Mutational Analysis of the Virion Host Shutoff Gene (UL41) of Herpes Simplex Virus (HSV): Characterization of HSV Type 1 (HSV-1)/HSV-2 Chimeras

DAVID N. EVERLY, JR., AND G. SULLIVAN READ*

School of Biological Sciences, University of Missouri—Kansas City, Kansas City, Missouri 64110

Received 5 May 1997/Accepted 26 June 1997

During lytic herpes simplex virus (HSV) infections, the half-lives of host and viral mRNAs are regulated by the HSV virion host shutoff (Vhs) protein (UL41). The sequences of the UL41 polypeptides of HSV type 1 (HSV-1) strain KOS and HSV-2 strain 333 are 87% identical. In spite of this similarity, HSV-2 strains generally shut off the host more rapidly and completely than HSV-1 strains. To examine type-specific differences in Vhs function, we compared the Vhs activities of UL41 alleles from HSV-1(KOS) and HSV-2(333) by assaying the ability of a transfected UL41 allele to inhibit expression of a cotransfected reporter gene. Both HSV-1 and HSV-2 alleles inhibited reporter gene expression over a range of vhs DNA concentrations. However, 40-fold less of the HSV-2 allele was required to yield the same level of inhibition as HSV-1, indicating that it is significantly more potent. Examination of chimeric UL41 alleles containing various combinations of HSV-1 and HSV-2 sequences identified three regions of the 333 polypeptide which increase the activity of KOS when substituted for the corresponding amino acids of the KOS protein. These are separated by two regions which have no effect on KOS activity, even though they contain 43 of the 74 amino acid differences between the parental alleles. In addition, alleles encoding a full-length KOS polypeptide with a 32-amino-acid N-terminal extension retain considerable activity. The results begin to identify which amino acid differences are responsible for type-specific differences in Vhs activity.

Controls of the rate of mRNA decay play an important role in eukaryotic gene expression (1, 3, 33). During lytic herpes simplex virus infections, the half-lives of both host and viral mRNAs are regulated by the product of the HSV virion host shutoff (vhs) gene (UL41) (30). At early times, copies of the Vhs polypeptide, which enter the cell as components of infecting virions, destabilize preexisting host mRNAs (10, 34, 38). This, together with the disruption of pre-mRNA splicing by the HSV immediate-early polypeptide ICP27 (15, 16), results in the shutoff of most host protein synthesis. In addition, following the onset of viral transcription, the Vhs protein ensures rapid turnover of viral mRNAs belonging to all kinetic classes of viral mRNA (22, 27, 28, 38). Thus, although it is apparently specific for mRNAs (20, 41), the Vhs protein is non-selective with regard to which mRNAs are targeted for degradation. As a generalized destabilizer of mRNAs, it plays two important roles during HSV infections: first, in redirecting the cell from synthesis of cellular to viral proteins; and second, in determining the levels of viral mRNAs and facilitating the sequential transition between expression of different classes of viral genes.

vhs (UL41) homologs have been identified in a number of alphaherpesviruses, including HSV types 1 and 2 (HSV-1 and -2) (6, 8, 9, 11, 25), varicella-zoster virus (5), pseudorabies virus (2), bovine herpesvirus, gallid herpesvirus, and equine herpesvirus 1 (7, 40). Of these, the most closely related, and also the most extensively studied, are the vhs genes of HSV-1 and HSV-2. Comparison of the predicted amino acid sequences of the UL41 polypeptides from HSV-1(17) and HSV-2(2-G) reveals that they are 87% identical (6). In spite of this similarity, HSV-2 strains generally exhibit more rapid and complete virion host shutoff than do HSV-1 strains (11, 17), and the transfer of UL41 alleles between strains transfers the host shutoff phenotype (9). The most straightforward explanation for these results is that Vhs (UL41) proteins from HSV-2 strains possess a more potent mRNA degradative activity than the homologous HSV-1 polypeptides. However, at present, one cannot rule out the possibility that the more rapid virion host shutoff of HSV-2 is due to more rapid and efficient release of the UL41 polypeptide from infecting virions.

To further examine type-specific differences in Vhs function, we compared the Vhs activities of UL41 alleles from HSV-1 (strain KOS) and HSV-2 (strain 333) by using a transient expression assay in which Vhs activity is measured by the ability of a transfected UL41 allele to inhibit expression of a cotransfected reporter gene. This assay has the advantage that the activities of different UL41 polypeptides can be compared in the absence of other viral gene products, circumventing any complications due to differences between the proteins with regard to packaging or release from virions (19, 29). Both HSV-1 and HSV-2 alleles inhibited reporter gene expression over a range of transfected vhs DNA concentrations. However, 40-fold less of the HSV-2 allele was required to yield the same level of inhibition as HSV-1, indicating that the HSV-2 allele possesses a significantly more potent Vhs activity than its HSV-1 homolog. The cotransfection assay was also used to compare the inhibitory activities of a series of chimeric UL41 alleles containing various mixtures of HSV-1 and HSV-2 sequences. The results identify three regions of the UL41 polypeptide that contribute to type-specific differences in Vhs activity. Furthermore, they indicate that more than half of the differences between the vhs alleles are unrelated to their differences in activity.

MATERIALS AND METHODS

Cells. Vero cells were purchased from the American Type Culture Collection and maintained in Eagle’s minimum essential medium (GIBCO) supplemented with 10% (vol/vol) calf serum and antibiotics as described previously (28).
FIG. 1. Construction of p333. The UL41-containing NotI-Not site fragment from HSV-2(333) was excised from plasmid pkCBglN and inserted between the corresponding sites of the vector pCDNAI, to yield the plasmid diagrammed in line 1. The shaded rectangle represents the CMV immediate-early and T7 promoters. The CMV and T7 transcriptional start sites are depicted by arrows. The plasmid shown in line 1 was partially digested with Smal to excise the short Smal fragment from the UL41 5′ untranslated region, and a BglII linker was inserted to generate the plasmid shown in line 2. This plasmid was digested with BglII and BglII to remove the short BglII fragment. The compatible ends generated by BglII and BglII were then religated to yield the plasmid p333, which is shown in line 3. The conserved restriction sites within UL41 which were used to construct the HSV-1HSV-2 chimeras are indicated. HSV-2 sequences are drawn to scale, while vector sequences are not.

Plasmids. (i) Plasmids encoding UL41 from HSV-2. Plasmid pkCBglN contains the 7.3-kb BglII fragment from HSV-2(333) cloned into the BglII site of pkC7 (12). It was provided by Denise Galloway. Construction of p333, in which UL41 from HSV-2(333) is cloned downstream from the cytomegalovirus (CMV) immediate-early and T7 RNA polymerase promoters, is diagrammed in Fig. 1. Briefly, the UL41-containing NotI-Not site fragment was excised from pkCBglN and inserted between the corresponding sites of the vector pCDNAI (Invitrogen). This plasmid was partially digested with Smal to excise the Smal fragment extending from 135 to 482 bp upstream from the UL41 start codon (6), and a BglII linker was inserted. The resulting plasmid was digested with BglII and BamHI to remove the short BamHI-BglII fragment from the upstream side of the gene; the plasmid was recircularized by ligation of the compatible BamHI- and BglII-generated ends. Sequencing of p333 confirmed that the authentic UL41 start codon is the first AUG from the 5′ end of mRNAs produced in vivo from the CMV immediate-early promoter or by in vitro transcription using T7 RNA polymerase.

(ii) Plasmids encoding UL41 from HSV-1. Construction of pKOS, which contains UL41 from HSV-1(KOS) cloned downstream from the CMV immediate-early and T7 promoters, is diagrammed in Fig. 2. Plasmid pWT6, described previously (29), contains the UL41-containing BstEII fragment of HSV-1(KOS) cloned into a modified form of the vector pSP64(polyA) (Promega). This plasmid was digested with Sall and BstEII to excise the short Sall-BstEII fragment from the upstream side of UL41, treated with mung bean nuclease to generate blunt ends, and recircularized by blunt-end ligation. A UL41-containing PstI-XbaI fragment was excised and subcloned between the corresponding sites of pCDNAI to yield pKOS. Sequencing of pKOS showed that UL41 is preceded on the upstream side by 89 bp of viral DNA, preceded by a single G:C base pair and then the PstI site from pCDNAI. Sequence analysis confirmed that the authentic UL41 start codon is the first AUG from the 5′ end of mRNAs produced from the CMV immediate-early promoter or by in vitro transcription using T7 RNA polymerase.

(iii) Plasmids encoding UL41 with an amino-terminal extension. pKOS was constructed by subcloning the UL41-containing PstI-XbaI fragment of pWT6 between the corresponding sites of pCDNAI (Fig. 3). Sequencing of pKOS revealed the presence of an in-frame AUG codon upstream from the authentic UL41 start codon, which was generated by the juxtaposition of viral and vector sequences. As a result, pKOS is predicted to encode a Vhs polypeptide consisting of the full-length UL41 product of HSV-1(KOS) with a 32-amino-acid N-terminal extension (Fig. 3). Consistent with this, a 62-kDa Vhs polypeptide is produced by in vitro transcription and translation of pKOS, as well as following transfection of cells with the pKOS allele (data not shown). This is compared to the 58-kDa product that is produced by in vitro transcription and translation of pKOS (data not shown) and which is seen in cells infected with wild-type HSV-1 or cells transfected with a plasmid encoding a wild-type UL41 polypeptide (29, 32).

(iv) Plasmids encoding chimeric UL41 polypeptides. Plasmids encoding chimeric UL41 alleles were constructed by exchanging fragments between p333 and pKOS or pKOS, using restriction sites that are conserved between the HSV-2 and HSV-1 alleles. To exchange fragments encoding amino-terminal portions of the proteins, the plasmids were cleaved in the 5′ polylinker with HindIII and with an enzyme that cleaves within UL41. To exchange carboxy-terminal fragments, the plasmids were digested in the 5′ polylinker with XbaI and with an enzyme that cleaves within UL41. Appropriate restriction fragments were exchanged, and the plasmids were religated. Four restriction sites were used to cleave within UL41. Digestion with NpsI excised the short NpsI fragment from HSV-1 and HSV-2. The HSV-1 allele is depicted in Fig. 1. Similarly, Spel, SacI, and XbaI were used to generate chimeric alleles with recombination junctions after amino acids 208, 243, and 365. Chimeric alleles were given designations that reflect the order of fragments from the parent alleles and the locations of the recombination junctions. For example, K/3/K(208,365) encodes a UL41 polypeptide containing KO5 sequences from amino acids 1 through 208, 333 sequences from amino acids 209 to 365, and KO5 sequences from amino acids 366 to 489. Since the KO5 and 333 polypeptides differ in length by three amino acids, the coordinates used to designate recombination junctions refer to the numbering of amino acids in the HSV-1 sequence. Chimeric alleles were sequenced across the junctions and analyzed by in vitro transcription and translation to confirm that they encode polypeptides of the predicted size which can be immunoprecipitated with UL41-specific rabbit antiserum (32).

DNA isolation and sequencing. Plasmids for use in transfections were prepared from bacterial lysates by using the Maxiprep system as recommended by the manufacturer (Qiagen Corp.). For DNA sequencing, UL41-containing plasmids were denatured, annealed with appropriate primers, and sequenced by using an Applied Biosystems model 377 DNA sequencer in the Molecular Biology Core Facility of the University of Missouri—Kansas City. Sequencing primers were designed based on the published sequences for the UL41 alleles of HSV-1(17) (25) and HSV-2(G) (6) and purchased from Integrated DNA Technologies (Coralville, Iowa).

Transient expression assay for Vhs activity. Vhs activity was measured by determining the ability of a transfected UL41 allele to inhibit expression of a cotransfected reporter gene. Transfections were performed as described previously (29) except that the reporter gene was lacZ rather than one encoding chloramphenicol acetyltransferase. Briefly, Vero cells were plated the day before...
transfection in 60-mm-diameter petri dishes at a density of 2.5 x 10^4 cells/cm^2.

Three to four hours before transfection, the medium was replaced with fresh Eagle's minimum essential medium containing 10% (vol/vol) calf serum. Cultures were transfected with 0.6-ml aliquots containing calcium phosphate coprecipitates of 3 mg of the reporter plasmid pSV-b-Galactosidase (Promega) and various amounts of a UL41-containing effector plasmid. Each transfection mixture also contained enough pcDNAI to maintain the amount of CMV promoter sequences (effector plasmid plus pcDNAI) equal to 0.73 pmol (3 mg of pKOS is 0.73 pmol) and enough salmon sperm carrier DNA to bring the total amount of DNA to 12 mg.

Cell extracts were prepared at 40 to 48 h after transfection and assayed for reporter gene expression by using a β-galactosidase enzyme assay system purchased from Promega. Briefly, cell extracts were aliquoted into 96-well trays and mixed with substrate, and the absorbance at 405 nm was determined at various times over a 2-h interval by using a Molecular Devices Thermo Max Microplate Reader. The β-galactosidase activity in each aliquot was determined from the initial velocity of the enzymatic reaction. For each experiment, triplicate cultures were transfected with each concentration of effector plasmid. For each culture, the amount of β-galactosidase activity was expressed as a fraction of that observed in transfections involving 0.73 pmol of pcDNAI and no UL41-containing

FIG. 2. Construction of pKOS. Plasmid pWT6 is diagrammed in line 1. The large open rectangle represents the UL41 open reading frame from HSV-1(KOS), and the thick lines represent viral sequences comprising the UL41 5' and 3' untranslated regions (UTR). The small shaded rectangles represent sequences derived from vectors. pWT6 was cut to completion with SalI and partially with BstEII to delete the short SalI-BstEII fragment from the 5' untranslated region. The remaining plasmid was digested with mung bean nuclelease and recircularized by blunt-end ligation to yield pKOS, which is shown in line 3. Zigzag lines represent the pcDNAI polylinker, and the small open rectangle represents the region of pcDNAI containing the CMV immediate-early and T7 promoters. The CMV and T7 transcriptional start sites are depicted by arrows. The conserved restriction sites within UL41 which were used to construct the HSV-1/HSV-2 chimeras are indicated. HSV-1 sequences are drawn to scale, while vector sequences are not.

FIG. 3. Structure of pxKOS. The large open rectangle represents the wild-type UL41 open reading frame from HSV-1(KOS), and the solid rectangle represents the 32-amino-acid N-terminal extension which is present in the Vhs protein encoded by pxKOS. The thick line represents viral sequences comprising part of the UL41 3' untranslated region, while the narrow open and shaded rectangles represent sequences from the polylinker of pWT6. Zigzag lines represent the pcDNAI polylinker, and the small open rectangle represents the region of pcDNAI containing the CMV immediate-early and T7 promoters. The CMV and T7 transcriptional start sites are depicted by arrows. HSV-1 sequences are drawn to scale, while vector sequences are not. The nucleotide sequence from the PstI site through the first five codons of the wild-type UL41 polypeptide is shown below the diagram, along with the predicted amino acid sequence of the UL41 polypeptide. The first five amino acids of the authentic UL41 polypeptide are shown in bold, preceded by the 32-amino-acid N-terminal extension in normal type. The ATG start codons utilized by the authentic UL41 polypeptide and by the polypeptide with the N-terminal extension are underlined, as are the PstI and BstEII sites. Nucleotides that are derived from the virus are shown in capital letters, while those derived from the plasmid vector are shown in lowercase. Nucleotide numbers are shown relative to the A of the start codon of the authentic UL41 polypeptide.
For each type of effector allele, the data were plotted to yield a dose-response curve showing inhibition of reporter gene expression as a function of the concentration of effector DNA. A curve was fitted to the data by third-order regression analysis using SigmaPlot version 2.02 (Jandel) and used to determine the concentration of effector DNA required to reduce reporter gene expression to 30% of the control value ([DNA]0.3). Replicate experiments were performed on different days, each yielding a separate dose-response curve and value of [DNA]0.3. These values were then averaged to yield the values of [DNA]0.3 that are reported in Fig. 6 and 7 and to calculate the standard errors of the mean.

Nucleotide sequence accession numbers. The DNA sequences of the UL41 alleles of HSV-1(KOS) and HSV-2(333) have been deposited in GenBank with accession no. AF007815 and AF007816, respectively.

RESULTS

Comparison of the UL41 sequences of HSV-1(KOS) and HSV-2(333). The sequences of the UL41 alleles of HSV-1(17) and HSV-2(G) have been published elsewhere (6, 25). Nevertheless, before comparing the activities of the UL41 alleles from HSV-1(KOS) and HSV-2(333), it was necessary to determine their sequences. On the basis of the nucleic acid sequence, HSV-1(KOS) is predicted to encode a 489-amino-acid UL41 polypeptide that is identical to that of HSV-1(17) except at amino acids 19, 317, 384, and 385 (Fig. 4). Interestingly, strain 17 has been reported to encode a particularly weak vhs function (9), suggesting that some of these changes may affect activity. In addition to the single-nucleotide changes which give rise to these differences in the protein sequence, the KOS allele contains six single-nucleotide changes that do not alter the amino acid sequence from that predicted for strain 17 (Table 1).

Comparison of the UL41 sequences of HSV-1(17) and HSV-2(333). The sequences of the UL41 alleles of HSV-1(17) and HSV-2(333) have been deposited in GenBank with accession no. AF007815 and AF007816, respectively.

![FIG. 4. Comparison of amino acid sequences of UL41 polypeptides encoded by various strains of HSV-1 and HSV-2. The predicted amino acid sequence of the UL41 polypeptide encoded by HSV-1(KOS) is shown in line 2 and compared to the published sequences of the UL41 polypeptides of HSV-1(17) (line 1) (25) and HSV-2(G) (line 4) (6), as well as to the sequence predicted for HSV-2(333) (line 3). Dashes in the sequences for strains 17, G, and 333 represent amino acids that are identical to those in KOS. Amino acids which differ between the UL41 polypeptides of KOS and strain 17 are shown in bold. The threonine at position 214 of the KOS polypeptide, which is changed to an isoleucine in the mutant vhs1, is shaded and underlined. Asterisks are introduced at three locations in the sequences of the HSV-1 strains to maintain maximal alignment with the polypeptides encoded by the HSV-2 strains, which are three amino acids longer. The amino acid numbers refer to the HSV-1 polypeptides. The single amino acid which differs between the UL41 polypeptides of HSV-2 strains 333 and G is shown in bold.](http://jvi.asm.org/ on August 28, 2017 by guest)
TABLE 1. Differences between the UL41 sequences of HSV-1(KOS) and HSV-1(17)*

<table>
<thead>
<tr>
<th>Nucleotide</th>
<th>Amino acid</th>
<th>Nucleotide</th>
<th>Amino acid</th>
</tr>
</thead>
<tbody>
<tr>
<td>A(56)</td>
<td>Q(19)</td>
<td>G(56)</td>
<td>R(19)</td>
</tr>
<tr>
<td>C(95)</td>
<td>I(31)</td>
<td>T(93)</td>
<td>I(31)</td>
</tr>
<tr>
<td>A(315)</td>
<td>Q(105)</td>
<td>G(315)</td>
<td>Q(105)</td>
</tr>
<tr>
<td>A(636)</td>
<td>T(212)</td>
<td>G(636)</td>
<td>T(212)</td>
</tr>
<tr>
<td>T(922)</td>
<td>L(308)</td>
<td>C(922)</td>
<td>L(308)</td>
</tr>
<tr>
<td>T(950)</td>
<td>M(317)</td>
<td>C(950)</td>
<td>T(317)</td>
</tr>
<tr>
<td>G(1154)</td>
<td>S(384)</td>
<td>A(1151)</td>
<td>K(384)</td>
</tr>
<tr>
<td>G(1154)</td>
<td>R(385)</td>
<td>C(1154)</td>
<td>P(385)</td>
</tr>
<tr>
<td>T(1353)</td>
<td>I(451)</td>
<td>C(1353)</td>
<td>I(451)</td>
</tr>
<tr>
<td>C(1405)</td>
<td>L(469)</td>
<td>T(1405)</td>
<td>L(469)</td>
</tr>
</tbody>
</table>

* Nucleotide numbers (in parentheses) are given relative to the A of the UL41 start codon. Amino acid numbers are shown in parentheses. Nucleotide differences that result in amino acid differences are shown in bold. The strain KOS sequence was determined in this study; the strain 17 sequence has been published elsewhere (25).

Comparison of the activities of UL41 alleles. During virus infections, interactions with other viral proteins are likely to influence the activity of the UL41 polypeptide. In particular, UL41 has been shown to interact with the viral transcriptional activator VP16 (32, 35, 36), and this interaction has been implicated as important for controlling the mRNA degradative activity. During virus infections, a domain which is sufficient for interaction with VP16 has been mapped to between amino acids 282 to 353, containing particularly high concentrations of nonidentical amino acids (Fig. 4).

TABLE 2. Differences between the UL41 sequences of HSV-2(333) and HSV-2(G)*

<table>
<thead>
<tr>
<th>Nucleotide</th>
<th>Amino acid</th>
<th>Nucleotide</th>
<th>Amino acid</th>
</tr>
</thead>
<tbody>
<tr>
<td>G(482)</td>
<td>W(161)</td>
<td>C(482)</td>
<td>S(161)</td>
</tr>
<tr>
<td>C(1044)</td>
<td>V(348)</td>
<td>T(1044)</td>
<td>V(348)</td>
</tr>
<tr>
<td>C(1296)</td>
<td>P(432)</td>
<td>A(1296)</td>
<td>P(432)</td>
</tr>
<tr>
<td>C(1306)</td>
<td>L(436)</td>
<td>T(1306)</td>
<td>L(436)</td>
</tr>
</tbody>
</table>

* Nucleotide numbers (in parentheses) are given relative to the A of the UL41 start codon. Amino acid numbers are shown in parentheses. Nucleotide differences that result in amino acid differences are shown in bold. The strain 333 sequence was determined in this study; the strain G sequence has been published elsewhere (6).

The cotransfection assay was next used to compare the Vhs activities of a number of chimeric UL41 alleles containing different mixtures of sequences from KOS and 333. Dose-response curves were determined for each of the chimeras; some examples of which are shown in Fig. 5, and used to determine Vhs activity. The chimeras 3/K(365), which encodes a polypeptide with the first 368 amino acids from strain 333 fused to amino acids 369 through 489 of strain KOS, inhibited lacZ expression as well as the parental strain 333 allele (Fig. 6, line 3). The same was true of 3/K(208) and 3/K(135), which encode UL41 polypeptides with the first 210 and 135 amino acids of strain 333 fused to KOS sequences from the recombination point to the carboxy terminus (Fig. 5; Fig. 6, lines 4 and 5). An important control was provided by 3/K1214(208), which is identical to 3/K(208) except that it encodes an isoleucine instead of threonine at position 214 in the KOS portion of the chimera (Fig. 7, line 4). This is due to the same point mutation as that carried by the mutant vhs 1 (23, 31). When present in a KOS background, this mutation inactivates Vhs activity both during virus infections (20, 28, 31) and in the cotransfection assay (29). As expected, 3/K1214(208) did not inhibit lacZ expression in the cotransfection assay (Fig. 7, line 4). The data indicate that differences were due, at least in part, to differences in the interaction of UL41 with VP16 or other viral proteins. In view of this, it was desirable to compare the activities of UL41 alleles by using an assay that allows measurement of Vhs activity in the absence of other viral gene products.

FIG. 5. Dose-response curves for the inhibition of reporter gene expression by wild-type and chimeric UL41 alleles. Replicate cultures were transfected with 3 μg of a plasmid carrying the lacZ reporter gene and the indicated amounts of various UL41 effector genes. LacZ expression was determined at 40 to 48 h after transfection and expressed as a fraction of that observed for transfections involving the pcDNAI vector and no UL41 effector gene. Error bars represent standard errors of the mean. For data points where no error bars are seen, the error bars were smaller than the data point.
within the first 135 amino acids of UL41 from strains KOS and 333 play a major role in the greater inhibitory activity of the strain 333 polypeptide. This region of the polypeptides contains only 10 nonidentical amino acids (Fig. 4).

The chimera K/3/K(135,208) encodes a UL41 polypeptide containing the first 135 amino acids from strain KOS fused to amino acids 136 through 210 of strain 333, followed by amino acids 209 to 489 of KOS (Fig. 6, line 6). This chimera exhibits an inhibitory activity that is indistinguishable from that of its KOS parent. Thus, the introduction of amino acids 136 and 210 from strain 333 into a KOS background does not increase the activity of the KOS polypeptide. This region contains a cluster of 11 nonidentical amino acids within a stretch of 20 residues, implying that these differences are unrelated to the difference in Vhs activity of KOS and 333.

The chimera K/3/K(208,365) encodes a UL41 polypeptide containing the first 208 amino acids from strain KOS fused to amino acids 211 through 368 of strain 333, followed by amino acids 366 to 489 of KOS (Fig. 6, line 7). The inhibitory activity of this allele was intermediate between those of its KOS and 333 parents, indicating that the introduction of residues between amino acids 211 and 368 of strain 333 is able to increase the activity of KOS somewhat. This improvement was due to residues between amino acids 210 and 245 of strain 333 because the chimera K/3/K(208,243) exhibited an inhibitory activity that was indistinguishable from that of K/3/K(208,365).
(Fig. 5; Fig. 6, line 8), while the activity K/3/K(243,365) was the same as that of the KOS parent (Fig. 5; Fig. 6, line 9). Interestingly, the region of the 333 polypeptide (amino acids 210 to 245) responsible for the improved activity contains only six amino acids that are nonidentical to those of KOS (Fig. 1). In contrast, the region from amino acids 246 to 368, which does not improve KOS activity, contains 31 nonidentical residues.

Analysis of the 3/K(365) chimera revealed another region of the strain 333 allele which improves the activity of the KOS allele when inserted into a KOS background. This allele encodes a UL41 polypeptide containing amino acids 1 through 365 from KOS fused to amino acids 369 through 492 of strain 333 (Fig. 6, line 10). It inhibited lacZ expression more efficiently than either the KOS parent or K/3/K(208,243) but not as well as strain 333, requiring six times as much transfected UL41 to achieve the same level of inhibition. Taken together, the data on the UL41 chimeras identify three regions of the strain 333 allele (encoding amino acids 1 to 135, 210 to 245, and 369 to 492) which improve the Vhs activity of the KOS allele when inserted into a KOS background. These are separated by two regions (encoding amino acids 136 to 209 and 246 to 368) which are unrelated to the greater Vhs activity of strain 333.

UL41 alleles encoding Vhs polypeptides with a 32-amino-acid N-terminal extension are active. During early attempts to clone the KOS gene downstream from the CMV immediate-early promoter, we inadvertently constructed a UL41 allele encoding a Vhs polypeptide with a 32-amino-acid N-terminal extension. This was due to the generation of an upstream AUG codon by the juxtaposition of viral and vector sequences (Fig. 3). When tested in the cotransfection assay, this allele inhibited reporter gene expression but required 50% higher concentrations of transfected UL41 than did KOS (Fig. 7, lines 1 and 5). KOS-333 chimeras that contained the N-terminal extension exhibited predictable Vhs activities. For example, xK/3(135), which encodes a UL41 polypeptide containing the 32-amino-
acid extension fused to amino acids 1 through 135 of KOS, followed by amino acids 136 through 492 of 333, inhibited lacZ expression at concentrations that were only fourfold higher than those required by the wild-type strain 333 allele (Fig. 7, lines 2 and 6). Similarly, xK/3(365) inhibited lacZ expression to the same extent as K/3(365) (Fig. 6, line 10; Fig. 7, line 7), while the activities of xK/3(K208,365) and K/3(K208,365) were indistinguishable (Fig. 6, line 7; Fig. 7, line 9). Furthermore, as predicted, the mutation changing threonine to isoleucine at position 214 abolished the activity of alleles containing the N-terminal extension (Fig. 7, line 8). Taken together, the data indicate that UL41 alleles containing the 32-amino-acid N-terminal extension retain considerable Vhs activity.

**DISCUSSION**

In this study, we demonstrate that UL41 from HSV-2(333) is significantly more active than the UL41 allele of HSV-1(KOS) at inhibiting expression of a cotransfected reporter gene in a transient expression assay in which no other viral gene products are present. This difference in UL41 activity parallels the type-specific difference in host shutoff that is observed during virus infections, in which HSV-2 strains generally shut off the host more rapidly and completely than HSV-1 strains. This implies that type-specific differences in host shut off are due primarily to intrinsic differences in the activities of the UL41 polypeptides rather than to differences in their interactions with other viral proteins or in the speed or efficiency with which they are released from infecting virions.

The transient expression assay also was used to characterize the Vhs activities of a series of chimeric UL41 alleles containing various mixtures of HSV-1 and HSV-2 sequences. The results identify three regions of the 333 polypeptide (amino acids 1 through 135, 210 through 245, and 369 through 492) which increase the activity of KOS when substituted for the corresponding amino acids of the KOS protein. These are separated by two regions of the 333 allele (amino acids 136 through 209 and 246 through 368) which have no effect on KOS activity when introduced into a KOS background. Although the KOS and 333 proteins differ at sites scattered throughout UL41, two clusters of amino acids (141 through 160 and 282 through 353) contain particularly high concentrations of nonidentical residues, accounting for 43 of the 74 differences between alleles. Interestingly, both clusters fall within the portions of the 333 polypeptide which have no effect on KOS activity, suggesting that these amino acid differences are unrelated to type-specific differences in activity. On the other hand, differences in relatively few amino acids in other portions of the protein can result in major type-specific differences in activity. Of particular note, a chimera encoding a UL41 polypeptide with the first 135 amino acids from strain 333 and the remainder from KOS exhibits a Vhs activity that is indistinguishable from that of 333, even though it differs from KOS at only 10 amino acids. Similarly, a chimera with amino acids 210 through 245 from 333 and the rest from KOS differs from KOS at only six amino acids yet exhibits a Vhs activity that is intermediate between those of KOS and 333.

These results are consistent with those of previous studies which examined the effects of various linker insertion mutations on the activity of UL41 from HSV-1(KOS) (19, 29). Those experiments (summarized in Fig. 6, line 1) identified three regions of UL41 in which linker insertion mutations abolish activity. These regions roughly correspond to the three portions of UL41 which were shown in the present study to be responsible for the type-specific differences in Vhs activity and which are highly conserved among the UL41 homologs of other alphaherpesviruses (2). The earlier studies also identified two regions of UL41 which tolerate linker insertion mutations without the loss of activity (19, 29); these fall within the two portions of UL41 which are unrelated to type-specific differences in activity (Fig. 6, line 1). In this light, it is interesting that the additional three-amino-acid length of the strain 333 polypeptide relative to that of KOS is due to the insertion of two amino acids after residue 150 and of one amino acid after residue 351 (Fig. 4). Both of these sites fall within the regions of UL41 which tolerate linker insertions and are unrelated to type-specific differences in activity. These regions are also entirely missing from the UL41 homologs of some alphaherpesviruses (2), further supporting the notion that their precise sequences are not critical to Vhs activity.

These experiments also demonstrate that UL41 alleles encoding polypeptides with a 32-amino-acid N-terminal extension retain considerable activity. Thus, although addition of the N-terminal extension to the KOS polypeptide increased the [DNA]0.3 by 50%, other alleles containing both the N-terminal extension and key regions of the 333 allele exhibited activities which were considerably greater than that of KOS. This result may be of practical importance for the purification of active Vhs protein, since it suggests that many UL41 polypeptides which have been modified by the addition of an epitope tag at the amino terminus will remain active.

The present results should be interpreted with the caveat that, because different UL41 alleles may express different amounts of the Vhs polypeptide in transfected cells, the transient expression assay does not provide a quantitative measure of the specific mRNA degradative activities of different UL41 polypeptides. For example, some chimeric proteins may differ in stability, leading to differences in the amounts that are present in transfected cells. In addition, the transient expression assay probably underestimates the difference between the activities of the KOS and 333 polypeptides. Because the UL41 polypeptide accelerates degradation of all mRNAs (30), it should be autoregulatory, degrading its own mRNA and decreasing the amount of UL41 protein that is produced in transfected cells. This effect should be greatest for the most active UL41 alleles. That this actually is the case is suggested by previous experiments which found several times more of the Vhs polypeptide in cells transfected with the inactive UL41 allele of the mutant vhs 1 than in cells transfected with the wild-type KOS allele (29). A qualitatively similar result has been obtained in studies using indirect immunofluorescence to visualize the UL41 polypeptide in cells transfected with the wild-type KOS allele and with the chimera 3/K(208), which exhibits an activity similar to that of 333. In these experiments, which used antisera raised against a UL41-LacZ fusion protein containing amino acids 239 through 489 of the KOS polypeptide (29) [a region that is common to both the KOS and 3/K(208) polypeptides], staining of cells transfected with 3/K(208) was much less intense than staining of those transfected with KOS (29a).

The three regions of the 333 polypeptide which increase KOS activity do so when substituted for the corresponding regions of KOS either individually or in combination. This finding is consistent with the possibility that these regions encode functionally independent domains of the protein that can be interchanged to yield functional UL41 proteins containing different combinations of KOS and 333 domains. In contrast, recent studies using site-directed mutagenesis of the KOS allele to change individual amino acids to their strain 333 counterparts have revealed one residue at which changing from the KOS to the 333 amino acid abolishes UL41 activity. However, if this change is made in conjunction with five other type-
specific changes within the same putative domain, the result is a chimeric protein with an activity that is significantly greater than that of KOS (6a), suggesting that the six type-specific residues are part of the same functional domain of the protein. If the UL41 polypeptide does, in fact, contain separate functional domains, the biochemical activities of those domains remain to be elucidated. Although obvious UL41 homologs exist in a number of alphaherpesviruses, computer searches of protein sequence databases have not revealed large-scale homologies between UL41 and known cellular proteins. However, comparison of short stretches of the UL41 polypeptide to cellular sequences reveals a region of 30 amino acids that is contained within the central conserved domain of UL41 and which is strikingly similar to sequences found in a number of cellular nucleases. The sequence of the UL41 polypeptide of HSV-1(KOS) from amino acids 191 through 220 is shown in line 13, aligned with the homologous sequences from the UL41 polypeptides of other alphaherpesviruses (lines 8 through 12). Homologous sequences from a number of cellular nucleases are shown in lines 1 through 7. Amino acids identical to those in the UL41 polypeptide of HSV-1(KOS) are shaded, while conservative changes are boldfaced and underlined. The location of the point mutation carried by the mutant vhs 1, which changes a threonine to an isoleucine at position 214 of the HSV-1(KOS) polypeptide and which inactivates Vhs activity, is shown by the arrows below line 13. BHS, bovine herpesvirus; PRV, pseudorabies virus; EVH-1, equine herpesvirus 1; VZV, varicella-zoster virus.

FIG. 8. Similarity between sequences of a conserved region of the UL41 polypeptides from alphaherpesviruses and sequences found in a number of cellular nucleases. The sequence of the UL41 polypeptide of HSV-1(KOS) from amino acids 191 through 220 is shown in line 13, aligned with the homologous sequences from the UL41 polypeptides of other alphaherpesviruses (lines 8 through 12). Homologous sequences from a number of cellular nucleases are shown in lines 1 through 7. Amino acids identical to those in the UL41 polypeptide of HSV-1(KOS) are shaded, while conservative changes are boldfaced and underlined. The location of the point mutation carried by the mutant vhs 1, which changes a threonine to an isoleucine at position 214 of the HSV-1(KOS) polypeptide and which inactivates Vhs activity, is shown by the arrows below line 13. BHS, bovine herpesvirus; PRV, pseudorabies virus; EVH-1, equine herpesvirus 1; VZV, varicella-zoster virus.

ACKNOWLEDGMENTS

We thank Mary Patterson for helpful discussions concerning all aspects of these experiments. We are indebted to Denise Galloway for providing plasmids, to Alfred Esser for allowing us to use his 96-well plate reader, and to J. T. Vida of the UMKC Molecular Biology Core Facility for sequencing the various UL41 alleles. We also thank Kelley Thomas for helpful discussions concerning DNA sequencing.

This work was supported by grant AI21501 from the National Institute of Allergy and Infectious Diseases and by a grant from the University of Missouri Research Board.

REFERENCES