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CA 2836987 C 2016/07/05

(11)(21) **2 836 987**

(12) BREVET CANADIEN / CANADIAN PATENT

(13) **C**

(22) **Date de dépôt/Filing Date:** 2005/05/24

(41) **Mise à la disp. pub./Open to Public Insp.:** 2005/12/15

(45) **Date de délivrance/Issue Date:** 2016/07/05

(62) **Demande originale/Original Application:** 2 567 094

(30) **Priorité/Priority:** 2004/05/26 (US60/574,851)

(51) **Cl.Int./Int.Cl.** ***C12N 7/01*** (2006.01), ***A61K 35/761*** (2015.01), ***A61P 35/00*** (2006.01), ***C12N 15/34*** (2006.01), ***C12N 15/861*** (2006.01)

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(54) **Titre : ADENOVIRUS CHIMERES A UTILISER DANS LE TRAITEMENT DU CANCER**
(54) **Title: CHIMERIC ADENOVIRUSES FOR USE IN CANCER TREATMENT**

(57) **Abrégé/Abstract:**
The present invention relates to oncolytic adenoviruses having therapeutic applications. Recombinant chimeric adenoviruses, and methods to produce them are provided. The chimeric adenoviruses of the invention comprise nucleic acid sequences derived from adenoviral serotypes classified within the subgroups B through F and demonstrate an enhanced therapeutic index.

Abstract

The present invention relates to oncolytic adenoviruses having therapeutic applications. Recombinant chimeric adenoviruses, and methods to produce them are provided. The chimeric adenoviruses of the invention comprise nucleic acid sequences derived from adenoviral serotypes classified within the subgroups B through F and demonstrate an enhanced therapeutic index.

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CHIMERIC ADENOVIRUSES FOR USE IN CANCER TREATMENT

This is a divisional application of Canadian Patent Application Serial No. 2,567,094 filed on May 24, 2005.

FIELD OF THE INVENTION

The invention described herein relates generally to the field of molecular biology, and more specifically to oncolytic adenoviruses having therapeutic applications. It should be understood that the expression "the invention" and the like used herein may refer to subject matter claimed in either the parent or the divisional applications.

BACKGROUND OF THE INVENTION

Cancer is a leading cause of death in the United States and elsewhere. Depending on the type of cancer, it is typically treated with surgery, chemotherapy, and/or radiation. These treatments often fail, and it is clear that new therapies are necessary, to be used alone or in combination with classical techniques.

One approach has been the use of adenoviruses, either alone or as vectors able to deliver anti-cancer therapeutic proteins to tumor cells. Adenoviruses are non-enveloped icosohedral double-stranded DNA viruses with a linear genome of approximately 36 kilobase pairs. Each end of the viral genome has a short sequence known as the inverted terminal repeat (or ITR), which is required for viral replication. All human adenovirus genomes examined to date have the same general organization; that is, the genes encoding specific functions are located at the same position on the viral genome. The viral genome contains five early transcription units (E1A, E1B, E2, E3, and E4), two delayed early units (IX and, Iva2), and one late unit (major late) that is processed to generate five families of late mRNAs (L1-L5). Proteins encoded by the early genes are involved in replication, whereas the late genes encode viral structural proteins. Portions of the viral genome can be readily substituted with DNA of foreign origin and recombinant adenoviruses are structurally stable, properties that make these viruses potentially useful for gene therapy (see Jolly, D. (1994) Cancer Gene Therapy 1:51-64).

Currently, the research efforts to produce clinically useful adenoviral therapy have focused on the adenoviral serotype, Ad5. The genetics of this human adenovirus are well-characterized and systems are well described for its molecular manipulation. High capacity production methods have been developed to support clinical applications, and some clinical experience with the agent is available. See, Jolly, D. (1994) Cancer

Gene Therapy, 1:51-64. Research related to the use of human adenoviruses (Ad) in cancer treatment has focused on the development of Ad5-based adenoviruses that have a higher potency in, or are preferentially targeted to, specific tumor cell types and there exists a need for generation of more potent oncolytic viruses if adenoviral therapy is to find practical application in a clinical setting.

Ad5 is only one of 51 currently known adenoviral serotypes, which are classified into subgroups A-F, based on various attributes including their hemagglutination properties ((see, Shenk, "Adenoviridae: The Viruses and Their Replication," in Fields Virology, Vol.2, Fourth Edition, Knipe, ea., Lippincott, Williams & Wilkins, pp. 2265-2267 (2001)). These serotypes differ at a variety of levels, e.g. pathology in humans and rodents, cell receptors used for attachment, but these differences have been largely ignored as potential means to develop more potent oncolytic adenoviruses (with the exception of fiber alterations, see Stevenson et al. (1997) *J.Virol.* 71:4782-4790; Krasnykh et al. (1996) *J. Virol.* 70:6839-6846; Wickham et al. (1997) *J.Virol.* 71:8221-8229; Legrand et al. (2002) Curr. Gene Ther. 2:323-329; Barnett et al. (2002) Biochim. Biophys. Acta 1-3:1-14; US Patent Application 2003/0017138).

Exploitation of differences among adenoviral serotypes may provide a source of more effective adenoviral-based therapeutics, using novel adenoviruses with increased selectivity and potency. There is a need for such improved adenoviral-based therapies.

SUMMARY OF THE INVENTION

The present invention provides novel chimeric adenoviruses, or variants or derivatives thereof, useful for viral-based therapy. In particular, the invention provides for chimeric adenoviruses, or variants or derivatives thereof, having a genome comprising an E2B region

wherein said E2B region comprises a nucleic acid sequence derived from a first adenoviral serotype and a nucleic acid sequence derived from a second adenoviral serotype;

wherein said first and second adenoviral serotypes are each selected from the adenoviral subgroups B, C, D, E, or F and are distinct from each other; and

wherein said chimeric adenovirus is oncolytic and demonstrates an enhanced therapeutic index for a tumor cell.

In one embodiment, the chimeric adenovirus further comprises regions encoding fiber, hexon, and penton proteins, wherein the nucleic acids encoding said proteins are all from the same adenoviral serotype. In another embodiment, the chimeric adenovirus of the invention comprises a modified E3 or E4 region.

In another embodiment, the chimeric adenovirus demonstrates an enhanced therapeutic index in a colon, breast, pancreas, lung, prostate, ovarian or hemopoietic tumor cell. In a particularly preferred embodiment, the chimeric adenovirus displays an enhanced therapeutic index in colon tumor cells.

In a preferred embodiment, the E2B region of the chimeric adenovirus comprises SEQ ID

NO: 3. In a particularly preferred embodiment, the chimeric adenovirus comprises SEQ ID NO: 1.

The present invention provides for a recombinant chimeric adenovirus, or a variant or derivative thereof, having a genome comprising an E2B region

wherein said E2B region comprises a nucleic acid sequences derived from a first adenoviral serotype and a nucleic acid second derived from a second adenoviral serotype;

wherein said first and second adenoviral serotypes are each selected from the adenoviral subgroups B, C, D, E, or F and are distinct from each other;

wherein said chimeric adenovirus is oncolytic and demonstrates an enhanced therapeutic index for a tumor cell; and

wherein said chimeric adenovirus has been rendered replication deficient through deletion of one or more adenoviral regions encoding proteins involved in adenoviral replication selected from the group consisting of E1, E2, E3 or E4.

In one embodiment, the chimeric adenovirus of the invention further comprises a heterologous gene that encodes a therapeutic protein, wherein said heterologous gene is expressed within a cell infected with said adenovirus. In a preferred embodiment, the therapeutic protein is selected from the group consisting of cytokines and chemokines, antibodies, pro-drug converting enzymes, and immunoregulatory proteins.

The present invention provides methods for using the chimeric adenoviruses of the invention for therapeutic purposes. In one embodiment, the chimeric adenoviruses can be used to inhibit the growth of cancer cells. In a particular embodiment, a chimeric adenovirus comprising SEQ ID NO: 1 is useful for inhibiting the growth of colon cancer cells.

In another embodiment, the adenoviruses of the invention are useful as vectors to deliver therapeutic proteins to cells.

The present invention provides a method for production of the chimeric adenoviruses of the invention, wherein the method comprises

a) pooling of adenoviral serotypes representing adenoviral subgroups B-F, thereby creating an adenoviral mixture;

b) passaging the pooled adenoviral mixture from step (a) on an actively growing culture of tumor cells at a particle per cell ratio high enough to encourage recombination between serotypes, but not so high as to produce premature cell death;

c) harvesting the supernatant from step (b);

d) infecting a quiescent culture of tumor cells with the supernatant harvested in step (c);

e) harvesting the cell culture supernatant from step (d) prior to any sign of CPE;

f) infecting a quiescent culture of tumor cells with the supernatant harvested in step (e); and

g) isolating the chimeric adenovirus from the supernatant harvested in step (f) by plaque purification.

According to one aspect of the invention there is provided a chimeric adenovirus having a genome comprising an E2B region, wherein said E2B region comprises a nucleic acid sequence derived from a first adenoviral serotype and a nucleic acid sequence derived from a second adenoviral serotype; wherein said first and second serotypes are each a different subgroup B,C, D, E, or F adenovirus; and wherein said chimeric adenovirus is oncolytic and demonstrates an enhanced therapeutic index for a tumor cell.

According to a further aspect of the invention there is provided a recombinant chimeric adenovirus having a genome comprising an E2B region, wherein said E2B region comprises a nucleic acid sequence derived from a first adenoviral serotype and a nucleic acid sequence derived from a second adenoviral serotype; wherein said first and second adenoviral serotypes are each a different subgroup B, C, D, E, or F adenovirus; wherein said chimeric adenovirus is oncolytic and demonstrates an enhanced therapeutic index for a tumor cell, and wherein said chimeric adenovirus has been rendered replication deficient through deletion of at least one adenoviral region encoding protein involved in adenoviral replication which is E1, E2, E3 or E4.

According to another aspect of the invention there is provided a method for isolating an adenovirus as described herein, wherein said method comprises:

a) pooling of adenoviral serotypes representing adenoviral subgroups B-F, thereby creating an adenoviral mixture;

b) passaging the pooled adenoviral mixture from step (a) on an actively growing culture of tumor cells at a particle per cell ratio high enough to encourage recombination between serotypes, but not so high as to produce premature cell death;

c) harvesting the supernatant from step (b);

d) infecting a quiescent culture of tumor cells with the supernatant harvested in step (c);

e) harvesting the cell culture supernatant from step (d) prior to any sign of CPE;

f) infecting a quiescent culture of tumor cells with the supernatant harvested in step (e); and

g) isolating the virus of the invention from the supernatant harvested in step (f) by plaque purification and sequencing to confirm identity.

According to yet another aspect of the invention there is provided a replication competent oncolytic adenovirus serotype 11 wherein the E3 transcription unit region and/or the E4orf4 gene contain a deletion and wherein the adenovirus has an enhanced therapeutic index.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. Ad retention time profiles on a TMAE HPLC column. A) Retention profiles for the individual Ad serotypes that were used to generate the original starting viral pool. B) Retention profiles of the passage 20 pools derived from HT-29, Panc-1, MDA-231, and PC-3 cell lines, respectively.

Figure 2. Cytolytic activity of the individual virus pools. A) HT-29, B) MDA-231, C) Panc-1 and D) PC-3 cells were infected with their respective viral pools at VP per cell ratios from 100 to 0.01. MTS assays were performed on differing days post infection (as indicated) dependent upon the cell line. Each data point in the panel represents an assay done in quadruplicate and the results are expressed as the means +/- SD. The panel depicts one representative experiment and all viral pools were assayed at least three independent times on the target tumor cell line (Figure Legend: —●— Ad5; —□— initial viral pool; —■— specific cell derived pool, passage 20).

Figure 3. Cytolytic activity of ColoAd1 and Ad5 on human tumor cell lines. An MTS assay was performed on A) a broad panel of human tumor cell lines and B) on a panel of human colon cancer cell lines to determine its potential potency specificity. The MTS assay was performed on differing days dependent upon the cell line. Each panel is a representative experiment that has been repeated at least three times. Each data point in the panel represents an assay done in quadruplicate and the results are expressed as the means +/- SD (Figure Legend: —●— Ad5; —□— ColoAd1).

Figure 4. Cytolytic activity of ColoAd1 and Ad5 on a panel of normal cells. HS-27, HUVEC and SAEC cells (primary fibroblast, endothelial, and epithelial cells, respectively) were infected with ColoAd1 and Ad5 at VP per cell ratios from 100 to 0.01. MTS assay was performed on differing days post infection dependent upon the cell and each panel is a representative experiment that has been repeated at least three times. Each data point in the panel represents an assay done in quadruplicate and the results are expressed as the means +/- SD (Figure Legend: —●— Ad5; —□— ColoAd1).

Figure 5. Cytolytic activity of ColoAd1, Ad5 and ONYX-015 on primary normal endothelial cells (HUVEC) and a colon tumor cell line (HT-29). Each panel is a representative experiment that has

been repeated at least three times. Each data point in the panel represents an assay done in quadruplicate and the results are expressed as the means +/- SD (Figure Legend: —●— Ad5; —□— ColoAd1; —■— Onyx-015).

Figure 6. Cytolytic activity of ColoAd1, Ad11p and Ad5 on a normal epithelial cell line (SAEC) and a human colon cancer cell line (HT-29). Each panel is a representative experiment that has been repeated at least three times. Each data point in the panel represents an assay done in quadruplicate and the results are expressed as the means +/- SD (Figure Legend: —●— Ad5; —□— Ad11p;
—■— ColoAd1).

Figure 7. Cytolytic activity of Recombinant Viruses. Recombinant viruses representing four viral populations (Adp11, ColoAd1, left end Ad11p/right end ColoAd1(ColoAd1.1) and left end ColoAd1/right end Ad11p (ColoAd1.2)) were constructed as described in Example 6. Cytolytic activity of each population in HT29 cells was determined as previously described. (Figure Legend: —●— Ad5; —□— Ad11p; —■— ColoAd1; —U— ColoAd1.1; —▲— ColoAd1.2).

DETAILED DESCRIPTION OF THE INVENTION

Definitions

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Generally, the nomenclature used herein and the laboratory procedures described below are those well known and commonly employed in the art.

As used herein, the term "adenovirus", "serotype" or "adenoviral serotype" refers to any of the 51 human adenoviral serotypes currently known, or isolated in the future. See, for example, Strauss, "Adenovirus infections in humans," in The Adenoviruses, Ginsberg, ea., Plenum Press, New York, NY, pp. 451-596 (1984). These serotypes are classified in the subgroups A-F (see, Shenk, "Adenoviridae: The Viruses and Their Replication," in Fields Virology, Vol.2, Fourth Edition, Knipe, ea., Lippincott Williams & Wilkins, pp. 2265-2267 (2001), as shown in Table 1.

Table 1

SubGroup	Adenoviral Serotype
A	12, 18, 31
B	3, 7, 11, 14, 16, 21, 34, 35, 51
C	1, 2, 5, 6
D	8-10, 13, 15, 17, 19, 20, 22-30, 32, 33, 36-39, 42-49, 50
E	4
F	40, 41

As used herein, "chimeric adenovirus" refers to an adenovirus whose nucleic acid sequence is comprised of the nucleic acid sequences of at least two of the adenoviral serotypes described above.

As used herein, "parent adenoviral serotype" refers to the adenoviral serotype which represents the serotype from which the majority of the genome of the chimeric adenovirus is derived.

As used herein, the term "homologous recombination" refers to two nucleic acid molecules, each having homologous sequences, where the two nucleic acid molecules cross over or undergo recombination in the region of homology.

As used herein, the term "potency" refers to the lytic potential of a virus and represents its ability to replicate, lyse, and spread. For the purposes of the instant invention, potency is a value which compares the cytolytic activity of a given adenovirus of the invention to that of Ad5 in the same cell line, i.e. potency = IC_{50} of AdX/IC_{50} of Ad5, where X is the particular adenoviral serotype being examined and wherein the potency of Ad5 is given a value of 1.

As used herein, the term "oncolytic virus" refers to a virus that preferentially kills cancer cells as compared with normal cells.

As used herein, the term "therapeutic index" or "therapeutic window" refers to a number indicating the oncolytic potential of a given adenovirus and is determined by dividing the potency of the adenovirus in a cancer cell line by the potency of the same adenovirus in a normal (i.e. non-cancerous) cell line.

As used herein, the term "modified" refers to a molecule with a nucleotide or amino acid sequence differing from a naturally-occurring, e.g. a wild-type nucleotide or amino acid sequence. A modified molecule can retain the function or activity of a wild-type molecule, i.e. a modified adenovirus may retain its oncolytic activity. Modifications include mutations to nucleic acids as described below.

As used herein, "mutation" with reference to a polynucleotide or polypeptide, refers to a naturally-occurring, synthetic, recombinant, or chemical change or difference to the primary, secondary, or tertiary structure of a polynucleotide or polypeptide, as compared to a reference polynucleotide or polypeptide, respectively (e.g., as compared to a wild-type polynucleotide or polypeptide). Mutations include such changes as, for example, deletions, insertions, or substitutions.

Polynucleotides and polypeptides having such mutations can be isolated or generated using methods well known in the art.

As used herein, "deletion" is defined as a change in either polynucleotide or amino acid sequences in which one or more polynucleotides or amino acid residues, respectively, are absent.

As used herein, "insertion" or "addition" is that change in a polynucleotide or amino acid sequence which has resulted in the addition of one or more polynucleotides or amino acid residues, respectively, as compared to the naturally occurring polynucleotide or amino acid sequence.

As used herein, "substitution" results from the replacement of one or more polynucleotides or amino acids by different polynucleotides or amino acids, respectively.

As used herein, the term "adenoviral derivative" refers to an adenovirus of the invention that has been modified such that an addition, deletion or substitution has been made to or in the viral genome, such that the resulting adenoviral derivative exhibits a potency and/or therapeutic index greater than that of the parent adenovirus, or in some other way is more therapeutically useful (i.e., less immunogenic, improved clearance profile). For example, a derivative of an adenovirus of the invention may have a deletion in one of the early genes of the viral genome, including, but not limited to, the E1A or E2B region of the viral genome.

As used herein, "variant" with reference to a polynucleotide or polypeptide, refers to a polynucleotide or polypeptide that may vary in primary, secondary, or tertiary structure, as compared to a reference polynucleotide or polypeptide, respectively (*e.g.*, as compared to a wild-type polynucleotide or polypeptide). For example, the amino acid or nucleic acid sequence may contain a mutation or modification that differs from a reference amino acid or nucleic acid sequence. In some embodiments, an adenoviral variant may be a different isoform or polymorphism. Variants can be naturally-occurring, synthetic, recombinant, or chemically modified polynucleotides or polypeptides isolated or generated using methods well known in the art. Changes in the polynucleotide sequence of the variant may be silent. That is, they may not alter the amino acids encoded by the polynucleotide. Where alterations are limited to silent changes of this type, a variant will encode a polypeptide with the same amino acid sequence as the reference. Alternatively, such changes in the polynucleotide sequence of the variant may alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide, resulting in conservative or non-conservative amino acid changes, as described below. Such polynucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence. Various codon substitutions, such as the silent changes that produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system.

As used herein, an "adenoviral variant" refers to an adenovirus whose polynucleotide sequence differs from a reference polynucleotide, e.g. a wild-type adenovirus, as described above. The differences are limited so that the polynucleotide sequences of the parent and the variant are similar overall and, in most regions, identical. As used herein, a first nucleotide or amino acid

sequence is said to be "similar" to a second sequence when a comparison of the two sequences shows that they have few sequence differences (i.e., the first and second sequences are nearly identical). As used herein, the polynucleotide sequence differences present between the adenoviral variant and the reference adenovirus do not result in a difference in the potency and/or therapeutic index.

As used herein, the term "conservative" refers to substitution of an amino acid residue for a different amino acid residue that has similar chemical properties. Conservative amino acid substitutions include replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, or a threonine with a serine. Insertions or deletions are typically in the range of about 1 to 5 amino acids.

As used herein, the term "nonconservative" refers to substituting an amino acid residue for a different amino acid residue that has different chemical properties. The nonconservative substitutions include, but are not limited to aspartic acid (D) being replaced with glycine (G); asparagine (N) being replaced with lysine (K); or alanine (A) being replaced with arginine (R).

The single-letter codes for amino acid residues include the following: A = alanine, R = arginine, N = asparagine, D = aspartic acid, C = cysteine, Q = Glutamine, E = Glutamic acid, G = glycine, H = histidine, I = isoleucine, L = leucine, K = lysine, M = methionine, F = phenylalanine, P = proline, S = serine, T = threonine, W = tryptophan, Y = tyrosine, V = valine.

It will be appreciated that polypeptides often contain amino acids other than the 20 amino acids commonly referred to as the 20 naturally occurring amino acids, and that many amino acids, including the terminal amino acids, may be modified in a given polypeptide, either by natural processes such as glycosylation and other post-translational modifications, or by chemical modification techniques which are well known in the art. Even the common modifications that occur naturally in polypeptides are too numerous to list exhaustively here, but they are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature, and they are well known to those of skill in the art. Among the known modifications which may be present in polypeptides of the present invention are, to name an illustrative few, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a polynucleotide or polynucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination.

Such modifications are well known to those of skill and have been described in great detail in the scientific literature. Several particularly common modifications, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, for

instance, are described in most basic texts, such as, for instance, I. E. Creighton, *Proteins-Structure and Molecular Properties*, 2nd Ed., W.H. Freeman and Company, New York, 1993. Many detailed reviews are available on this subject, such as, for example, those provided by Wold, F., in *Posttranslational Covalent Modification of Proteins*, B. C. Johnson, Ed., Academic Press, New York, pp 1-12, 1983; Seifter et al., *Meth. Enzymol.* 182: 626-646, 1990 and Rattan et al., *Protein Synthesis: Posttranslational Modifications and Aging,* Ann. N.Y. Acad. Sci. 663: 48-62, 1992.

It will be appreciated, as is well known and as noted above, that polypeptides are not always entirely linear. For instance, polypeptides may be branched as a result of ubiquitination, and they may be circular, with or without branching, generally as a result of posttranslational events, including natural processing events and events brought about by human manipulation which do not occur naturally. Circular, branched and branched circular polypeptides may be synthesized by non-translational natural processes and by entirely synthetic methods, as well.

Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. In fact, blockage of the amino or carboxyl group in a polypeptide, or both, by a covalent modification, is common in naturally occurring and synthetic polypeptides and such modifications may be present in polypeptides of the present invention, as well. For instance, the amino terminal residue of polypeptides made in *E. coli*, prior to proteolytic processing, almost invariably will be N-formylmethionine.

The modifications that occur in a polypeptide often will be a function of how it is made. For polypeptides made by expressing a cloned gene in a host, for instance, the nature and extent of the modifications in large part will be determined by the host cell posttranslational modification capacity and the modification signals present in the polypeptide amino acid sequence. For instance, as is well known, glycosylation often does not occur in bacterial hosts such as *E. coli*. Accordingly, when glycosylation is desired, a polypeptide should be expressed in a glycosylating host, generally a eukaryotic cell. Insect cells often carry out the same posttranslational glycosylations as mammalian cells and, for this reason, insect cell expression systems have been developed to efficiently express mammalian proteins having native patterns of glycosylation, *inter alia*. Similar considerations apply to other modifications.

It will be appreciated that the same type of modification may be present to the same or varying degree at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications.

As used herein, the following terms are used to describe the sequence relationships between two or more polynucleotide or amino acid sequences: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", "substantial identity", "similarity", and "homologous". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing or may comprise a complete cDNA or gene sequence. Generally, a reference sequence is at least 18 nucleotides or 6

amino acids in length, frequently at least 24 nucleotides or 8 amino acids in length, and often at least 48 nucleotides or 16 amino acids in length. Since two polynucleotides or amino acid sequences may each (1) comprise a sequence (i.e., a portion of the complete polynucleotide or amino acid sequence) that is similar between the two molecules, and (2) may further comprise a sequence that is divergent between the two polynucleotides or amino acid sequences, sequence comparisons between two (or more) molecules are typically performed by comparing sequences of the two molecules over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a conceptual segment of at least 18 contiguous nucleotide positions or 6 amino acids wherein a polynucleotide sequence or amino acid sequence may be compared to a reference sequence of at least 18 contiguous nucleotides or 6 amino acid sequences and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions, deletions, substitutions, and the like (i.e., gaps) of 20 percent or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for aligning a comparison window may be conducted, for example, by the local homology algorithm of Smith and Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman and Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson and Lipman, *Proc. Natl. Acad. Sci. (U.S.A .)* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, (Genetics Computer Group, 575 Science Dr., Madison, Wis.), VectorNTI from Informatix, Geneworks, or MacVector software packages), or by inspection, and the best alignment (i. e., resulting in the highest percentage of homology over the comparison window) generated by the various methods is selected.

As used herein, the term "sequence identity" means that two polynucleotide or amino acid sequences are identical (i.e., on a nucleotide-by-nucleotide or residue-by-residue basis) over the comparison window. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A, T, C, G, U, or I) or 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 comparison window (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The terms "substantial identity" as used herein denotes a characteristic of a polynucleotide or amino acid sequence, wherein the polynucleotide or amino acid comprises a sequence that has at least 85 percent sequence identity, preferably at least 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison window of at least 18 nucleotide (6 amino acid) positions, frequently over a window of at least 24-48 nucleotide (8-16 amino acid) positions, wherein the percentage of sequence identity is calculated by comparing the reference sequence to the sequence which may include deletions or additions which total 20 percent or less of the reference sequence

over the comparison window. The reference sequence may be a subset of a larger sequence. The term "similarity", when used to describe a polypeptide, is determined by comparing the amino acid sequence and the conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. The term "homologous", when used to describe a polynucleotide, indicates that two polynucleotides, or designated sequences thereof, when optimally aligned and compared, are identical, with appropriate nucleotide insertions or deletions, in at least 70% of the nucleotides, usually from about 75% to 99%, and more preferably at least about 98 to 99% of the nucleotides.

As used herein, "homologous", when used to describe a polynucleotide, indicates that two polynucleotides, or designated sequences thereof, when optimally aligned and compared, are identical, with appropriate nucleotide insertions or deletions, in at least 70% of the nucleotides, usually from about 75% to 99%, and more preferably at least about 98 to 99% of the nucleotides.

As used herein, "polymerase chain reaction" or "PCR" refers to a procedure wherein specific pieces of DNA are amplified as described in U.S. Pat. No. 4,683,195. Generally, sequence information from the ends of the polypeptide fragment of interest or beyond needs to be available, such that oligonucleotide primers can be designed; these primers will point towards one another, and will be identical or similar in sequence to opposite strands of the template to be amplified. The 5' terminal nucleotides of the two primers will coincide with the ends of the amplified material. PCR can be used to amplify specific DNA sequences from total genomic DNA, cDNA transcribed from total cellular RNA, plasmid sequences, etc. (See generally Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51: 263, 1987; Erlich, ed., *PCR Technology*, Stockton Press, NY, 1989).

As used herein, "stringency" typically occurs in a range from about T_m (melting temperature)-5°C (5° below the T_m of the probe) to about 20°C to 25°C below T_m. As will be understood by those of skill in the art, a stringent hybridization can be used to identify or detect identical polynucleotide sequences or to identify or detect similar or related polynucleotide sequences. As herein used, the term "stringent conditions" means hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences.

As used herein, "hybridization" as used herein, shall include "any process by which a polynucleotide strand joins with a complementary strand through base pairing" (Coombs, J., *Dictionary of Biotechnology*, Stockton Press, New York, N.Y., 1994).

As used herein, the term "therapeutically effective dose" or "effective amount" refers to that amount of adenovirus which ameliorates the symptoms or conditions of a disease. A dose is considered a therapeutically effective dose in the treatment of cancer or its metastasis when tumor or metastatic growth is slowed or stopped, or the tumor or metastasis is found to shrink in size, so as to lead to an extension in life-span for the subject.

Adenoviruses of the Invention

The present invention provides chimeric adenoviruses, or variants or derivatives thereof, having a genome in which the nucleotide sequence of the E2B region of the chimeric adenovirus comprises nucleic acid sequences derived from at least two adenoviral serotypes, which serotypes are each selected from the adenoviral subgroups B, C, D, E and F and are distinct from each other. A chimeric adenovirus of the invention is oncolytic and demonstrates an enhanced therapeutic index for a tumor cell.

Isolation of Chimeric Adenoviruses

The chimeric adenoviruses of the invention, or variants or derivatives thereof, can be produced using modification of a technique referred to as "bioselection", in which an adenovirus with desired properties, such as enhanced oncogenicity or cell type specificity, is generated through the use of genetic selection under controlled conditions (Yan et al. (2003) *J. Virol.* 77:2640-2650).

In the present invention, a mixture of adenoviruses of differing serotypes is pooled and is passaged, preferably at least twice, on a subconfluent culture of tumor cells at a particle per cell ratio high enough to encourage recombination between serotypes, but not so high as to produce premature cell death. A preferred particle per cell ratio is approximately 500 particles per cell, and is easily determined by one skilled in the art. As used herein, a "subconfluent culture" of cells refers to a monolayer or suspension culture in which the cells are actively growing. For cells grown as a monolayer, an example would be a culture where approximately 50% to 80% of the area available for cell growth is covered with cells. Preferred is a culture where approximately 75% of the growth area is covered with cells.

In a preferred embodiment, the adenoviral mixture is one that includes adenoviral serotypes representative of the adenoviral subgroups B, C, D, E and F. Group A adenoviruses are not included in the mixture as they are associated with tumor formation in rodents. Preferred tumor cell lines useful in the bioselection process include, but are not limited to, those derived from breast, colon, pancreas, lung and prostate. Some examples of solid tumor cell lines useful for the "bioselective" passaging of the adenoviral mixture include, but are not limited to, MDA231, HT29, PAN-1 and PC-3 cells. Hemopoietic cell lines include, but are not limited to, the Raji and Daudi B-lymphoid cells, K562 erythroblastoid cells, U937 myeloid cells, and HSB2 T-lymphoid cells.

Adenoviruses produced during these initial passages are used to infect quiescent tumor cells at a particle to cell ratio low enough to permit the infection of a cell by no more than one adenovirus. After up to 20 passages under these conditions, the supernatant from the last passage is harvested prior to visible cytopathic effect (CPE, see Fields Virology, Vol.2, Fourth Edition, Knipe, ea., Lippincott Williams & Wilkins, pp. 135-136) to increase selection of highly potent viruses. The harvested supernatant can be concentrated by techniques well known to those skilled in the art. A preferred method for attaining quiescent cells, i.e. ones in which active cell growth has stopped, in a

monolayer culture is to allow the culture to grow for 3 days following confluence, where confluence means that the entire area available for cell growth is occupied (covered with cells). Similarly, suspension cultures can be grown to densities characterized by the absence of active cell growth.

The serotype profile of the concentrated supernatant, which contains the bioselected adenoviral pool, can be examined by measuring the retention times of the harvested viral pool on an anion exchange column, where different adenoviral serotypes are known to have characteristic retention times (Blanche et al. (2000) *Gene Therapy* 7:1055-1062); see Example 3, Figures 1A and B. Adenoviruses of the invention can be isolated from the concentrated supernatant by dilution and plaque purification, or other techniques well know in the art, and grown for further characterization. Techniques well known in the art are used to determine the sequence of the isolated chimeric adenoviruses (see Example 5).

An example of a chimeric adenovirus of the invention is the chimeric adenovirus ColoAd1, which was isolated using HT29 colon cells in the bioselection process. ColoAd1 has the nucleic acid sequence of SEQ ID NO: 1. The majority of the nucleotide sequence of ColoAd1 is identical to the nucleotide sequence of the Ad11 serotype (SEQ ID NO: 2) (Stone et al. (2003) *Virology* 309:152-165; Mei et al. (2003) *J. Gen. Virology* 84:2061-2071). There are two deletions in the ColoAd1 nucleotide sequence as compared with Ad11, one 2444 base pairs in length within the E3 transcription unit region of the genome (base pairs 27979 to 30423 of SEQ ID NO: 2) and a second, smaller deletion, 25 base pairs in length (base pairs 33164 to 33189 of SEQ ID NO: 2), within the E4orf4 gene. The E2B transcription unit region (SEQ ID NO: 3) of ColoAd1, which encodes the adenoviral proteins DNA polymerase and terminal protein, is located between base pairs 5067 and 10354 of SEQ ID NO: 1, and is an area of homologous recombination between the Ad11 and Ad3 serotypes. Within this region of ColoAd1, there are 198 base pair changes, as compared with the sequence of Ad11 (SEQ ID NO: 1). The changes result in stretches of nucleotides within the E2B region of ColoAd1 which are homologous to the sequence within a portion of the E2B region of Ad3 (SEQ ID NO: 8), with the longest stretch of homology between ColoAd1 and Ad3 being 414 bp in length. The E2B region of ColoAd1 (SEQ ID NO: 3) confers enhanced potency to the ColoAd1 adenovirus as compared to unmodified Ad11 adenovirus (see Example 6; Fig 7). In other embodiments, a chimeric adenovirus of the invention can comprise nucleic acid sequences from more than two adenoviral serotypes.

A chimeric adenovirus of the invention, or a variant or derivative thereof, can be evaluated for its selectivity in a specific tumor type by examination of its lytic potential in a panel of tumor cells derived from the same tissue upon which the adenoviral pool was initially passaged. For example, the chimeric adenovirus ColoAd1 (SEQ ID NO: 1), which was initially derived from an adenoviral pool passaged on HT-29 colon tumor cell lines, was re-examined both in HT-29 cells and in a panel of other colon-derived tumor cells lines, including DLD-1, LS174T, LS1034, SW403, HCT116, SW48, and Colo320DM (see Figure 3B). Any available colon tumor cell lines would be equally useful for such an evaluation. Isolated adenoviral clones from adenoviral pools selected on other tumor cell

types can be similarly tested in a suitable tumor cell panel, including, but not limited to, prostate cell lines (e.g. DU145 and PC-3 cell lines); pancreatic cell lines (e.g. the Panc-1 cell line); breast tumor cell lines (e.g. the MDA231 cell line) and ovarian cell lines (e.g. the OVCAR-3 cell line). Other available tumor cell lines are equally useful in isolating and identifying adenoviruses of the invention.

The chimeric adenoviruses of the invention have an enhanced therapeutic index as compared with the adenoviral serotypes from which it is derived. (see Figure 6, which compares the cytolytic activity of the chimeric adenovirus ColoAd1 with Ad11p).

The invention also encompasses chimeric adenoviruses that are constructed using recombinant techniques well-known to those skilled in the art. Such chimeric adenoviruses comprise a region of nucleotide sequence derived from one adenoviral serotype which is incorporated by recombinant techniques into the genome of a second adenoviral serotype. The incorporated sequence confers a property, e.g. tumor specificity or enhanced potency, to the parental adenoviral serotype. For example, the E2B region of ColoAd1 (SEQ ID NO: 3) can be incorporated into the genome of Ad35 or Ad9.

<u>Adenoviral Derivatives</u>

The invention also encompasses a chimeric adenovirus of the invention that is modified to provide other therapeutically useful chimeric adenoviruses. Modifications include, but are not limited to, those described below.

One modification is production of derivatives of the chimeric adenovirus of the invention substantially lacking the ability to bind p53, as a result of a mutation in the adenoviral gene that encodes the E1B-55K protein. Such viruses generally have some, or all, of the E1B-55K region deleted. (see U.S. Patent No. 5,677,178). U.S. Patent No. 6,080,578 describes, among other things, Ad5 mutants that have deletions in the region of the E1B-55K protein that is responsible for binding p53. Another preferred modification to the chimeric adenoviruses of the instant invention are mutations in the E1A region, as described in U.S. Patent Nos. 5,801,029 and 5,972,706. These types of modifications provide derivatives of the chimeric adenoviruses of the invention with greater selectivity for tumor cells.

Another example of a modification encompassed by the invention is a chimeric adenovirus which exhibits an enhanced degree of tissue specificity due to placement of viral replication under the control of a tissue specific promoter as described in U.S. Patent No. 5,998,205. Replication of a chimeric adenovirus of the invention can also be put under the control of an E2F responsive element as described in United States Patent 7,001,596. This modification affords a viral replication control mechanism based on the presence of E2F, resulting in enhanced tumor tissue specificity, and is distinct from the control realized by a tissue specific promoter. In both of these embodiments, the tissue specific promoter and the E2F responsive element are operably linked to an adenoviral gene that is essential for the replication of the adenovirus.

Another modification encompassed by the invention is use of a chimeric adenovirus of the invention, e.g. ColoAd1, as the backbone for production of novel replication-deficient adenoviral vectors. As described in Lai et al. ((2002) *DNA Cell Bio.* 21:895-913), adenoviral vectors which are replication deficient can be used to deliver and express therapeutic genes. Both first generation (in which the E1 and E3-regions are deleted) and second generation (in which the E4 region is additionally deleted) adenoviral vectors derived from the chimerc adenoviruses of the invention are provided herein. Such vectors are easily produced using techniques well known to those skilled in the art (see Imperiale and Kochanek (2004) *Curr. Top. Microbiol. Immunol.* 273:335-357; Vogels et al. (2003) *J. Virol.* 77:8263-8271).

A further modification encompassed by the invention is the insertion of a heterologous gene, useful as a marker or reporter for tracking the efficiency of viral infection. One embodiment of this type of modification is insertion of the thymidine kinase (TK) gene. The expression of TK within infected cells can be used to track the level of virus remaining in cells following viral infection, using radiolabeled subtrates of the TK reaction (Sangro et al. (2002) *Mol. Imaging Biol.* 4:27-33).

Methods for the construction of the modified chimeric adenoviruses are generally known in the art. See, Mittal, S. K. (1993) *Virus Res.* 28:67-90 and Hermiston, T. et al. (1999) Methods in Molecular Medicine: Adenovirus Methods and Protocols, W.S.M. Wold, ed, Humana Press. Standard techniques are used for recombinant nucleic acid methods, polynucleotide synthesis, and microbial culture and transformation (e.g., electroporation, lipofection). Generally, enzymatic reactions and purification steps are performed according to the manufacturer's specifications. The techniques and procedures are generally performed according to conventional methods in the art and various general references (see generally, Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd. edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.) which are provided throughout this document. The nomenclature used herein and the laboratory procedures in analytical chemistry, organic synthetic chemistry, and pharmaceutical formulation described below are those well known and commonly employed in the art.

Determination of Therapeutic Potential

Chimeric adenoviruses of the invention, or variants or derivatives thereof, can be evaluated for their therapeutic utility by examination of their lytic potential in tumor cells derived from tissues of interest as therapeutic targets. Tumor cell lines useful for testing such adenoviruses include, but are not limited to, colon cell lines, including but not limited to, DLD-1, HCT116, HT29, LS1034 and SW48 cell lines; prostate cell lines, including but not limited to, DU145 and PC-3 cell lines; pancreatic cell lines, including but not limited to, the Panc-1 cell line; breast tumor cell lines, including but not limited to, the MDA231 cell line and ovarian cell lines, including but not limited to, the OVCAR-3 cell line. Hemopoietic cell lines include, but are not limited to, the Raji and Daudi B-lymphoid cells, K562 erythroblastoid cells, U937 myeloid cells, and HSB2 T-lymphoid cells. Any other tumor cell lines

that are available can be used in evaluating and identifying adenoviruses of the invention for use in the treatment of neoplasia.

The cytolytic activity of adenoviruses of the invention can be determined in representative tumor cell lines and the data converted to a measurement of potency, with an adenovirus belonging to subgroup C, preferably Ad5, being used as a standard (i.e. given a potency of 1). A preferred method for determining cytolytic activity is an MTS assay (see Example 4, Figure 2).

The therapeutic index of an adenovirus of the invention in a particular tumor cell line can be calculated by comparison of the potency of the given adenovirus in a tumor cell line with the potency of that same adenovirus in a non-cancerous cell line. Preferred non-cancerous cell lines are SAEC cells, which are epithelial in origin, and HUVEC cells which are endothelial in origin (see Figure 4). These two cell types represent normal cells from which organs and vasculature, respectively, are derived, and are representative of likely sites of toxicity during adenoviral therapy, depending on the mode of delivery of the adenovirus. However, practice of the invention is not limited to the use of these cells, and other non-cancerous cell lines (e.g. B cells, T cells, macrophages, monocytes, fibroblasts) may also be used.

The chimeric adenoviruses of the invention can be further evaluated for their ability to target neoplastic cell growth (i.e. cancer) by their capacity to reduce tumorigenesis or neoplastic cell burden in nude mice harboring a transplant of neoplastic cells, as compared to untreated mice harboring an equivalent neoplastic cell burden (see Example 7).

Evaluation of the adenoviruses of the invention can also be performed using primary human tumor explants (Lam et al. (2003) *Cancer Gene Therapy* ; Grill et al. (2003) *Mol. Therapy* 6:609-614), which provide test conditions present in tumors that cannot normally be produced using the tumor xenograft studies.

Therapeutic Utility

The present invention provides for the use of chimeric adenoviruses of the invention for the inhibition of tumor cell growth, as well as for the use of adenoviral vectors derived from these chimeric adenoviruses to deliver therapeutic proteins useful in the treatment of neoplasia and other disease states.

Pharmaceutical Compositions and Administration

The present invention also relates to pharmaceutical compositions which comprise the chimeric adenoviruses of the invention, including variants and derivatives thereof, formulated for therapeutic administration to a patient. For therapeutic use, a sterile composition containing a pharmacologically effective dosage of adenovirus is administered to a human patient or veterinary non-human patient for treatment, for example, of a neoplastic condition. Generally, the composition will comprise about 10^{11} or more adenovirus particles in an aqueous suspension. A pharmaceutically acceptable carrier or excipient is often employed in such sterile compositions. A

variety of aqueous solutions can be used, e.g. water, buffered water, 0.4% saline, 0.3% glycine and the like. These solutions are sterile and generally free of particulate matter other than the desired adenoviral vector. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g. sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, etc. Excipients which enhance infection of cells by adenovirus may be included. (see U.S. Patent No. 6,392,069)

Adenoviruses of the invention may also be delivered to neoplastic cells by liposome or immunoliposome delivery; such delivery may be selectively targeted to neoplastic cells on the basis of a cell surface property present on the neoplastic cell population (e.g., the presence of a cell surface protein which binds an immunoglobulin in an immunoliposome). Typically, an aqueous suspension containing the virions are encapsulated in liposomes or immunoliposomes. For example, a suspension of adenovirus virions can be encapsulated in micelles to form immunoliposomes by conventional methods (U.S. Patent No. 5,043,164, U.S. Patent No. 4,957,735, U.S. Patent No. 4,925,661; Connor and Huang, (1985) *J. Cell Biol.* 101: 581; Lasic D.D. (1992) *Nature* 355: 279; Novel Drug Delivery (eds. Prescott and Nimmo, Wiley, New York-, 1989); Reddy et al. (1992) *J. Immunol.* 148:1585). Immunoliposomes comprising an antibody that binds specifically to a cancer cell antigen (e.g., CALLA, CEA) present on the cancer cells of the individual may be used to target virions to those cells (Fisher (2001) *Gene Therapy* 8:341-348).

To further increase the efficacy of the adenoviruses of the invention, they may be modified to exhibit enhanced tropism for particular tumor cell types. For example, as shown in PCT WO 1998/040508, a protein on the exterior coat of an adenovirus may be modified to display a chemical agent, preferably a polypeptide, that binds to a receptor present on tumor cells to a greater degree than normal cells. (See also, U. S. Patent Nos. 5,770,442 and 5,712,136). The polypeptide can be an antibody, and preferably is a single chain antibody.

Adenoviral Therapy

The adenoviruses of the invention, or pharmaceutical compositions thereof, can be administered for therapeutic treatment of neoplastic disease or cancer. In therapeutic applications, compositions are administered to a patient already affected by the particular neoplastic disease, in an amount sufficient to cure or at least partially arrest the condition and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose" or "efficacious dose". Amounts effective for this use will depend upon the severity of the condition, the general state of the patient, and the route of administration.

For example, but not by way of limitation, a human patient or non-human mammal having a solid or haemotologic neoplastic disease, (e.g. pancreatic, colon, ovarian, lung, or breast carcinoma, leukemia or multiple myeloma) may be treated by administering a therapeutically effective dosage of an appropriate adenovirus of the invention, i.e. one which has been shown to have an improved

therapeutic index for that tissue type. For example, a preferred chimeric adenovirus for the treatment of colon cancer would be the adenovirus ColoAd1 (SEQ ID NO: 1). Suspensions of infectious adenovirus particles may be delivered to neoplastic tissue by various routes, including intravenous, intraperitoneal, intramuscular, subdermal, and topical. An adenovirus suspension containing about 10^3 to 10^{12} or more virion particles per ml may be administered by infusion (e.g., into the peritoneal cavity for treating ovarian cancer, into the portal vein for treating hepatocarcinoma or liver metastases from other non-hepatic primary tumors) or other suitable route, including direct injection into a tumor mass (e.g.. a breast tumor), enema (e.g., colon cancer), or catheter (e.g., bladder cancer). Other routes of administration may be suitable for carcinomas of other origins, i.e. inhalation as a mist (e.g., for pulmonary delivery to treat bronchogenic carcinoma, small- cell lung carcinoma. non-small cell lung carcinoma, lung adenocarcinoma. or laryngeal cancer) or direct application to a tumor site (e.g., bronchogenic carcinoma, nasopharyngeal carcinoma, laryngeal carcinoma, cervical carcinoma).

Adenoviral therapy using the adenoviruses of the instant invention may be combined with other antineoplastic protocols, such as conventional chemotherapy or x-ray therapy to treat a particular cancer. Treatment can be concurrent or sequential. A preferred chemotherapeutic agent is cisplatin, and the preferred dose may be chosen by the practitioner based on the nature of the cancer to be treated, and other factors routinely considered in administering cisplatin. Preferably, cisplatin will be administered intravenously at a dose of 50-120 mg/m^2 over 3-6 hours. More preferably it is administered intravenously at a dose of 80 mg/m^2 over 4 hours. A second preferred chemotherapeutic agent is 5-fluorouracil, which is often administered in combination with cisplatin. The preferred dose of 5-fluorouracil is 800-1200 mg/m^2 per day for 5 consecutive days.

Adenoviral therapy using the adenoviruses of the instant invention as adenoviral vectors may also be combined with other genes known to be useful in viral based therapy. See U. S. Patent No. 5,648,478. In such cases, the chimeric adenovirus further comprises a heterologous gene that encodes a therapeutic protein, incorporated within the viral genome, such that the heterologous gene is expressed within an infected cell. A therapeutic protein, as used herein, refers to a protein that would be expected to provide some therapeutic benefit when expressed in a given cell.

In one embodiment, the heterologous gene is a pro-drug activator gene, such as cytosine deaminase (CD) (See, U.S. Patent Nos. 5,631,236; 5,358,866; and 5,677,178). In other embodiments, the heterologous gene is a known inducer of cell-death, e.g apoptin or adenoviral death protein (ADP), or a fusion protein, e.g. fusogenic membrane glycoprotein (Danen-Van Oorschot et al. (1997) *Proc. Nat. Acad. Sci.* 94:5843-5847; Tollefson et al.(1996) *J. Virol.* 70:2296-2306; Fu et al. (2003) *Mol. Therapy* 7: 48-754, 2003; Ahmed et al. (2003) *Gene Therapy* 10:1663-1671; Galanis et al. (2001) *Human Gene Therapy* 12(7): 811-821).

Further examples of heterologous genes, or fragments thereof, include those that encode immunomodulatory proteins, such as cytokines or chemokines. Examples include interleukin 2, U.S. Patent Nos. 4,738,927 or 5,641,665; interleukin 7, U. S. Patent Nos. 4,965,195 or 5,328,988; and

interleukin 12, U. S. Patent No. 5,457,038; tumor necrosis factor alpha, U. S. Patent Nos. 4,677,063 or 5,773,582; interferon gamma, U.S. Patent Nos. 4,727,138 or 4,762,791; or GM CSF, U.S. Patent Nos. 5,393,870 or 5,391,485, Mackensen et al. (1997) *Cytokine Growth Factor Rev.* 8:119-128). Additional immunomodulatory proteins further include macrophage inflammatory proteins, including MIP- 3. Monocyte chemotatic protein (MCP-3 alpha) may also be used; a preferred embodiment of a heterologous gene is a chimeric gene consisting of a gene that encodes a protein that traverses cell membranes, for example, VP22 or TAT, fused to a gene that encodes a protein that is preferably toxic to cancer but not normal cells.

The chimeric adenoviruses of the invention can also be used as vectors to deliver genes encoding therapeutically useful RNA molecules, i.e. siRNA (Dorsett and Tuschl (2004) *Nature Rev Drug Disc* 3:318-329).

In some cases, genes can be incorporated into a chimeric adenovirus of the invention to further enhance the ability of the oncolytic virus to eradicate the tumor, although not having any direct impact on the tumor itself - these include genes encoding proteins that compromise MHC class I presentation (Hewitt et al. (2003) *Immunology* 110: 163-169), block complement, inhibit IFNs and IFN-induced mechanisms, chemokines and cytokines, NK cell based killing (Orange et al., (2002) *Nature Immunol.* 3: 1006-1012; Mireille et al. (2002) *Immunogenetics* 54: 527-542; Alcami (2003) *Nature Rev. Immunol.* 3: 36-50; down regulate the immune response (e.g. IL-10, TGF- Beta, Khong and Restifo (2002) *Nature Immunol.* 3: 999-1005; 2002) and metalloproteases which can breakdown the extracelluar matrix and enhance spread of the virus within the tumor (Bosman and Stamenkovic (2003) *J. Pathol.* 2000: 423-428; Visse and Nagase (2003) *Circulation Res.* 92: 827-839).

Kits

The invention further relates to pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, reflecting approval by the agency of the manufacture, use or sale of the product for human administration.

The present invention is further described by the following examples, which are illustrative of specific embodiments of the invention, and various uses thereof. These exemplifications, which illustrating certain specific aspects of the invention, do not portray the limitations or circumscribe the scope of the disclosed invention.

Unless otherwise indicated, the practice of the present invention employs conventional techniques of cell culture, molecular biology, microbiology, recombinant DNA manipulation, immunology science, which are within the skill of the art. Such techniques are explained fully in the

literature. See, e.g. Cell Biology: a Laboratory Handbook: J. Celis (Ed).Academic Press. N.Y. (1996); Graham, F.L. and Prevec, L. Adenovirus-based expression vectors and recombinant vaccines. In: Vaccines: New Approaches to Immunological Problems. R.W. Ellis (ed) Butterworth. Pp 363-390; Grahan and Prevec Manipulation of adenovirus vectors. In: Methods in Molecular Biology, Vol. 7: Gene Transfer and Expression Techniques. E.J. Murray and J.M. Walker (eds) Humana Press Inc., Clifton, N.J. pp 109-128, 1991; Sambrook et al. (1989), Molecular Cloning, A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press; Sambrook et al. (1989), and Ausubel et al. (1995), Short Protocols in Molecular Biology, John Wiley and Sons.

EXAMPLES

Methods

Standard techniques are used for recombinant nucleic acid methods, polynucleotide synthesis, and microbial culture and transformation (e.g., electroporation, lipofection). Generally, enzymatic reactions and purification steps are performed according to the manufacturer's specifications. The techniques and procedures are generally performed according to conventional methods in the art and various general references (see generally, Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd. edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.) which are provided throughout this document. The nomenclature used herein and the laboratory procedures in analytical chemistry, organic synthetic chemistry, and pharmaceutical formulation and delivery, and treatment of patients. Methods for the construction of adenoviral mutants are generally known in the art. See, Mittal, S. K., Virus Res.,1993, vol: 28, pages 67-90; and Hermiston, T. et al., Methods in Molecular Medicine: Adenovirus Methods and Protocols, W.S.M. Wold, ed, Humana Press, 1999. Further, the adenovirus 5 genome is registered as Genbank 10 accession #M73260, and the virus is available from the American Type Culture Collection, Rockville, Maryland, U. S. A., under accession number VR-5.

Viruses and Cell Lines

The Ad serotypes Ad3 (GB strain), Ad4 (RI-67 strain), Ad5 (Adenoid 75 strain), Ad9 (Hicks strain), Ad11p (Slobitski strain), Ad16 (Ch. 79 strain) and all the cell lines, with the exception of the following were all purchased from the ATCC: MDA231-mt1 (a derivative isolated by Dr. Deb Zajchowski from a rapidly growing subcutaneous implanted xenograft of MDA231 cells) and Panc1-sct (derived by Dr. Sandra Biroc from a rapidly growing subcutaneous implanted xenograft of Panc1 cells), HUVEC (Vec Technologies, Rensselaer, NY), and SAEC (Clonetics, Walkersville, MD). Ad40 was a kind gift from Dr. William S.M. Wold at St. Louis University.

Example 1 - Viral Purification and Quantitation

Viral stocks were propagated on 293 cells and purified on CsCl gradients (Hawkins et al., 2001). The method used to quantitate viral particles is based on that of Shabram et al. (1997) *Human Gene Therapy* 8:453-465, with the exception that the anion-exchanger TMAE Fractogel™ was used instead of Resource Q. In brief, a 1.25 ml column was packed with Fractogel EMD TMAE-650 (S) (catalog # 116887-7 EM Science, Gibbstown, NJ 08027). HPLC separation was performed on an Agilent™ HP 1100 HPLC using the following conditions: Buffer A = 50 mM HEPES, pH 7.5; Buffer B = 1.0 M NaCl in Buffer A; flow rate of 1 ml per minute. After column equilibration for not less than 30 minutes in Buffer A, approximately 10^9-10^{11} viral particles of sample were loaded onto the column in 10-100 ul volume, followed by 4 column volumes of Buffer A. A linear gradient extending over 16 column volumes and ending in 100% Buffer B was applied.

The column effluent was monitored at A260 and A280 nm, peak areas calculated, and the 260 to 280 nm ratio determined. Viral peaks were identified as those peaks having a A260/A280 ratio close to 1.33. A virus standard was included with each sample series. The number of viral particles per ml of the standard had been determined using the method of Lehmberg et al. (1999) *J. Chrom. B*, 732:411-423}. In the viral concentration range used, the A260 nm peak area of each sample is directly proportional to the number of viral particles in the sample. The number of viral particles per ml in each test sample was calculated by multiplying the known number of viral particles per ml in the standard by the ratio of the A260 nm viral peak area of the sample to the A260 nm viral peak area of the standard.

The column was regenerated after each sample gradient by washing with two column volumes of 0.5 N NaOH followed by two column volumes of 100% Buffer A, 3 column volumes of 100% Buffer B, and then 4 column volumes of 100% Buffer A.

Example 2 – Bioselection

Viral serotypes representing subgroups Ads B-F were pooled and passaged on sub-confluent cultures of the target tumor cell lines at a high particle-per-cell ratio for two rounds to invite recombination to occur between serotypes. Supernatant (1.0, 0.1 0.01, 0.001 ml) from the second round of the high viral particle-per-cell infection, subconfluent cultures, was then used to infect a series of over-confluent T-75 tissue culture flasks of target tumor cell lines PC-3, HT-29, Panc-1 and MDA-231. To achieve over-confluency, each cell line was seeded at split ratios that allowed that cell line to reach confluency between 24 and 40 hours post seeding, and the cells were allowed to grow a total of 72 hours post seeding prior to infection. This was done to maximize the confluency of the cells to mimic growth conditions in human solid tumors.

Cell culture supernatant was harvested from the first flask in the 10-fold dilution series that did not show any sign of CPE at day 3 or 4 post-infection (in the case of HT-29 and PC-3, this was modified for passages 10-20 to harvest of the second flask, i.e. harvest 100–fold below the dilution in which CPE were detectable by day 3 post-infection). Each harvest served as the starting material for the successive passage of the virus. This process was repeated until the viral pool achieved 20 bioselective passages.

Individual viruses from each bioselected pool were isolated by two rounds of plaque purification on A549 cells using standard methods (Tollefson, A., Hermiston, T.W., and Wold, W.S.M.; "Preparation and Titration of CsCl-banded Adenovirus Stock" in Adenovirus Methods and Protocols, Humana Press, 1999, pp 1-10, W.S.M. Wold, Ed). In brief, dilutions of the supernatant harvested from the 20th passage on each target tumor line were used to infect A549 cells in a standard plaque assay. Well-individuated plaques were harvested, and the same plaque assay method was used to generate a second round of individual plaques from these harvests. Well isolated plaques from the second round of plaque purification were deemed pure, infected cultures were prepared using these purified plaques, and the oncolytic potency of these culture supernatants determined by MTS assay as described.

Example 3 - Serotype Characterization

The parental adenoviral serotypes comprising the viral pools or the isolated ColoAd1 adenovirus were identified using anion-exchange chromatography similar to that described in Shabram et al. (1997) *Human Gene Therapy* 8:453:465, with the exception that the anion-exchanger TMAE Fractogel media (EM Industries, Gibbstown, NJ) was used instead of Resource Q, as described in Example 1 (see Figure 1).

Adenovirus type 5 eluted at approximately 60% Buffer B during the gradient. The other serotypes (3,4, 9, 11p, 16, 35, and 40) each eluted at a characteristic retention time consistent with the retention times on Q Sepharose^{tm} XL published by Blanche et al. (2000) *Gene Therapy* 7:1055-1062.

Example 4 - Cytolytic assay

The viral lytic capacity was measured by using a modification of the MTT assay (Shen et al., 2001). Briefly, the MTS assay (Promega, CellTiter 96® Aqueous Non-Radioactive Cell Proliferation Assay) was used in place of the MTT assay since conversion of MTS by cells into aqueous, soluble formazan reduces time and eliminates the use of a volatile organic solvent associated with the MTT assay.

To perform the assay, cells were seeded at a defined density for each tumor cell line that generated a confluent monolayer within 24 hr. These densely seeded cells were allowed to grow for 2 additional days prior to exposure to the test virus(es). Infections of both tumor and primary normal cells were carried out in quadruplicate with serial three fold dilutions of the viruses starting at a particle per cell ratio of 100 and ending at a particle per cell ratio of 0.005. Infected cells were incubated at 37^{0} C and the MTS assay was performed at the time points indicated for the individual primary cells or tumor cell lines. Mock-infected cells served as negative controls and established the 100% survival point for the given assay.

Example 5 - DNA sequencing

DNA sequencing of the Ad11p (SEQ ID NO: 2) and ColoAd1 (SEQ ID NO: 1) genomic DNAs was performed as follows. Briefly, purified adenovirus DNA from ColoAd1 and Ad11p was partially digested with the restriction endonuclease Sau3A1 and shotgun cloned into the plasmid vector pBluescript II (Stratagene, La Jolla, CA). Positive clones were propagated and sequenced using the primers M13R and KS (Stratagene, La Jolla, CA). Individual sequence reactions were trimmed, edited and assembled using Sequencher^{tm} (Gene Codes Corp., Ann Arbor, Michigan). Gaps in coverage were amplified with custom oligonucleotide primers and sequenced. The ends of the viral genomes were sequenced directly off the adenoviral DNA. In all, each genome was sequenced at 3X+ coverage and 431 bases at 2X coverage.

To determine the origin of the ColoAd1 E2B region, two primer sets were generated, one to the E2B pTP gene (bp9115, 5'GGGAGTTTCGCGCGGACACGG3' (SEQ ID NO: 4) and bp 9350, 5' GCGCCGCCGCCGCGGAGAGGT3' (SEQ ID NO: 5)) and one to the DNA polymerase gene (bp 7520 5'CGAGAGCCCATTCGTGCAGGTGAG3' (SEQ ID NO: 6) and bp 7982, 5'GCTGCGACTACTGCGGCCGTCTGT3' (SEQ ID NO: 7) and used to PCR isolate DNA fragments from the various serotypes (Ad3,4,5,9,11p,16 and 40) using reagents from the Advantage^{tm} 2 PCR kit (Clonetics, Walkersville, MD; Cat #K1910-Y) and run on a PTC-200^{tm} thermocycler from MJ Research (Watertown, MA). These fragments were subsequently sequenced along with the DNA sequence of Ad3 using dye terminator sequencing on as ABI 3100 genetic analyzer.

The E2B region of Ad3 was sequenced using isolated Ad3 DNA and overlapping primers. Sequence information was analyzed using the Vector NTI^{tm} program (Informatix).

Example 6 - Construction of recombinant viruses

Genomic DNAs of Ad11p (SEQ ID NO: 2) and ColoAd1 (SEQ ID NO: 1) were purified from CsCl gradient-banded virus particles. The genomic DNAs were digested with PacI which cuts each

only once within the viral genome. The Pac1 cut occurs at base 18141 on ColoAd1 nucleotide sequence (SEQ ID NO: 1) and at base 18140 on the Ad11 nucleotide sequence (SEQ ID NO: 2). Digested DNAs were mixed in equal amounts and ligated in the presence of T4 DNA ligase at 16° C overnight. This ligation mixture was transfected into A549 cells using the $CaPO_4$ transfection kit from Invitrogen, Carlsbad, CA (Cat #K2780-01). Isolated plaques were picked and screened by restriction enzyme digestion and PCR analysis to distinguish the four viral populations (Ad11p, ColoAd1, left end Ad11p/right end ColoAd1 (ColoAd1.1) and left end ColoAd1/right end Ad11p(ColoAd1.2)).

The viral lytic capacity of each population was determined in several cell lines, including HT29 and HUVEC cell lines, as described in Example 3. The results demonstrated the order of potency, from least potent to most potent, as Ad11p, ColoAd1.2, ColoAd1.1, ColoAd1 (see Figure 7 for the results in HT29 cells).

Also constructed were chimeric adenoviruses pCJ144 and pCJ146, which contain the full-length ColoAd1 genome in which the wild-type Ad11p E3 and E4 region, respectively, has been restored. These modifications were introduced by homologous recombination into BJ5183 E. Coli (Chartier *et al.* (1996) *J. Virol.* 70:4805-4810). Both of these chimeric adenoviruses demonstrated reduced lytic capacity in HT29 and HUVEC cells compared to ColoAd1 or ColoAd1.2.

Example 7 - *In Vivo* Efficacy of Adenovirus

In a typical human tumor xenograft nude mouse experiment, animals are injected with 5 x 10^6 cells subcutaneously into the hind flank of the mouse. When the tumors reach 100-200 ul in size, they are injected with vehicle (PBS) or with virus at 2 x 10^{10} particles for five consecutive days (1 x 10^{11} particles total). A reduction in the size of the tumor would be noted relative to the PBS control and additional control viruses (Ad5, ONYX-015).

Example 8 – ColoAd1 Selectivity on Primary Human Tissue Explants

Tissue specimens from colorectal tumors and adjacent normal tissues removed during surgery were placed in culture media and infected with equal numbers of either ColoAd1 or Ad5 viruses. Culture supernatants were collected at 24 hours post infection and the number of virus particles produced was determined. ColoAd1 produced more virus particles per input particle than Ad5 on tumor tissue, while it produced fewer particles per input particle than Ad5 on normal tissue.

DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 2

NOTE: Pour les tomes additionels, veillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE THAN ONE VOLUME.

THIS IS VOLUME 1 OF 2

NOTE: For additional volumes please contact the Canadian Patent Office.

The embodiments of the invention in which an exclusive property or privilege is claimed are defined as follows:

1. A replication competent oncolytic type B adenovirus comprising the genome of Ad11, wherein said genome defines a deletion in the base pairs comprising:

(1) an E3 region deletion comprising base pairs 27979 to 30423, numbered according to SEQ ID NO:2,

(2) an E4orf4 gene deletion comprising base pairs 33164 to 33189, numbered according to SEQ ID NO:2, or

(3) a combination of (1) and (2),

wherein the adenovirus has an enhanced therapeutic index for a tumour cell.

2. A replication competent oncolytic type B adenovirus according to claim 1, wherein the adenovirus comprises the deletion in the E3 region.

3. A replication competent oncolytic type B adenovirus according to claim 2, wherein the adenovirus comprises the deletion in the E4orf4 gene.

4. A replication competent oncolytic type B adenovirus according to claim 1, wherein the adenovirus comprises the deletion in the E4orf4 gene.

5. A pharmaceutical composition comprising a replication competent type B adenovirus as defined in any one of claims 1 to 4, together with a pharmaceutically acceptable diluent or carrier.

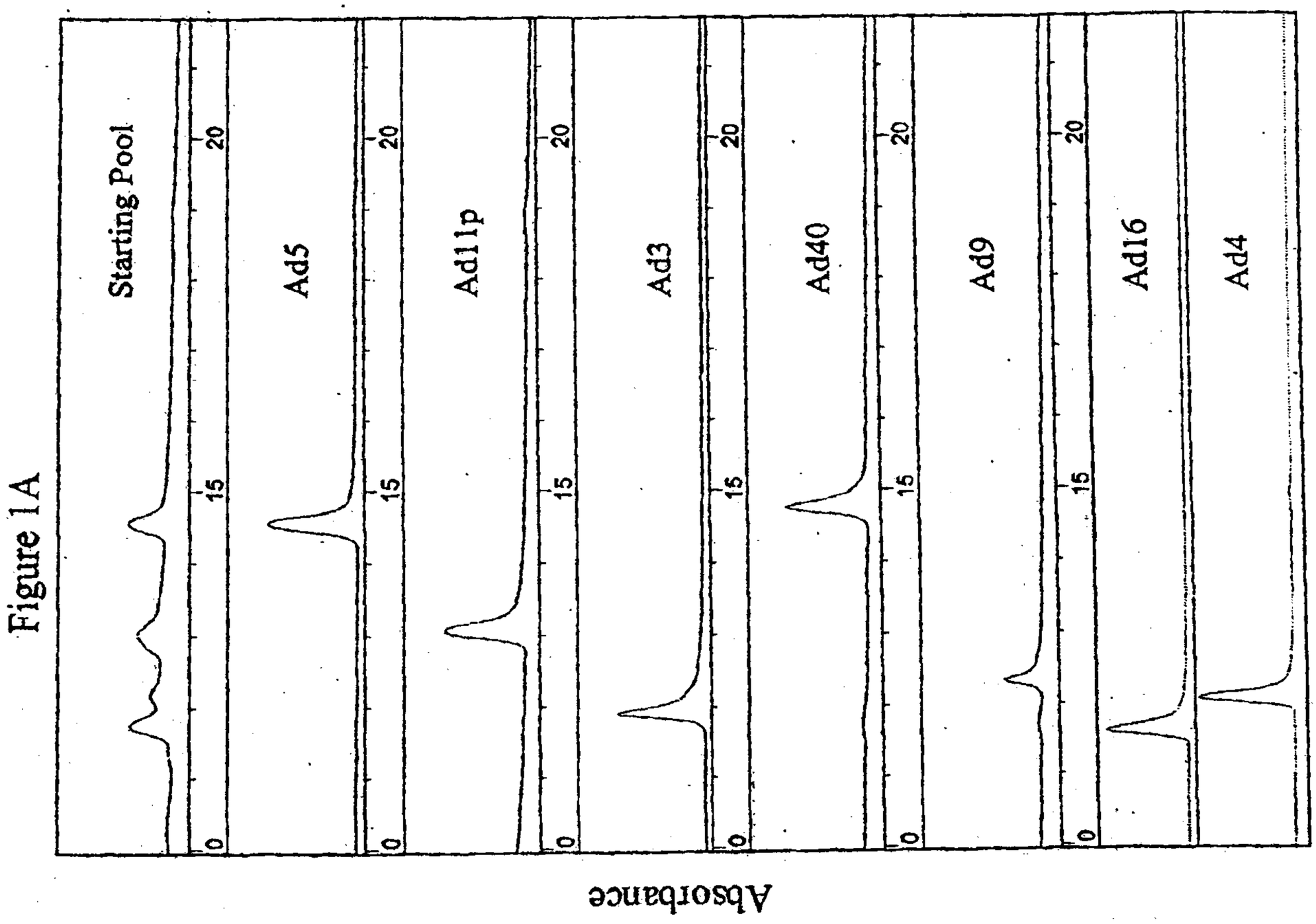

Starting Pool
Ad5
Ad11p
Ad3
Ad40
Ad9
Ad16
Ad4
20
15
0
Absorbance
Retention Time (minutes)

Figure 1A

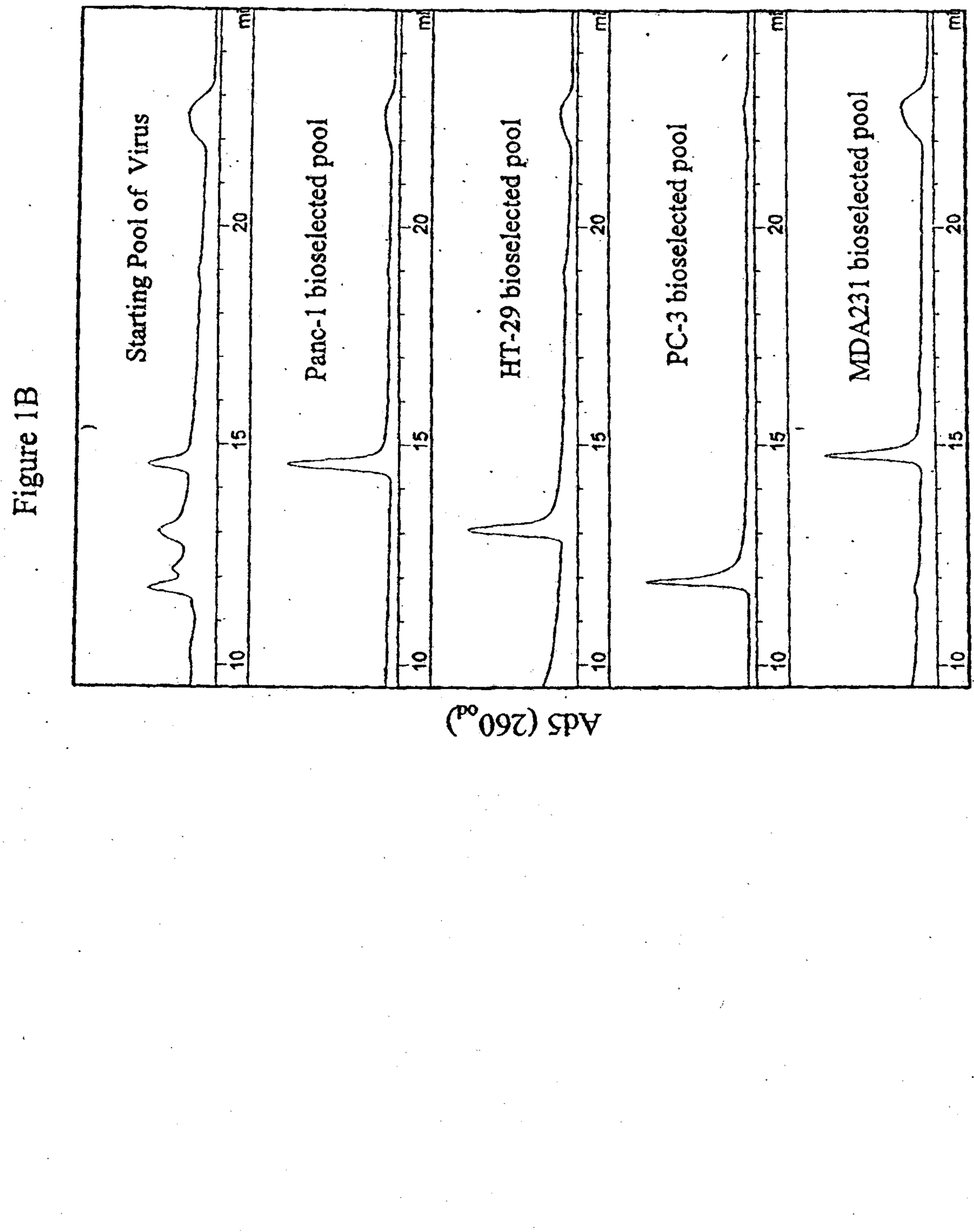

Starting Pool of Virus
Panc-1 bioselected pool
HT-29 bioselected pool
PC-3 bioselected pool
MDA231 bioselected pool
20
15
10
Retention Time (minutes)
Ads (260nm)

Figure 1B

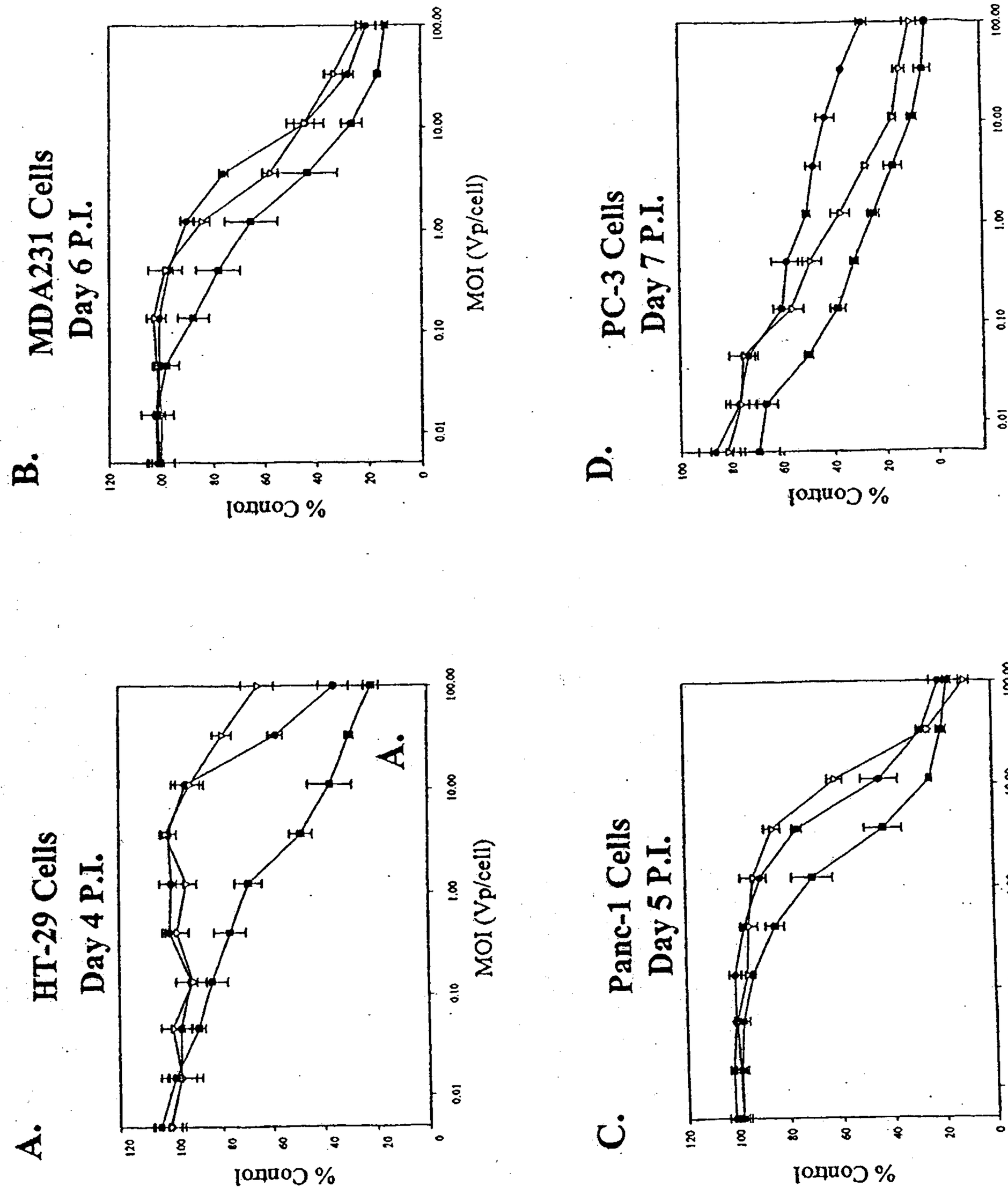

A.
HT-29 Cells
Day 4 P.I.
B.
MDA231 Cells
Day 6 P.I.
C.
Panc-1 Cells
Day 5 P.I.
D.
PC-3 Cells
Day 7 P.I.
% Control
MOI (Vp/cell)
0
20
40
60
80
100
120
0.01
0.10
1.00
10.00
100.00

Figure 2

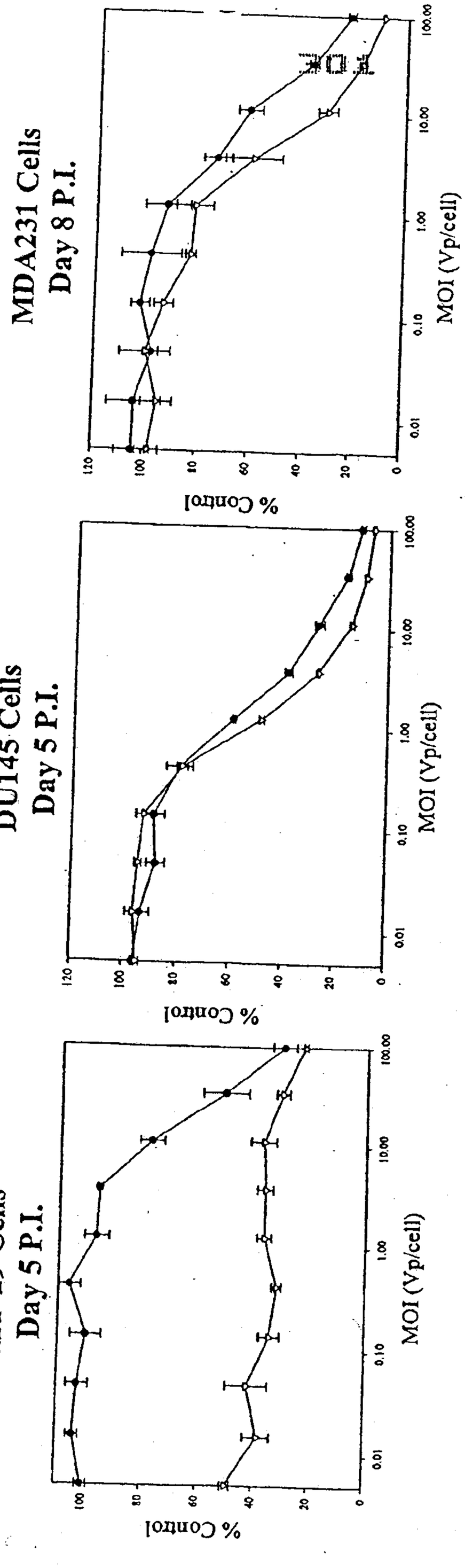

MDA231 Cells
Day 8 P.I.
DU145 Cells
Day 5 P.I.
HT-29 Cells
Day 5 P.I.
PC-3 Cells
Day 5 P.I.
Panc-1 Cells
Day 6 P.I.
OVCAR-3 Cells
Day 7 P.I.
% Control
MOI (Vp/cell)
120
100
80
60
40
20
0
100.00
10.00
1.00
0.10
0.01

Figure 3A

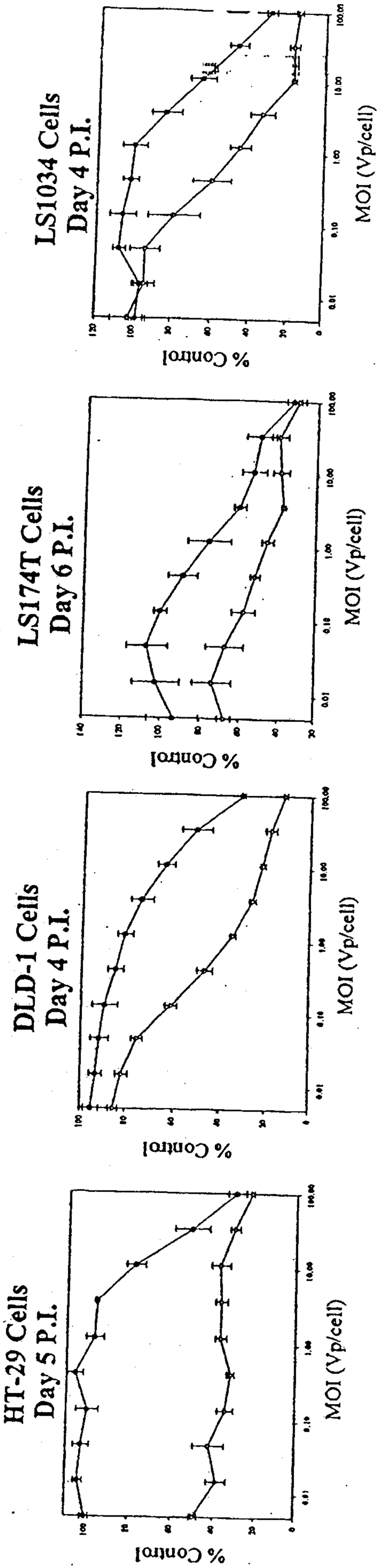
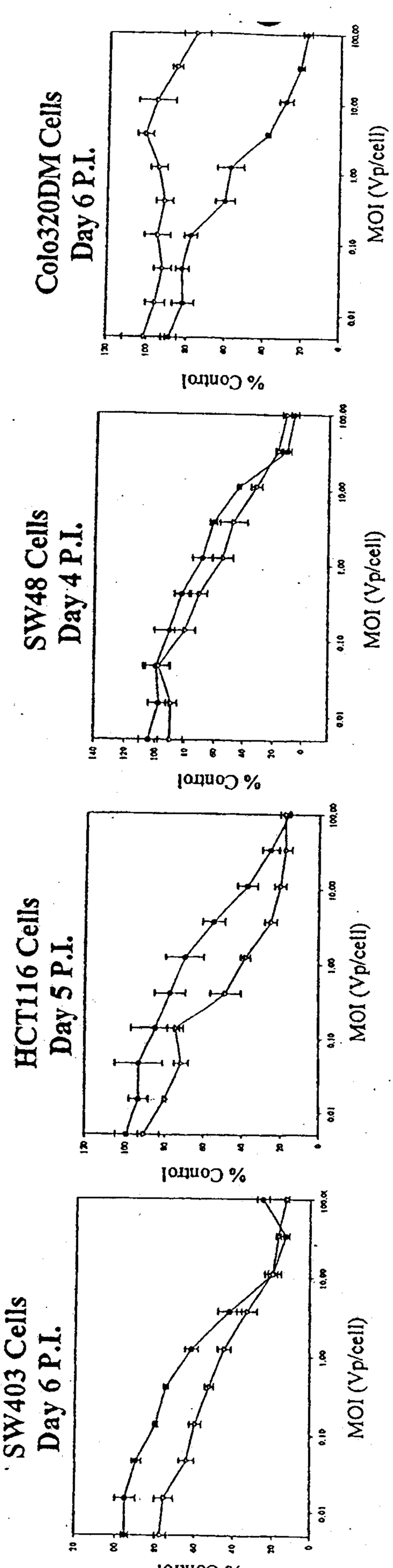

LS1034 Cells
Day 4 P.I.
% Control
MOI (Vp/cell)
LS174T Cells
Day 6 P.I.
% Control
MOI (Vp/cell)
DLD-1 Cells
Day 4 P.I.
% Control
MOI (Vp/cell)
HT-29 Cells
Day 5 P.I.
% Control
MOI (Vp/cell)

Figure 3B


Colo320DM Cells
Day 6 P.I.
% Control
MOI (Vp/cell)
SW48 Cells
Day 4 P.I.
% Control
MOI (Vp/cell)
HCT116 Cells
Day 5 P.I.
% Control
MOI (Vp/cell)
SW403 Cells
Day 6 P.I.
% Control
MOI (Vp/cell)

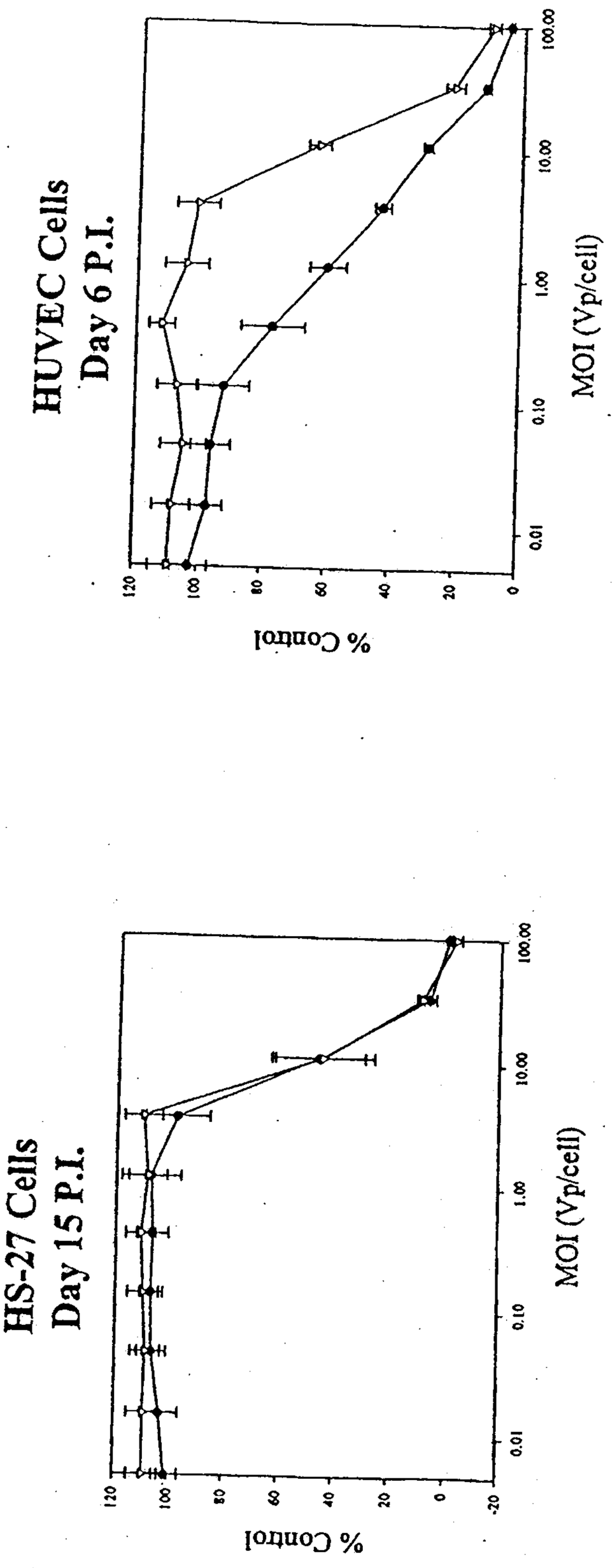

HUVEC Cells
Day 6 P.I.
% Control
MOI (Vp/cell)
HS-27 Cells
Day 15 P.I.
% Control
MOI (Vp/cell)
SAEC Cells
Day 6 P.I.
% Control
MOI (Vp/cell)

Figure 4

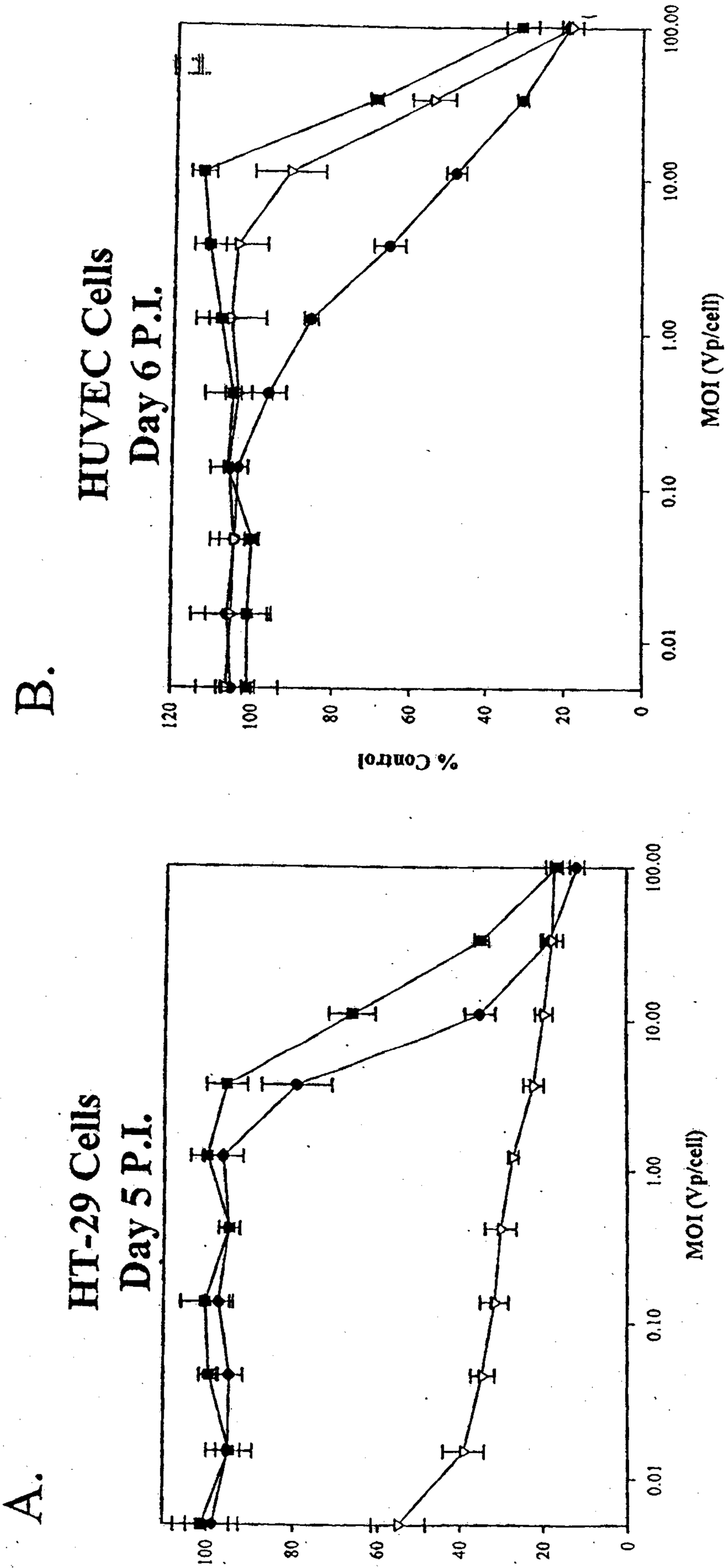

B.
HUVEC Cells
Day 6 P.I.
% Control
120
100
80
60
40
20
0
0.01
0.10
1.00
10.00
100.00
MOI (Vp/cell)
A.
HT-29 Cells
Day 5 P.I.
% Control
100
80
60
40
20
0
0.01
0.10
1.00
10.00
100.00
MOI (Vp/cell)

Figure 5

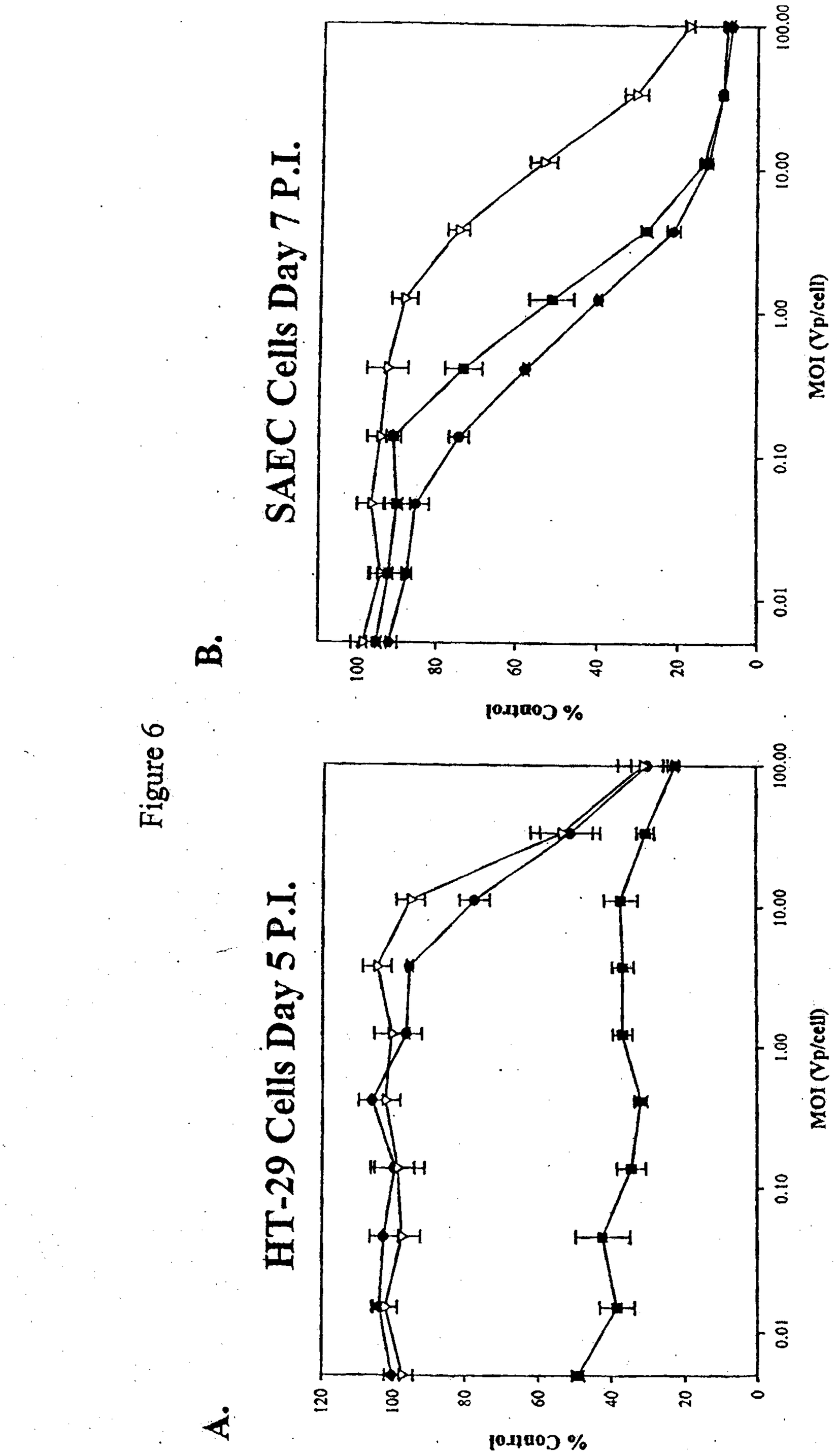
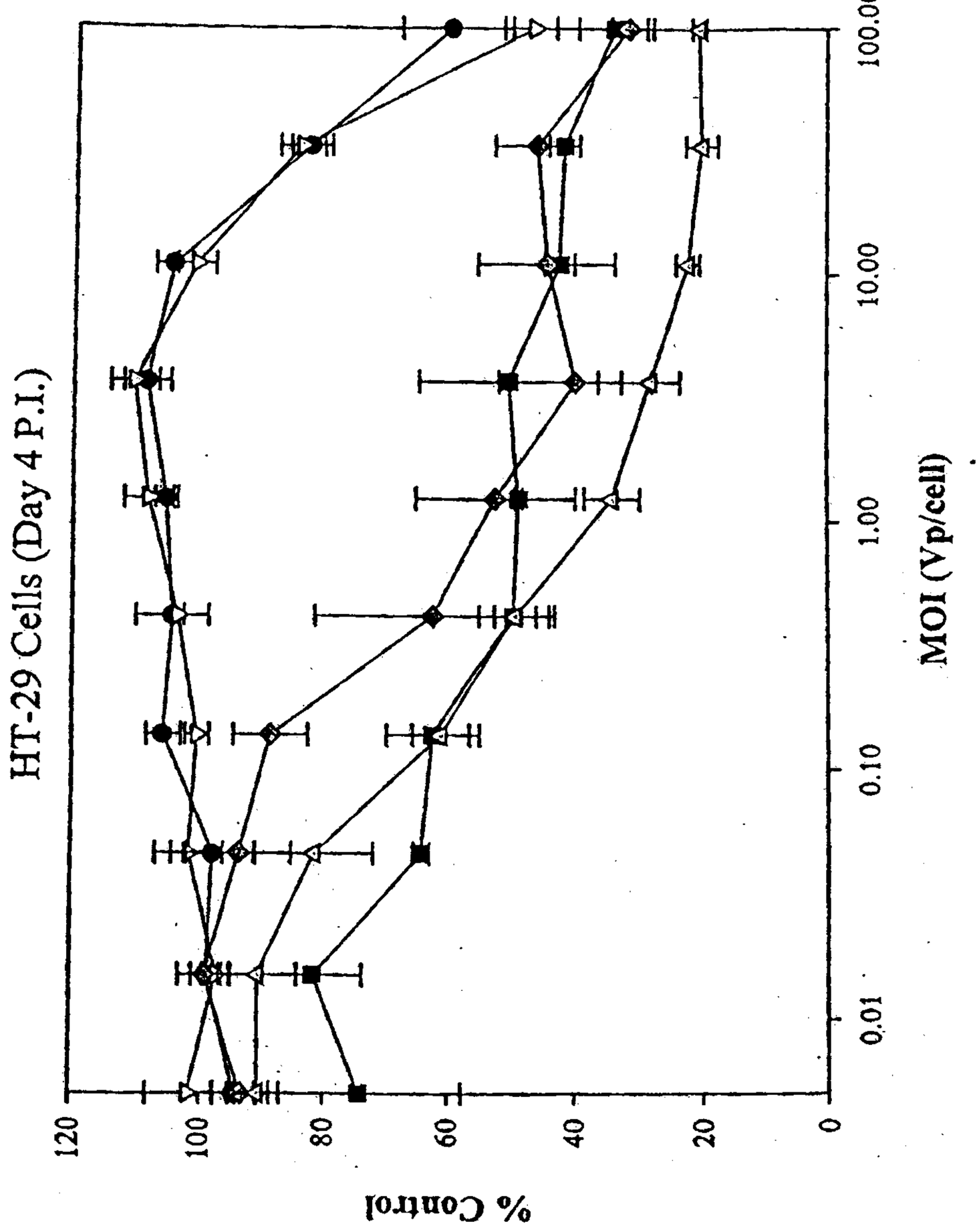

B.
SAEC Cells Day 7 P.I.
% Control
100
80
60
40
20
0
0.01
0.10
1.00
10.00
100.00
MOI (Vp/cell)
A.
HT-29 Cells Day 5 P.I.
% Control
120
100
80
60
40
20
0
0.01
0.10
1.00
10.00
100.00
MOI (Vp/cell)

Figure 6

Figure 7


HT-29 Cells (Day 4 P.I.)
% Control
120
100
80
60
40
20
0
MOI (Vp/cell)
100.00
10.00
1.00
0.10
0.01