2–5).

One feature of antigenic sites is that they usually contain a large number of charged and polar aa. Hydrophilicity analysis and secondary structure prediction have been utilized to identify antigenic determinants. Typical contiguous antigenic determinants are hydrophilic stretches of aa adjacent to regions having potential for secondary structures involving β-turns. Hydropathic plots and protein secondary-structure predictions indicate that there are two domains; aa residues 116–134 (Fig. 6, domain 1) and 152–166 (Fig. 6, domain 2) possess the features of typical antigenic determinants. Homologous comparison with the gB-equivalent gp of other herpesviruses indicates that the hydrophilic stretches are the less conserved region.

(e) Conclusions

Nucleotide sequence analysis has revealed an ORF of 2940 bp. An analysis of the deduced aa sequence indicated that an antigenic determinant for a monoclonal anti-gp14 antibody was present in the N terminus of the protein. Alignment of aa sequences indicates strong homology to the gB-equivalent gp of other herpesviruses. Since no intron has been discovered in herpesvirus genes, these data suggest that the ORF codes for gp14 which was the counterpart of herpesvirus gB.

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