



US008765444B2

(12) **United States Patent**
He et al.

(10) **Patent No.:** **US 8,765,444 B2**
(45) **Date of Patent:** **Jul. 1, 2014**

(54) **COMPOSITIONS AND METHODS USING
HERPES SIMPLEX VIRUS**

(75) Inventors: **Bin He**, Chicago, IL (US); **Dustin
Verpooten**, Schererville, IN (US); **Yijie
Ma**, Chicago, IL (US)

(73) Assignee: **The Board of Trustees of the
University of Illinois**, Urbana, IL (US)

(*) Notice: Subject to any disclaimer, the term of this
patent is extended or adjusted under 35
U.S.C. 154(b) by 479 days.

(21) Appl. No.: **12/836,856**

(22) Filed: **Jul. 15, 2010**

(65) **Prior Publication Data**

US 2011/0052630 A1 Mar. 3, 2011

Related U.S. Application Data

(60) Provisional application No. 61/225,710, filed on Jul.
15, 2009, provisional application No. 61/225,736,
filed on Jul. 15, 2009.

(51) **Int. Cl.**
C12N 7/00 (2006.01)
C12N 7/04 (2006.01)
A61K 39/245 (2006.01)

(52) **U.S. Cl.**
USPC **435/235.1**; 435/236; 424/231.1

(58) **Field of Classification Search**
CPC A61K 39/12; C12N 2710/16011;
C12N 2710/16021; C12N 2710/16034; C12N
2710/16062; C12N 15/00
See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

5,585,096 A * 12/1996 Martuza et al. 424/93.2
7,264,814 B2 * 9/2007 Nishiyama 424/199.1

OTHER PUBLICATIONS

Chou et al., Science, 1990, 250:1262-1266.*
EMULSIGEN®-D Technical Bulletin, available from www.mvp-
technologies.com/adjuvants/Emulsigen_D.pdf, 2 pages, copyright
2006.*

* cited by examiner

Primary Examiner — Stacy B. Chen

(74) *Attorney, Agent, or Firm* — Polsinelli PC; Teddy C.
Scott, Jr.; Ron Galant

(57) **ABSTRACT**

Provided herein are methods and compositions for use in
treating HSV-related conditions and diseases.

9 Claims, 14 Drawing Sheets

Figure 1

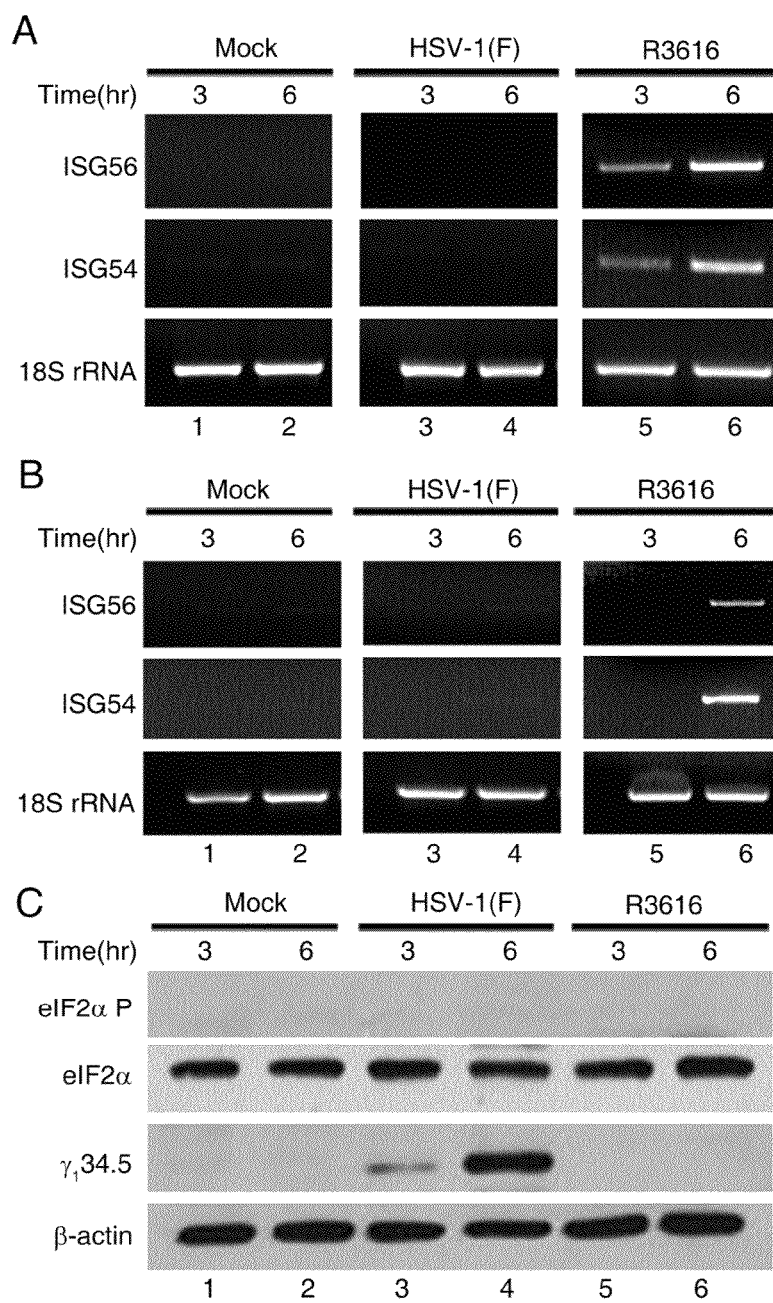


Figure 2

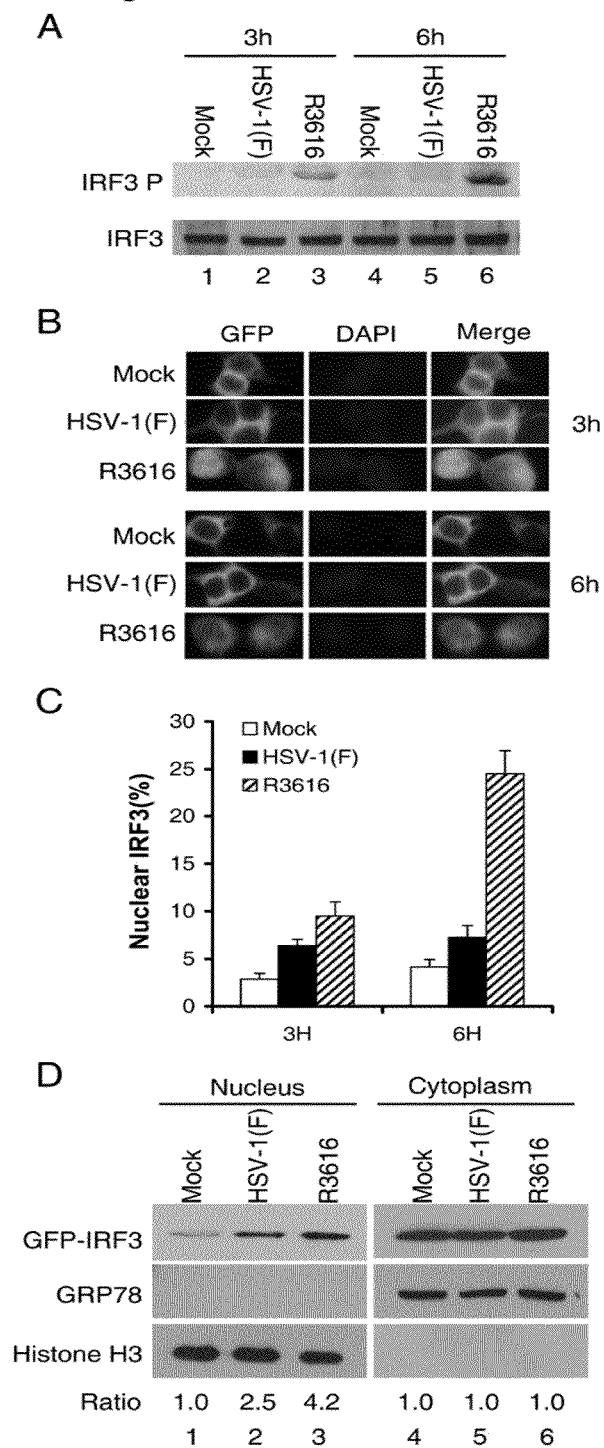


FIG. 3

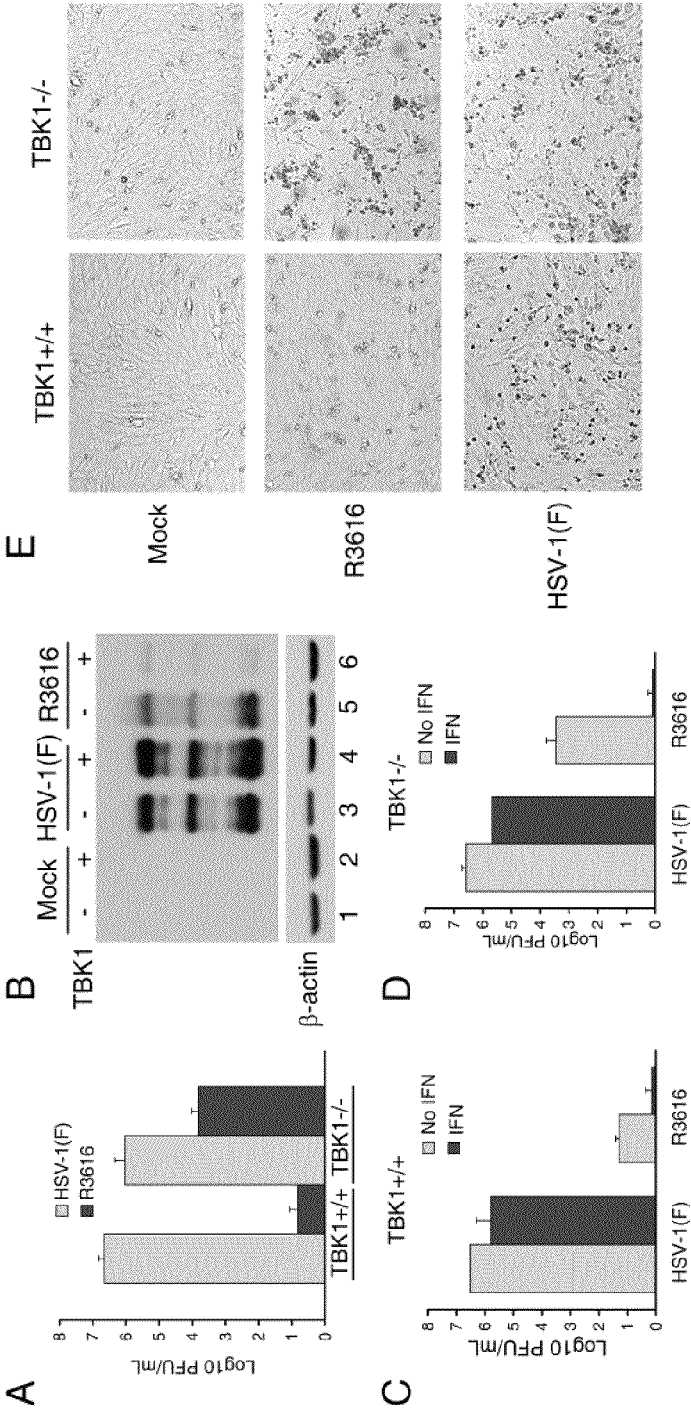


FIG. 4

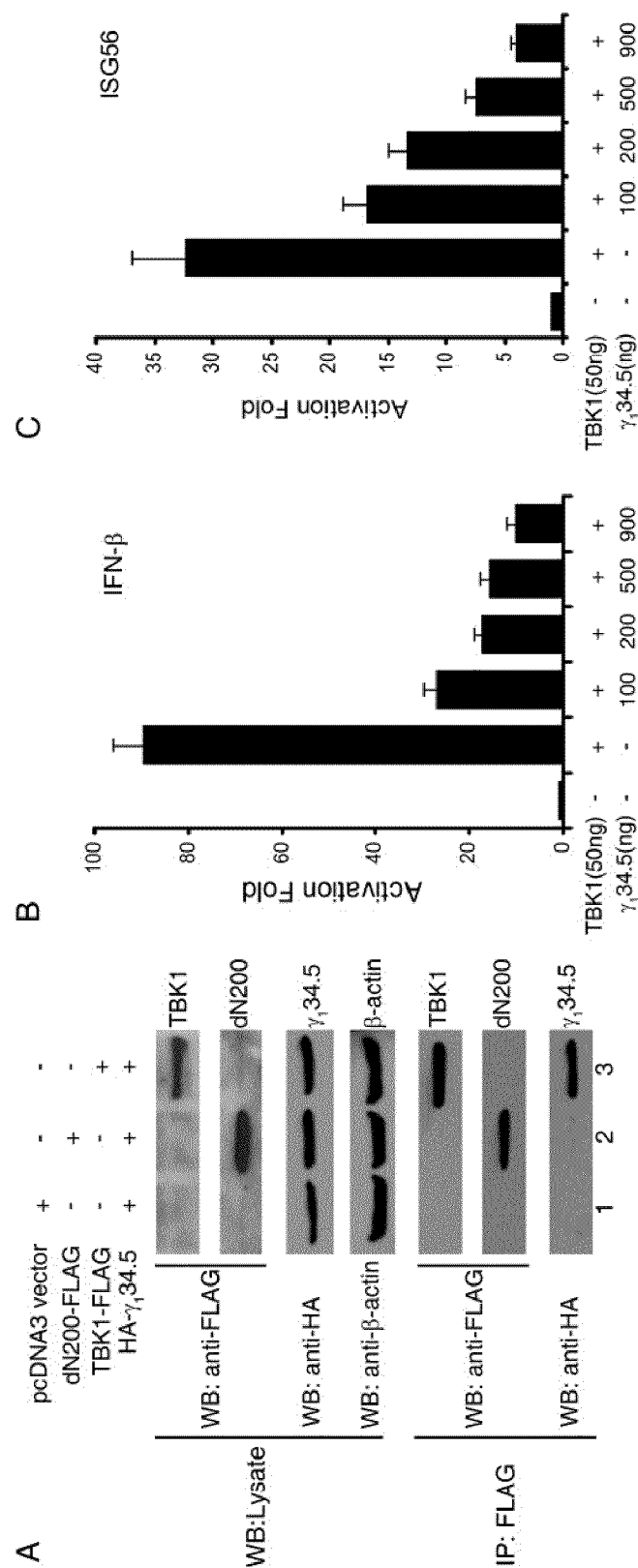


Figure 5

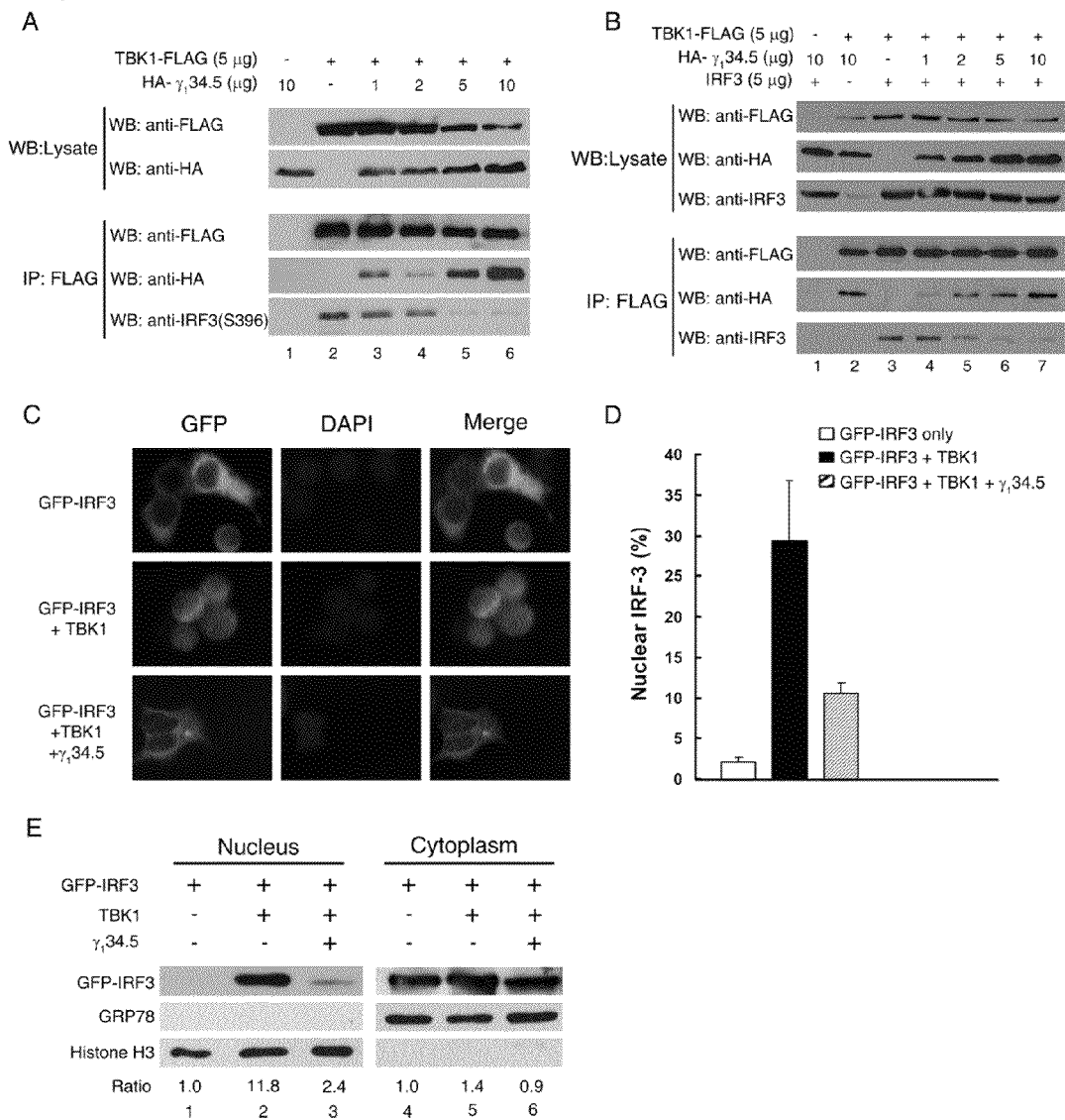


FIG. 6

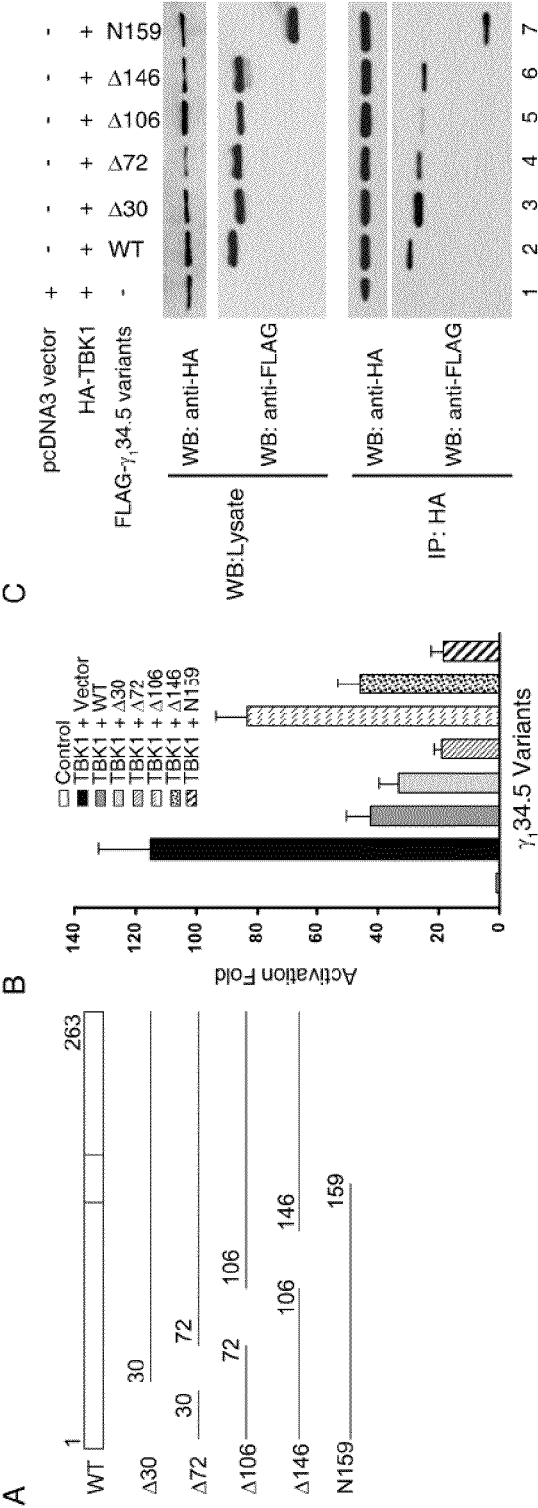


FIG. 7

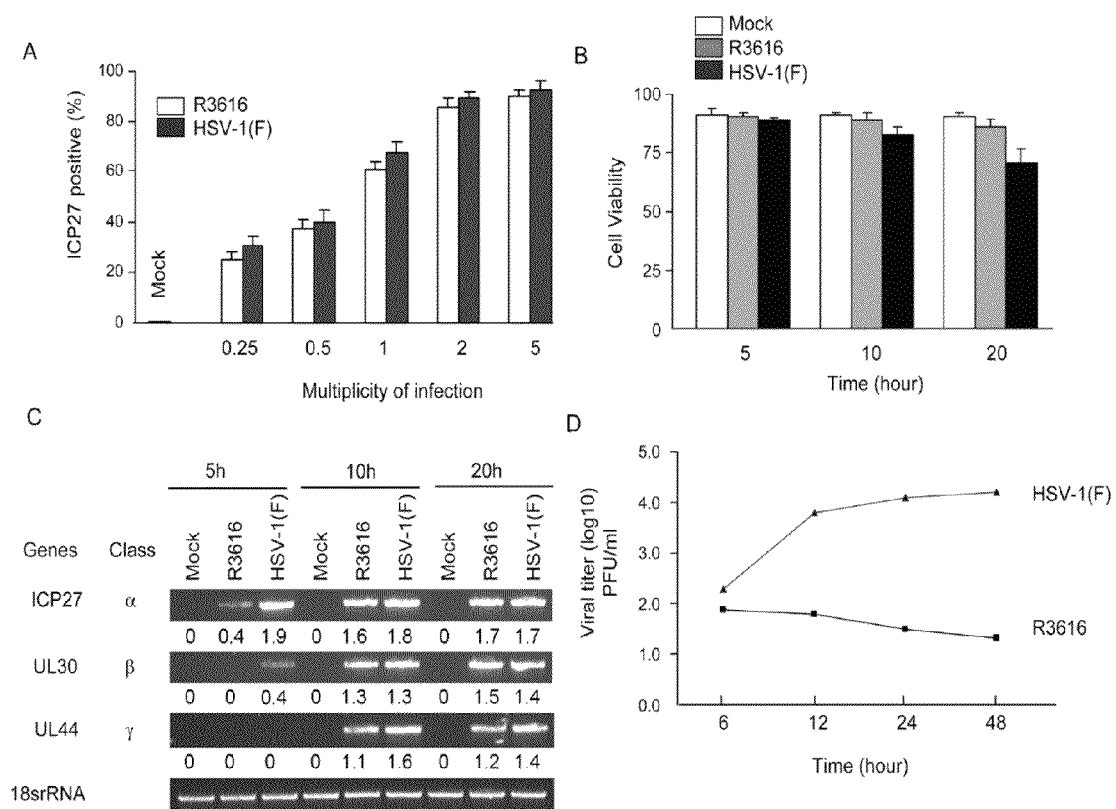


FIG. 8

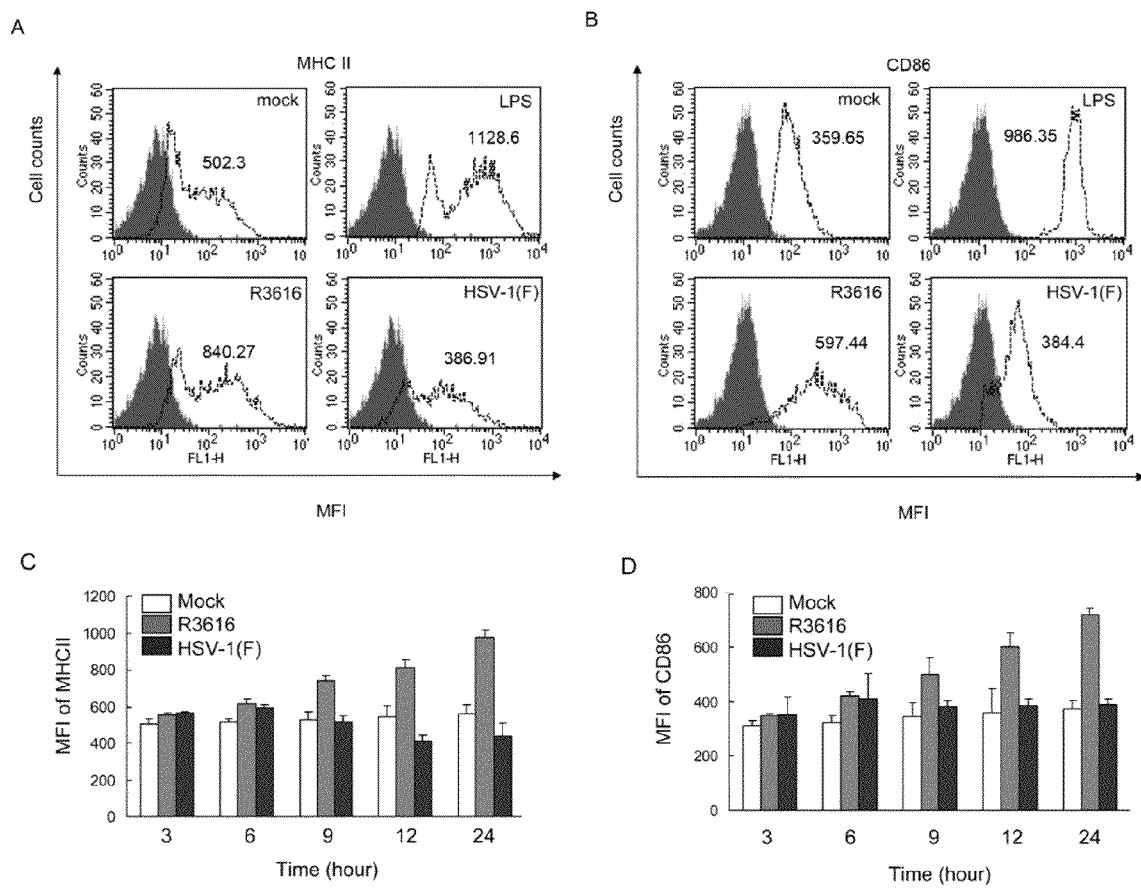


FIG. 9

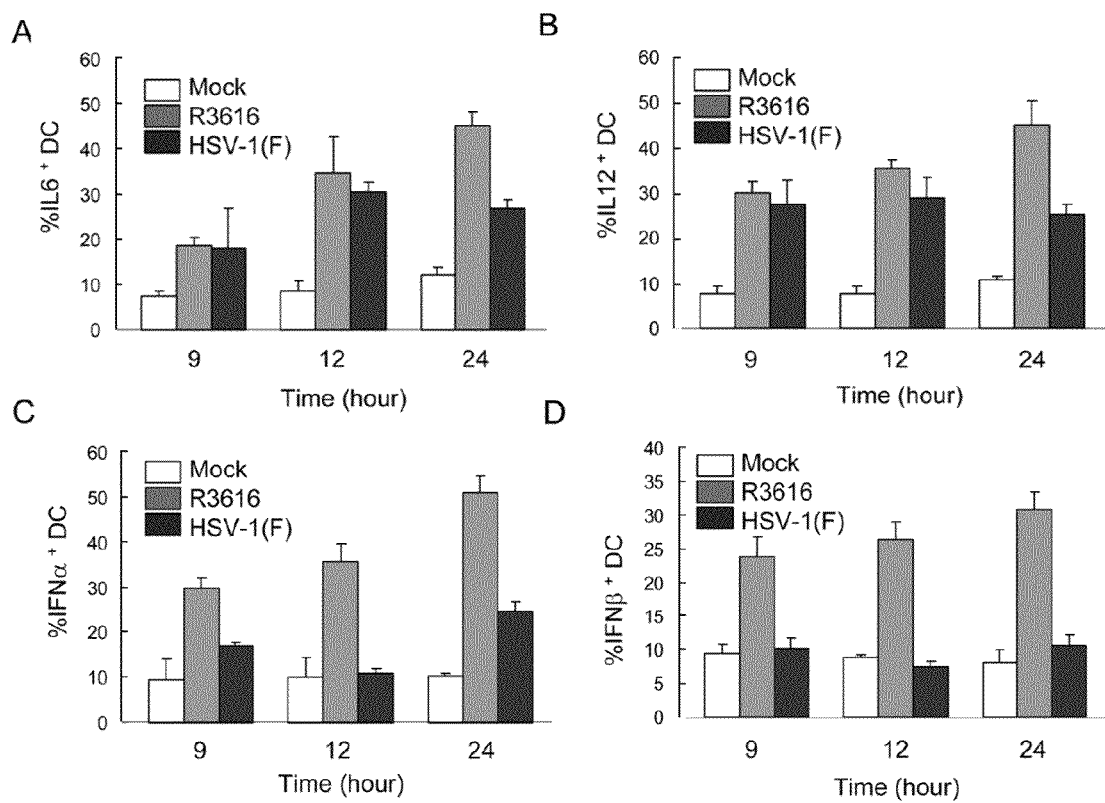


FIG. 10

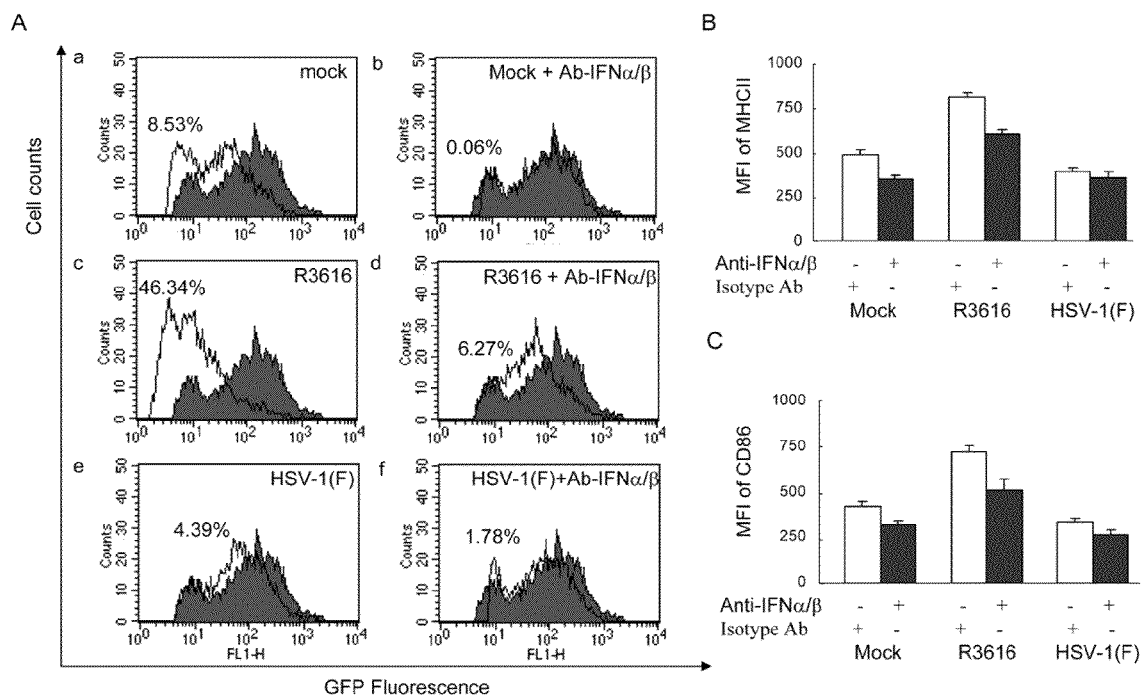


FIG. 11

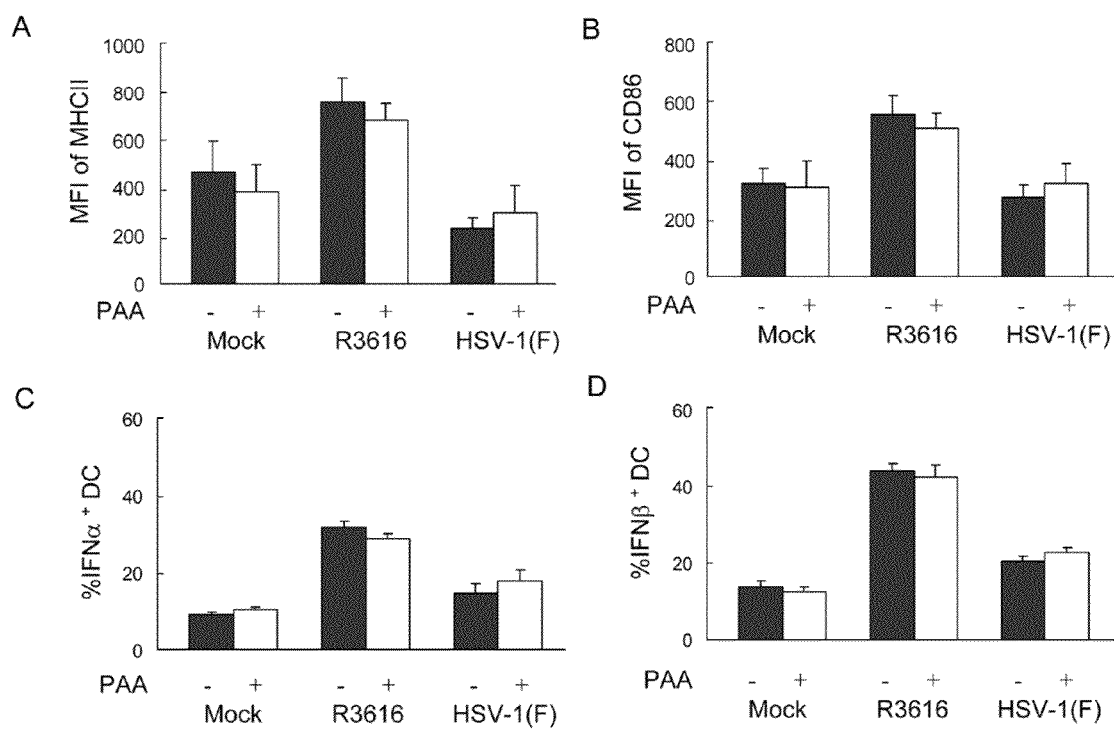
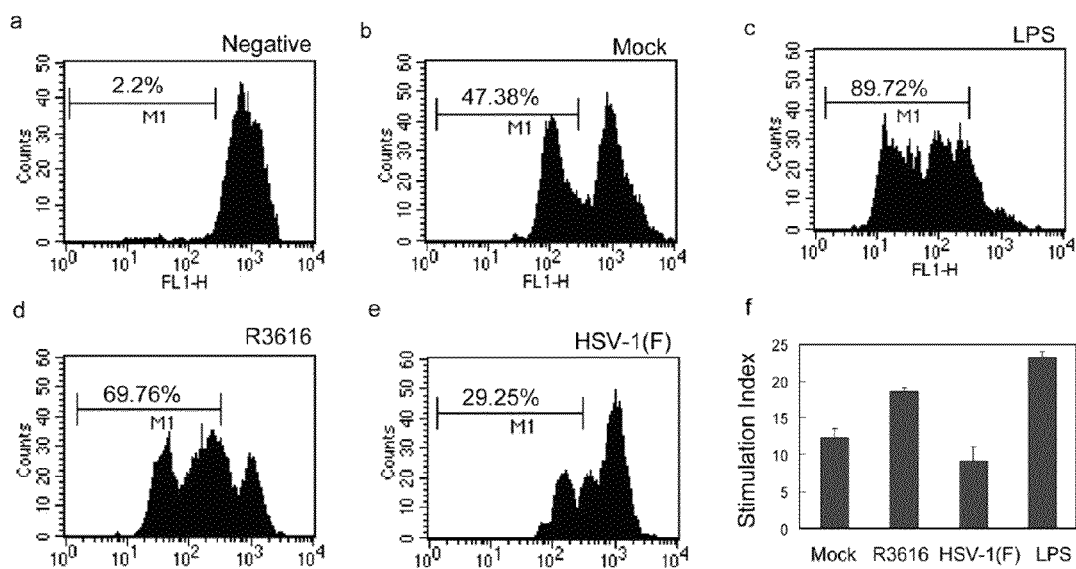


FIG. 12

A



B

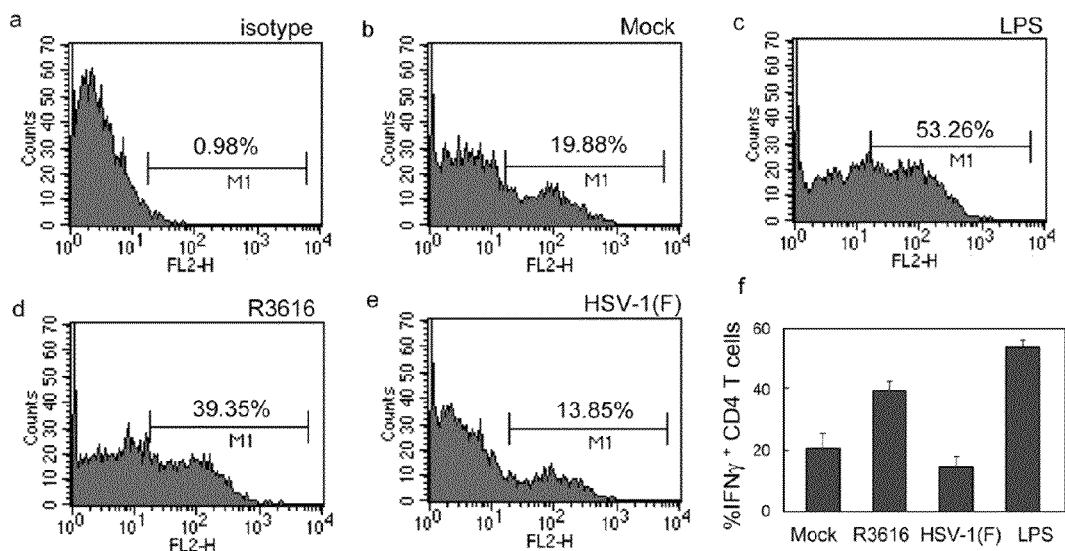


FIG. 13

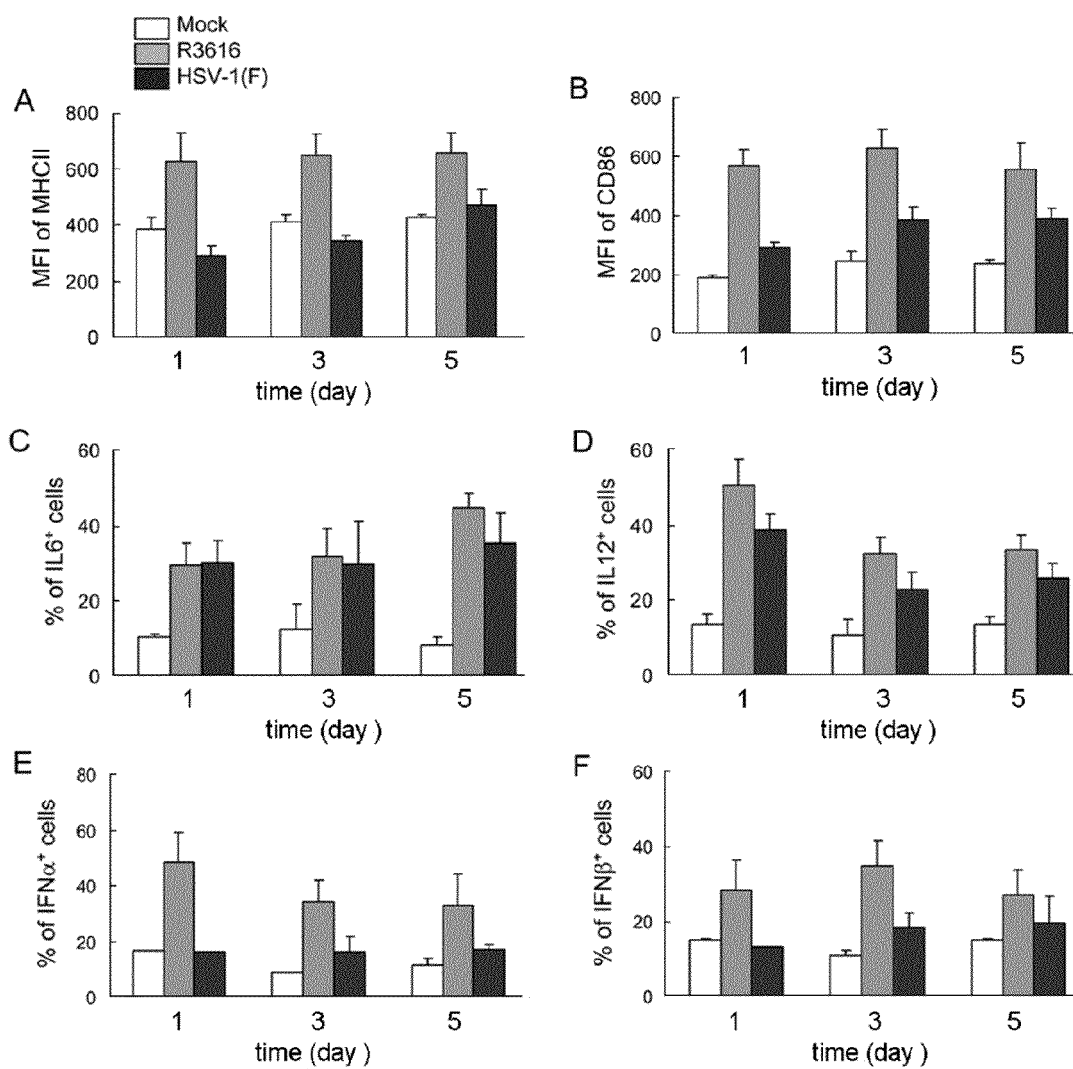
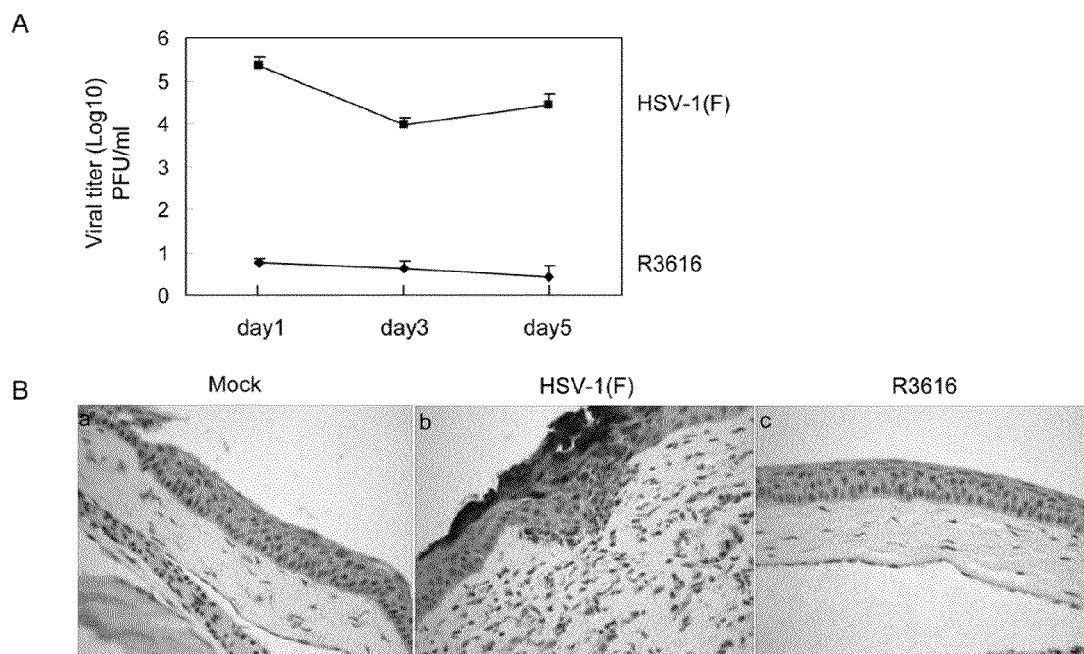


FIG. 14



1

COMPOSITIONS AND METHODS USING HERPES SIMPLEX VIRUS

FEDERALLY SPONSORED RESEARCH

This invention was made with government support under the National Institutes of Health grant number NIH AI 046665. The government has certain rights in the invention.

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. Provisional Application Nos. 61/225,710, filed on Jul. 15, 2009, and 61/225,736, also filed on Jul. 15, 2009, which are both incorporated by reference in their entirety.

FIELD OF THE INVENTION

The present invention relates to the development and use of γ_1 34.5 nucleic acid and protein from HSV-1 and/or TANK-binding kinase-1 (TBK1) for identifying compounds for use in preventing or treating HSV-related conditions and diseases.

REFERENCE TO THE SEQUENCE LISTING

Applicant hereby makes reference to the sequence listing, which is contained in a file named "SequenceListing.txt" (18 Kb, created Feb. 15, 2013) and incorporated herein by reference.

BACKGROUND

HSV-1 infections are common and affect between 70 and 80 percent of the total population in the United States. Several manifestations of HSV disease cause significant morbidity and mortality. For example, HSV disease in an immunocompromised host will often result in progressive infection, particularly in stem cell transplant recipients. HSV infection is also a risk factor in HIV infection and transmission. HSV-1 is a human pathogen responsible for localized mucocutaneous lesions and encephalitis, and is transmitted via body secretions and/or direct oral and sexual contact.

During infection of a cell, expression of HSV proteins interferes with the induction of antiviral immunity. One such protein, the γ_1 34.5 protein, consists of 263 amino acids and is essential in the pathogenesis of HSV infection. In the targeted/infected host cell, TBK1 is a key component of Toll-like receptor-dependent and -independent signaling pathways. In response to microbial components, TBK1 activates interferon regulatory factor 3 (IRF3) and cytokine expression.

While the γ_1 34.5 protein of HSV-1 has been extensively studied and sequenced in various HSV strains, there is scant evidence to show how the γ_1 34.5 protein is a critical determinant of viral replication. Accordingly, effective use of the γ_1 34.5 protein for treating HSV-related conditions and diseases has been slight. A method to identify compounds that can prevent or treat HSV-1 and HSV-2-related conditions and diseases is desired. Further, a γ_1 34.5 protein-based vaccine having enhanced immunogenicity over other HSV-1 related vaccines is also desired.

SUMMARY OF THE INVENTION

Provided herein is a method for screening for a modulator of γ_1 34.5. The method may comprise providing a cell, which

2

contains TBK1, contacting the cell with a γ_1 34.5 nucleic acid or HSV, and a candidate modulator compound, and measuring a HSV infection biological parameter. The HSV may be HSV-1 or HSV-2. The γ_1 34.5 nucleic acid may be contained within a vector, which is contacted with the cell. The HSV may contain a nucleic acid encoding γ_1 34.5. A modulator of γ_1 34.5 is identified by a change in one or more HSV-1 infection biological parameters as compared to a control. Such parameters include virus yield, interferon regulatory factor-3 (IRF3) phosphorylation, interferon regulatory factor-7 (IRF7) phosphorylation, nuclear translocation of IRF3, TBK1 phosphorylation, interferon expression, and interferon stimulated gene expression. The cell may be a mammalian cell, such as a mammalian dendritic cell, a Vero cell, a 293T cell, a HEL cell, a CHO cell, or a HeLa cell. The cell may express TBK1 and/or IRF3 from one or more transfected nucleic acids and/or from endogenous nucleic acid. The HSV may be contacted with the cell before or after the candidate modulator compound is contacted with the cell.

Also provided herein is a method for screening for a modulator of TBK1. Similarly to the above-described method for screening for modulators of γ_1 34.5, a cell is provided that comprises TBK1. However, the cell is then contacted with a γ_1 34.5 null or γ_1 34.5 truncation HSV mutant and a candidate modulator compound. A modulator is again identified by a change in one or more HSV infection biological parameters as compared to a control. Such parameters include virus yield, interferon regulatory factor-3 (IRF3) phosphorylation, nuclear translocation of IRF3, TBK1 phosphorylation, interferon expression, and interferon stimulated gene expression. The cell may be a mammalian cell, such as a mammalian dendritic cell, a Vero cell, a 293T cell, a HEL cell, a CHO cell, or a HeLa cell. The cell may express TBK1 and/or IRF3 from one or more transfected nucleic acids and/or from endogenous nucleic acid. The HSV-1 may be contacted with the cell before or after the candidate modulator compound is contacted with the cell.

Also provided herein is an attenuated HSV-1 virus that comprises a deletion, which removes a fragment of the amino-terminal domain of γ_1 34.5. This deletion is present in at least one copy of the polynucleotides or genes encoding γ_1 34.5. The removed fragment may consist of amino acid 1 to amino acid 30 or amino acid 30 to amino acid 72 of SEQ ID NO:3. The removed fragment may not be from the amino-terminal domain of γ_1 34.5. Such a fragment may consist of amino acid 159 to amino acid 263 of SEQ ID NO:3.

The attenuated HSV-1 virus may be combined with an adjuvant to form an immunogenic composition. This composition may be used to provoke an immune response against HSV strains in a subject and/or to prevent or reduce the incidence of or severity of a clinical sign associated with HSV infection. Examples of clinical signs include keratitis, gingivostomatitis, pharyngitis, encephalitis, and mucocutaneous lesions.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows the inhibition of ISG54 and ISG56 induction in infected mouse embryonic fibroblasts by HSV-1 γ_1 34.5 protein.

FIG. 2 shows the inhibition of phosphorylation of endogenous IRF3 in infected cells by γ_1 34.5 protein.

FIG. 3 shows viral replication in TBK1^{+/+} and TBK1^{-/-} cells.

FIG. 4 shows association between γ_1 34.5 protein and TBK1.

3

FIG. 5 shows inhibition of TBK1 directed phosphorylation of IRF3 by γ_1 34.5 protein.

FIG. 6 shows various γ_1 34.5 protein variants and their ability to bind TBK1.

FIG. 7 shows effects of viral infection of immature dendritic cells.

FIG. 8 shows effects of γ_1 34.5 on the expression of cell surface molecules.

FIG. 9 shows effects of γ_1 34.5 on cytokine expression

FIG. 10 shows effects of HSV infection on IFN secretion in dendritic cells.

FIG. 11 shows effect of viral DNA replication inhibitor on dendritic cell maturation.

FIG. 12 shows activation of naïve CD4 T cells by dendritic cells.

FIG. 13 shows modulation of dendritic cell maturation by γ_1 34.5 in vivo.

FIG. 14 shows viral replication in the eye.

DETAILED DESCRIPTION

The inventor has discovered that TBK1 is a cellular target of the γ_1 34.5 protein and that γ_1 34.5 protein-TBK1 interaction is necessary for HSV infection and replication. The inventor has used this discovery to develop methods of screening for compounds that modulate the activity of the γ_1 34.5 protein; to develop methods of screening for compounds that modulate the activity of TBK1; and to identify mutant forms of the γ_1 34.5 protein, which can be used as vaccine platforms. Compounds that modulate either of γ_1 34.5 protein or TBK1 may be used in methods to treat HSV-related conditions and diseases including cancer.

1. DEFINITIONS

The terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting. As used in the specification and the appended claims, the singular forms “a,” “and” and “the” include plural references unless the context clearly dictates otherwise.

For the recitation of numeric ranges herein, each intervening number there between with the same degree of precision is explicitly contemplated. For example, for the range of 6-9, the numbers 7 and 8 are contemplated in addition to 6 and 9, and for the range 6.0-7.0, the number 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, and 7.0 are explicitly contemplated.

a. Fragment

“Fragment” as used herein may mean a portion or a nucleic acid that encodes a polypeptide. The fragments may be DNA fragments selected from at least one of the various encoding nucleotide sequences of the present invention, including SEQ ID NOS: 2 and 4. The DNA fragments may be 30 or more nucleotides in length, 45 or more, 60 or more, 75 or more, 90 or more, 120 or more, 150 or more, 180 or more, 210 or more, 240 or more, 270 or more, 300 or more, 360 or more, 420 or more, 480 or more, 540 or more, 600 or more, 660 or more, 720 or more, 780 or more, 840 or more, 900 or more, 960 or more, 1020 or more, 1080 or more, 1140 or more, 1200 or more, 1260 or more, 1320 or more, 1380 or more, 1440 or more, 1500 or more, 1560 or more, 1620 or more, 1680 or more, 1740 or more, 1800 or more, 1860 or more, 1820 or more, 1880 or more, 1940 or more, 2000 or more, 2600 or more, 2700 or more, 2800 or more, 2900 or more, 2910 or more, 2920 or more, 2930 or more, 2931 or more, 2932 or more, 2933 or more, 2934 or more, 2935 or more, 2936 or more, 2937 or more, or 2938 or more in length

4

DNA fragments may be fewer than 10 nucleotides, fewer than 20, fewer than 30, fewer than 40, fewer than 50, fewer than 60, fewer than 75, fewer than 90, fewer than 120, fewer than 150, fewer than 180, fewer than 210, fewer than 240, fewer than 270, fewer than 300, fewer than 360, fewer than 420, fewer than 480, fewer than 540, fewer than 600, fewer than 660, fewer than 720, fewer than 780, fewer than 840, fewer than 900, fewer than 960, fewer than 1020, fewer than 1080, fewer than 1140, fewer than 1200, fewer than 1260, fewer than 1320, fewer than 1380, fewer than 1440, fewer than 1500, fewer than 1560, fewer than 1620, fewer than 1680, or fewer than 1740 nucleotides, fewer than 1800, fewer than 1860, fewer than 1820, fewer than 1880, fewer than 1940, fewer than 2000, fewer than 2600, fewer than 2700, fewer than 2800, fewer than 2900, fewer than 2910, fewer than 2920, fewer than 2930, fewer than 2931, fewer than 2932, fewer than 2933, fewer than 2934, fewer than 2935, fewer than 2936, fewer than 2937, or fewer than 2938.

“Fragment” may also mean a polypeptide fragment. The fragment may be polypeptide fragment selected from at least one of the various encoding polypeptide sequences of the present invention, including SEQ ID NOS: 1 and 3. The polypeptide fragments may be 30 or more amino acids in length, 45 or more, 60 or more, 75 or more, 90 or more, 120 or more, 150 or more, 180 or more, 210 or more, 240 or more, 270 or more, 300 or more, 360 or more, 420 or more, 480 or more, 540 or more, 600 or more, 660 or more, or 710 amino acids or more in length

Polypeptide fragments may be fewer than 10 amino acids, fewer than 20, fewer than 30, fewer than 40, fewer than 50, fewer than 60, fewer than 75, fewer than 90, fewer than 120, fewer than 150, fewer than 180, fewer than 210, fewer than 240, fewer than 270, fewer than 300, fewer than 360, fewer than 420, fewer than 480, fewer than 540, fewer than 600, fewer than 660, fewer than 700, fewer than 701, fewer than 702, fewer than 703, fewer than 704, fewer than 705, fewer than 706, fewer than 707, fewer than 708, fewer than 709, or fewer than 710 amino acids in length.

b. Identical

“Identical” or “identity” as used herein in the context of two or more nucleic acids or polypeptide sequences, may mean that the sequences have a specified percentage of residues that are the same over a specified region. The percentage may be calculated by optimally aligning the two sequences, comparing the two sequences over the specified region, determining the number of positions at which the identical residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the specified region, and multiplying the result by 100 to yield the percentage of sequence identity. In cases where the two sequences are of different lengths or the alignment produces one or more staggered ends and the specified region of comparison includes only a single sequence, the residues of single sequence are included in the denominator but not the numerator of the calculation. When comparing DNA and RNA, thymine (T) and uracil (U) may be considered equivalent. Identity may be performed manually or by using a computer sequence algorithm such as BLAST or BLAST 2.0.

c. Immune Response

“Immune response” as used herein may mean the activation of a host’s immune system, e.g., that of a mammal, in response to the introduction of a γ_1 34.5 protein, or variant thereof, or exogenous gene thereof, via the provided HSV-related vaccines. The immune response can be in the form of a cellular or humoral response, or both.

d. Nucleic Acid

"Nucleic acid" or "oligonucleotide" or "polynucleotide" as used herein may mean at least two nucleotides covalently linked together. The depiction of a single strand also defines the sequence of the complementary strand. Thus, a nucleic acid also encompasses the complementary strand of a depicted single strand. Many variants of a nucleic acid may be used for the same purpose as a given nucleic acid. Thus, a nucleic acid also encompasses substantially identical nucleic acids and complements thereof. A single strand provides a probe that may hybridize to a target sequence under stringent hybridization conditions. Thus, a nucleic acid also encompasses a probe that hybridizes under stringent hybridization conditions.

Nucleic acids may be single stranded or double stranded, or may contain portions of both double stranded and single stranded sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine and isoguanine. Nucleic acids may be obtained by chemical synthesis methods or by recombinant methods.

A nucleic acid will generally contain phosphodiester bonds, although nucleic acid analogs may be included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoramidate linkages and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Pat. Nos. 5,235,033 and 5,034,506, which are incorporated by reference. Nucleic acids containing one or more non-naturally occurring or modified nucleotides are also included within one definition of nucleic acids. The modified nucleotide analog may be located for example at the 5'-end and/or the 3'-end of the nucleic acid molecule. Representative examples of nucleotide analogs may be selected from sugar- or backbone-modified ribonucleotides. It should be noted, however, that also nucleobase-modified ribonucleotides, i.e. ribonucleotides, containing a non-naturally occurring nucleobase instead of a naturally occurring nucleobase such as uridines or cytidines modified at the 5-position, e.g. 5-(2-amino)propyl uridine, 5-bromo uridine; adenosines and guanosines modified at the 8-position, e.g. 8-bromo guanosine; deaza nucleotides, e.g. 7-deaza-adenosine; O- and N-alkylated nucleotides, e.g. N6-methyl adenosine are suitable. The 2'-OH-group may be replaced by a group selected from H, OR, R, halo, SH, SR, NH₂, NHR, NR₂ or CN, wherein R is C₁-C₆ alkyl, alkenyl or alkynyl and halo is F, Cl, Br or I. Modified nucleotides also include nucleotides conjugated with cholesterol through, e.g., a hydroxyprolinol linkage as described in Krutzfeldt et al., *Nature* (Oct. 30, 2005), Soutschek et al., *Nature* 432:173-178 (2004), and U.S. Patent Publication No. 20050107325, which are incorporated herein by reference. Modified nucleotides and nucleic acids may also include locked nucleic acids (LNA), as described in U.S. Patent No. 20020115080, which is incorporated herein by reference. Additional modified nucleotides and nucleic acids are described in U.S. Patent Publication No. 20050182005, which is incorporated herein by reference. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments, to enhance diffusion across cell membranes, or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs may be

made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

e. Operably Linked

"Operably linked" as used herein may mean that expression of a gene is under the control of a promoter with which it is spatially connected. A promoter may be positioned 5' (upstream) or 3' (downstream) of a gene under its control. The distance between the promoter and a gene may be approximately the same as the distance between that promoter and the gene it controls in the gene from which the promoter is derived. As is known in the art, variation in this distance may be accommodated without loss of promoter function.

f. Promoter

"Promoter" as used herein may mean a synthetic or naturally-derived molecule which is capable of conferring, activating or enhancing expression of a nucleic acid in a cell. A promoter may comprise one or more specific transcriptional regulatory sequences to further enhance expression and/or to alter the spatial expression and/or temporal expression of same. A promoter may also comprise distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A promoter may be derived from sources including viral, bacterial, fungal, plants, insects, and animals. A promoter may regulate the expression of a gene component constitutively, or differentially with respect to cell, the tissue or organ in which expression occurs or, with respect to the developmental stage at which expression occurs, or in response to external stimuli such as physiological stresses, pathogens, metal ions, or inducing agents. Representative examples of promoters include the bacteriophage T7 promoter, bacteriophage T3 promoter, SP6 promoter, lac operator-promoter, tac promoter, SV40 late promoter, SV40 early promoter, RSV-LTR promoter, CMV IE promoter, SV40 early promoter or SV40 late promoter and the CMV IE promoter.

g. Variant

"Variant" used herein with respect to a nucleic acid may mean (i) a portion or fragment of a referenced nucleotide sequence; (ii) the complement of a referenced nucleotide sequence or portion thereof; (iii) a nucleic acid that is substantially identical to a referenced nucleic acid or the complement thereof; or (iv) a nucleic acid that hybridizes under stringent conditions to the referenced nucleic acid, complement thereof, or a sequences substantially identical thereto.

"Variant" with respect to a peptide or polypeptide that differs in amino acid sequence by the insertion, deletion, or conservative substitution of amino acids, but retain at least one biological activity. Variant may also mean a protein with an amino acid sequence that is substantially identical to a referenced protein with an amino acid sequence that retains at least one biological activity. A conservative substitution of an amino acid, i.e., replacing an amino acid with a different amino acid of similar properties (e.g., hydrophilicity, degree and distribution of charged regions) is recognized in the art as typically involving a minor change. These minor changes can be identified, in part, by considering the hydropathic index of amino acids, as understood in the art. Kyte et al., *J. Mol. Biol.* 157:105-132 (1982). The hydropathic index of an amino acid is based on a consideration of its hydrophobicity and charge. It is known in the art that amino acids of similar hydropathic indexes can be substituted and still retain protein function. In one aspect, amino acids having hydropathic indexes of ± 2 are substituted. The hydrophilicity of amino acids can also be used to reveal substitutions that would result in proteins retaining biological function. A consideration of the hydrophilicity of amino acids in the context of a peptide permits

calculation of the greatest local average hydrophilicity of that peptide, a useful measure that has been reported to correlate well with antigenicity and immunogenicity. U.S. Pat. No. 4,554,101, incorporated fully herein by reference. Substitution of amino acids having similar hydrophilicity values can result in peptides retaining biological activity, for example immunogenicity, as is understood in the art. Substitutions may be performed with amino acids having hydrophilicity values within ± 2 of each other. Both the hydrophobicity index and the hydrophilicity value of amino acids are influenced by the particular side chain of that amino acid. Consistent with that observation, amino acid substitutions that are compatible with biological function are understood to depend on the relative similarity of the amino acids, and particularly the side chains of those amino acids, as revealed by the hydrophobicity, hydrophilicity, charge, size, and other properties.

2. METHODS OF SCREENING

Provided herein is a method for screening for compounds that modulate the $\gamma_1 34.5$. The method comprises providing a cell that comprises TBK1, contacting the cell with a $\gamma_1 34.5$ nucleic acid or HSV-1, which contains a polynucleotide that expresses $\gamma_1 34.5$, and a candidate modulator compound, and measuring an infection biological parameter.

Also provided herein is a method for screening for modulators of TBK1. The method comprises providing a cell that comprises TBK1, contacting the cell with a variant of HSV-1, which is null for $\gamma_1 34.5$, and a candidate modulator compound, and measuring a HSV-1 infection biological parameter. A modulator of the $\gamma_1 34.5$ protein or TBK1 may be identified by a change in the HSV-1 infection parameter as compared to a control. The herein described screening methods may be performed in a variety of formats, including in vitro, cell-based, and in vivo assays.

a. TBK1

TBK1 is a kinase that plays a necessary role in cellular antiviral mechanisms that operate in a cell-type and time-dependent manner. TBK1 is an essential kinase that phosphorylates interferon regulatory factor 3 (IRF3) as well as the closely related interferon regulatory factor 7 (IRF7), each of which translocates to the nucleus and induces antiviral genes, such as interferon- α/β and interferon-stimulated gene 56 (ISG56).

TBK1 and IRF3 belong to a signaling pathway that mediates induction of gene expression, including a mixture of secreted factors, which, in concert, mediate proliferative activity toward endothelial cells. TBK1 governs this pathway and is expressed at significant levels in many solid tumors. This pattern of expression and the decreased expression of angiogenic factors in cultured cells upon RNA-interference-mediated ablation has previously identified TBK1 as an important protein for vascularization and subsequent tumor growth and a target for cancer therapy. See, for example, Korherr et al., PNAS (Mar. 14, 2006) Vol. 103(11) pp. 4240-4245. Accordingly, the identification of modulators of TBK1 may be useful in methods for treating cancer.

The method for screening candidate modulator compounds of TBK1 or $\gamma_1 34.5$ employs the use of TBK1, or a variant thereof. TBK1 may have the amino acid sequence provided in SEQ ID NO:1. TBK1 may be encoded by SEQ ID NO:2. A variant of TBK1 may be 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:1. A variant of TBK1 may be between 80% and 95% identical to SEQ ID NO:1. TBK1 may be expressed from an endogenous or exogenous nucleic acid. A cell may be transfected with an exogenous nucleic acid encoding TBK1. The exogenous nucleic acid may be a vector comprising SEQ ID NO:2, or a variant thereof. An endogenously expressed TBK1 may be expressed from the cell genome.

TABLE 1

SEQ ID NO: 1	MQSTSNHLWLLSDILGGGATANVFRGRHKK
TBK1 Amino Acid Sequence	TGDLFAIKVFNNIS
	FLRPVDVQMRFEFVLKKNLHKNIIVKLFAIEE
	ETTRHKVLIMEFCPCGSLYTVLEEPS
	NAYGLPESEFLIIVLRDVVGGMNLRENGIVH
	RDIKPGNIMRVIGEDGQSVYKLTDFGA
	ARELEDEQFVSLYGTEEYLHPDMYERAVAL
	RKDHQKKYGATVDLWSIGVTFYHAATGS
	LPPFPFEGPRRNKEVMYKIIITGKPSGAISGVQ
	KAENGPIDWSGDMFVSCSLSRGLQVL
	LTPVLANILEADQEKCWGFDQFFAETSDILH
	RMVIHVFSLQQMTAHKIYIHSYNTATI
	FHELVIYKQTKIISSNQELIYEGRRLVLEPGRL
	AQHFPKTEENPIFVVSREPLNTIGL
	IYEKISLPKVHPRYDLGDASMAKAITGVVC
	YACRIASTLLLYQELMRKGIRWLIELI
	KDDYNETVHKKTEVVI TLDFCIRNIEKTVKV
	YEKLKMINLEAELGEISDIHTKLLRL
	SSSQGTIETSLQDIDSRLSPGGS LADAWAHQE
	GTHPKDRNVEKLQVLLNCMTETIYYQF
	KKDKAERRLAYNEEQIHKFDKQKLYYHATK
	AMTHFTDECVKKYEAFLNKSEEWIRKML
	HLRKQLLSLTNQCFDIEEVSKYQEYTNELQ
	ETLPQKMFTASSGIKHTMTP IYPSNT

TABLE 1-continued

		LVENTLGMKKLKEEMEGVVKELAENNHILE RFGSLTMDGGLRNVDCI			
SEQ ID NO: 2		gccggcggtg	gcgcggcgga	gacccggctg	gtataacaag
TBK1 Nucleic Acid Sequence		aggattgcct	gatccagcca	agatgcagag	cacttctaata
		catctgtggc	ttttatctga	tatttttaggc	caaggagcta
		ctgcaaatgt	ctttcgtgga	agacataaga	aaactgggtga
		tttatttgct	atcaaatgat	ttataaacaat	aagcttcctt
		cgtccagtgg	atgttcaaat	gagagaattt	gaagtgttga
		aaaaactcaa	tcacaaaaat	attgtcaaat	tatttgctat
		tgaagaggag	acaacaacaa	gacataaagt	acttattatg
		gaattttgtc	catgtgggag	tttatacact	gttttagaag
		aaccttctaa	tgcttatgga	ctaccagaat	ctgaattcct
		aattgttttg	cgagatgtgg	tgggtggaat	gaatcatcta
		cgagagaatg	gtatagtga	ccgtgatata	aagccaggaa
		atatcatgcg	tgttataggg	gaagatggac	agtctgtgta
		caaaactcaca	gattttgggtg	cagctagaga	attagaagat
		gatgagcagt	ttgtttctct	gtatggcaca	gaagaatatt
		tgacccctga	tatgtatgag	agagcagtgc	taagaaaaga
		tcacagaaag	aaatatggag	caacagtgtga	tctttggagc
		attggggtaa	cattttacca	tgacagctact	ggatcactgc
		catttagacc	ctttgaaggg	cctcgtagga	ataaagaagt
		gatgtataaa	ataattacag	gaaagccttc	tggtgcaata
		tctggagtac	agaaaagcaga	aaatggacca	attgactgga
		gtggagacat	gcctgtttct	tgacgtcttt	ctcggggtct
		tcagggttcta	cttaccctcg	ttcttgcaaa	catccttgaa
		gcagatcagg	aaaagtgttg	gggttttgac	cagttttttg
		cagaaactag	tgatataact	caccgaatgg	taattcatgt
		tttttcgcta	caacaaatga	cagctcataa	gatttatatt
		catagctata	atactgctac	tatatattcat	gaactggat
		ataaacaac	caaaattatt	tcttcaaatc	aagaacttat
		ctacgaaggg	cgacgcttag	tcttagaacc	tggaggctg
		gcacaacatt	tccttaaaac	tactgaggaa	aacctatat
		ttgtagtaag	ccgggaacct	ctgaatacca	taggattaat
		atatgaaaaa	atttcctccc	ctaaagtaca	tccacgttat
		gatttagacg	gggatgctag	catggctaag	gcaataacag
		gggttgtgtg	ttatgcctgc	agaattgcc	gtaccttact
		gctttatcag	gaattaatgc	gaaaggggat	acgatggctg
		attgaattaa	ttaaagatga	ttacaatgaa	actgttcaca
		aaaagacaga	agttgtgatc	acattggatt	tctgtatcag
		aaacattgaa	aaaactgtga	aagtatatga	aaagtgtgatg
		aagatcaacc	tggaaagcgc	agagttagg	gaaatttcag
		acatacacac	caaattgttg	agactttcca	gttctcagg
		aacaatagaa	accagtcctc	aggatatoga	cagcagatta
		tctccagggtg	gatcactggc	agacgcacatg	gcacatcaag
		aaggcactca	tccgaaagac	agaaatgtag	aaaaactaca
		agtccctgtta	aattgcactga	cagagattta	ctatcagttc
		aaaaaagaca	aagcagaacg	tagattagct	tataatgaag
		aacaaatcca	caaatttgat	aagcaaaaac	tgtattacca
		tgccacaaaa	gctatgacgc	actttacaga	tgaatgtggt
		aaaaagtatg	aggcattttt	gaataagtca	gaagaatgga
		taagaaagat	gcttcatctt	aggaaacagt	tattatcgct
		gactaatcag	tgttttgata	ttgaagaaga	agtatcaaaa
		tatcaagaat	ataactaatga	gttacaagaa	actctgcctc
		agaaaatggt	tacagcttcc	agtggaaatca	aacataccat
		gaccccaatt	tatccaagtt	ctaaccacatt	agtagaaatg
		actcttggtg	tgaagaaatt	aaaggaagag	atggaaaggg
		tggttaaaga	acttgctgaa	aataaccaca	tttagaaaag
		gtttggctct	ttaaccatgg	atgggtggcct	tccgaacggt
		gactgtcttt	agctttctaa	tagaagttta	agaaaagt
		ccgtttgcac	aagaaaataa	cgcttgggca	ttaaatgaat
		gcctttatag	atagtcactt	gtttctacaa	ttcagtat
		gatgtggtcg	tgtaaatatg	tacaatattg	taaaacata
		aaaaatatac	aaatttttgg	ctgctgtgaa	gatgtaatt
		tatcttttaa	cattttataat	tatatgagga	aaatttgacct
		cagtgtacac	gagaagaaaag	ccatgaccga	ccaatatggt
		gacatactga	tcctctactc	tgagtggggc	taaataagtt
		atcttctctg	accgcctact	ggaaatattt	ttaagtggaa
		ccaaaatagg	catccttaca	aatcaggaag	actgacttga
		cacgtttgta	aatggtagaa	cggtggctac	tgtgagtggg
		gagcagaacc	gcaccactgt	tatactggga	taacaatttt
		tttgagaagg	ataaagtggc	attattttat	tttacaaggt
		gccagatcc	cagttatcct	tgtatccatg	taatttcaga
		tgaattatta	agcaaacatt	ttaaagtga	ttcattatta
		aaaactattc	atctttttcc	ttggccata	aatgtgtaat
		tgtcattaaa	attctaatgt	catttcaact	gttttaagct
		gtatatttct	ttaattctgc	ttactatttc	atggaaaaaa
		ataaatttct	caattttaat	gt	

11

b. γ_1 34.5 and HSV

The herein described methods for screening candidate modulator compounds of the γ_1 34.5 protein or TBK1 may employ the use of the γ_1 34.5 protein, a variant thereof, and/or a vector comprising a nucleic acid encoding the γ_1 34.5 pro-

12

interacts with TBK1. This interaction blocks IRF3 activation and also blocks the subsequent induction of antiviral genes early in HSV infection. γ_1 34.5 protein may prevent translational arrest mediated by double-stranded (ds) RNA-activated protein kinase PKR (eIF2aK2) in a cell.

TABLE 2

SEQ ID NO: 3	MARRRRHRGPRRPRPPGPTGAVPTAQSQVTS
γ_1 34.5 Amino Acid Sequence	TPNSEPAVRSAPA
	AAPPPPPASGPPPPCSLLLRQWLHPESASDD
	DDDDWDPSPPPEPAPEARPTAAAPR
	PRSPPPGAGPGGGANPSHPPSRPRLPPRLAL
	RLRVTAEHLARLRLRRAGGEGAPEPP
	ATPATPATPATPATPATPATPATPATPATPAR
	VRFSPHVRVRHLVWASAARLARRGS
	WARERADRARFRRRVAEAEAVIGPCLGPEA
	RARALARGAGFANSV
SEQ ID NO: 4	tttaaagtcg cggcgcgcca gcccgggccc ccccgggccc
γ_1 34.5 Nucleic Acid Sequence	agacgagcga gttagacagg caagcactac tcgcctctgc
	acgcacatgc ttgcctgtca aactctacca ccccggcacg
	ctctctgtct ccatggcccg cgcgcgcgcg catcgcgccc
	cccgccgccc cggcgcgccc gggcccaagg gcgcgcgtccc
	aaccgcacag tcccaggtaa cctccacgcc caactcggaa
	cccgcggtca ggagcgcgcc cgcggcgccc cgcgcgcgcg
	cccccgccag tgggcccccg ccttcttgtt cgetgctgct
	gcgcagtggt ctccacgttc ccgagtcgcg gtccgacgac
	gacgatgacg acgactggcc ggacagcccc cgcgcgcgac
	cggcgccaga ggccccgccc accgcgcgcg ccccccgccc
	ccggtcccca cgcgcgcgcg cgggcccggg gggcggggct
	aacccctccc acccccccct acgccccttc cgccttcgcg
	cgcgcctcgc cctccgctcg cgcgtcacgg cagagcacct
	ggcgcgctcg cgcctgcgac gcgcggcgcg ggaggggcg
	ccggagcccc cgcgcacccc cgcgcacccc gcgacccccg
	cgacccccgc gacccccgcg acccccgcga cccccgcgac
	ccccgcgacc cccgcgaccc cgcgcggggt gcgcttctcg
	ccccacgtcc ggggtcgcca cctggtgtgc tgggctctcg
	ccgcccgcct ggcgcgccgc ggtcgtggg cccgcgagcg
	ggcgagacgg gctcggttcc ggcgccgggt ggcgaggcc
	gaggcggtca tcgggcccgt cctggggccc gaggcccggt
	cccgggccct ggcccccgga gccggcccgg cgaactcggt
	ctaacgttac acccgaggcg gctgggtct tccgcggagc
	tcccgggagc tccgcaccaa gccgctctcc ggagagacga
	tggcaggagc cgcgcataa tacgctggga gccggcccgc
	ccccgaggcg ggccccccct cggaggcgcg gactggccaa
	tggcgggccc ccagcgcggc ggggcccggc caaccagcgt
	ccgcgcagtc ttcggggccc ggcccactgg gcgggagtta
	ccgcccagtg ggccggggcg cccacttccc ggtatggtaa
	ttaaaaactt acaagaggcc ttgttccgct tcccggtatg
	gtaattagaa actcattaat gggcgggccc ggccgcgcctt
	ccgcttccg gcaattcccg cggcccttaa tgggcaaccc
	cggatttccc cgcctcccgc gccgcgcgta accactccct
	tgggggttccg gggtatgcta attgcttttt tggcggaat

tein (SEQ ID NO:4) or TBK1 (SEQ ID NO:2), or variants thereof. A variant of γ_1 34.5 may be 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:3 or SEQ ID NO:4. A variant of γ_1 34.5 may be between 80% and 95% identical to SEQ ID NO:3 or SEQ ID NO:4. A variant γ_1 34.5 may be truncated. A variant γ_1 34.5 may have a fragment removed from the amino-terminal domain. The removed fragment may correspond to amino acid 1 to amino acid 30 of SEQ ID NO:3, amino acid 1 to amino acid 146 of SEQ ID NO:3, amino acid 30 to amino acid 72 of SEQ ID NO:3, or amino acid 159 to 263 of SEQ ID NO:3. The HSV may be null for γ_1 34.5.

The nucleic acid encoding the γ_1 34.5 protein may be endogenous to HSV. See SEQ ID NO:4.

The HSV may be HSV-1 or HSV-2. Upon infecting a cell, HSV may or may not express γ_1 34.5 protein or a variant thereof. Upon HSV infection, if γ_1 34.5 is expressed, γ_1 34.5

c. Cell

Provided herein is a cell that comprises a TBK1. The cell may be any eukaryotic cell. The eukaryotic cell may be any mammalian cell, such as a mammalian dendritic cell, a HeLa cell, a CHO cell, a yeast cell, a human embryonic kidney cell, a HEL cell, or a 293T cell.

The cell may comprise a vector. The vector may express any member of a peptide or cDNA library, or any other peptide or nucleic acid, may be introduced into the cell by any convenient method, which will vary depending on the vector-host system employed. Generally, a vector may be introduced into a host cell by transformation or infection (also known as "transfection") with a virus (e.g., phage) bearing the vector. Yeast cells may be transformed using polyethylene glycol, for example, as taught by Hinnen (1978) *Proc. Natl. Acad. Sci. USA*, 75:1929-33. Mammalian cells are conveniently transformed using the calcium phosphate precipitation method

described by Graham, et al. (1978) *Virology*, 52:546 and by Gorman, et al. (1990) *DNA and Prot. Eng. Tech.*, 2:3-10. However, other known methods for introducing DNA into host cells, such as nuclear injection, electroporation, protoplast fusion, and other means also are acceptable for use in the invention.

Cell culture conditions may allow transcription, translation, and protein transport between cellular compartments. Factors that affect these processes are well-known and include, for example, DNA/RNA copy number; factors that stabilize DNA; nutrients, supplements, and transcriptional inducers or repressors present in the culture medium; temperature, pH and osmolarity of the culture; and cell density. The adjustment of these factors to promote expression in a particular vector-host cell system is within the level of skill in the art. Principles and practical techniques for maximizing the productivity of in vitro mammalian cell cultures, for example, may be found in *Mammalian Cell Biotechnology: a Practical Approach* (Butler ed., IRL Press (1991)).

Any of a number of well-known techniques for large- or small-scale production of proteins may be employed in expressing the candidate modulator. These may include the use of a shaken flask, a fluidized bed bioreactor, a roller bottle culture system, and a stirred tank bioreactor system. Cell culture may be carried out in a batch, fed-batch, or continuous mode.

(1) Cell Contact

The cell may be contacted with a nucleic acid encoding γ_1 34.5 protein, or a variant thereof, an HSV virus containing a nucleic acid encoding γ_1 34.5 protein, or a variant thereof, a nucleic acid encoding TBK1, or a variant thereof, a candidate modulator compound, and/or a nucleic acid encoding a candidate modulator compound.

The time of contact may vary depending upon the nucleic acid or compound and any accompanying reagents employed in the method and can readily be determined by the person using the method.

d. Candidate Modulator

A candidate modulator compound may be any compound wherein the characterization of the compound's ability to modulate is desirable. Exemplary candidate compounds or substrates include small molecules, peptides, nucleic acids, antibodies, polypeptides, drugs, and organic compounds.

The candidate modulator may be present within a library (i.e., a collection of compounds). Such candidates may, for example, be encoded by DNA molecules within an expression library. Test substances may be present in conditioned media or in cell extracts. Other such test substances include compounds known in the art as "small molecules," which have molecular weights less than 10^5 daltons, preferably less than 10^4 daltons and still more preferably less than 10^3 daltons. Such test substances may be provided as members of a combinatorial library, which includes synthetic agents (e.g., peptides) prepared according to multiple predetermined chemical reactions. Those having ordinary skill in the art will appreciate that a diverse assortment of such libraries may be prepared according to established procedures, and members of a library of substances can be simultaneously or sequentially screened as described herein.

The screening methods may be performed in a variety of formats, including in vitro, cell-based and in vivo assays. Any cells may be used with cell-based assays.

Methods for recovery of the candidate compound(s) are well-known and vary depending on the expression system employed. A compound including a signal sequence may be recovered from the culture medium. The compound may also be expressed intracellularly and recovered from cell lysates.

The modulator compound, or candidate modulator compound, may be purified from culture medium or a cell lysate by any method capable of separating the compound from one or more components of the host cell or culture medium. The compound may be separated from host cell and/or culture medium components that would interfere with the intended use of the compound. As a first step, the culture medium or cell lysate may be centrifuged or filtered to remove cellular debris. The supernatant may then typically be concentrated or diluted to a desired volume or diafiltered into a suitable buffer to condition the preparation for further purification.

The compound may then be further purified using well-known techniques. The technique chosen will vary depending on the properties of the compound. For example, the compound may be purified using an affinity column containing the cognate binding partner of a binding member of the compound. For instance, the compound fused with green fluorescent protein, hemagglutinin, or FLAG epitope tags or with hexahistidine or similar metal affinity tags may be purified by fractionation on an affinity column. Any of TBK1, γ_1 34.5 protein, or candidate modulator compounds may be fused to one or more such tags.

Modulators of TBK1 or γ_1 34.5 protein can also be further evaluated, detected, cloned, sequenced, and the like, either in solution or after binding to a solid support. For recovery of an expressed candidate compound, the host cell may be cultured under conditions suitable for cell growth and expression and the expressed compound recovered from a cell lysate or, if the candidate compounds are secreted, from the culture medium. In particular, the culture medium may contain appropriate nutrients and growth factors for the host cell employed. The nutrients and growth factors are, in many cases, well known or may be readily determined empirically by those skilled in the art. Suitable culture conditions for mammalian host cells, for instance, are described in *Mammalian Cell Culture* (Mather ed., Plenum Press 1984) and in Barnes and Sato (1980) *Cell* 22:649.

e. Nucleic Acid Vector

Also provided herein is a vector that comprises a nucleic acid that encodes γ_1 34.5 protein, or a variant thereof, TBK1, or a variant thereof, and/or a candidate modulator compound.

The vector may be a nucleic acid sequence containing an origin of replication. A vector may be a vector, bacteriophage, bacterial artificial chromosome or yeast artificial chromosome. A vector may be a DNA or RNA vector. A vector may be either a self-replicating extrachromosomal vector or a vector which integrates into a host genome.

The vector may be an expression vector, which may include one or more control sequences capable of effecting and/or enhancing the expression of the proteins, or variants thereof, as discussed herein. Control sequences for expression in eukaryotic cells may include a promoter, an enhancer, and a transcription termination sequence, for example a polyadenylation signal).

The vector may also include other sequences, such as, for example, nucleic acid sequences encoding a signal sequence or an amplifiable gene. A signal sequence may direct the secretion of a polypeptide fused thereto from a cell expressing the protein. In the expression vector, nucleic acid encoding a signal sequence may be linked to a polypeptide coding sequence so as to preserve the reading frame of the polypeptide coding sequence.

f. Infection Parameters

Candidate modulator compounds of γ_1 34.5 protein or TBK1 may be determined to be modulators based upon measuring any one or more of HSV virus infection parameters and comparing to a control. These parameters may be biochemi-

cal. These parameters may include interferon expression, interferon stimulated gene (ISG) expression, virus yield, TBK1 phosphorylation, phosphorylation or targeting of one or more proteins downstream of TBK1, such as IRF-3 or IRF-7, and/or nuclear translocation of IRF3. Virus yield may be measured in plaque forming units (pfu). As compared to a control cell, the virus yield of a cell comprising TBK1, and contacted with HSV and a candidate modulator compound, may be higher or lower than the control cell. For example, when the modulator and a γ_1 34.5 null HSV virus are brought into contact with a cell comprising TBK1, the modulator of TBK1 may result in an increase in virus yield, as compared to a control.

g. Control Cells

The method of screening and identifying modulators of γ_1 34.5 protein or TBK1 may use control cells in the analysis. Control calls may be contacted by the candidate modulator compound and compared with cells comprising TBK1 and contacted with an HSV. The control cells can be used to aid in the identification of γ_1 34.5 protein or TBK1 modulating compounds from a pool or library of candidates. For example, a positive control cell for identifying a candidate modulator that inhibits γ_1 34.5 protein may be an HSV virus-infected cell that does not express or comprise TBK1. A negative control in a screen for modulators of TBK1 may comprise contacting the candidate modulator compound with a cell that does not express TBK1. Other controls may include the use of known TBK1 or γ_1 34.5 protein inhibitors.

3. VACCINE PLATFORM

a. HSV Vaccine

Provided herein is an attenuated HSV virus for use as an immunogenic composition for the prevention or amelioration of HSV infection. The HSV virus may be characterized by having a fragment deleted from one or both N-termini of the γ_1 34.5 nucleotide sequences. The fragment that is deleted from one or both N-termini of the γ_1 34.5 nucleotide sequences may contain amino acid 1 to amino acid 10 of SEQ ID NO:3, amino acid 1 to amino acid 15 of SEQ ID NO:3, amino acid 1 to amino acid 20 of SEQ ID NO:3, amino acid 1 to amino acid 25 of SEQ ID NO:3, amino acid 31 to amino acid 72 of SEQ ID NO:3, amino acid 35 to amino acid 70 of SEQ ID NO:3, amino acid 40 to amino acid 65 of SEQ ID NO:3, amino acid 165 to amino acid 263 of SEQ ID NO:3, amino acid 170 to amino acid 263 of SEQ ID NO:3, amino acid 180 to amino acid 263 of SEQ ID NO:3, amino acid 200 to amino acid 263 of SEQ ID NO:3, and/or amino acid 230 to amino acid 263 of SEQ ID NO:3.

The γ_1 34.5 fragment that is deleted from one or both N-termini may contain amino acid 1 to amino acid 30 of SEQ ID NO:3; amino acid 1 to amino acid 146 of SEQ ID NO:3; amino acid 30 to amino acid 72 of SEQ ID NO:3; or amino acid 159 to amino acid 263 of SEQ ID NO:3. The deletion detrimentally affects virulence while retaining the immunogenic character of HSV.

Adjuvant substances that stimulate immunogenicity may be mixed with the attenuated virus in order to improve the immune response to the virus. Examples of adjuvants include EMULSIGEN®-D, monophosphoryl lipid A (MPL) and Freund. Immunological adjuvants have generally been divided into two basic types: aluminum salts and oil emulsions. Aluminum phosphate and hydroxide (alum) adjuvants induce elevated levels of antibody against antigens in alum-based vaccines above those obtained with the corresponding aqueous vaccine. Numerous alum-based vaccines, including

methods of preparation thereof, were developed as, for example, disclosed in U.S. Pat. Nos. 5,747,653, 6,013,264, 6,306,404 and 6,372,223. EMULSIGEN®-D is a sterile oil-in-water emulsion free of animal origin ingredients, containing uniformly dispersed, micron size oil droplets and dimethyldioctadecylammonium bromide.

Alternatively, an oil based adjuvant may be used. The main components of the oil-based adjuvants are: oil, emulsifier and immunostimulant. Examples of emulsified oil-based adjuvants are Incomplete Freund's Adjuvant (IFA), consisting of an approximately 50:50 water-in-oil emulsion, and complete Freund's adjuvant (CFA), a similar preparation with inclusion of killed mycobacteria. Examples of improved emulsions as vaccine adjuvants, by enhancing the immunogenicity of the antigen, include submicron emulsions as disclosed in U.S. Pat. No. 5,961,970 and solid fat nanoemulsions as disclosed in U.S. Pat. No. 5,716,637, for example.

The vaccine may be administered orally, intravenously, intramuscularly or subcutaneously. The pharmaceutical composition of the invention may also be administered to other mucous membranes. The pharmaceutical composition is then provided in the form of a suppository, nasal spray or sublingual tablet.

The uptake of the attenuated virus may be facilitated by a number of methods. For instance, a non-toxic derivative of the cholera toxin B subunit, or of the structurally related subunit B of the heat-labile enterotoxin of enterotoxigenic *Escherichia coli* may be added to the composition, as disclosed in U.S. Pat. No. 5,554,378.

These attenuated viruses offer several advantages over other known HSV viruses developed for prophylactic treatment of HSV: (1) the deletions were selectively chosen to avoid over-attenuation of the HSV virus such that the resulting virus would be efficacious for prophylactic treatment of HSV infections and conditions as well as safe; (2) the deletions related to the N-terminus of the coding sequence for the γ_1 34.5 protein was selected to ensure replication incompetence yet enhance immunogenicity and efficacy of the virus.

The attenuated virus may be used in therapeutic and/or immunogenic compositions for preventing and treating HSV-related conditions and diseases. The pharmaceutical compositions can be used for the prophylactic treatment of an HSV-related disease or condition and comprises an immunizingly effective amount of an attenuated HSV virus in a suitable pharmaceutical vehicle. The composition may be used to generate a neutralizing immune response to HSV infection, for prophylactic treatment of HSV infection, and for prevention of recurrent HSV disease symptoms.

The composition may be used in a method to reduce the incidence of or severity of a clinical sign associated with HSV infection. Such a method may comprise the step of administering the immunogenic composition to a subject in need thereof, wherein the reduction of the incidence of or the severity of a clinical sign is relative to a subject not receiving the immunogenic composition. Examples of clinical signs include gingivostomatitis, pharyngitis, encephalitis, and mucocutaneous lesions.

A mammal can be inoculated intramuscularly or subcutaneously with a composition comprising an immunity-inducing dose of one or more of the herein described viruses. Other modes of inoculation include surface scarification or inoculation of a body cavity. An effective immunization of a human host may be achieved by one to several inoculations of between 10 and 1,000,000 pfu each, as measured in a susceptible human or nonhuman primate cell lines. Each inoculation may have between 1,000 and 1,000,000, or between 10,000

and 1,000,000, or between 100,000 and 1,000,000, or between 500,000 and 1,000,000 pfu.

Notwithstanding the foregoing, pharmaceutical compositions suitable for use in context of the present invention include compositions wherein the active ingredients are contained in an amount effective to achieve the intended purpose. All formulations for administration should be in dosages suitable for the chosen route of administration. More specifically, a "therapeutically effective" dose means an amount of a compound effective to prevent, alleviate or ameliorate symptoms of a disease of the subject being treated. Determination of a therapeutically effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

Toxicity and therapeutic efficacy of the compositions described herein can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., by determining the IC_{50} (the concentration which provides 50% inhibition) and the maximal tolerated dose for a subject compound. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage may vary depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. Depending on the severity and responsiveness of the condition to be treated, dosing can also be a single administration of a slow release composition, with course of treatment lasting from several days to several weeks or until cure is effected or diminution of the disease state is achieved. The amount of a composition to be administered will, of course, be dependent on the subject being treated, the severity of the affliction, the manner of administration, the judgment of the prescribing physician, and all other relevant factors.

The present invention can be utilized as illustrated by the following non-limiting example.

Example 1

Materials and Methods for Examples 2-6

Cells and Viruses—Vero, HEL, and 293T cells were from the American Type Culture Collection. TBK1+/+ and TBK1-/- MEF were gifts from Dr. Wen-Chen Yeh. Cells were propagated in Dulbecco's modified Eagle's medium supplemented with 5% (Vero and 293T) or 10% (MEF and HEL) fetal bovine serum. HSV-1(F) is a prototype HSV-1 strain used in this study. In recombinant virus R3616, a 1 kb fragment from the coding region of the $\gamma_1 34.5$ gene was deleted. These viral strains were gifts from Dr. Bernard Roizman (University of Chicago).

Plasmids—Plasmids pcDNA3, pTK-Luc and dN200 have been described elsewhere. The FLAG- $\gamma_1 34.5$ plasmids, WT, $\Delta 30$, $\Delta 72$, $\Delta 106$, $\Delta 146$, and N159, were constructed by inserting PCR amplified fragments into the BamHI and XhoI sites of pcDNA3. To construct GST-IRF3, a DNA fragment encoding amino acids 380 to 427 from IRF3 was ligated into the BamHI and EcoRI sites of pGEX4-T1. pISG56-Luc was a gift from Ganes Sen (The Cleveland Clinical Research Foundation). Plasmids IFNB and FLAG-TBK1 were gifts from R. Lin, J. Hiscott (McGill University), and U. Siebenlist (NIH). Plasmid GFP-IRF3 was a gift from Nancy Reich (State University of New York, Stony Brook). Plasmid HA- $\gamma_1 34.5$ was a gift from Youjia Cao (Nankai University). To construct HA-TBK1, the TBK1 insert was PCR amplified and cloned into the BamHI and XhoI sites of pcDNA3.

Viral Infections—Cells were infected with viruses at 0.05, 5 or 10 pfu per cell. At indicated time points, virus yields were determined on Vero cells. For interferon assays, cells were untreated or treated with mouse alpha interferon (100 U/ml; Sigma) for 20 h. Cells were then infected with viruses. After adsorption for 2 h, the monolayers were overlaid with DMEM medium and incubated at 37° C. At indicated time points post infection, samples were harvested, viruses were released by three cycles of freezing and thawing, and then titrated on Vero cells. For radioisotope labeling, cells were labeled with [³⁵S] methionine (50 μ Ci/ml; ICN) in DMEM lacking methionine but supplemented with 2% fetal bovine serum 1 h before harvest. At indicated time points, lysates of cell were subjected to electrophoresis and autoradiography.

RT-PCR and Reporter Assays—Cells were mock infected or infected with viruses at 5 pfu per cell in serum free DMEM. At 1 h after infection, cells were grown in DMEM with 1% fetal bovine serum. At the indicated time points, total RNA was harvested from cells using RNeasy kit (Qiagen). RT-PCR analysis was performed with one-step RT-PCR system according to manufacture protocols (Invitrogen). Primers used were as follows: mouse ISG54 (ATGAGTACAAC-GAGTAAG (SEQ ID NO:5) and (CTAGTATTCAGCACCT-GCTT (SEQ ID NO:6)), mouse ISG56 (ATGGGAGAGAAT-GCTGATGG (SEQ ID NO:7)) and (TCAGAATGCAGGGTTCATTT (SEQ ID NO:8)), Human SG54 (ATGAGTGAGAACATAAGAA (SEQ ID NO:9)) and (TCATTCCCCATTCCAGCTTG (SEQ ID NO:10)), human ISG56 (ATGAGTACAAATGGTGATGATCATCAG (SEQ ID NO:11) and ATTGCCTGCTTCTATATACATTCT-TGC (SEQ ID NO:12)), human or mouse 18S rRNA (CG-CAGCTAG GAA TAA TGG AA (SEQ ID NO:13)) and (TTA TGACCGCACTT ACTGG (SEQ ID NO:14)). Luciferase reporter assays were performed as described previously. Briefly, 293T cells grown on 12-well plate were transfected with a control plasmid or plasmid vector expressing TBK1 and $\gamma_1 34.5$ variants, along with IFN- β or ISG56 reporter plasmid expressing firefly luciferase using Lipofectamine 2000 (Invitrogen). Total levels of transfected DNA were kept constant with empty vector plasmid. As a control for transfection efficiency, a plasmid containing the *Renilla* luciferase gene driven by the HSV-1 TK promoter was included. At 36 h after transfection, cells were harvested and luciferase activities were measured using the Promega's dual luciferase assay system.

Immunoblotting and Immunoprecipitation Analyses—To analyze protein expression, cells were washed, harvested, and solubilized in disruption buffer containing 50 mM Tris-HCl (pH 7.1), 5% 2-mercaptoethanol, 2% sodium dodecyl sulfate (SDS), and 2.75% sucrose. Samples were then sonicated, boiled, subjected to electrophoresis on denaturing 12% polyacrylamide gels, transferred to nitrocellulose membranes, blocked with 5% nonfat milk, and reacted with antibodies against eIF2 α , phosphorylated eIF2 α (Cell Signaling Tech.), β -actin (Sigma), HSV-1 (Dako Inc.), FLAG (Sigma), HA (Santa Cruz Biotech), IRF3 (Santa Cruz Biotech), phosphorylated IRF3 (ser396) (Cell Signaling Tech.), and $\gamma_1 34.5$. The membranes were rinsed in phosphate-buffered saline and reacted with donkey anti-rabbit immunoglobulin conjugated to horseradish peroxidase. Protein bands were detected by enhanced chemiluminescence (Amersham Pharmacia Biotech Inc.). To examine protein interactions, 293T cells were transfected with indicated amounts of pcDNA3, FLAG-TBK1, HA- $\gamma_1 34.5$, FLAG-dN200, and IRF3. At 40 h after transfection, cells were harvested and lysed in 50 mM Tris-HCl (pH 7.4) buffer containing 1% NP-40; 0.25% Na-deoxycholate; 150 mM NaCl; 1 mM EDTA; 1 mM 4-(2-Aminoet-

hyl)benzenesulfonyl fluoride hydrochloride; 1 μ g/ml Aprotinin/leupeptin/pepstatin; 1 mM Na_3VO_4 ; 1 mM NaF. Lysates were incubated overnight at 40°C with anti-FLAG M2 affinity gel (Sigma) or anti-HA antibody (Applied Biological Materials Inc.) plus protein A/G agarose beads (Santa Cruz Biotechnology). Immunocomplexes captured on the affinity gel or protein A/G agarose beads were subjected to electrophoresis and immunoblotting analysis.

Kinase Assays—Recombinant GST-IRF3 fusion protein was purified from bacterial lysates by affinity chromatography. 293T cells were transfected with pcDNA3, FLAG-TBK1, and HA- $\gamma_134.5$. At 40 h after transfection, cell lysates were prepared in 20 mM Tris-HCl (pH 7.4) containing 137 mM NaCl; 10% glycerol; 1% Triton X-100; 2 mM EDTA; 50 mM sodium glycerophosphate; 20 mM sodium pyrophosphate; 5 μ g/ml aprotinin; 5 μ g/ml leupeptin; 1 mM Na_3VO_4 and 5 mM benzamide. TBK1 was immunoprecipitated with anti-FLAG affinity gel (Sigma). Immunocomplexes were incubated with recombinant GST-IRF3 (380-427) for 20 min at 30°C in 25 mM Hepes buffer (pH 7.5) containing 10 mM MgCl_2 , 25 mM sodium- β -glycerophosphate, 5 mM benzamide, 1 mM Na_3VO_4 , 0.5 mM dithiothreitol, and 100 μ M ATP. Samples were subjected to electrophoresis and immunoblotting analysis with rabbit anti-phospho IRF3 (Ser396).

Fluorescence Microscopy—After transfection or infection, cells were washed with phosphate-buffer saline and fixed with ice cold methanol and acetone for 5 min. Following this step, cells were washed with phosphate-buffer saline and stained with 4',6-diamidino-2-phenylindole (DAPI) (1.5 μ g/ml) in the VECTASHIELD mounting medium. Samples were visualized under a fluorescent microscope and images were captured with Zeiss AxioCam MRm camera.

Cell Fractionation Assays—Infected or transfected cells were lysed in phosphate-buffer saline containing 0.4% Nonidet P-40 and protease inhibitor cocktails (Sigma) and kept on ice with gentle inversion. After centrifugation for 3 min, and the nuclei were pelleted and supernatant were transferred to a tube. The nuclei were resuspended in phosphate-buffer saline with 0.4% NP-40 and frozen at -80°C for 30 min. The cytoplasmic and nuclear fractions were then solubilized in disruption buffer. Samples were subjected to electrophoresis and Western blot analysis with antibodies against IRF3 (Santa Cruz Biotech), GRP78 (BD Transduction Laboratories), and histone H3 (Cell Signaling), respectively.

Example 2

34.5 Null Mutant Activates Antiviral Immunity Early in HSV Infection

Although expressed as a leaky late gene, $\gamma_134.5$ is also detectable early in infection. To explore the biological function of $\gamma_134.5$, we measured the induction of ISG54 and ISG56 early in HSV infected cells. Mouse embryonic fibroblasts (MEF) were either mock infected or infected with viruses and mRNA levels were determined by RT-PCR. As illustrated in FIG. 1A, the induction of ISG54 as well as ISG56 was seen in cells infected with the $\gamma_134.5$ null mutant R3616. The mRNA levels of ISG54 and ISG56 increased as virus infection progressed from 3 h to 6 h. This stimulation was not observed in cells mock infected or infected with wild type HSV-1(F) although comparable levels of 18sRNA were noted in all cells. In correlation, wild type virus, but not the $\gamma_134.5$ null mutant, expressed the $\gamma_134.5$ protein at 3 and 6 h after infection (FIG. 1C). Similar results were obtained in human lung fibroblasts (HEL) albeit there was a delay in the kinetics of ISG54 and ISG56 induction by R3616 (FIG. 1B).

Since the onset of viral DNA replication triggers the shutoff of protein synthesis mediated by dsRNA dependent protein kinase PKR, we next asked whether the induction of ISG54 and ISG56 by R3616 was linked to this event. As measured by [35S]methionine labeling, at 3 or 6 h after infection, profiles of protein synthesis were similar in HEL cells infected with HSV-1(F) or R3616 (data not shown). Although eIF-2 α was constitutively expressed at comparable levels, there was no detectable eIF-2 α phosphorylation regardless of $\gamma_134.5$ expression (FIG. 1C), suggesting that PKR is not activated early in HSV infection. These phenotypes were also seen in MEF cells. Hence, the expression of $\gamma_134.5$ abrogated the induction of ISG54 and ISG56 by HSV, which was independent of eIF2 α phosphorylation and the shutoff of protein synthesis.

Previous work has demonstrated that IRF3 activation stimulates ISG56 expression in HSV infected cells. We further evaluated phosphorylation of endogenous IRF3 in infected cells. As revealed by immunoblotting analysis (FIG. 2A), IRF3 was constitutively expressed in HEL cells. Unlike HSV-1(F), R3616 infection resulted in an appearance of the IRF3 phosphoserine-396 isoform at 3 h after infection (lane 3). This response became evident at 6 h after infection (lane 6). To monitor the cellular localization of IRF3, 293T cells expressing a GFP-IRF3 fusion protein were infected with viruses (FIGS. 2B&C). GFP-IRF3 predominantly localized to the cytoplasm in cells mock infected or infected with HSV-1(F). However, as viral infection proceeded, a significant portion of IRF3 was redistributed to the nucleus in cells infected with R3616 at 6 h after infection. These phenotypes were also seen in cell fractionation analysis. As shown in FIG. 2D, GFP-IRF3 was present in the cytoplasmic fraction of mock infected or virus infected cells. However, little GFP-IRF3 was seen in the nuclear fraction of mock infected cells. In virus infected cells, R3616 stimulated more nuclear translocation of GFP-IRF3 than HSV-1(F). As expected, control proteins GRP78 and histone H3 were detected in the cytoplasmic and nuclear fractions, respectively. Together, these results indicate that early expression of $\gamma_134.5$ is required to suppress phosphorylation and nuclear translocation of IRF3 in HSV infection.

Example 3

34.5 Null Mutant Replicates More Efficiently in TBK1^{-/-} Cells than in TBK1^{+/+} Cells

While HSV induction of antiviral responses involves different components, this process requires TBK1. We hypothesized whether there is a possible link between $\gamma_134.5$ and the TBK1 pathway. To test this, we investigated viral growth properties in TBK1^{+/+} and TBK1^{-/-} MEF cells. Specifically, cells were infected with either HSV-1(F) or R3616. At 24 h post infection, virus yields were determined. As shown in FIG. 3A, HSV-1(F) replicated efficiently in both TBK1^{+/+} and TBK1^{-/-} cells, reaching titers of 4.6×10^6 and 1×10^6 pfu/ml, respectively. In striking contrast, R3616 replicated poorly in TBK1^{+/+} cells, with a virus yield less than 10 pfu/ml. There was approximately 10^5 -fold decrease in viral growth as compared to HSV-1(F). This reduction was attributable to the lack of $\gamma_134.5$ in R3616. Strikingly, R3616 replicated more efficiently in TBK1^{-/-} cells, with a titer reaching 6.6×10^3 pfu/ml. There was approximately 10^3 -fold restoration in viral yield. This increase was partial but significant when compared to the replication seen in TBK1^{+/+} cells. These phenotypes were mirrored by cytopathic effects after viral infection. As illustrated in FIG. 3E, mock-infected cells

21

formed a monolayer, with most cells displaying spindle morphology. HSV-1(F) induced morphological changes in both TBK1+/+ and TBK1-/- cells, where cells formed clumps, indicative of viral replication. In contrast, R3616 induced cytopathic effects only in TBK1-/- cells. Immunoblot analysis revealed that HSV-1(F) produced high levels of viral polypeptides in both TBK1+/+ and TBK1-/- cells, whereas R3616 produced a substantial amount of viral polypeptides only in TBK1-/- cells (FIG. 3B). Collectively, these results show that HSV infection invokes host responses via TBK1 which restricts viral replication in the absence of a γ_1 34.5 blockade.

To examine whether interferon was able to restore the antiviral activity in the absence of TBK1, we assessed viral responses to IFN- α . As indicated in FIGS. 3C&D, HSV-1(F) replicated well in both TBK1+/+ and TBK1-/- cells, with titers ranging from 3.2×10^6 to 3.9×10^6 pfu/ml at 24 h after infection. Treatment with IFN- α had a marginal effect on viral replication. As expected, R3616 replicated more efficiently in untreated TBK1-/- than in TBK1+/+ cells, with a titer of 2.8×10^3 pfu/ml. When cells were treated with IFN- α R3616 barely replicated, with minimal infectious virus produced. Thus, addition of IFN- α in TBK1-/- cells restored the antiviral activity to R3616. The growth pattern of R3616 resembled that seen in TBK1+/+ cells. Thus, TBK1-induced downstream antiviral molecules likely contribute to the inhibitory effect on viral replication.

Example 4

34.5 Protein Associates with TBK1 and Inhibits Activation of IFN- β and ISG56 Promoters

The functional link between TBK1 and γ_1 34.5 raised a possibility that γ_1 34.5 may interact with TBK1 and suppress its activity. To test this hypothesis, we carried out co-immunoprecipitation experiments in 293T cells transfected with a vector, HA- γ_1 34.5, FLAG-TBK1, and FLAG-dN200, a truncated form of Ebola VP35. As shown in FIG. 4A, the γ_1 34.5 protein was co-immunoprecipitated with TBK1, but not with the control protein dN200. Levels of protein expression were comparable in lysates of transfected cells. This data indicates that the γ_1 34.5 protein specifically associates with TBK1. As TBK1 activates the expression of ISG56 and IFN- β , we also performed luciferase reporter assays in 293T cells. As indicated in FIG. 4B, the expression of TBK1 activated the IFN- β promoter by approximately 90-fold. However, co-expression of γ_1 34.5 inhibited this induction in a dose dependent manner. Likewise, the γ_1 34.5 protein suppressed the induction of the ISG56 promoter by TBK1 (FIG. 4C). We conclude that in the absence of any other HSV proteins, the γ_1 34.5 protein associates with TBK1 and prevents the activation of ISG56 and IFN- β promoters.

Example 5

34.5 Protein is Sufficient to Block Phosphorylation and Nuclear Translocation of IRF3

When bound to IRF3, TBK1 phosphorylates the carboxyl terminus of IRF3, which permits nuclear translocation and activation of IRF3 (7,34). To gain insight into γ_1 34.5 function, we examined whether the γ_1 34.5 protein directly disrupted this process. Lysates of 293T cells transfected with FLAG-TBK1 and HA- γ_1 34.5 were immunoprecipitated with anti-FLAG antibody. Immunocomplexes were subjected to in vitro kinase assays with recombinant GST-IRF3 (FIG. 5A). It

22

is notable that there were some variations in TBK1 expression. Nonetheless, as the expression of γ_1 34.5 was elevated, IRF3 phosphorylation was reduced, indicating that the γ_1 34.5 protein inhibits IRF3 activation. A simple explanation for the inhibitory effect of the γ_1 34.5 protein is that it sequesters TBK1 in an inactive complex and blocks the access of IRF3. To test this idea, we analyzed the TBK1 complex by immunoprecipitation. 293T cells were transfected with FLAG-TBK1, IRF3, and HA- γ_1 34.5. Protein expression was detected in cell lysates (FIG. 5B, upper panels). In parallel, the TBK1 complex was immunoprecipitated with anti-FLAG antibody and subsequently analyzed for the presence of TBK1, γ_1 34.5, and IRF3 (FIG. 5B, lower panels). Although TBK1 remained at similar levels in immunoprecipitates, IRF3 and γ_1 34.5 displayed different patterns. In the absence of γ_1 34.5, IRF3 associated with TBK1 (lane 3). As the level of γ_1 34.5 increased, the amount of IRF3 associated with TBK1 diminished (lanes 4-7). Thus, expression of the γ_1 34.5 protein displaced IRF3 in the TBK1 complex. To determine whether γ_1 34.5 blocked nuclear translocation of IRF3 stimulated by TBK1, a cellular localization experiment was performed in 293T cells expressing GFP-IRF3 or in combination with TBK1 and γ_1 34.5 (FIG. 5C). When expressed alone, IRF3 remained in the cytoplasm. Addition of TBK1 induced IRF3 redistribution to the nucleus in approximately 30% of GFP-IRF3 positive cells. This response was suppressed to less than 10% upon expression of the γ_1 34.5 protein as illustrated among cells from different fields (FIG. 5D). Further analysis by cell fractionation revealed similar phenotypes. As illustrated in FIG. 5E, TBK1 strongly stimulated nuclear translocation of GFP-IRF3. However, addition of γ_1 34.5 drastically reduced nuclear accumulation of GFP-IRF3. Control proteins GRP78 and histone H3 remained in the cytoplasmic and nuclear fractions, respectively. These results suggest that the γ_1 34.5 protein blocks IRF3 phosphorylation and nuclear translocation.

Example 6

Deletions in the Amino Terminus of 34.5 Disrupt its Activity on TBK1

The γ_1 34.5 protein consists of 263 amino acids, with a large amino terminal domain, a linker of triplet repeats, and a carboxyl-terminal domain. To map the functional domain, we constructed a series of γ_1 34.5 variants with deletions in either the amino-terminus or the carboxyl terminus (FIG. 6A). N159 has a deletion in the region spanning amino acids 159 to 263, whereas Δ 30, Δ 72, Δ 106, and Δ 146 have deletions in regions encompassing amino acids 1 to 30, 30 to 72, 72 to 106, and 106 to 146, respectively. We first evaluated these mutants in reporter assays with an IFN- β promoter construct (FIG. 6B). Like wild type γ_1 34.5, N159 suppressed the induction of IFN- β by TBK1 efficiently, indicating that deletion of the carboxyl-terminal domain has no effect. Similarly, Δ 30, Δ 72, and Δ 146 inhibited the IFN- β promoter activity to different degrees. Hence, deletions from amino acids 1 to 72 or from 106 to 146 had little effect on the γ_1 34.5 activity. In contrast, Δ 106 failed to inhibit TBK1 effectively (FIG. 6B). Therefore, deletion of amino acids 72 to 106 in γ_1 34.5 substantially relieved its inhibitory effect. We next assessed the ability of γ_1 34.5 to bind TBK1 by immunoprecipitation. As illustrated in FIG. 6C, all γ_1 34.5 variants, except Δ 106, co-precipitated with TBK1. These activities paralleled with the phenotypes seen in reporter assays. These results indicate that the region spanning amino acids 72 to 106 in the γ_1 34.5 protein is indispensable to inhibit TBK1.

In addition to the foregoing, our data shows that a γ_1 34.5 N-terminal deletion mutant (lacking amino acids 1-146) is impaired for replication and stimulates interferon expression in cell culture as well as in a mouse model.

Example 7

Materials and Methods Used for Examples 8-13

Mice. BALB/c and C57BL/6 mice were purchased from Harlan Sprague Dawley Inc. and housed under specific pathogen free conditions in biosafety level 2 containment. Groups of five week-old mice were selected for this study. Experiments were performed in accordance with the guideline of the University of Illinois at Chicago.

Cells and viruses. Vero cells were obtained from the American Type Culture Collection and propagated in Dulbecco's modified Eagle's medium supplemented with 10% fetal bovine serum. Myeloid DCs were generated as previously described. Briefly, bone marrow cells were removed from the tibias and femurs of BALB/c mice. Following red blood cell lysis and washing, progenitor cells were plated in RPMI-1640 medium (Invitrogen, Auckland, NZ) supplemented with 10% FBS, 0.1 mM nonessential amino acids, 1 mM sodium pyruvate and 20 ng/ml granulocyte-macrophage colony stimulating factor (GM-CSF, Biosource, Camarillo, Calif.) in 6-well plates at 4×10^6 /well. Cells were supplemented with 2 ml fresh medium every other day. On day 8, DCs were positively selected for surface CD11c expression using magnetic beads (Miltenyi Biotec, Auburn, Calif.) to give >97% pure population of CD11c⁺MHCII⁺ cells. DCs displayed low levels of CD40, CD80, CD86, and major histocompatibility complex class II (MHC class II) molecules, characteristic of immature DC. Purified CD11c⁺DCs were cultured in fresh medium with FBS and GM-CSF and used in subsequent experiments.

HSV-1(F) is a prototype HSV-1 strain used in these studies. In recombinant virus R3616, a 1 kb fragment from the coding region of the γ_1 34.5 gene was deleted.

Viral infection. Purified CD11c⁺DCs were plated in 12 well plates (5×10^5 cells/well) and infected with HSV-1(F) or R3616 at indicated multiplicities of infection. After 2 h incubation, cells were washed with phosphate-buffer saline (PBS) and resuspended in RPMI 1640 supplemented with 10% FBS and 20 ng/ml GM-CSF. At different time points after infection, cells were harvested for analyses. For in vivo analysis, groups of five mice were anesthetized by intraperitoneal injection of ketamine (100 mg/kg) and xylazine (5 mg/kg). HSV-1(F) or R3616 (2×10^5 pfu) was inoculated on the surface of scarified corneas of Balb/C mice bilaterally. On day 1, 3, and 5, whole eyes were collected from sacrificed mice. The corneas were digested with collagenase type 1 (Invitrogen, Garlsbad, Calif.) at 3 mg/ml for 2 h at 37° C. The digested tissues were passed through a 70- μ m nylon cell strainer and spun down at 2000 rpm for 5 min at 4° C. The final pellet was re-suspended in complete RPMI 1640 medium and the single cell suspension was used for further analysis.

RT-PCR analysis. Total RNA from mock infected or virus-infected DCs was extracted using the RNeasy kit (Qiagen Inc. Valencia Calif.). Equal amounts of RNA from each sample were employed to synthesize cDNA using random primers as suggested by manufacturer (Invitrogen, Garlsbad, Calif.). cDNAs were then subjected to PCR amplification for ICP27, UL30, UL44, and 18s rRNA using the specific primers (primers for 18s rRNA were CGCAGCTAGGAATAATGGAA (SEQ ID NO:15) and TTATGACCCGCACTTACTGG (SEQ ID NO:16); primers for ICP27 were CTGGAATCGGACAG-

CAGCCGG (SEQ ID NO:17) and GAGGCGCGACCACA-CACTGT (SEQ ID NO:18); primers for UL30 were ACT-AACTTCGACTGGCCCTTC (SEQ ID NO:19) and CCGTACATGTCGATGTTCAAC (SEQ ID NO:20); primers for UL44 were GCCGCCGCCTACTACCC (SEQ ID NO:21) and GCTGCCGCGATCGTGATG (SEQ ID NO:22)). PCR products were separated on a 1.5% agarose gel and visualized with ethidium bromide under ultraviolet light.

Mixed lymphocyte reaction. Spleens were harvested from C57BL/6 mice by cervical dislocation. Single splenocyte suspensions were prepared by forcing tissue through a fine wire mesh using a syringe plunger followed by repeated pipetting in culture medium. After RBC depletion, CD4⁺ T cells were purified by using the micro-beads (Miltenyi Biotec, Auburn, Calif.) according to the manufacturer's instructions and used as the responder cells. Stimulator cells were bone marrow derived DCs from BALB/c mice and further treated with ultraviolet light before use. The responder cells (1×10^6) were labeled with carboxyfluorescein diacetate succinimidyl ester (CFSE, Invitrogen, Garlsbad, Calif.) and co-cultured with the DCs stimulator cells (2×10^5) in 2 ml media. After 48 h, proliferation of the responder CD4⁺ T cells were analyzed using FACS Calibur and data were analyzed by gating of CFSE positive cells with Cell Questpro software (BD).

Flow cytometry. Cells were stained with fluorescein isothiocyanate (FITC) or phycoerythrin (PE)-linked monoclonal antibodies according to the manufacturer's instruction. Briefly, cells were blocked with Fcy monoclonal antibody (0.5 μ g/ml) for 30 min at 4° C. After washing with phosphate buffer saline (PBS), cells were stained with isotype-matched antibodies, anti-CD11c-PE, anti-MHCII-FITC and anti-CD86-FITC antibodies for 30 min on ice with gentle shaking (eBioscience, San Diego, Calif.). Samples were processed and screened using FACS Calibur and data were analyzed with Cell Questpro software (BD).

Flow cytometry of intracellular cytokine production of IL-6, IL-12, IFN- α and IFN- β in cells were performed as follows. Single-cell suspension were stimulated in 96-well plates with anti-CD3 (5 μ g/ml) and anti-CD28 (5 μ g/ml) mAb for 12 h at 37° C. in 5% CO₂, followed by the addition of Monensin (2 μ g/ml) for 4 h. After washing two times with PBS, cells were blocked with 1 μ l of Fc mAb (0.5 μ g/ml) for 30 min at 4° C. and fixed with 4% of paraformaldehyde at 4° C. for 15 min before permeabilizing with buffer (eBioscience, San Diego, Calif.) at 4° C. for 10 min. After washing once with PBS, cells were stained with appropriate isotype controls, anti-IL-6-FITC, anti-IL-12-FITC, anti-IFN- α -FITC and IFN- β -FITC antibodies (PBL Laboratories, Piscataway, N.J.). Samples were processed and screened using FACS Calibur and data were analyzed with Cell Questpro software (BD).

To determine viral infectivity, DCs mock infected or infected with viruses were fixed in 4% paraformaldehyde (sigma) and permeabilized in permeabilizing buffer (ebioscience, San Diego, Calif.). Cells were blocked with 5% normal mouse serum (sigma), incubated with a monoclonal antibody against HSV-1 ICP27 (Virusys, Sykesville, Md.) and reacted with a goat anti-mouse FITC-conjugated antibody (Santa Cruz biotech, CA). ICP27 expression was determined by flow cytometry.

Interferon bioassay. Culture media from mock infected or virus infected DCs were collected and treated with ultraviolet light to inactivate virus. Where indicated, 30 μ g/ml neutralizing antibodies specific to mouse IFN α / β (PBL Laboratories, Piscataway, N.J.) were added to media. Samples were incubated with Vero cells overnight and washed with phosphate-buffer saline. Vero cells were subjected to infection

with VSV-GFP (10 pfu/cell). At 10 h after infection, cells were harvested and analyzed by flow cytometry using FACS Calibur and data were analyzed with Cell Questpro software (BD).

Plaque assay. To determine the titer of infectious virus, virus infected DCs were harvested, freeze-thawed three times. Eye tissues were collected from mice and mechanically homogenized. Samples were serially diluted in 199v medium and viral yields were titrated on Vero cells at 37° C.

Immunohistochemistry Analysis. Tissue sections for immunohistochemistry were deparaffinized with xylene and rehydrated through a series of graded ethanols. Endogenous peroxidase activity was quenched using a 0.3% H₂O₂-methanol bath followed by several washes with phosphate buffered saline. HSV-1 antigens were detected using a 1:1000 dilution of an HSV-1-specific antiserum raised in a rabbit (DAKO) as previously described. Tissue sections were incubated with primary antibody at 43° C. prior to the addition of biotinylated anti-rabbit immunoglobulin secondary antibody, avidin-horseradish peroxidase, and 3,3'-diaminobenzidine tetrahydrochloride (0.04%) in 0.05 M Tris-HCL (pH 7.4) and 0.025% H₂O₂ as a chromogen (Ventana Medical Systems, Tucson, Ariz.).

Example 8

HSV-1 Lacking the 34.5 Gene is Capable of Infecting Immature Dendritic Cells (DCs)

As an initial step, we sought to compare the susceptibilities of DCs to infection with the 34.5 null mutant and wild-type virus. Purified CD11c+ DCs were generated from bone marrow in the presence of GM-CSF. These cells, constituting 95% of CD11c+ CD11b+ conventional DCs, were exposed to wild-type HSV-1(F) and R3616 which lacks the γ_1 34.5 gene. ICP27 expression, as a measure of infectivity, was examined by fluorescence-activated cell sorter analysis. As shown in FIG. 7A, the number of ICP27-positive cells increased in a multiplicity-of-infection-dependent manner. At a multiplicity of infection of 2, more than 85% of cells were positive for ICP27 expression. A higher dose did not increase infectivity. HSV-1(F) and R3616 infected DCs comparably. A cell viability assay showed that at a multiplicity of infection of 2, 90% of DCs infected with R3616 were viable throughout infection (FIG. 7B). A similar result for HSV-1(F)-infected DCs at 5 or 10 h postinfection was seen. There was a slight reduction in the viability of HSV-1(F)-infected cells at 20 h, when 75% of cells were viable.

To assess viral gene expression, total RNA extracted from infected DCs was subjected to RT-PCR amplification (FIG. 7C). At the early time point (5 h), ICP27 expression was detectable in both HSV-1(F)- and R3616-infected cells, but its level was 3.75-fold higher in HSV-1(F)-infected cells. UL30 was expressed only weakly in HSV-1(F)-infected cells, and its level was 3.75-fold lower than that of ICP27. No UL44 was detectable. As virus infection progressed to late time points (10 and 20 h), basically the same levels of ICP27 and UL30 were observed. Levels of UL44 were 14 to 30% higher in HSV-1(F)-infected cells than in R3616-infected cells. We further measured the production of infectious virus in immature DCs infected at 2 PFU per cell. The results presented in FIG. 7D shown that HSV-1(F) replicated to a titer of 6.2×10^3 PFU/ml at 12 h postinfection and increased to 1.9×10^4 PFU/ml at 48 h postinfection. In contrast, R3616 barely grew, with virus yields remaining at approximately 1.2×10^2 PFU/ml over the course of infection. Wild-type virus and the γ_1 34.5

null mutant were able to infect immature DCs and express viral RNA, but the γ_1 34.5 null mutant was severely impaired in viral production.

Example 9

34.5 Protein is Required to Suppress HSV-Induced Maturation of Dendritic Cells

Based on the above-described analysis, we assessed the impact of γ_1 34.5 on DC maturation. Immature CD11c+ DCs, mock infected or infected with viruses (2 PFU/cell), were subjected to fluorescence-activated cell sorter analysis at 12 h after infection (FIGS. 8A and 8B). We chose to use a multiplicity of infection of 2 because the majority of cells (>85%) are infected and viable after virus infection at this level. As expected, lipopolysaccharide (LPS) induced the up-regulation of MHC-II and CD86 expression compared to that in control mock-infected cells. R3616 also stimulated the expression of MHC-II and CD86, although the magnitude was lower than that for LPS. In contrast, HSV-1(F) reduced the expression of MHC-II slightly and had no stimulatory effect on CD86. To monitor the kinetics of costimulatory-molecule up-regulation, virus-infected DCs were analyzed over a 24-h period. As illustrated in FIGS. 8C and 8D, in HSV-1(F)-infected cells, the expression of MHC-II and CD86 was maintained at basal levels, which were comparable to or slightly lower than those in mock-infected cells at the time points examined. Similar phenotypes in cells infected with R3616 were seen at 3 and 6 h after infection. As infection progressed to 9 h, R3616 stimulated MHC-II and CD86 expression significantly, and expression and further increased at 12 and 24 h after infection. These results suggest that γ_1 34.5 is required to suppress HSV-induced upregulation of costimulatory molecules in immature DCs.

We next analyzed cytokine production by intracellular staining with antibodies against IL-6, IL-12, IFN- α , and IFN- β . As shown in FIGS. 9A and 9B, both HSV-1(F) and R3616 stimulated the expression of IL-6 and IL-12 throughout infection compared to that in mock-infected cells. At 24 h after infection, R3616 induced more cells to produce IL-6 and IL-12 than HSV-1(F). However, the expression patterns for IFN- α and IFN- β were different (FIGS. 9C and 9D). Compared to the proportion among mock-infected cells, HSV-1(F) infection modestly increased the proportion of IFN- α positive DCs. This effect was not seen for IFN- β positive cells at any of the time points examined. In striking contrast, R3616 infection increased IFN- α and IFN- β -positive cells drastically. Thus, unlike wild-type virus, the γ_1 34.5 null mutant stimulated IFN- α/β expression in DCs. These results suggest that γ_1 34.5 is involved in blocking the maturation of DCs during HSV infection.

Example 10

The Interference of 34.5 with Dendritic Cell Maturation is Linked to Reduced IFN Secretion

We further evaluated the IFN- α/β secretion among DCs by a bioassay. CD11c+ DCs were mock infected or infected with HSV-1(F) or R3616, and the media were collected and irradiated with UV. The conditioned media, irradiated with UV, were incubated with Vero cells in the presence or absence of neutralizing antibodies against IFN- α/β . Vero cells were then subjected to infection with VSV-GFP, a virus sensitive to IFN. In this assay, the GFP signal inversely correlates with the IFN level. As revealed by flow cytometry analysis (FIG.

10A), in the absence of neutralizing antibodies against IFN- α/β , only 8.4% of mock-infected or 4.4% of HSV-1(F)-infected cells remained GFP negative. In contrast, 46.3% of R3616-infected cells were GFP negative, indicative of increased IFN secretion. Remarkably, the addition of antibodies against IFN- α/β to R3616-infected cells reduced GFP-negative cells to 6.27%. Neutralizing antibodies had modest effects on cells mock infected or infected with HSV-1(F), which is due likely to a low level of IFN production. We conclude that the $\gamma_1 34.5$ null mutant indeed stimulated IFN- α/β production in DCs and that wild-type virus suppressed IFN- α/β expression.

To determine whether IFN secretion was required for DC maturation, DCs, mock infected or infected with viruses, were treated or left untreated with anti-IFN- α/β antibodies. At 12 h after treatment, cells were analyzed for MHC-II and CD86 expression. As shown in FIGS. 10B and 10C, R3616 but not HSV-1(F) stimulated the expression of MHC-II and CD86 in DCs untreated with anti-IFN- α/β . Notably, treatment with anti-IFN- α/β antibodies led to a decrease in MHC-II and CD86 expression when DCs were infected with R3616. This reduction was partial but statistically significant (33%). Treatment with anti-IFN- α/β antibodies had a minor effect on HSV-1(F)-infected or mock-infected cells. Hence, these results suggest that the inhibition of IFN production by $\gamma_1 34.5$ contributes to impaired DC maturation. In addition, $\gamma_1 34.5$ appears to exert its activity independently of IFN production.

Example 11

Viral Modulation of Dendritic Cell Maturation is Independent of Viral DNA Replication

To test whether viral DNA replication is linked to DC maturation, DCs were mock infected or infected with viruses in the presence or absence of PAA (400 $\mu\text{g/ml}$), a viral DNA polymerase inhibitor. At 12 h post infection, cells were stained for expression of MHC class II, CD86, IFN- α , and IFN- β , respectively. As shown in FIG. 11A, unlike mock infected or HSV-1(F) infected cells, R3616 stimulated MHC class II expression. Similarly, R3616 but not HSV-1(F) stimulated the expression of CD86 (FIG. 11B), IFN- α (FIG. 11C) and IFN- β (FIG. 11D). Notably, these phenotypes were not affected by PAA, an inhibitor of viral DNA replication (data not shown), suggesting that HSV modulation of DC maturation is independent of viral DNA replication.

Example 12

34.5 Protein Attenuates the Capacity of Dendritic Cells to Stimulate T-Cell Activation

Because functional DCs stimulate T cell responses, we determined the effect of $\gamma_1 34.5$ on T cell activation. Immature DCs were mock infected or infected with viruses at 2 pfu per cell. At 12 h after infection, cells were treated with UV light to inactivate viruses. In parallel, a set of uninfected cells were stimulated with LPS as a control. The cells were co-cultured with allogeneic CD4+T cells for 48 h and cell proliferation was analyzed by flow cytometry. As shown in FIG. 12A, CD4+T cells alone exhibited 2.2% spontaneous proliferation whereas LPS stimulated a strong proliferation, with 89.72% of CD4+T cells being activated. Mock infected DCs activated T cell proliferation by 47.38%, which represents a background level. Compared to mock infected cells, R3616 infected DCs induced a significantly higher level of T cell

proliferation (67.7%). However, wild type HSV-1(F) infected DCs stimulated T cell proliferation weakly (29.25%).

We next measured IFN- γ expression by CD4+ T cells after co-culture with DCs (FIG. 12B). As expected, T cells alone showed a background level of IFN- γ production (0.98%), LPS induced the expression of IFN- γ (53.26%). Similarly, R3616-infected DCs induced a higher percentage of IFN- γ positive T cells (39.35%) than mock-infected DCs (19.88%). However, HSV-1(F) infected DCs induced a background level of IFN- γ (13.85%). Together, these results suggest that the $\gamma_1 34.5$ protein is required to inhibit naïve T cells to express IFN- γ and differentiate to Th1 cells by modulating DC maturation.

Example 13

34.5 Protein is Required to Suppress the Maturation of Dendritic Cells In Vivo

To further examine $\gamma_1 34.5$, we assessed DC maturation in an ocular infection model. Mice were mock infected or infected with viruses (2×10^5 pfu/eye). Single cell suspensions were prepared from the eye tissues after infection and phenotypes of DC11c⁺ DCs were analyzed by flow cytometry. As depicted in FIGS. 13A and 13B, on day 1, 3, and 5, R3616 consistently stimulated higher levels of MHCII, and CD86 on DCs as compared to mock infection. In contrast, HSV-1(F) expressed lower levels of MHC class II and CD86. Thus, the $\gamma_1 34.5$ protein blocked the expression of costimulatory molecules in DCs of infected mice.

Cytokine assays revealed that less than 10% of DCs from mock-infected mice expressed IL-6 and IL-12 on day 1, 3, and 5 (FIGS. 13C and 13D). However, infection with both R3616 and HSV-1(F) resulted in increased number of DCs producing IL-6 and IL-12. Notably, HSV-1(F) induced a slightly less IL-12 over the course of infection. In addition, there was a low level of IFN producing cells (less than 10%) in DCs from mock infected mice (FIGS. 13E and 13F). A similar pattern was seen in DCs from mice infected with HSV-1(F) throughout infection. In contrast, there was a prominent increase in IFN positive DCs from R3616 infected mice, which was evident on day 1 and 3. These results indicate that $\gamma_1 34.5$ is involved in blocking viral induction of type I IFN in DCs in vivo.

As a parallel approach, we determined viral replication in the eye. As illustrated in FIG. 14A, HSV-1(F) replicated efficiently in the eye, with titers reaching 5.5×10^5 pfu/ml on day 1, 3.9×10^4 pfu/ml on day 3, and 4.4×10^4 pfu/ml on day 5, respectively. In contrast, R3616 barely replicated over the course of infection. There was a 1000-fold reduction in viral yield as compared to that for HSV-1(F). These phenotypes were also mirrored by immunohistochemistry analysis (FIG. 14B). Viral antigens were only detectable in the eye infected with wild type virus. Thus, viral replication correlated with the inhibition of DC maturation by $\gamma_1 34.5$ in vivo.

While the present invention is described in connection with what is presently considered to be the most practical and preferred embodiments, it should be appreciated that the invention is not limited to the disclosed embodiments, and is intended to cover various modifications and equivalent arrangements included within the spirit and scope of the claims. Modifications and variations in the present invention may be made without departing from the novel aspects of the invention as defined in the claims. The appended claims should be construed broadly and in a manner consistent with the spirit and the scope of the invention herein.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 22

<210> SEQ ID NO 1

<211> LENGTH: 729

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

```

Met  Gln  Ser  Thr  Ser  Asn  His  Leu  Trp  Leu  Leu  Ser  Asp  Ile  Leu  Gly
1      5      10      15

Gln  Gly  Ala  Thr  Ala  Asn  Val  Phe  Arg  Gly  Arg  His  Lys  Lys  Thr  Gly
20     25     30

Asp  Leu  Phe  Ala  Ile  Lys  Val  Phe  Asn  Asn  Ile  Ser  Phe  Leu  Arg  Pro
35     40     45

Val  Asp  Val  Gln  Met  Arg  Glu  Phe  Glu  Val  Leu  Lys  Lys  Leu  Asn  His
50     55     60

Lys  Asn  Ile  Val  Lys  Leu  Phe  Ala  Ile  Glu  Glu  Glu  Thr  Thr  Thr  Arg
65     70     75     80

His  Lys  Val  Leu  Ile  Met  Glu  Phe  Cys  Pro  Cys  Gly  Ser  Leu  Tyr  Thr
85     90     95

Val  Leu  Glu  Glu  Pro  Ser  Asn  Ala  Tyr  Gly  Leu  Pro  Glu  Ser  Glu  Phe
100    105    110

Leu  Ile  Val  Leu  Arg  Asp  Val  Val  Gly  Gly  Met  Asn  His  Leu  Arg  Glu
115    120    125

Asn  Gly  Ile  Val  His  Arg  Asp  Ile  Lys  Pro  Gly  Asn  Ile  Met  Arg  Val
130    135    140

Ile  Gly  Glu  Asp  Gly  Gln  Ser  Val  Tyr  Lys  Leu  Thr  Asp  Phe  Gly  Ala
145    150    155    160

Ala  Arg  Glu  Leu  Glu  Asp  Asp  Glu  Gln  Phe  Val  Ser  Leu  Tyr  Gly  Thr
165    170    175

Glu  Glu  Tyr  Leu  His  Pro  Asp  Met  Tyr  Glu  Arg  Ala  Val  Leu  Arg  Lys
180    185    190

Asp  His  Gln  Lys  Lys  Tyr  Gly  Ala  Thr  Val  Asp  Leu  Trp  Ser  Ile  Gly
195    200    205

Val  Thr  Phe  Tyr  His  Ala  Ala  Thr  Gly  Ser  Leu  Pro  Phe  Arg  Pro  Phe
210    215    220

Glu  Gly  Pro  Arg  Arg  Asn  Lys  Glu  Val  Met  Tyr  Lys  Ile  Ile  Thr  Gly
225    230    235    240

Lys  Pro  Ser  Gly  Ala  Ile  Ser  Gly  Val  Gln  Lys  Ala  Glu  Asn  Gly  Pro
245    250    255

Ile  Asp  Trp  Ser  Gly  Asp  Met  Pro  Val  Ser  Cys  Ser  Leu  Ser  Arg  Gly
260    265    270

Leu  Gln  Val  Leu  Leu  Thr  Pro  Val  Leu  Ala  Asn  Ile  Leu  Glu  Ala  Asp
275    280    285

Gln  Glu  Lys  Cys  Trp  Gly  Phe  Asp  Gln  Phe  Phe  Ala  Glu  Thr  Ser  Asp
290    295    300

Ile  Leu  His  Arg  Met  Val  Ile  His  Val  Phe  Ser  Leu  Gln  Gln  Met  Thr
305    310    315    320

Ala  His  Lys  Ile  Tyr  Ile  His  Ser  Tyr  Asn  Thr  Ala  Thr  Ile  Phe  His
325    330    335

Glu  Leu  Val  Tyr  Lys  Gln  Thr  Lys  Ile  Ile  Ser  Ser  Asn  Gln  Glu  Leu
340    345    350

Ile  Tyr  Glu  Gly  Arg  Arg  Leu  Val  Leu  Glu  Pro  Gly  Arg  Leu  Ala  Gln
355    360    365

```

His 370	Pro	Lys	Thr	Thr	Glu 375	Glu	Asn	Pro	Ile	Phe 380	Val	Val	Ser	Arg	
Glu 385	Pro	Leu	Asn	Thr	Ile 390	Gly	Leu	Ile	Tyr	Glu 395	Lys	Ile	Ser	Leu	Pro 400
Lys	Val	His	Pro	Arg 405	Tyr	Asp	Leu	Asp	Gly 410	Asp	Ala	Ser	Met	Ala 415	Lys
Ala	Ile	Thr	Gly 420	Val	Val	Cys	Tyr	Ala 425	Cys	Arg	Ile	Ala	Ser	Thr	Leu
Leu	Leu	Tyr 435	Gln	Glu	Leu	Met	Arg 440	Lys	Gly	Ile	Arg	Trp 445	Leu	Ile	Glu
Leu	Ile 450	Lys	Asp	Asp	Tyr	Asn 455	Glu	Thr	Val	His 460	Lys	Lys	Thr	Glu	Val
Val 465	Ile	Thr	Leu	Asp	Phe 470	Cys	Ile	Arg	Asn	Ile 475	Glu	Lys	Thr	Val	Lys 480
Val	Tyr	Glu	Lys 485	Leu	Met	Lys	Ile	Asn	Leu 490	Glu	Ala	Ala	Glu	Leu 495	Gly
Glu	Ile	Ser	Asp 500	Ile	His	Thr	Lys	Leu 505	Leu	Arg	Leu	Ser	Ser	Ser	Gln
Gly	Thr	Ile 515	Glu	Thr	Ser	Leu	Gln 520	Asp	Ile	Asp	Ser	Arg 525	Leu	Ser	Pro
Gly 530	Gly	Ser	Leu	Ala	Asp 535	Ala	Trp	Ala	His	Gln 540	Glu	Gly	Thr	His	Pro
Lys 545	Asp	Arg	Asn	Val	Glu 550	Lys	Leu	Gln	Val	Leu 555	Leu	Asn	Cys	Met	Thr 560
Glu	Ile	Tyr	Tyr 565	Gln	Phe	Lys	Lys	Asp	Lys 570	Ala	Glu	Arg	Arg	Leu 575	Ala
Tyr	Asn	Glu 580	Glu	Gln	Ile	His	Lys	Phe 585	Asp	Lys	Gln	Lys	Leu	Tyr 590	Tyr
His	Ala 595	Thr	Lys	Ala	Met	Thr	His 600	Phe	Thr	Asp	Glu	Cys 605	Val	Lys	Lys
Tyr 610	Glu	Ala	Phe	Leu	Asn 615	Lys	Ser	Glu	Glu	Trp 620	Ile	Arg	Lys	Met	Leu
His 625	Leu	Arg	Lys	Gln	Leu 630	Leu	Ser	Leu	Thr	Asn 635	Gln	Cys	Phe	Asp	Ile 640
Glu	Glu	Glu	Val 645	Ser	Lys	Tyr	Gln	Glu	Tyr 650	Thr	Asn	Glu	Leu	Gln 655	Glu
Thr	Leu	Pro 660	Gln	Lys	Met	Phe	Thr 665	Ala	Ser	Ser	Gly	Ile 670	Lys	His	Thr
Met	Thr 675	Pro	Ile	Tyr	Pro	Ser	Ser 680	Asn	Thr	Leu	Val	Glu 685	Met	Thr	Leu
Gly 690	Met	Lys	Lys	Leu	Lys 695	Glu	Glu	Met	Glu	Gly 700	Val	Val	Lys	Glu	Leu
Ala 705	Glu	Asn	Asn	His	Ile 710	Leu	Glu	Arg	Phe	Gly 715	Ser	Leu	Thr	Met	Asp 720
Gly	Gly	Leu	Arg 725	Asn	Val	Asp	Cys	Leu							

<400> SEQUENCE: 2

gccggcggtg gcgcggcgga gaccgcgctg gtataacaag aggattgcct gatccagcca 60

-continued

agatgcagag cacttcta	catctgtggc	ttttatctga	tatttttaggc	caaggagcta	120
ctgcaaatgt ctttcgtgga	agacataaga	aaactgggtga	tttatttgct	atcaaagtat	180
ttaataacat aagcttcctt	cgtccagtgg	atgttcaaat	gagagaattt	gaagtgttga	240
aaaaactcaa tcacaaaaat	attgtcaaat	tatttgctat	tgaagaggag	acaacaacaa	300
gacataaagt acttattatg	gaattttgtc	catgtgggag	tttatacact	gttttagaag	360
aaccttctaa tgccatgga	ctaccagaat	ctgaattctt	aattgttttg	cgagatgtgg	420
tgggtggaat gaatcatcta	cgagagaatg	gtatagtgc	ccgtgatatc	aagccaggaa	480
atatcatgcg tgttataggg	gaagatggac	agtctgtgta	caaactcaca	gattttgggtg	540
cagctagaga attagaagat	gatgagcagt	ttgtttctct	gtatggcaca	gaagaatatt	600
tgcacctga tatgtatgag	agagcagtgc	taagaaaaga	tcatcagaag	aaatatggag	660
caacagttga tctttggagc	attggggtaa	cattttacca	tgacgctact	ggatcactgc	720
catttagacc ctttgaaggg	cctcgtagga	ataaagaagt	gatgtataaa	ataattacag	780
gaaagccttc tgggtgcaata	tctggagtag	agaaagcaga	aaatggacca	attgactgga	840
gtggagacat gcctgtttct	tgacgtcttt	ctcggggctc	tcagggttcta	cttacccttg	900
ttcttgcaaa catccttgaa	gcagatcagg	aaaagtgttg	gggttttgac	cagttttttg	960
cagaaactag tgatatactt	caccgaatgg	taattcatgt	tttttcgcta	caacaaatga	1020
cagctcataa gatttatatt	catagctata	atactgtac	tatatttcat	gaactgggtat	1080
ataaacaac caaaattatt	tcttcaaatc	aagaacttat	ctacgaaggg	cgacgcttag	1140
tcttagaacc tggaaggctg	gcacaacatt	tccctaaaac	tactgaggaa	aacctatat	1200
ttgtagtaag ccgggaacct	ctgaatacca	taggattaat	atatgaaaaa	atttcctctc	1260
ctaaagtaca tccacgttat	gatttagacg	gggatgctag	catggctaag	gcaataacag	1320
gggttgtgtg ttatgcctgc	agaattgcc	gtaccttact	gctttatcag	gaattaatgc	1380
gaaaggggat acgatggctg	attgaattaa	ttaaagatga	ttacaatgaa	actgttcaca	1440
aaaagacaga agttgtgatc	acattggatt	tctgtatcag	aaacattgaa	aaaactgtga	1500
aagtatatga aaagtgtgat	aagatcaacc	tggaagcggc	agagttaggt	gaaatttcag	1560
acatacacac caaattgttg	agactttcca	gttctcaggg	aacaatagaa	accagctctc	1620
aggatatcga cagcagatta	tctccaggtg	gatcactggc	agacgcattg	gcacatcaag	1680
aaggcactca tccgaaagac	agaaatgtag	aaaaactaca	agtcctgtta	aattgcatga	1740
cagagattta ctatcagttc	aaaaaagaca	aagcagaacg	tagattagct	tataatgaag	1800
aacaaatcca caaatttgat	aagcaaaaac	tgtattacca	tgccacaaaa	gctatgacgc	1860
actttacaga tgaatgtggt	aaaaagtatg	aggcattttt	gaataagtca	gaagaatgga	1920
taagaaagat gcttcactct	aggaaacagt	tattatcgct	gactaatcag	tgttttgata	1980
ttgaagaaga agtatcaaaa	tatcaagaat	atactaata	gttacaagaa	actctgcctc	2040
agaaaatggt tacagcttcc	agtggaaatc	aacataccat	gaccccaatt	tatccaagtt	2100
ctaacacatt agtagaaatg	actcttggtg	tgaagaaatt	aaaggaagag	atggaagggg	2160
tgggttaaaga acttgctgaa	aataaccaca	ttttagaag	gtttggctct	ttaacctatg	2220
atggtggcct tcgcaacgtt	gactgtcttt	agctttctaa	tagaagttta	agaaaagttt	2280
ccgtttgcac aagaaaataa	cgtttgggca	ttaaatgaat	gcctttatag	atagtcactt	2340
gtttctacaa ttcagtattt	gatgtggctg	tgtaaatatg	tacaatattg	taaatacata	2400
aaaaatatac aaatttttgg	ctgctgtgaa	gatgtaattt	tatcttttaa	cattttataat	2460

-continued

tatatgagga aatttgacct cagtgatcac gagaagaaag ccatgaccga ccaatatgtt	2520
gacatactga tectctactc tgagtggggc taaataagtt atttctctg accgcctact	2580
ggaaatattt ttaagtggaa ccaaaatagg catccttaca aatcaggaag actgacttga	2640
cacgtttgta aatggtagaa cgttggtctac tgtgagtggg gaggagaacc gcaccactgt	2700
tatactggga taacaatttt ttgagaagg ataaagtggc attattttat ttacaaggt	2760
gccagatcc cagttatcct tgtatccatg taatttcaga tgaattatta agcaaacatt	2820
ttaaagttaa ttcattatta aaaactattc atttttttcc ttggccata aatgtgtaat	2880
tgtcattaaa attctaaggt catttcaact gttttaagct gtatatttct ttaattctgc	2940
ttactatttc atggaaaaaa ataaatttct caattttaat gt	2982

<210> SEQ ID NO 3

<211> LENGTH: 263

<212> TYPE: PRT

<213> ORGANISM: Herpes simplex virus 1

<400> SEQUENCE: 3

Met Ala Arg Arg Arg Arg His Arg Gly Pro Arg Arg Pro Arg Pro Pro	1	5	10	15
Gly Pro Thr Gly Ala Val Pro Thr Ala Gln Ser Gln Val Thr Ser Thr	20	25	30	
Pro Asn Ser Glu Pro Ala Val Arg Ser Ala Pro Ala Ala Ala Pro Pro	35	40	45	
Pro Pro Pro Ala Ser Gly Pro Pro Pro Ser Cys Ser Leu Leu Leu Arg	50	55	60	
Gln Trp Leu His Val Pro Glu Ser Ala Ser Asp Asp Asp Asp Asp Asp	65	70	75	80
Asp Trp Pro Asp Ser Pro Pro Pro Glu Pro Ala Pro Glu Ala Arg Pro	85	90	95	
Thr Ala Ala Ala Pro Arg Pro Arg Ser Pro Pro Pro Gly Ala Gly Pro	100	105	110	
Gly Gly Gly Ala Asn Pro Ser His Pro Pro Ser Arg Pro Phe Arg Leu	115	120	125	
Pro Pro Arg Leu Ala Leu Arg Leu Arg Val Thr Ala Glu His Leu Ala	130	135	140	
Arg Leu Arg Leu Arg Arg Ala Gly Gly Glu Gly Ala Pro Glu Pro Pro	145	150	155	160
Ala Thr Pro Ala Thr Pro Ala Thr Pro Ala Thr Pro Ala Thr Pro Ala	165	170	175	
Thr Pro Ala Thr Pro Ala Thr Pro Ala Thr Pro Ala Thr Pro Ala Arg	180	185	190	
Val Arg Phe Ser Pro His Val Arg Val Arg His Leu Val Val Trp Ala	195	200	205	
Ser Ala Ala Arg Leu Ala Arg Arg Gly Ser Trp Ala Arg Glu Arg Ala	210	215	220	
Asp Arg Ala Arg Phe Arg Arg Val Ala Glu Ala Glu Ala Val Ile	225	230	235	240
Gly Pro Cys Leu Gly Pro Glu Ala Arg Ala Arg Ala Leu Ala Arg Gly	245	250	255	
Ala Gly Pro Ala Asn Ser Val	260			

-continued

```

<210> SEQ ID NO 4
<211> LENGTH: 1399
<212> TYPE: DNA
<213> ORGANISM: Herpes simplex virus 1

<400> SEQUENCE: 4

tttaaagtcg cggcggcgca gcccgggccc ccgcgggccc agacgagcga gttagacagg      60
caagcactac tcgcctctgc acgcacatgc ttgcctgtca aactetacca ccccggcacg      120
ctctctgtct ccatggcccg ccgcgcgcgc catcgcggcc ccgcgcgcgc ccggccgccc      180
gggcccacgg gcgcgcgtcc aaccgcacag tcccaggtaa cctccacgcc caactcggaa      240
cccgcggtca ggagcgcgcg cgcggcgcgc ccgcgcgcgc ccccgccag tgggcccccg      300
ccttcttggt cgctgctgct gcgccagtgg ctccacgttc ccgagtcgcg gtccgacgac      360
gacgatgacg acgactggcc ggacagcccc ccgcgcgagc cggcgccaga ggccccggcc      420
accgcgcgcg cccccgcgcg ccggtcccca ccgcgcgcgc cgggccccgg gggcggggct      480
aacccctccc accccccctc acgccccttc cgccttcgcg cgcgcctcgc cctccgcctg      540
cgcgctcaccg cagagcaact ggcgcgccctg cgctgcgac gcgcggggcg ggagggggcg      600
ccggagcccc ccgcgacccc cgcgaccccc gcgacccccg cgacccccgc gacccccgcg      660
acccccgcga cccccgcgac ccccgcgacc ccgcgacccc ccgcgcgggt gcgcttctcg      720
ccccacgtcc ggggtcgcca cctgggtggtc tgggcctcgg ccgcccgcct ggcgcgccgc      780
ggctcgtggg ccgcgcgagc ggccgacccg gctcgggttc ggcgccgggt ggcgagggcc      840
gaggcggtca tcgggcccgt cctggggccc gaggcccggt cccgggcccct ggcccccgga      900
gccggccccg cgaactcggc ctaacgttac acccgaggcg gcctgggtct tcgcgggagc      960
tcccgggagc tccgcaccaa gccgctctcc ggagagacga tggcaggagc cgcgcatata      1020
tacgtgggga gccggcccgcc ccccgaggcg ggccccccct cggagggcgg gactggccaa      1080
tcggcgcccg ccagcgcggc ggggccccgc caaccagcgt ccgcgcgagc ttcggggccc      1140
ggcccactgg gcgggagtta ccgccagtg ggccggggcg cccacttccc ggtatggtaa      1200
ttaaaaaactt acaagaggcc ttgttcgct tcccggtatg gtaattagaa actcattaat      1260
gggcggcccc ggcgccctt cccgcttcg gcaattcccg cggcccttaa tgggcaaccc      1320
cggatttccc cgcctccgcg gccgcgcgta accactccct tgggggttcg ggttatgcta      1380
attgcttttt tggcggaat                                     1399

```

```

<210> SEQ ID NO 5
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

```

```

<400> SEQUENCE: 5

atgagtacaa cgagtaag                                     18

```

```

<210> SEQ ID NO 6
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

```

```

<400> SEQUENCE: 6

ctagtattca gcacctgctt                                     20

```

-continued

<210> SEQ ID NO 7
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 7

atgggagaga atgctgatgg 20

<210> SEQ ID NO 8
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 8

tcagaatgca gggttcattt 20

<210> SEQ ID NO 9
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 9

atgagtgaga acaataagaa 20

<210> SEQ ID NO 10
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 10

tcattcccca ttccagcttg 20

<210> SEQ ID NO 11
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 11

atgagtacaa atggtgatga tcatcag 27

<210> SEQ ID NO 12
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 12

attgcctgct tctatataca ttcttgc 27

<210> SEQ ID NO 13
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

-continued

<400> SEQUENCE: 13

cgcagctagg aataatggaa

20

<210> SEQ ID NO 14

<211> LENGTH: 19

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 14

ttatgaccgc acttactgg

19

<210> SEQ ID NO 15

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 15

cgcagctagg aataatggaa

20

<210> SEQ ID NO 16

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Primer'

<400> SEQUENCE: 16

ttatgaccgc cacttactgg

20

<210> SEQ ID NO 17

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 17

ctggaatcgg acagcagccg g

21

<210> SEQ ID NO 18

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 18

gaggcgcgac cacacactgt

20

<210> SEQ ID NO 19

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 19

actaacttcg actggccctt c

21

<210> SEQ ID NO 20

-continued

<hr/>	
<211> LENGTH: 21	
<212> TYPE: DNA	
<213> ORGANISM: Artificial	
<220> FEATURE:	
<223> OTHER INFORMATION: Primer	
<400> SEQUENCE: 20	
c c g t a c a t g t c g a t g t t c a a c	21
<210> SEQ ID NO 21	
<211> LENGTH: 17	
<212> TYPE: DNA	
<213> ORGANISM: Artificial	
<220> FEATURE:	
<223> OTHER INFORMATION: Primer	
<400> SEQUENCE: 21	
g c c g c c g c c t a c t a c c c	17
<210> SEQ ID NO 22	
<211> LENGTH: 18	
<212> TYPE: DNA	
<213> ORGANISM: Artificial	
<220> FEATURE:	
<223> OTHER INFORMATION: Primer	
<400> SEQUENCE: 22	
g c t g c c g c g a t c g t g a t g	18
<hr/>	

- We claim:
- 1. An attenuated HSV-1 virus comprising a deletion that removes a fragment of only the amino-terminal domain of the γ_1 34.5 protein, wherein the γ_1 34.5 protein comprising the deletion is capable of being expressed by the virus, and wherein the γ_1 34.5 protein does not interact with TBK1.
 - 2. The attenuated HSV-1 virus of claim 1, wherein the deletion is present in at least one copy of a γ_1 34.5 polynucleotide.
 - 3. The attenuated HSV-1 virus of claim 1, wherein the deletion comprises a fragment selected from the group consisting of amino acid 1 to amino acid 146 of SEQ ID NO: 3 and amino acid 72 to amino acid 106 of SEQ ID NO: 3.
 - 4. An immunogenic composition comprising the virus of claim 1 and an adjuvant.
 - 5. The composition of claim 4, wherein the adjuvant is selected from the group consisting of a sterile oil-in-water emulsion free of animal origin ingredients, wherein the emulsion comprises uniformly dispersed, micron size oil droplets and dimethyldioctadecylammonium bromide; monophosphoryl lipid A (MPL); and Freund.
 - 6. A method of provoking an immune response against a HSV-1 strain in a subject comprising the step of administering to the subject the immunogenic composition of claim 4.
 - 7. The method of claim 6, wherein the subject is human.
 - 8. The attenuated HSV-1 virus of claim 3, wherein the deletion consists of amino acid 72 to amino acid 106 of SEQ ID NO: 3.
 - 9. The attenuated HSV-1 virus of claim 3, wherein the deletion consists of amino acid 1 to amino acid 146 of SEQ ID NO: 3.

* * * * *