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(54) Titre : COMPOSITION POUR LE TRAITEMENT D'UNE INFECTION PAR LE VIRUS DE L'HEPATITE B
(54) Title: COMPOSITION FOR TREATING HBV INFECTION

(57) Abrégé/Abstract:
The present invention provides a composition comprising hepatitis B virus (HBV) component(s), and which may be either nucleic acid- or polypeptide-based as well as nucleic acid molecules and vectors encoding such HBV component(s). It also relates to infectious viral particles and host cells comprising such nucleic acid molecules or vectors. It also provides composition and kits of parts comprising such nucleic acid molecules, vectors, infectious viral particles or host cells and the therapeutic use thereof for preventing or treating HBV infections.

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(54) **Title**: COMPOSITION FOR TREATING HBV INFECTION

(57) **Abstract**: The present invention provides a composition comprising hepatitis B virus (HBV) component(s), and which may be either nucleic acid- or polypeptide-based as well as nucleic acid molecules and vectors encoding such HBV component(s). It also relates to infectious viral particles and host cells comprising such nucleic acid molecules or vectors. It also provides composition and kits of parts comprising such nucleic acid molecules, vectors, infectious viral particles or host cells and the therapeutic use thereof for preventing or treating HBV infections.

Composition for treating HBV infection

The present invention relates to immunogenic compositions with hepatitis B virus (HBV) component(s), and which may be either nucleic acid- or polypeptide-based. Said immunogenic compositions can be used for stimulating or enhancing an immune response to HBV with the goal of providing a protective or therapeutic effect against HBV infection and any condition or disease caused by or associated with an HBV infection. The present invention also relates to expression vectors for expressing such HBV component(s) and their therapeutic or prophylactic use. The invention is of very special interest in the field of immunotherapy, and more particular for treating patients infected with HBV, especially those chronically infected.

BACKGROUND

Hepatitis B is a major public health problem with more than 350 million persons chronically infected worldwide, 20 to 40% of them being at risk of developing chronic liver disease, cirrhosis and hepatocellular carcinoma. Despite the existence of effective preventive vaccines, the hepatitis B virus (HBV) infection is still rampant in many countries, even developed ones, with an estimation of 4.5 millions of new cases of infection per year worldwide. Unlike the WHO recommendation which is to implement universal vaccination, the coverage of full course preventive vaccination varies from 25% in Asia to 75-90% in Europe. Currently hepatitis B is the 10^{th} cause of mortality (around 1 million of deaths/year) and HBV related liver carcinoma, the 5^{th} most frequent cancer. Geographic repartition of HBV infection is uneven with prevalence lower than 1% in Western countries to more than 10% in South Eastern countries, most part of Africa and Equatorial South America. In high HBV chronic carrier prevalence area, vertical transmission from infected mother to neonate is the most frequent mode of contamination and almost always results in chronic hepatitis (90% of cases). This rate can be lowered to 15% by preventive vaccination of infected babies immediately after birth. In Western countries, infection occurs most likely during adulthood through horizontal transmission, via body fluids such as blood, semen, saliva, resulting in acute and self recovering infection in 85% of patients but nevertheless to chronic infection in 15% of cases.

Hepatitis B virus (HBV) is a member of the hepadnaviridae and primarily infects the liver, replicating in hepatocytes. The infectious particles are the so called 42-45nm "Dane particles" which consist of an outer lipoprotein envelope which contains three different surface proteins (HBs) and an inner nucleocapsid, the major structural protein of which is the core protein (HBcAg). Within the nucleocapsid is a single copy of the HBV genome linked to the viral polymerase protein (P). In addition to 42–45-nm virions, the blood of HBV-infected patients contains 20-nm spheres made of HBsAg and host-derived lipids which are released from infected cells. These spheres outnumber the virions by a factor of 10^4–10^6.

The HBV genome is a relaxed circular partially double-stranded DNA of approximately 3,200 nucleotides consisting of a full-length negative strand and a shorter positive strand. It contains 4 overlapping open reading frames (ORFs), C, S, P and X. The C ORF encodes the core protein (or HBcAg), a 183 amino acid-long protein which constitutes the HBV nucleocapsid and a second protein found in the serum of patients during virus replication known as HBeAg which contains a precore N-terminal extension and a part of HBcAg. The C-terminus of the core protein is very basic and contains 4 Arg-rich domains which are predicted to bind nucleic acids as well as numerous phosphorylation sites (the phosphorylation state of core is associated with conformational changes in the capsid particle as described in Yu and Sommers, 1994, J. Virol. 68:2965). The S ORF encodes three surface proteins all of which have the same C terminus but differ at their N-termini due to the presence of three in-frame ATG start codons that divide the S ORF into three regions, S (226 amino acids), pre-S2 (55 amino acids) and pre-S1 (108 amino acids), respectively. The large-surface antigen protein (L) is produced following translation initiation at the first ATG start codon and comprises 389 amino acid residues (preS1-preS2-S). The middle surface antigen protein (M) results from translation of the S region and the pre-S2 region starting at the second start ATG whereas the small surface antigen protein of 226 amino acids (S, also designated HBsAg) results from translation of the S region initiated at the third start ATG codon. The HBV surface proteins are glycoproteins with carbohydrate side chains (glycans) attached by N-glycosidic linkages. The P ORF encodes the viral polymerase and the X ORF contains a protein known as the X protein, which is thought to be a transcriptional activator.

After virions enter hepatocytes, by an as-yet-unknown receptor, nucleocapsids transport the genomic HBV DNA to the nucleus, where the relaxed circular DNA is converted to covalently closed circular DNA (cccDNA). The cccDNA functions as the template for the

transcription of four viral RNAs, which are exported to the cytoplasm and used as mRNAs for translation of the HBV proteins. The longest (pre-genomic) RNA also functions as the template for HBV replication, which occurs in nucleocapsids in the cytoplasm. Some of the HBV DNA and polymerase-containing capsids are then transported back to the nucleus, where they release the newly generated relaxed circular DNA to form additional cccDNA. With a half-life longer than the one of hepatocytes, the cccDNA is responsible for the persistence of HBV. Other capsids are enveloped by budding into the endoplasmic reticulum and secreted after passing through the Golgi complex.

A number of preclinical and clinical studies have emphasized the importance of CD4+ and CD8+ T cell immune responses for effective anti-viral response (Ferrari et al, 1990, J Immul, 145:3442 ; Penna et al, 1996, J Clin Invest, 98:1185 ; Penna et al, 1997, Hepatology, 25:1022). That is to say, patients naturally having recovered from hepatitis B mounted multi-specific and sustained responses mediated by T helper (T_H) and cytotoxic T (CTL) lymphocytes which are readily detectable in peripheral blood. Upon recognition of viral peptides, CTL acquire the capacity to either cure HBV-infected cells via a non-cytopathic, cytokine mediated inhibition of HBV replication and/or to kill them via perforin-Fas ligand and TNFα-mediated death pathways. Both effector functions have been observed during resolution of acute hepatitis B and this type 1 T-cell (Th1) response persists after clinical recovery. It often coincides with an elevation of serum alanine-aminotransferase (ALT) levels and with appearance of HBcAg specific IgM and IgG. Anti-HBe and anti-HBs antibodies appear later and indicate a favorable outcome of infection. HBsAg-specific antibodies are neutralizing, mediate protective immunity and persist for life after clinical recovery. Chronic HBV infection is, however, only rarely resolved by the immune system. When this occurs, viral clearance is associated with increased CTL activity and increased ALT levels caused by a destruction of infected hepatocytes by the immune system. However, the vast majority of chronically infected patients show weak and temporary CD4 and CD8 T cell immune responses that are antigenically restricted and ineffective to clear viral infection, although individual HBV-specific T-cell clones have been isolated and expanded from liver biopsies. The reason for this alteration of the effector functions of the cellular immune response in chronic hepatitis B is currently not known. However it was shown that functional T cell responses can be partially restored in some patients when the viral load is below a threshold of 10^6 IU/mL (Webster et al 2004, J. Virol. 78:5707). These data are clearly encouraging and

emphasize the need for immunomodulatory strategies capable of inducing an effective T-cell response.

Ideally, treatment of chronic viral hepatitis B should first permit to suppress HBV replication before irreversible liver damage, so as to eliminate the virus, prevent disease progression to cirrhosis or liver cancer and improve patient survival. Conventional treatment of chronic hepatitis B includes pegylated interferon-alpha (IFNa) and nucleoside/nucleotide analogues (NUCs) such as lamivudine, and more recently entecavir, telbivudine, adefovir and tenofovir (EASL Clinical Practice Guidelines: management of chronic hepatitis B, 2009). IFNa is a potent antiviral molecule, whereby inhibiting viral replication, which however, causes serious side effects in merely 25 - 30% of patients. NUCs act as competitive inhibitors of HBV polymerase aimed to inhibit the reverse transcription of the pre-genomic RNA into the negative DNA strand and then the double stranded viral DNA. They limit the formation of new virions, but are ineffective to eliminate the supercoiled cccDNA hidden in the nucleus of infected hepatocytes which constitutes a source of new progeny viruses. This can explain why NUC efficacy is temporary and viral rebound occurs immediately after cessation of treatment, requiring patients to stay life long under treatment. In addition, long-term efficacy is also limited due to emergence of resistant HBV mutants (more than 24% after one year and approximately 66% after four years of lamivudine treatment as discussed in Leung et al., 2001, Hepatology 33:1527) although newer NUCs (entecavir, telbivudine and tenofovir) showed much fewer occurrences of drug-resistant HBV mutants, while increasing suppression of HBV DNA. Long-term treatment data with these new drugs are, however, limited and this higher efficacy has not been correlated with a significantly higher rate of HBs-seroconversion.

Besides antiviral therapies, efforts are currently made to develop supplemental therapies aiming at improved host's immune responses, specifically those mediated by cytotoxic T and helper T lymphocytes. A large majority of existing immunotherapy approaches have focused on the use of HBV surface protein(s), S preS1 and/or preS2 (Smith et al., 1983, Nature 302:490; Lubeck et al., 1989, Proc. Natl Acad. Sci. USA 86 :6763 ; Adkins et al., 1998, BioDrugs 10 :137 ; Loirat et al., 2000, J. Immunol. 165:4748; Funuy-Ren et al. 2003, J. Med. Virol. 71:376; Kasaks et al., 2004, J. Gen. Virol. 85:2665; Xiangming Li et al., 2005, Intern. Immunol. 17:1293; Mancini-Bourguine et al., 2006, Vaccine 24:4482; Vandepapeliere et al., 2007, Vaccine 25:8585). Encouraging results were obtained at least with respect to the stimulation of immune responses. For example, Mancini-Bourguine et al. (2006, Vaccine

24:4482) reported induction and/or recall T cell responses in HBV chronically infected patients injected with a preS2-S-encoding DNA vaccine, which is a good indication that the immune system is still operational in these patients.

HBcAg was also used as an immunogen (Yi-Ping Xing et al., 2005, World J. Gastro. 11:4583) as well as chimeric HBcAg capsids bearing foreign epitopes on their surface (WO92/11368; WO00/32625; Koletzki et al., 1997, J. Gen. Virol. 78:2049). The most promising location for inserting epitopes from the point of view of immunogenicity seems to be the site of an outer loop predicted to be on the surface of HBcAg in the vinicity of position 80 (Argos et al. 1988, EMBO J. 7:819). Schodel et al. (1992, J. Virol. 66:106) and Borisova et al. (1993, J. Virol. 67:3696) were able to insert preS1 and HBsAg epitopes in this region and reported successful immunization with the chimeric particles.

Multivalent vaccine candidates aimed to simultaneously target multiple HBV antigens have also been investigated. Notably, a polyepitope DNA vaccine encoding a fusion polypeptide of multiple cytotoxic T-lymphocytes (CTL) and helper T-lymphocyte (HTL) epitopes present in envelope, core and polymerase proteins was shown to elicit multiple CTL and HTL responses in preclinical mouse models (Depla et al., 2008, J. Virol. 82:435). Several vaccine formulations based on a mixture of DNA plasmids encoding HBsAg, HBcAg and HBV polymerase were developed (WO2005/056051; WO2008/020656) and demonstrated specific anti-HBV cellular and humoral responses in transgenic mouse model of chronic hepatitis B (Chae Young Kim et al., 2008, Exp. Mol. Medicine 40:669). Phase I clinical trials were initiated in South Korea in HBV carriers in combination with lamivudine treatment (Yang et al., 2006, Gene Ther. 13:1110).

Accordingly, there still exists a need for alternative immunotherapeutic approaches for inducing immune responses in a more potent and effective manner, especially cell-mediated immune responses, in an individual in need thereof such as an HBV chronically infected patient. Moreover, there is a need to provide vector-based composition capable of expressing the HBV antigen in a stable and sustained manner.

This technical problem is solved by the provision of the embodiments as defined in the claims.

Other and further aspects, features and advantages of the present invention will be apparent from the following description of the presently preferred embodiments of the invention. These embodiments are given for the purpose of disclosure.

SUMMARY OF THE INVENTION

Accordingly, in a first aspect, the present invention provides an immunogenic composition comprising at least one polypeptide or a nucleic acid molecule encoding said at least one polypeptide, wherein said at least one polypeptide is selected from the group consisting of:

(i) A polymerase moiety comprising at least 450 amino acid residues of a polymerase protein originating from a first HBV virus;

(ii) A core moiety comprising at least 100 amino acid residues of a core protein originating from a second HBV virus; and

(iii) An env moiety comprising one or more immunogenic domain(s) of 15 to 100 consecutive amino acid residues of a HBsAg protein originating from a third HBV virus; or

Any combination of said polymerase moiety, core moiety, env moiety, said nucleic acid molecule encoding said polymerase moiety, said nucleic acid molecule encoding said core moiety and/or said nucleic acid molecule encoding said env moiety.

Definitions

As used herein throughout the entire application, the terms "a" and "an" are used in the sense that they mean "at least one", "at least a first", "one or more" or "a plurality" of the referenced compounds or steps, unless the context dictates otherwise. For example, the term "a cell" includes a plurality of cells including a mixture thereof.

The term "and/or" wherever used herein includes the meaning of "and", "or" and "all or any other combination of the elements connected by said term".

The term "about" or "approximately" as used herein means within 10%, preferably within 8%, and more preferably within 5% of a given value or range.

As used herein, when used to define products, compositions and methods, the term "comprising" (and any form of comprising, such as "comprise" and "comprises"), "having" (and any form of having, such as "have" and "has"), "including" (and any form of including,

such as "includes" and "include") or "containing" (and any form of containing, such as "contains" and "contain") are open-ended and do not exclude additional, unrecited elements or method steps. "Consisting essentially of" means excluding other components or steps of any essential significance. Thus, a composition consisting essentially of the recited components would not exclude trace contaminants and pharmaceutically acceptable vehicles. "Consisting of" means excluding more than trace elements of other components or steps. For example, a polypeptide "consists of" an amino acid sequence when the polypeptide does not contain any amino acids but the recited amino acid sequence. A polypeptide "consists essentially of" an amino acid sequence when such an amino acid sequence is present with eventually only a few additional amino acid residues. A polypeptide "comprises" an amino acid sequence when the amino acid sequence is at least part of the final amino acid sequence of the polypeptide. Such a polypeptide can have a few up to several hundred additional amino acids residues.

The terms "amino acids", "residues" and "amino acid residues" are synonyms and encompass natural amino acids as well as amino acid analogs (e.g. non-natural, synthetic and modified amino acids, including D or L optical isomers).

The terms "polypeptide", "peptide" and "protein" are used herein interchangeably to refer to polymers of amino acid residues which comprise nine or more amino acids bonded via peptide bonds. The polymer can be linear, branched or cyclic and may comprise naturally occurring and/or amino acid analogs and it may be interrupted by non-amino acids. As a general indication, if the amino acid polymer is long (e.g. more than 50 amino acid residues), it is preferably referred to as a polypeptide or a protein whereas if it is 50 amino acids long or less, it is referred to as a "peptide".

Within the context of the present invention, the terms "nucleic acid", "nucleic acid molecule", "polynucleotide" and "nucleotide sequence" are used interchangeably and define a polymer of any length of either polydeoxyribonucleotides (DNA) (e.g., cDNA, genomic DNA, plasmids, vectors, viral genomes, isolated DNA, probes, primers and any mixture thereof) or polyribonucleotides (RNA) molecules (e.g., mRNA, antisense RNA) or mixed polyribo-polydeoxyribonucleotides. They encompass single or double-stranded, linear or circular, natural or synthetic polynucleotides. Moreover, a polynucleotide may comprise non-naturally occurring nucleotides, such as methylated nucleotides and nucleotide analogs (see US 5,525,711, US 4,711,955 or EPA 302 175 as examples of modifications) and may be

interrupted by non-nucleotide components. If present, modifications to the nucleotide may be imparted before or after polymerization.

As used herein, the term "immunogenic composition" refers to a formulation which comprises 1, 2, 3, 4 or more component(s) described hereinafter (e.g. the polymerase moiety, the core moiety, the env moiety, the nucleic acid molecule encoding the polymerase moiety, the nucleic acid molecule encoding the core moiety and/or the nucleic acid molecule encoding the env moiety) and optionally other components (e.g. adjuvant, carrier, diluent, etc). The immunogenic composition of the present invention will typically be in a form that is capable of being administered to a host organism and induces a protective or therapeutic immune response sufficient to induce or stimulate anti-HBV immunity, resulting in a therapeutic benefit such as prevent an HBV infection, reduce and/or ameliorate at least one condition caused by or associated with an HBV infection (e.g. reduce the viral load, reduce or delay the risk of hepatic lesions such as cirrhosis or liver cancer, improve liver history, etc), and/or reduce serum HBeAg or HBsAg level or both, and/or induce HBe seroconversion, HBs seroconversion or both and/or enhance the efficacy of another anti-HBV therapy or prophylaxis. Upon introduction in a host organism, the immunogenic composition of the present invention is able to provoke an immune response including, but not limited to, the production of antibodies and/or cytokines and/or the activation of cytotoxic T cells, B, T-lymphocytes, antigen presenting cells, helper T cells, dendritic cells, NK cells, leading to the production of innate immune response and/or specific humoral and/or cellular immune responses against at least one HBV antigen/epitope.

An "immunogenic domain" refers to a structural portion of an HBV protein capable of being bound by an antibody or T cell receptor. Typically, such an immunogenic domain contains one or more B and/or T epitope(s), in particular. CTL or T_H epitopes or both, and are involved in recognition by a particular antibody, or in the context of an MHC (Major Histocompatibility Complex), by T-cell receptors. An "epitope" corresponds to a minimal peptide motif (usually a set of 9-11 amino acid residues) that together form a site recognized by an antibody, T-cell receptor or HLA molecule. Those residues can be consecutive (linear epitope) or not (conformational epitope that includes residues that are not immediately adjacent to one another). Recognition of a T-cell epitope by a T-cell is generally believed to be via a mechanism wherein T-cells recognize peptide fragments of antigens which are bound to class I or class II MHC molecules expressed on antigen-presenting cells.

As used herein, "HBV" and "hepatitis B virus" are used interchangeably and refer to any member of the hepadnaviridae (see e.g. Ganem and Schneider in Hepadnaviridae (2001) "The viruses and their replication" (pp2923-2969), Knipe DM et al., eds. Fields Virology, 4th ed. Philadelphia, Lippincott Williams & Wilkins or subsequent edition). Extensive phylogenetic analyses have led to the classification of hepatitis B viruses into 8 major genotypes (A to H). which show sequence divergence by at least 8%. The various HBV genotypes show distinct geographic distribution and can display heterogeneous disease symptoms and/or clinical outcome. The various HBV were classified in nine different subtypes (*ayw1, ayw2, ayw3, ayw4, ayr, adw2, adw4, adrq+ and adqr-)* in connection with HBsAg-associated serology (see review by Mamum-Al Mahtab et al., 2008, Hepatobiliary Pancrease Dis Int 5:457; Schaeffer, 2007, World Gastroenterol. 7:14; Norder et al., 1993, J. Gen Virol.74:1341). Each genotype and serotype encompasses different HBV strains and isolates. An isolate corresponds to a specific virus isolated from a particular source of HBV (e.g. a patient sample or other biological HBV reservoir) whereas a strain encompasses various isolates which are very close each other in terms of genomic sequences.

A number of HBV suitable for use in the context of the present invention are described in the art, especially in Genbank. Exemplary HBV of genotype A include without limitation isolate HB-JI444AF and strain HB-JI444A (accession number AP007263). Exemplary HBV of genotype B include without limitation clone pJDW233 (accession number D00329),, isolate HBV/14611 (accession number AF121243), HBV-B1 identified in 2001 by Hou, et al. (GenBank accession number AF282917.1), HBV strain Whutj-37 (GenBank accession number AY2933309.1) identified by Zhang et al. (2005, Arch. Virol. 150, 721-741), the Chinese HBV strain GDH1 identified by He et al. (GenBank accession number AY766463.1) and HBV isolate 57-1 subtype adw identified by Jiang et al. (GenBank accession number AY518556.1). Exemplary HBV of genotype C include without limitation isolate AH-1-ON980424 (accession number AB113879), strain HCC-3-TT (accession number AB113877), HBV isolate SWT3.3 identified by Fang et al. (GenBank accession number EU916241.1), HBV isolate H85 identified by Zhu et al. (GenBank accession number AY306136.1), HBV strain C1248 identified by Tu et al. (GenBank accession number DQ975272.1), HBV isolate CHN-H155 (GenBank accession number DQ478901.1) identified by Wang et al. (2007, J. Viral Hepat 14, 426-434) and HBV isolate GZ28-1 identified by Zhou et al. (GenBank accession number EF688062). Exemplary HBV of genotype D include without limitation

isolates KAMCHATKA27 (accession number AB188243), ALTAY136 (accession number AB188245) and Y07587 described in Stoll-Becker et al. (1997, J. Virol. 71:5399) and available at Genbank under accession number Y07587 as well as the HBV isolate described under accession number AB267090. Exemplary HBV of genotype E include without limitation isolate HB-JI411F and strain HB-JI411 (accession number AP007262). Exemplary HBV of genotype F include without limitation isolates HBV-BL597 (accession number AB214516) and HBV-BL592 (accession number AB166850). Exemplary HBV of genotype G include without limitation isolate HB-JI444GF and strain HB-JI444G (accession number AP007264). Exemplary HBV of genotype H include without limitation isolate HBV ST0404 (accession number AB298362) and isolate HB-JI260F and strain HB-JI260 (accession number AP007261). However, the present invention is not limited to these exemplary HBV. Indeed the nucleotide and amino acid sequences can vary between different HBV isolates and genotypes and this natural genetic variation is included within the scope of the invention as well as non-natural modification(s) such as those described below.

As used herein, a "native HBV protein" refers to a protein, polypeptide or peptide (e.g. the polymerase protein, the core protein or the HBsAg, etc) that can be found, isolated, obtained from a source of HBV in nature as distinct from one being artificially modified or altered by man in the laboratory. Thus, this term would include naturally-occurring HBV proteins polypeptides or peptides unless otherwise specified. Such sources in nature include biological samples (e.g. blood, plasma, sera, semen, saliva, tissue sections, biopsy specimen etc.) collected from a subject infected or that has been exposed to HBV, cultured cells (such as HepG2.2.15, HuH6-C15 (Sureau et al., 1986, Cell 47:37; Sells et al., 1987, Proc. Natl. Acad. Sci. 84(4):1005); HuH7.TA61 or HuH7.TA62 (Sun et al., 2006, J Hepatol. 45(5):636), tissue cultures as well as recombinant materials. Recombinant materials include without limitation HBV isolate (e.g. available in depositary institutions), HBV genome, genomic RNA or cDNA libraries, plasmids containing HBV genome or fragment(s) thereof or any prior art vector known to include such elements.

Nucleotide sequences encoding the various HBV proteins can be found in specialized data banks (e.g. those mentioned above) and in the literature (see e.g. Valenzuela et al., 1980, The nucleotide sequence of the hepatitis B viral genome and the identification of the major viral genes (pp57-70) in "Animal Virus Genetics"; eds B. Fields, et al.; Academic Press Inc., New York and Vaudin et al., 1988, J. Gen. Virol. 69:1383). Representative examples of native

polymerase, core and HBsAg polypeptides are set forth in SEQ ID NO: 1-3, respectively (SEQ ID NO: 1 provides the amino acid sequence of the native polymerase protein of HBV isolate Y07587, SEQ ID NO: 2 provides the amino acid sequence of the native core protein of HBV isolate Y07587 and SEQ ID NO: 3 provides the amino acid sequence of the native env (HBsAg) of HBV isolate Y07587). Nucleotide sequences encoding the native polymerase, core and HBsAg of Y07587 HBV are shown for illustrative purposes in SEQ ID NO: 4, 5 and 6, respectively. However, as discussed above, the HBV proteins are not limited to these exemplary sequences and genetic variation is included in the scope of the invention.

As used herein, the term "moiety" (e.g. polymerase, core and/or env moieties) refers to a protein, polypeptide or peptide that originates from a native HBV protein, polypeptide or peptide after being artificially modified or altered by man in the laboratory as described herein. The term "modified" encompasses deletion, substitution or addition of one or more nucleotide/amino acid residue(s), any combination of these possibilities (e.g. degeneration of the native nucleotide sequence to reduce homology between the HBV sequences encoded by the composition of the invention, introduction of appropriate restriction sites) as well as non natural arrangements (e.g. fusion between two or more HBV proteins, polypeptides or peptides or moiety/ies). When several modifications are contemplated, they can concern consecutive residues and/or non consecutive residues. Modification(s) can be generated by a number of ways known to those skilled in the art, such as site-directed mutagenesis (e.g. using the Sculptor™ *in vitro* mutagenesis system of Amersham, Les Ullis, France), PCR mutagenesis, DNA shuffling and by chemical synthetic techniques (e.g. resulting in a synthetic nucleic acid molecule). The modification(s) contemplated by the present invention encompass silent modifications that do not change the amino acid sequence of the encoded HBV polypeptides, as well as modifications that are translated into the encoded polypeptide resulting in a modified amino acid sequence as compared to the corresponding native one. The term "originate" (or originating) is used to identify the original source of a molecule but is not meant to limit the method by which the molecule is made which can be, for example, by chemical synthesis or recombinant means.

Preferably, each of the HBV moieties in use in the present invention retains a high degree of amino acid sequence identity with the corresponding native HBV protein, over either the full length protein or portion(s) thereof. The percent identity between two polypeptides is a function of the number of identical positions shared by the sequences, taking into account the

number of gaps which need to be introduced for optimal alignment and the length of each gap. Various computer programs and mathematical algorithms are available in the art to determine the percentage of identity between amino acid sequences, such as for example the Blast program (e.g. Altschul et al., 1997, Nucleic Acid Res. 25:3389; Altschul et al., 2005, FEBS J. 272:5101) available at NCBI. The same can be applied for nucleotide sequences. Programs for determining nucleotide sequence homology are also available in specialized data base (Genbank or the Wisconsin Sequence Analysis Package), for example BESTFIT, FASTA and GAP programs.

For example, further to the modifications described hereinafter (e.g. reduced enzymatic activities, etc), any or all of the HBV moieties comprised or encoded by the composition of the invention can be modified so as to be representative of a specific genotype, and thus comprise an amino acid sequence corresponding to a consensus or near consensus sequence which is typically determined after sequence alignment of various HBV polypeptides of a particular genotype.

The term "combination" as used herein refers to any kind of combination between at least two of the components comprised or encoded by the immunogenic composition of the invention and any arrangement possible of the various components with a specific preference for 2 or 3 of the said components. This encompasses mixture of two or more polypeptides, mixture of two or more nucleic acid molecules/vectors, mixture of one or more polypeptide(s) and one or more nucleic acid molecules/vectors, as well as fusion of two or more nucleic acid molecules so as to provide a single polypeptide chain bearing two or more HBV moieties (e.g. non natural arrangement).

In a preferred embodiment, the immunogenic composition of the invention comprises a combination of at least two of said polymerase moiety, core moiety, env moiety or of at least two of said nucleic acid molecules encoding said polymerase moiety, said nucleic acid molecule encoding said core moiety and/or said nucleic acid molecule encoding said env moiety. A particularly preferred composition of the invention is selected from the group consisting of (i) a composition comprising a combination of a polymerase moiety and a core moiety as defined herein or a combination of nucleic acid molecules encoding said polymerase moiety and said core moiety; (ii) a composition comprising a combination of a core moiety and a env moiety as defined herein or a combination of nucleic acid molecules

encoding said core moiety and said env moiety; and (iii) a composition comprising a combination of a polymerase moiety, a core moiety and a env moiety as defined herein or a combination of nucleic acid molecules encoding said polymerase moiety, said core moiety and said env moiety.

The term "fusion" or "fusion protein" as used herein refers to the combination with one another of at least two polypeptides (or fragment(s) thereof) in a single polypeptide chain. Preferably, the fusion between the various polypeptides is performed by genetic means, i.e. by fusing in frame the nucleotide sequences encoding each of said polypeptides. By "fused in frame", it is meant that the expression of the fused coding sequences results in a single protein without any translational terminator between each of the fused polypeptides. The fusion can be direct (i.e. without any additional amino acid residues in between) or through a linker. The presence of a linker may facilitate correct formation, folding and/or functioning of the fusion protein. The present invention is not limited by the form, size or number of linker sequences employed and multiple copies of a linker sequence may be inserted at the junction between the fused polypeptides. Suitable linkers in accordance with the invention are 3 to 30 amino acids long and composed of repeats of amino acid residues such as glycine, serine, threonine, asparagine, alanine and/or proline (see for example Wiederrecht et al., 1988, Cell 54, 841; Aumailly et al., 1990 FEBS Lett. 262, 82; and Dekker et al., 1993, Nature 362, 852), e.g. Ser-Gly-Ser or Gly-Ser-Gly-Ser-Gly linker.

As used herein, the term "heterologous hydrophobic sequence" refers to a peptide of hydrophobic nature (that contains a high number of hydrophobic amino acid residues such as Val, Leu, Ile, Met, Phe, Tyr and Trp residues). "Heterologous" refers to a sequence that is foreign to the native HBV protein, polypeptide or peptide from which originate the selected HBV moiety. It can be a peptide foreign to an HBV virus (e.g. a peptide from a measle or a rabies virus) or a peptide from an HBV virus but in a position in which it is not ordinarily found within the viral genome. The heterologous hydrophobic sequence can be fused in frame at the N-terminus, at the C-terminus or within an HBV moiety and may play a role in polypeptide trafficking, facilitate polypeptide production or purification, prolong half-life, among other things. Suitable heterologous hydrophobic sequences in accordance with the invention are 15 to 100 amino acids long and contain a highly hydrophobic domain.

The term "vector" as used herein refers to both expression and non-expression vectors and includes viral as well as non viral vectors, including extrachromosomal vectors (e.g. multicopy plasmids) and integrating vectors designed for being incorporated into the host chromosome(s). Particularly important in the context of the invention are vectors for transferring nucleic acid molecule(s) in a viral genome (so-called transfer vectors), vectors for use in immunotherapy (i.e. which are capable of delivering the nucleic acid molecules to a host organism) as well as expression vectors for use in various expression systems or in a host organism.

As used herein, the term "viral vector" encompasses vector DNA as well as viral particles generated thereof. Viral vectors can be replication-competent, or can be genetically disabled so as to be replication-defective or replication-impaired. The term "replication-competent" as used herein encompasses replication-selective and conditionally-replicative viral vectors which are engineered to replicate better or selectively in specific host cells (e.g. tumoral cells).

As used herein, the term "regulatory sequence" refers to any sequence that allows, contributes or modulates the expression of a nucleic acid molecule in a given host cell or organism, including replication, duplication, transcription, splicing, translation, stability and/or transport of the nucleic acid or one of its derivative (i.e. mRNA) into a host cell or organism.

As used herein, the term "host cell" should be understood broadly without any limitation concerning particular organization in tissue, organ, or isolated cells. Such cells may be of a unique type of cells or a group of different types of cells and encompass bacteria, lower and higher eukaryotic cells as well as cultured cell lines, primary cells and proliferative cells. This term includes cells which can be or has been the recipient of the composition(s), nucleic acid molecule(s), vector(s) or infectious viral particle(s) of the invention and progeny of such cells.

The term "host organism" refers to a vertebrate, particularly a member of the mammalian species and especially domestic animals, farm animals, sport animals, and primates including humans. Preferably, the host organism is a patient suffering from a chronic HBV infection. The infecting HBV can be from the same genotype or serotype as at least one of the first, second or third HBV in use in the present invention.

As used herein, the term "isolated" refers to a protein, polypeptide, peptide, nucleic acid molecule, host cell or virus that is removed from its natural environment (i.e. separated from at least one other component(s) with which it is naturally associated).

As used herein a "therapeutically effective amount" is a dose sufficient for the alleviation of one or more symptoms normally associated with an HBV infection or any disease or condition caused by or associated with an HBV infection. When prophylactic use is concerned, this term means a dose sufficient to prevent or to delay the establishment of an HBV infection. "Therapeutic" compositions are designed and administered to a host organism already infected by an HBV with the goal of reducing or ameliorate at least one disease or condition caused by or associated with said HBV infection, eventually in combination with one or more conventional therapeutic modalities as described herein (e.g. treatment with nucleoside or nucleotide analogs). For example, a therapeutically effective amount for inducing an immune response could be that amount necessary to cause activation of the immune system (e.g. resulting in the development of an anti-HBV response). The term "cancer" encompasses any cancerous conditions including diffuse or localized tumors, metastasis, cancerous polyps as well as preneoplastic lesions (e.g. cirrhosis).

As used herein, a "pharmaceutically acceptable vehicle" is intended to include any and all carriers, solvents, diluents, excipients, adjuvants, dispersion media, coatings, antibacterial and antifungal agents, and absorption delaying agents, and the like, compatible with pharmaceutical administration

In accordance with the present invention, said polymerase, core and/or env moieties comprised or encoded by the composition of the invention may originate independently from any HBV genotype, strain or isolate identified at present time, such as those described above in connection with the term "HBV". Further, each of the polymerase, core and env moieties may originate from a native corresponding HBV protein or from a modified HBV polypeptide (e.g. modified so as to be representative of a specific genotype). Thus, the first, second and third HBV virus from which originate the polymerase, core and env moieties comprised or encoded by the composition of the present invention can be independently from the same or different genotypes, serotypes and/or isolates. For example, using HBV moieties originating from two or three different HBV genotypes permits to provide protection against a broader range of HBV genotypes.

In one embodiment, it could be interesting to adapt the immunogenic composition of the invention to a specific geographic region by using at least one HBV moiety from HBV genotype(s) that is/are endemic in this region. For illustrative purposes, genotypes A and C are the most prevalent in the United States whereas patients from Western European countries are infected mostly with genotypes A and D and those in the Mediterranean basin by genotype D. Limited data from India suggest that genotypes A and D are most common in India. On the other hand, genotypes B and C are the most prevalent in China. For example, a composition of the invention destined to European countries may comprise a polymerase moiety which originates from genotype A and core and env moieties which originate from genotype D or vice versa. Alternatively, the polymerase and core moieties can be from genotype A and env moiety from genotype D. As another example, a composition of the invention destined to European countries and the USA may comprise polymerase, core and env moieties which independently originate from genotype A, C and D. On the other hand, a composition of the invention destined to China may comprise or encode polymerase, core and env moieties which independently originate from genotype B and/or C.

One may also adapt the immunogenic composition of the invention to the population of patients to be treated. For example, genotype A is more common among American Whites and African Americans and those with sexually acquired HBV infections whereas genotypes B and C, on the other hand, are common among Asian Americans, patients born in Asia and those with maternal to infant transmission of HBV infection. HBV genotypes have also been associated with different clinical outcomes (Schaeffer et al., 2005, J. Viral. Hepatitis 12:111) with genotypes D and F being associated with more severe disease progression and a worse prognosis than genotype A (Sanchez-Tapias et al., 2002, Gastroenterology 123:1848). It is within the reach of the skilled person to adapt the composition of the invention according to the population and/or geographic region to be treated by choosing appropriate HBV genotypes, serotypes, strain and/or isolates.

According to an advantageous embodiment, at least two of the first, second and third HBV viruses, and preferably all, are from the same HBV genotype, and particularly from genotype D. Independently, they can originate from the same isolate, with a specific preference for the first, second and third HBV viruses being from HBV isolate Y07587. Preferably, the polymerase moiety in use in the present invention comprises an amino acid sequence which

exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with the amino acid sequence shown in SEQ ID NO: 1 or part(s) thereof comprising at least 450 amino acid residues. Alternatively or in combination, the core moiety in use in the present invention comprises an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with the amino acid sequence shown in SEQ ID NO: 2 or part(s) thereof comprising at least 100 amino acid residues. Alternatively or in combination, the one or more immunogenic domains of the env moiety in use in the present invention comprises an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with part(s) of 15-100 amino acid residues within the amino acid sequence shown in SEQ ID NO: 3.

Polymerase moiety

According to one embodiment, the polymerase moiety comprised or encoded by the composition of the invention is modified as compared to the corresponding native HBV polymerase.

An appropriate modification is the truncation of at least 20 amino acid residues and at most 335 amino acid residues normally present at the N-terminus of a native HBV polymerase. This modification is particularly relevant for compositions of the invention also comprising a second polypeptide so as to reduce or delete the overlapping portions between polymerase and core moieties. It is within the reach of the skilled person to adapt the truncation to the composition of the invention within the recited range at least 20 amino acid residues and at most 335 amino acid residues. With respect to a native HBV polymerase, the polymerase moiety used in the context of the present invention is advantageously truncated by at least 30 amino acid residues and at most 200 amino acid residues, desirably by at least 35 amino acid residues and at most 100 amino acid residues, preferably by at least 40 amino acid residues and at most 60 amino acid residues, and more preferably at least 45 and at most 50 amino acid residues, with a special preference for a truncation including the first 47 or the 46 amino acid residues following the initiator Met residue located at the N-terminus of a native HBV polymerase. Preferably, the truncation extends from position 1 (Met initiator) or 2 to position 47 of SEQ ID NO: 1.

A preferred embodiment is directed to a polymerase moiety comprising an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with the portion of the amino acid sequence shown in SEQ ID NO: 1 extending from approximately position 48 to approximately position 832; and even more preferably to a polymerase moiety comprising an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with the amino acid sequence shown in SEQ ID NO: 7.

Alternatively or in combination, the polymerase moiety in use in the invention is modified so as to exhibit a reduced reverse-transcriptase (RTase) enzymatic activity with respect to a native HBV polymerase. Advantageously, said reduction of RTase activity is provided by one or more mutation(s) in the domain responsible for RTase enzymatic activity.

Structural and functional organization of HBV polymerases was investigated almost 20 years ago (see for example Radziwill et al., 1990, J. Virol. 64:613). They are multifunctional proteins with three functional domains that catalyze the major steps in HBV replication (priming, DNA synthesis and removal of RNA templates) and a non essential spacer which are arranged in the following order:

- the first domain extending from position 1 to approximately position 177 is responsible for HBV terminal protein activity,
- the spacer is located from approximately position 178 to approximately position 335,
- the DNA polymerase domain extending from approximately position 336 to approximately position 679 is responsible for RTase activity, and
- the RNase H domain from approximately position 680 to the C-terminus (approximately position 832) is involved in RNase H activity.

Four residues have been involved in the RTase activity, forming a motif "YMDD" (for Tyr, Met, Asp and Asp residues) generally present from approximately position 538 to approximately position 541 of a native HBV polymerase (e.g. corresponding to positions 538, 539, 540 and 541 in SEQ ID NO: 1 and to positions 492, 493, 494 and 495 in SEQ ID NO: 7) and the present invention encompasses any mutation(s) in this motif or elsewhere in the

RTase domain that correlate with a significant reduction (i.e. at least a 10 fold reduction) or ablation of the RTase activity while retaining immunogenic properties. Representative examples of suitable RTase-deficient polymerase mutants are described in the literature, e.g. in Radziwill et al. (1990, J. Virol. 64:613), in Bartenschlager et al. (1990, J. Virol. 64:5324) and in Jeong et al. (1996, Biochem Bioph Res Commun. 223(2):264). Preferably, the polymerase moiety in use in the present invention comprises the substitution of the first Asp residue of the YMDD motif (corresponding to position 540 in SEQ ID NO: 1 and to position 494 of SEQ ID NO: 7) or of the amino acid residue located in an equivalent position in a native HBV polymerase to any amino acid residue other than Asp, with a special preference for a substitution to a His residue (D540H mutation). Reduction or ablation of RTase activity can be performed using assays well known in the art (e.g. the endogenous polymerase assays described in Radziwill et al., 1990, J Virol. 64:613).

Alternatively or in combination, the polymerase moiety in use in the present invention is modified so as to exhibit a reduced RNase H enzymatic activity with respect to a native HBV polymerase. Advantageously, said reduction of RNase H activity is provided by one or more mutation(s) in the domain responsible for RNase H enzymatic activity. As discussed above, the functional domain involved in RNase H activity has been mapped within the C-terminal portion of HBV polymerase, more particularly from position 680 to the C-terminal position 832 and the present invention encompasses any mutation(s) in this domain that correlate with a significant reduction (i.e. at least a 10 fold reduction) or ablation of the RNase H activity and which is not deleterious to immunogenic properties. Representative examples of suitable RNase H-deficient polymerase mutants are described in the literature, e.g. in Radziwill et al. (1990, J. Virol. 64:613), in Bartenschlager at al. (1990, J. Virol. 64:5324). Preferably, the polymerase moiety in use in the present invention comprises the substitution of the Glu residue corresponding to position 718 in SEQ ID NO: 1 and to position 672 of SEQ ID NO: 7 or of the amino acid residue located in an equivalent position in a native HBV polymerase to any amino acid residue other than Glu, with a special preference for a substitution to a His residue (E718H mutation). Reduction or ablation of RNase H activity can be performed using assays well known in the art (e.g. in vitro RNaseH activity assays or DNA-RNA tandem molecule analysis described in Radziwill et al., 1990, J Virol. 64:613 or in Lee et al., 1997, Biochem. Bioph. Res. Commun. 233(2):401).

Preferably, the polymerase moiety in use in the present invention is mutated so as to reduce or ablate both the RTase and the RNase activities and comprises the modifications discussed above in connection with these enzymatic functions, with a special preference for mutations D540H and E718H.

A preferred embodiment of the present invention is directed to a polymerase moiety comprising, alternatively essentially consisting of or alternatively consisting of an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with the amino acid sequence shown in SEQ ID NO: 8 or with the amino acid sequence shown in SEQ ID NO: 7 with the substitution of the Asp residue in position 494 to an His residue and the substitution of the Glu residue in position 672 to an His residue.

In another and preferred embodiment, the polymerase moiety in use in the present invention is fused in frame to heterologous hydrophobic sequence(s) so as to improve synthesis, and/or stability, and/or presentation at the surface of the expressing host cells and/or presentation to host's MHC class I and/or MHC class II antigens. Suitable heterologous hydrophobic sequences include sequences such as signal and/or trans-membrane peptides permitting to target the polymerase moiety in the secretion pathway. Such peptides are known in the art. Briefly, signal peptides are generally present at the N-terminus of membrane-presented or secreted polypeptides and initiate their passage into the endoplasmic reticulum (ER). They comprise 15 to 35 essentially hydrophobic amino acids which are then removed by a specific ER-located endopeptidase to give the mature polypeptide. Trans-membrane peptides are usually highly hydrophobic in nature and serve to anchor the polypeptides in the cell membrane (see for example Branden and Tooze, 1991, in Introduction to Protein Structure p. 202-214, NY Garland; WO99/03885). The choice of the trans-membrane and/or signal peptides which can be used in the context of the present invention is vast. They may be obtained from any membrane-anchored and/or secreted polypeptide (e.g. cellular or viral polypeptides) such as those of immunoglobulins, tissue plasminigen activator, insulin, rabies glycoprotein, the HIV virus envelope glycoprotein or the measles virus F protein or may be synthetic. The preferred site of insertion of the signal peptide is the N-terminus downstream of the codon for initiation of translation and that of the trans-membrane peptide is the C-

terminus, for example immediately upstream of the stop codon. Moreover, a linker peptide can be used to connect the signal and/or trans-membrane peptides to the polymerase moiety.

Other hydrophobic sequence(s) can be employed in the context of the invention, such as those generally present in envelope or membrane bound proteins, including HBsAg. Of particular interest in the context of the present invention is the fusion of the polymerase moiety with one or more of the immunogenic domains described herein (env1, env2, env3 and/or env4) which are of hydrophobic nature. The one or more hydrophobic domain(s) can be fused in frame at the N-terminus, at the C-terminus or within the polymerase moiety.

Preferably, in the context of the invention, the polymerase moiety in use in the invention is fused in frame to the signal and trans-membrane peptides of the rabies glycoprotein. As illustrated in the appended example section, said rabies signal sequence is fused in frame at the N terminus and said rabies transmembrane sequence is fused in frame at the C-terminus of said polymerase moiety. A most preferred embodiment is directed to a polymerase moiety comprising, alternatively essentially consist of, or alternatively consists of an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, particularly at least 90% of identity, preferably at least 95% of identity and more preferably 100% identity with the amino acid sequence shown in SEQ ID NO: 9.

Core moiety

Alternatively or in combination with the composition described above, the present invention also provides a composition comprising a core moiety originating from a second HBV. As described herein in connection with HBV virus, the core moiety in use in the invention originates from an HBV which is the same or different of the HBV virus from which originates the polymerase moiety. Preferably, the core and the polymerase moieties both originate from a genotype D HBV, with a special preference for the Y07587 HBV isolate or alternatively, from a HBV genotype prevalent in China (e.g. genotype B or C).

According to one embodiment, the core moiety in use in this invention can be a native HBV core (e.g. that shown in SEQ ID NO: 2) or a modified core as compared to the corresponding native HBV core that retains at least 100 amino acid residues of a core protein, with a specific preference for a core moiety comprising from 120 to 180 amino acid residues, desirably from

125 to 148 amino acid residues and preferably from 130 to 143 amino acid residues (e.g. approximately 140 amino acid residues).

An appropriate modification is a truncation. Desirably, the truncation encompasses at least 10 amino acid residues and at most 40 amino acid residues normally present at the C-terminus of a native HBV core or within the C-terminal part (i.e. the portion encompassing the last 40 amino acid residues). This modification is particularly relevant for compositions of the invention also comprising a polymerase moiety so as to reduce or delete the overlapping portions between polymerase and core moieties. It may also be relevant for deleting a NLS (nuclear localization signal) within this region of core and/or for inhibiting interaction with HBV polymerase. It is within the reach of the skilled person to adapt the truncation to the composition of the invention within the recited range at least 10 amino acid residues and at most 40 amino acid residues. Appropriate truncations include 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39 or 40 consecutive amino acid residues normally present at the C-terminus of a native HBV core or within its C-terminal portion. With respect to a native HBV core, the core moiety used in the context of the present invention is advantageously truncated by at least 20 amino acid residues and at most 40 amino acid residues, preferably by at least 30 amino acid residues and at most 38 amino acid residues, and more preferably by at least 34 amino acid residues and at most 37 amino acid residues located at the C-terminus of a native HBV or within the C-terminal part with a special preference for a truncation including the last 35 amino acid residues of a native HBV core (in other terms, the truncation extends from approximately position 149 to the C-terminus of the core polypeptide).

Of particular interest is a core moiety comprising an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with the portion of the amino acid sequence shown in SEQ ID NO: 2 extending from position 1 to approximately position 148 and even more preferably a core moiety comprising an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with the amino acid sequence shown in SEQ ID NO: 10.

Alternatively or in combination, the core moiety is modified so as to exhibit a reduced recognition of and/or interaction with an HBV envelope protein with respect to a native HBV core. Advantageously, said reduction of recognition/interaction is provided by one or more mutation(s) in a region located internally in the vinicity of residue 80 that is predicted to form an outer loop exposed on the surface of core particles (Argos et al., 1988, EMBO J. 7:819). Reduction or ablation of recognition of or interaction with a env protein can be performed using assays well known in the art (such as electron microscopy, analysis of nucleocapsids formation in cells, secreted virions following transient transfection in HuH7, as described in Seitz et al., 2007, EMBO J., 26: 416 or in Ponsel et al., 2003, J. Virol.77(1): 416).

A preferred modification comprises deletion of one or more amino acid residues in the region of the core extending from approximately position 75 to approximately position 85 (corresponding to residues 75-85 of SEQ ID NO: 2 and SEQ ID NO: 10), with a special preference for the deletion of the portion of the core moiety extending from approximately position 77 to approximately position 84 (corresponding to residues 77-84 of SEQ ID NO: 2 and SEQ ID NO: 10). A preferred core moiety comprises, alternatively essentially consists of or alternatively consists of an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with the amino acid sequence shown in SEQ ID NO: 11 or with the amino acid sequence shown in SEQ ID NO: 2 lacking residues 77-84.

Env moiety

Alternatively or in combination with the composition described above, the present invention also provides a composition comprising an env moiety. Said env moiety comprises one or more immunogenic domain(s) of at least 15 consecutive amino acid residues present in a HBs protein originating from a third HBV virus. Preferably, each of said immunogenic domains corresponds to a portion of at least 20 amino acids and at most 100 amino acids present in a HBsAg protein either a native one or a modified one (e.g. modified so as to be representative of a specific genotype). Each of the immunogenic domains can originate from the same or different HBV virus(es) which can be the same or different with respect to HBV viruses from which originate the core and polymerase moieties. Preferably, each of the env immunogenic domains originates from a genotype D HBV, and especially from the Y07587 HBV isolate or alternatively, from a HBV genotype prevalent in China (e.g. genotype B or C).

Advantageously, each of the one or more immunogenic domains comprises T cell epitopes specific for T helper (T_H) cells and/or for cytotoxic T (CTL) cells which can be restricted to various MHC class I and/or class II antigens (e.g. A2, A24, DR, DP, etc). Such epitopes have been described in the art (WO93/03764; WO94/19011; Desombere et al., 2000, Clin. Exp. Immunol 122:390; Loirat et al., 2000, J. Immunol. 165:4748; Schirmbeck et al., 2002, J. Immunol 168:6253; Depla et al., 2008, J. Virol. 82 :435) and it is within the reach of the skilled person to design suitable immunogenic domain(s) as described herein within the recited range of 15 to 100 amino acid residues which include(s) B, T_H and/or CTL epitopes from a native env protein (e.g. that shown in SEQ ID NO: 3). Preferably, the env moiety comprised in or encoded by the composition of the invention does not include any immunogenic domain(s) originating from preS1 and preS2 regions.

The present invention encompasses env moiety comprising one immunogenic domain as well as those comprising two, three or more.

Desirably, the one or more immunogenic domain(s) in use in the present invention is/are selected from the group consisting of:

- The portion of an env protein (HBsAg) extending from position 14-51 (env 1 domain);
- The portion of an env protein (HBsAg) extending from position 165-194 (env 2 domain);
- The portion of an env protein (HBsAg) extending from position 81-106 (env 3 domain);
- The portion of an env protein (HBsAg) extending from position 202-226 (env 4 domain); and
- Any combination thereof

Particularly suitable immunogenic domain(s) for use in the present invention comprises, alternatively essentially consists of or alternatively consists of an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with any of the amino acid sequences shown in SEQ ID NO: 12-15.

In the context of the invention, the combination of immunogenic domains can be in the form of a mixture of individual immunogenic domains in the composition of the invention or in the form of a fusion in frame between two or more immunogenic domains in any arrangement possible (e.g. fusion or mixture of env1-env2, env2-env1, env1-env3, env3-env1, env1-env4, env4-env1, env2-env-3, env3-env2, env2-env4, env4-env2, env3-env4, env4-env3, env1-env2-env3, env2-env1-env3, env1-env2-env4, etc.). Moreover, the combination can comprise a single copy or several copies thereof (e.g. env1-env-2-env1, env1-env-4, env1, etc. The fusion between each immunogenic domain can be direct or through a linker.

Env moieties of particular interest in the context of the invention comprise the fusion of two or three immunogenic domains shown in SEQ ID NO: 12-15, with a special preference for an env1-env2 fusion comprising, alternatively essentially consisting of or alternatively consisting of an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with the amino acid sequence shown in SEQ ID NO: 16 or an env1-env2-env4 fusion comprising, alternatively essentially consisting of or alternatively consisting of an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with the amino acid sequence shown in SEQ ID NO: 17.

According to a specific embodiment, the polymerase, core and/or env moieties comprised in or encoded by the composition of the invention can be fused in frame by pairs or all together. For example, one may envisage the fusion of the polymerase and env moieties in a single polypeptide chain. Alternatively, the core and env moieties can be fused in frame in a single polypeptide chain. Here again, the encoding nucleic acid sequences can be fused either directly or through a linker. Advantageously, the env moiety is fused in frame to the C-terminus of the core or polymerase moiety.

Preferred examples of fusion polypeptides of the core moiety with the env moiety are selected from the group consisting of:

- A polypeptide comprising, or alternatively consisting essentially of, or alternatively consisting of an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more

preferably at least 95% of identity, and even more preferably 100% identity with the amino acid sequence shown in SEQ ID NO: 18 (core*t-env1);

- A polypeptide comprising, or alternatively consisting essentially of, or alternatively consisting of an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with the amino acid sequence shown in SEQ ID NO: 19 (core*t-env1-env2); and
- A polypeptide comprising, or alternatively consisting essentially of, or alternatively consisting of an amino acid sequence which exhibits at least 80% of identity, advantageously at least 85% of identity, preferably at least 90% of identity, more preferably at least 95% of identity, and even more preferably 100% identity with the amino acid sequence shown in SEQ ID NO: 20 (core-env1-env2-env4) or with the portion of the amino acid sequence shown in SEQ ID NO: 20 starting at residue 1 and ending at residue 251 (core-env1-env2) or with the portion of the amino acid sequence shown in SEQ ID NO: 20 starting at residue 1 and ending at residue 221 (core-env1); or deleted versions thereof lacking residues 77-84 in the core moiety.

In the context of the invention, the polymerase moiety, the core moiety and/or the env moiety comprised or encoded by the composition of the invention may further comprise additional modifications. Suitable modifications are those which are beneficial to the synthesis, processing, stability and solubility of the resulting polypeptide (e.g. those aimed to modify potential cleavage sites, potential glycosylation sites and/or membrane anchorage as described herein) as well as those which are beneficial to the immunogenicity of the resulting composition (e.g. incorporation or fusion with one or more compounds capable of enhancing immunogenic properties). Such compounds capable of enhancing immunogenic properties have been described in the literature and include, without limitation, calreticulin (Cheng et al., 2001, J. Clin. Invest. 108:669), Mycobacterium tuberculosis heat shock protein 70 (HSP70) (Chen et al., 2000, Cancer Res. 60:1035), ubiquitin (Rodriguez et al., 1997, J. Virol. 71:8497), bacterial toxin such as the translocation domain of Pseudomonas aeruginosa exotoxin A (ETA(dIII)) (Hung et al., 2001 Cancer Res. 61:3698) as well as T helper epitope(s) such as Pan-Dr peptide (Sidney et al., 1994, Immunity 1:751), pstS1 GCG epitope (Vordermeier et al., 1992, Eur. J. Immunol. 22:2631), tetanus toxoid peptides P2TT (Panina-Bordignon et al., 1989, Eur. J. Immunol. 19:2237) and P30TT (Demotz et al., 1993, Eur. J. Immunol. 23:425),

influenza epitope (Lamb et al., 1982, Nature 300:66) and hemaglutinin epitope (Rothbard et al., 1989, Int. Immunol. 1:479).

Nucleic acid molecule

The present invention also provides isolated nucleic acid molecules encoding independently or in combination the polymerase, core and env moieties in use in the present invention as well as compositions comprising such nucleic acid molecule(s).

Of particular interest are:

- Nucleic acid molecules which encode polymerase moieties as described herein, with a special preference for those comprising the amino acid sequence shown in any of SEQ ID NO: 7, 8, 9 or the amino acid sequence shown in SEQ ID NO: 7 with the substitution of the Asp residue in position 494 to an His residue and the substitution of the Glu residue in position 672 to an His residue;
- Nucleic acid molecules which encode core moieties described herein, with a special preference for those comprising the amino acid sequence shown in SEQ ID NO: 10 or 11;
- Nucleic acid molecules which encode env moieties described herein, with a special preference for those comprising the amino acid sequence shown in any of SEQ ID NO: 12-17; and
- Nucleic acid molecules which encode fused core and env moieties described herein, with a special preference for those comprising the amino acid sequence shown in any of SEQ ID NO: 18, 19 or 20 or the portion of the amino acid sequence shown in SEQ ID NO: 20 starting at residue 1 and ending at residue 251 (core-env1-env2) or the portion of the amino acid sequence shown in SEQ ID NO: 20 starting at residue 1 and ending at residue 221 (core-env1); or deleted versions thereof lacking core residues 77-84 of SEQ ID NO: 20.

Desirably, the nucleic acid molecules of the invention can be optimized for providing high level expression in a particular host cell or organism, e.g. mammalian, yeast (e.g. *Saccharomyces cerevisiae*, *Saccharomyces pombe* or *Pichia pastoris*) or bacteria (e.g. *E. coli*, *Bacillus subtilis* or *Listeria*). It has been indeed observed that, when more than one codon is available to code for a given amino acid, the codon usage patterns of organisms are highly non-random (see for example Wada et al., 1992, Nucleic Acids Res. 20:2111) and the utilisation of codons may be markedly different between different hosts (see for example

Nakamura et al., 1996, Nucleic Acids Res. 24:214). As the nucleotide sequences used in the invention are mostly of viral origin (HBV), they may have an inappropriate codon usage pattern for efficient expression in host cells such as bacterial, lower or higher eukaryotic cells. Typically, codon optimisation is performed by replacing one or more "native" (e.g. HBV) codon corresponding to a codon infrequently used in the host cell of interest by one or more codon encoding the same amino acid which is more frequently used. It is not necessary to replace all native codons corresponding to infrequently used codons since increased expression can be achieved even with partial replacement. Moreover, some deviations from strict adherence to optimised codon usage may be made to accommodate the introduction of restriction site(s) into the resulting nucleic acid molecule.

Further to optimization of the codon usage, expression in the host cell or organism can further be improved through additional modifications of the nucleotide sequence. For example, the nucleic acid molecule of the invention can be modified so as to prevent clustering of rare, non-optimal codons being present in concentrated areas and/or to suppress or modify at least partially negative sequence elements which are expected to negatively influence expression levels. Such negative sequence elements include without limitation the regions having very high (>80%) or very low (<30%) GC content; AT-rich or GC-rich sequence stretches; unstable direct or inverted repeat sequences; RNA secondary structures; and/or internal cryptic regulatory elements such as internal TATA-boxes, chi-sites, ribosome entry sites, and/or splicing donor/acceptor sites. Another embodiment of the invention pertains to fragments of the nucleic acid molecule of the invention, e.g. restriction endonuclease and PCR-generated fragments. Such fragments can be used as probes, primers or fragments encoding an immunogenic portion of the first and/or second polypeptide.

A preferred nucleic acid molecule according to the invention is selected from the group consisting of:

- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 21 (encoding the truncated Pol of SEQ ID NO: 7);
- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 22 (encoding the mutated Pol of SEQ ID NO: 8);

- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 21 with the substitution of the G nucleotide in position 1480 to a C, of the G nucleotide in position 2014 to a C and of the A nucleotide in position 2016 to a T (encoding the truncated Pol of SEQ ID NO: 7 with the substitution of the D540H and E718H mutations);
- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 23 (encoding the truncated and mutated Pol-TMR of SEQ ID NO: 9);
- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 24 (encoding core*t-env1 of SEQ ID NO: 18);
- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 25 (encoding core*t-env1-env2 of SEQ ID NO: 19); and
- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 26 (encoding core-env1-env2-env4 of SEQ ID NO: 20) or with the portion of the nucleotide sequence shown in SEQ ID NO: 26 starting at nucleotide 1 and ending at nucleotide 753 (encoding core-env1-env2) or with the portion of the nucleotide sequence shown in SEQ ID NO: 26 starting at nucleotide 1 and ending at nucleotide 663 (encoding core-env1); or deleted versions thereof lacking the portion extending from the G in position 229 to the A in position 252 of SEQ ID NO: 26 (corresponding to deletion of residues 77-84 in the core moiety).

The nucleic acid molecules of the present invention can be generated using sequence data accessible in the art and the sequence information provided herein. The DNA sequence coding for each of the HBV polypeptides can be isolated directly from HBV-containing cells, cDNA and genomic libraries, viral genomes or any prior art vector known to include it, by conventional molecular biology or PCR techniques, and can be modified (e.g. as described herein). Alternatively, the nucleic acid molecule of the invention can also be generated by chemical synthesis in automatised process (e.g. assembled from overlapping synthetic oligonucleotides as described for example in Edge, 1981, Nature 292, 756; Nambair et al., 1984, Science 223:1299; Jay et al., 1984, J. Biol. Chem. 259:6311).

Also provided by the present invention are vectors comprising one or more nucleic acid molecule(s) of the present invention as well as compositions comprising such vector(s).

A variety of host-vector systems may be used in the context of the present invention, including bacteriophage, plasmid or cosmid vectors adapted to expression in prokaryotic host organisms such as bacteria (e.g. *E. coli, Bacillus subtilis or Listeria*); vectors adapted to expression in yeast (e.g. *Saccharomyces cerevisiae*, *Saccharomyces pombe*, *Pichia pastoris*); virus expression vectors (e.g. baculovirus) adapted to expression in insect cell systems (e.g. Sf 9 cells); virus or plasmid expression vectors (e.g. Ti plasmid, cauliflower mosaic virus CaMV; tobacco mosaic virus TMV) adapted to expression in plant cell systems; as well as plasmid and viral vectors adapted to expression in higher eukaryotes cells or organisms. Such vectors are largely described in the literature and commercially available (e.g. in Stratagene, Amersham Biosciences, Promega, etc.). Representative examples of suitable plasmid vectors include, without limitation, pREP4, pCEP4 (Invitrogene), pCI (Promega), pCDM8 (Seed, 1987, Nature 329, 840) and pMT2PC (Kaufman et al., 1987, EMBO J. 6:187), pVAX and pgWiz (Gene Therapy System Inc; Himoudi et al., 2002, J. Virol. 76:12735). A number of viral vectors can also be utilized in the context of the invention derived from a variety of different viruses (e.g. retrovirus, adenovirus, AAV, poxvirus, herpes virus, measle virus, foamy virus, alphavirus, vesicular stomatis virus and the like).

Of particular interest are adenoviral vectors which have a number of well-documented advantages for gene transfer or for recombinant production (for a review, see "Adenoviral vectors for gene therapy", 2002, Ed D. Curiel and J. Douglas, Academic Press). The adenoviral vectors for use in accordance with the present invention can be derived from a variety of human or animal sources (e.g. canine, ovine, simian adenovirus, etc). Any serotype can be employed with a special preference for human adenoviruses and a specific preference for subgenus C such as Ad2 (Ad2), 5 (Ad5), 6 (Ad6), subgenus B such as 11 (Ad11), 34 (Ad34) and 35 (Ad35) and subgenus D such as 19 (Ad19), 24 (Ad24), 48 (Ad48) and 49 (Ad49). It may also be advantageous to use animal Ad with a special preference for chimp Ad, such as chimp Ad3 (Peruzzi et al., 2009, Vaccine 27:1293) and chimp Ad63 (Dudareva et al., 2009, vaccine 27:3501) The cited adenovirus are available from the American Type Culture Collection (ATCC, Rockville, Md.) or have been the subject of numerous publications describing their sequence, organization and methods of producing, allowing the artisan to apply them (see for example US 6,133,028; US 6,110,735; WO 02/40665; WO

00/50573; EP 1016711; Vogels et al., 2003, J. Virol. 77:8263; WO00/70071; WO02/40665; WO2004/001032; WO2004/083418; WO2004/097016; WO2005/010149).

In one embodiment, the adenoviral vector of the present invention is replication-defective. Preferred replication-defective adenoviral vectors are E1-defective (see for example US 6,136,594 and US 6,013,638), with an E1 deletion extending from approximately positions 459 to 3328 or from approximately positions 459 to 3510 (by reference to the sequence of the human adenovirus type 5 disclosed in the GeneBank under the accession number M 73260 and in Chroboczek et al., 1992, Virol. 186:280). The cloning capacity can further be improved by deleting additional portion(s) of the adenoviral genome (all or part of the non essential E3 region or of other essential E2, E4 regions as described in WO94/28152; Lusky et al., 1998, J. Virol 72:2022).

The nucleic acid molecule(s) of the present invention can be inserted in any location of the adenoviral genome, with a specific preference for insertion in replacement of the E1 region. It/they may be positioned in sense or antisense orientation relative to the natural transcriptional direction of the region in question.

Other suitable viral vectors in the context of the invention are derived from poxviruses (see for example Cox et al. in "Viruses in Human Gene Therapy" Ed J. M. Hos, Carolina Academic Press). In the context of the present invention, a poxviral vector may be obtained from any member of the poxviridae, in particular canarypox, fowlpox and vaccinia virus, the latter being preferred. Suitable vaccinia viruses include without limitation the Copenhagen strain (Goebel et al., 1990, Virol. 179:247 and 517; Johnson et al., 1993, Virol. 196:381), the Wyeth strain and the modified Ankara (MVA) strain (Antoine et al., 1998, Virol. 244:365). The general conditions for constructing recombinant poxvirus are well known in the art (see for example EP 206 920; Mayr et al., 1975, Infection 3:6; Sutter and Moss, 1992, Proc. Natl. Acad. Sci. USA 89:10847; US 6,440,422). The nucleic acid molecule of the present invention is preferably inserted within the poxviral genome in a non-essential locus. Thymidine kinase gene is particularly appropriate for insertion in Copenhagen vaccinia vectors (Hruby et al., 1983, Proc. Natl. Acad. Sci USA 80:3411; Weir et al., 1983, J. Virol. 46:530) and deletion II or III for insertion in MVA vector (Meyer et al., 1991, J. Gen. Virol. 72:1031; Sutter et al., 1994, Vaccine 12:1032).

The present invention also encompasses vectors (e.g. plasmid DNA) complexed to lipids or polymers to form particulate structures such as liposomes, lipoplexes or nanoparticles. Such technologies are available in the art (see for example Arangoa et al., 2003, Gene Ther. 10:5; Eliaz et al., 2002, Gene Ther. 9:1230 and Betageri et al., 1993, "Liposome drug delivery systems", Technomic Publishing Company, Inc).

According to a preferred embodiment, the vectors of the invention comprise the nucleic acid molecule(s) of the invention in a form suitable for expression in a host cell or organism, which means that the nucleic acid molecule(s) is/are placed under the control of one or more regulatory sequences, appropriate to the vector and/or the host cell. It will be appreciated by those skilled in the art that the choice of the regulatory sequences can depend on such factors as the host cell, the level of expression desired, etc.

The promoter is of special importance and suitable promoters useful in the context of the present invention include constitutive promoters which direct expression of the nucleic acid molecule(s) in many types of host cell and those which direct expression of the nucleic acid molecule(s) only in certain host cells (e.g. liver-specific regulatory sequences) or in response to specific events or exogenous factors (e.g. by temperature, nutrient additive, hormone or other ligand).

Promoters suitable for constitutive expression in mammalian cells include but are not limited to the cytomegalovirus (CMV) immediate early promoter (Boshart et al., 1985, Cell 41:521), the RSV promoter, the adenovirus major late promoter, the phosphoglycero kinase (PGK) promoter (Adra et al., 1987, Gene 60:65), and the thymidine kinase (TK) promoter of herpes simplex virus (HSV)-1. Vaccinia virus promoters are particularly adapted for expression in poxviral vectors. Representative example include without limitation the vaccinia 7.5K, H5R, 11K7.5 (Erbs et al., 2008, Cancer Gene Ther. 15:18), TK, p28, p11 and K1L promoter, as well as synthetic promoters such as those described in Chakrabarti et al. (1997, Biotechniques 23:1094, in connection with the pSE/L promoter), Hammond et al. (1997, J. Virological Methods 66:135) and Kumar and Boyle (1990, Virology 179:151) as well as early/late chimeric promoters. Liver-specific promoters include without limitation those of HMG-CoA reductase (Luskey, 1987, Mol. Cell. Biol. 7:1881); sterol regulatory element 1 (SRE-1; Smith et al., 1990, J. Biol. Chem. 265:2306); albumin (Pinkert et al., 1987, Genes Dev. 1:268); phosphoenol pyruvate carboxy kinase (PEPCK) (Eisenberger et al., 1992, Mol. Cell Biol.

12:1396); human C-reactive protein (CRP) (Li et al., 1990, J. Biol. Chem. 265:4136); human glucokinase (Tanizawa et al., 1992, Mol. Endocrinology 6:1070); cholesterol 7-alpha hydroylase (CYP-7) (Lee et al., 1994, J. Biol. Chem. 269:14681); alpha-1 antitrypsin (Ciliberto et al., 1985, Cell 41:531); insulin-like growth factor binding protein (IGFBP-1) (Babajko et al., 1993, Biochem Biophys. Res. Comm. 196:480); human transferrin (Mendelzon et al., 1990, Nucleic Acids Res. 18:5717); collagen type I (Houglum et al., 1994, J. Clin. Invest. 94:808) and FIX (US 5,814,716) genes.

Those skilled in the art will appreciate that the regulatory elements controlling the expression of the nucleic acid molecule(s) of the invention may further comprise additional elements for proper initiation, regulation and/or termination of transcription (e.g. polyA transcription termination sequences), mRNA transport (e.g. nuclear localization signal sequences), processing (e.g. splicing signals), and stability (e.g. introns and non-coding 5' and 3' sequences), translation (e.g. an initiator Met, tripartite leader sequences, ribosome binding sites, Shine-Dalgamo sequences, etc.) into the host cell or organism and purification steps (e.g. a tag).

In accordance with the present invention, the nucleic acid molecules of the present invention encoding said polymerase moiety, said core moiety and/or said env moiety can be carried by the same vector or at least two vectors (e.g. two or three independent vectors). Thus the present invention encompasses a vector that carries the nucleic acid molecules encoding said polymerase moiety, said core moiety and said env moiety as well as independent vectors, each carrying only one or two of the nucleic acid molecules encoding said polymerase moiety, said core moiety and said env moiety. Such vector(s) are also provided by the present invention as well as compositions comprising such vector(s). When using different vectors, they can be from different origin or from the same origin. For example, one may envisage expression of one HBV moiety from a defective poxvirus (e.g. MVA) and expression of the two other moieties from another poxvirus vector (e.g. a Copenhagen vector). As another example, one may envisage a composition comprising an adenoviral vector encoding the polymerase moiety and an adenoviral vector encoding the core and env moieties. Alternatively, expression from different viral vectors (e.g. expression of the polymerase moiety from an adenoviral vector and expression of core and/or env moieties from MVA or vice versa) is also suitable in the context of the invention as well as expression of the HBV moieties from plasmid and viral vector(s).

Preferred embodiments of the invention are directed to vectors selected from the group consisting of:

(i) A MVA vector comprising a nucleic acid molecule placed under the control of a vaccinia promoter such as the 7.5K promoter, and encoding a polymerase moiety comprising an amino acid sequence as shown in SEQ ID NO: 7, 8 or 9 or in SEQ ID NO: 7 with the substitution of the Asp residue in position 494 to an His residue and the substitution of the Glu residue in position 672 to an His residue. Preferably, said nucleic acid molecule is inserted in deletion III of the MVA genome.

(ii) A MVA vector comprising a nucleic acid molecule placed under the control of a vaccinia promoter such as the pH5r promoter and encoding a core moiety and an env moiety comprising an amino acid sequence as shown in SEQ ID NO: 18 or 19. Preferably, said nucleic acid molecule is inserted in deletion III of the MVA genome.

(iii) An E1-defective Ad vector comprising inserted in place of the E1 region a nucleic acid molecule placed under the control of the CMV promoter and encoding a polymerase moiety comprising an amino acid sequence as shown in SEQ ID NO: 7, 8 or 9 or in SEQ ID NO: 7 with the substitution of the Asp residue in position 494 to an His residue and the substitution of the Glu residue in position 672 to an His residue.

(iv) An E1-defective Ad vector comprising inserted in place of the E1 region a nucleic acid molecule placed under the control of the CMV promoter and encoding a core moiety and an env moiety comprising an amino acid sequence as shown in SEQ ID NO: 18, 19 or 20 or the portion of SEQ ID NO: 20 starting at residue 1 and ending at residue 251 (core-env1-env2) or the portion of SEQ ID NO: 20 starting at residue 1 and ending at residue 221 (core-env1).

As well as to a composition comprising vectors (i) and (ii) or (iii) and (iv).

If needed, the vector or composition of the invention can further comprise one or more transgene(s), e.g. a gene of interest to be expressed together with the nucleic acid molecule(s) of the invention in a host cell or organism. Desirably, the expression of the transgene has a therapeutic or protective activity to an HBV infection or any disease or condition caused by or associated with an HBV infection or is able to enhance immunogenicity of the composition of the invention. Suitable transgenes include without limitation one or more additional HBV polypeptide(s)/peptide(s) or encoding nucleic acid molecule(s) such as the X protein or fragment thereof, immunomodulators such as cytokine (e.g. IL-2, IL-7, IL-12, IL-15, IL-18,

IL-21, IFNg), fusion of cytokines (such as those described in WO2005/14642) or their encoding nucleic acid molecules as well as suicide gene products or encoding nucleic acid molecules particularly useful in the context of treating liver carcinoma (such as cytosine deaminase (CDase), uracil phosphoribosyl transferase (UPRTase), the *FCU-1* gene product (described in WO 99/54481) and derivatives thereof (described in WO2006/048768) which are to be used with the prodrug 5-fluorocytosine (5-FC). If a transgene is used, it can be expressed in the form of a fusion with any of the nucleic acid molecule of the invention or be expressed independently under the control of appropriate regulatory elements. Further, it can be inserted in any location of the vector of the invention or in an independent vector which is used in combination with the vector(s) or composition of the invention.

In another aspect, the present invention provides infectious viral particles comprising the nucleic acid molecules or vectors of the present invention as well as compositions comprising such infectious viral particles.

Typically, such viral particles are produced by a process comprising the steps of:

(a) introducing the viral vector of the invention into a suitable cell line,

(b) culturing said cell line under suitable conditions so as to allow the production of said infectious viral particle,

(c) recovering the produced infectious viral particle from the culture of said cell line, and

(d) optionally purifying said recovered infectious viral particle.

When the viral vector is defective, the infectious particles are usually produced in a complementation cell line or via the use of a helper virus, which supplies *in trans* the non functional viral genes. For example, suitable cell lines for complementing E1-deleted adenoviral vectors include the 293 cells (Graham et al., 1997, J. Gen. Virol. 36, 59-72) as well as the HER-96 and PER-C6 cells (e.g. Fallaux et al., 1998, Human Gene Ther. 9, 1909-1917; WO97/00326). Cells appropriate for propagating poxvirus vectors are avian cells, and most preferably primary chicken embryo fibroblasts (CEF) prepared from chicken embryos obtained from fertilized eggs.

The infectious viral particles may be recovered from the culture supernatant or from the cells after lysis. They can be further purified according to standard techniques (chromatography,

ultracentrifugation in a cesium chloride gradient as described for example in WO96/27677, WO98/00524, WO98/22588, WO98/26048, WO00/40702, EP1016700 and WO00/50573).

The present invention also encompasses vectors or viral particles that have been modified to allow preferential targeting to a particular target cell (see for example Wickam et al., 1997, J. Virol. 71, 8221-8229; Arnberg et al., 1997, Virol. 227, 239-244; Michael et al., 1995, Gene Therapy 2, 660-668; WO94/10323; WO02/96939 and EP 1 146 125). A characteristic feature of targeted vectors and viral particles of the invention is the presence at their surface of a ligand capable of recognizing and binding to a cellular and surface-exposed component such as a cell-specific marker (e.g. an HBV-infected cell), a tissue-specific marker (e.g. a liver-specific marker), as well as a viral (e.g. HBV) antigen. Examples of suitable ligands include antibodies or fragments thereof directed to an HBV antigenic domain. Cell targeting can be carried out by genetically inserting the ligand into a polypeptide present on the surface of the virus (e.g. adenoviral fiber, penton, pIX or vaccinia p14 gene product).

The invention also relates to host cells which comprise the nucleic acid molecules, vectors or infectious viral particles of the invention as well as compositions comprising such host cells. In the context of the invention, host cells include prokaryotic cells, lower eukaryotic cells such as yeast, and other eukaryotic cells such as insect cells, plant and mammalian (e.g. human or non-human) cells as well as complementing cells capable of complementing at least one defective function of a replication-defective vector of the invention (e.g. adenoviral vector) such as 293 and PERC.6 cells.

According to a specific embodiment of the invention, the host cell can be further encapsulated. Cell encapsulation technology has been previously described (Tresco et al., 1992, ASAIO J. 38, 17-23; Aebischer et al., 1996, Human Gene Ther. 7, 851-860).

Still a further aspect of the present invention is a method for producing recombinant polymerase, core and/or env moieties, employing the vectors, infectious viral particles and/or host cells of the invention. The method of the present invention comprises (a) introducing a vector or an infectious viral particle of the invention into a suitable host cell to produce a transfected or infected host cell, (b) culturing *in-vitro* said transfected or infected host cell under conditions suitable for growth of the host cell, (c) recovering the polymerase, core

and/or env moiety(ies) from the cell culture, and (d) optionally, purifying the recovered polypeptide(s).

It is expected that those skilled in the art are knowledgeable in the numerous expression systems available for producing the HBV moiety(ies) in appropriate host cells and of the methods for introducing a vector or an infectious viral particle into a host cell. Such methods include, but are not limited to, microinjection (Capechi et al., 1980, Cell 22:479), $CaPO_4$-mediated transfection (Chen and Okayama, 1987, Mol. Cell Biol. 7:2745), DEAE-dextran-mediated transfection, electroporation (Chu et al., 1987, Nucleic Acid Res. 15:1311), lipofection/liposome fusion (Felgner et al., 1987, Proc. Natl. Acad. Sci. USA 84 :7413), particle bombardement (Yang et al., 1990, Proc. Natl. Acad. Sci. USA 87:9568), gene guns, transduction, viral infection as well as direct administration into a host organism via various means.

The vectors of the invention can be used in association with transfection reagents in order to facilitate introduction of the vector in the host cell, such as polycationic polymers (e.g. chitosan, polymethacrylate, PEI, etc) and cationic lipids (e.g.DC-Chol/DOPE, transfectam lipofectin now available from Promega). Moreover, as discussed above, recombinant DNA technologies can be used to improve expression of the nucleic acid molecule(s) in the host cell or organism, e.g. by using high-copy number vectors, substituting or modifying one or more transcriptional regulatory sequences (e.g. promoter, enhancer and the like), optimising the codon usage of the nucleic acid molecule(s) to the host cell, and suppressing negative sequences that may destabilize the transcript.

Host cells of the present invention can be cultured in conventional fermentation bioreactors, flasks, and petri plates. Culturing can be carried out at a temperature, pH and oxygen content appropriate for a given host cell. No attempts to describe in detail the various methods known for the production of proteins in prokaryote and eukaryote cells will be made here.

The HBV moiety(ies) can then be purified by well-known purification methods including ammonium sulfate precipitation, acid extraction, gel electrophoresis; filtration and chromatographic methods (e.g. reverse phase, size exclusion, ion exchange, affinity, phosphocellulose, hydrophobic-interaction, hydroxylapatite, or high performance liquid chromatography). The conditions and technology to be used depend on factors such as net

charge, molecular weight, hydrophobicity, hydrophilicity and will be apparent to those having skill in the art. Moreover, the level of purification will depend on the intended use.

In another aspect, this invention provides a composition comprising at least one of the polymerase, core and/or env moiety(ies), the encoding nucleic acid molecules, the vector(s), the infectious viral particle(s), or the host cell of the invention (also referred herein to "active agent") or any combination thereof (e.g. combination of polypeptides or vectors/viral particles encoding various HBV moieties as described herein or combination of different genotypes). Preferably, the composition is a pharmaceutical composition which comprises a pharmaceutically acceptable vehicle further to a therapeutically effective amount of the active agent(s).

Suitably, the composition of the invention comprises a diluent appropriate for human or animal use. It is preferably isotonic, hypotonic or weakly hypertonic and has a relatively low ionic strength. Representative examples include sterile water, physiological saline (e.g. sodium chloride), Ringer's solution, glucose, trehalose or saccharose solutions, Hank's solution, and other aqueous physiologically balanced salt solutions (see for example the most current edition of Remington : The Science and Practice of Pharmacy, A. Gennaro, Lippincott, Williams&Wilkins). The composition of the invention is suitably buffered in order to be appropriate for human use at a physiological or slightly basic pH (e.g. from approximately pH 7 to approximately pH 9). Suitable buffers include without limitation phosphate buffer (e.g. PBS), bicarbonate buffer and/or Tris buffer.

The composition can also contain other pharmaceutically acceptable excipients for providing desirable pharmaceutical or pharmacodynamic properties, including for example modifying or maintaining the pH, osmolarity, viscosity, clarity, colour, sterility, stability, rate of dissolution of the formulation, modifying or maintaining release or absorption into an the human or animal organism, promoting transport across the blood barrier or penetration in a particular organ (e.g. liver). Suitable excipients include amino acids.

The pharmaceutically acceptable vehicles included in the composition of the invention must also permit to preserve its stability under the conditions of manufacture and long-term storage (i.e. at least one month) at freezing (e.g. -70°C, -20°C), refrigerated (e.g. 4°C) or ambient

temperatures. In this respect, formulations which are particularly adapted to the composition of the invention include:

- 1M saccharose, 150 mM NaCl, 1mM $MgCl_2$, 54 mg/l Tween 80, 10 mM Tris pH 8.5 (especially when the active agent is an adenoviral vector), and
- 10 mg/ml mannitol, 1 mg/ml HSA, 20 mM Tris, pH 7.2, and 150 mM NaCl
- physiological saline

In addition, the composition of the invention may comprise one or more adjuvant(s) suitable for systemic or mucosal application in humans. Preferably, the adjuvant is capable of stimulating immunity to the composition of the invention, especially a T cell-mediated immunity e.g. through the toll-like receptors (TLR), such as TLR-7, TLR-8 and TLR-9. Representative examples of useful adjuvants include without limitation alum, mineral oil emulsion such as Freunds complete and incomplete (IFA), lipopolysaccharide or a derivative thereof (Ribi et al., 1986, Immunology and Immunopharmacology of Bacterial Endotoxins, Plenum Publ. Corp., NY, p407-419), saponins such as QS21 (Sumino et al., 1998, J.Virol. 72:4931; WO 98/56415), imidazo-quinoline compounds such as Imiquimod (Suader, 2000, J. Am Acad Dermatol. 43:S6), S-27609 (Smorlesi, 2005, Gene Ther. 12:1324) and related compounds such as those described in WO2007/147529, cytosine phosphate guanosine oligodeoxynucleotides such as CpG (Chu et al., 1997, J. Exp. Med. 186:1623; Tritel et al., 2003, J. Immunol. 171:2358) and cationic peptides such as IC-31 (Kritsch et al., 2005, J. Chromatogr Anal. Technol Biomed Life Sci 822:263).

The composition of the present invention is suitable for a variety of modes of administration, including systemic, topical and localized administration. Injection can be performed by any means, for example by subcutaneous, intradermal, intramuscular, intravenous, intraperitoneal, intratumoral, intravascular, intraarterial injection or by direct injection into an artery (e.g. by hepatic artery infusion) or a vein feeding liver (e.g. injection into the portal vein). Injections can be made with conventional syringes and needles, or any other appropriate devices available in the art. Alternatively the composition of the present invention may be administered via a mucosal route, such as the oral/alimentary, intranasal, intratracheal, intrapulmonary, intravaginal or intra-rectal route. Administration in the respiratory tract can be performed through nebulisation or aerosolization of droplet, spray, or dry powdered compositions using a pressured container (e.g. with a suitable propellant such as dichlorodifluoromethane, propane, nitrogen and the like), or in a non-pressurized dispenser.

Topical administration can also be performed using transdermal means (e.g. patch and the like). In the context of the invention, a preferred composition is formulated for intramuscular and subcutaneous routes.

The composition of the invention can be in various forms, e.g. solid, liquid or frozen. Solid (e.g. dry powdered or lyophilized) compositions can be obtained by a process involving vacuum drying and freeze-drying. For mucosal administration, the compositions can be formulated as gastroresistant capsules and granules for oral administration, suppositories for rectal or vaginal administration, eventually in combination with absorption enhancers useful to increase the pore size of the mucosal membranes. Such absorption enhancers are typically substances having structural similarities to the phospholipid domains of the mucosal membranes such as sodium deoxycholate, sodium glycocholate, dimethyl-beta-cyclodextrin, lauryl-1-lysophosphatidylcholine).

The appropriate dosage can be adapted as a function of various parameters, in particular the mode of administration; the composition employed; the age, health, and weight of the host organism; the nature and extent of symptoms; kind of concurrent treatment; the frequency of treatment; and/or the need for prevention or therapy. Further refinement of the calculations necessary to determine the appropriate dosage for treatment is routinely made by a practitioner, in the light of the relevant circumstances. For general guidance, suitable dosage for a virus-comprising composition varies from about 10^5 to about 10^{13} vp (viral particles), iu (infectious unit) or pfu (plaque-forming units) depending on the vector and the quantitative technique used. Techniques available to evaluate the quantity of vp, iu and pfu present in a sample are conventional in the art. For example, the number of adenoviral particles (vp) is usually determined by measuring the A260 absorbance, iu titers by quantitative DBP immunofuorescence and pfu by counting the number of plaques following infection of permissive cells. Preferably the vp/iu ratio is below 100 in accordance with FDA guidelines. Doses from about $5x10^5$ to about 10^9 pfu are preferred for MVA-based composition with a specific preference for doses of about 10^7, about $5x10^7$, about 10^8 or about $5x10^8$ pfu. Concerning Ad-based compositions, preferred doses contain from about 10^6 to about 10^{12} vp, with a specific preference for doses of about 10^9, about $5x10^9$, about 10^{10}, about $5x10^{10}$ vp or about 10^{11} vp. A composition based on vector plasmids may be administered in doses of between 10 µg and 20 mg, advantageously between 100 µg and 2 mg. A protein composition may be administered in one or more doses of between 10 ng and 20 mg, with a special

preference for a dosage from about 0.1 µg to about 2 mg of the therapeutic protein per kg body weight. The administration may take place in a single dose or a dose repeated one or several times after a certain time interval.

The composition of the invention may be employed in methods for treating a variety of diseases and pathologic conditions, especially those caused by or associated with an HBV infection. As used herein, the term "treatment" or "treating" encompasses prophylaxis and/or therapy. It is especially useful for treating HBV chronic infection and/or liver lesions in HBV-infected patients including cirrhosis and liver cancer. Preferably, upon introduction into a host organism according to the modalities described herein, the composition of the invention provides a therapeutic benefit to the treated host as compared to before treatment. The therapeutic benefit can be evidenced by a number of ways, for instance a decrease of HBV viral load detected in blood, plasma, sera or liver of an infected subject, and/or by the detection of an anti-HBV immune response (e.g. production of anti-HBV antibodies and/or T cell-mediated immunity) or by the delay of the symptoms associated with an HBV infection (e.g. delay in the development of liver cirrhosis or cancer), or by a decrease of liver inflammation/steatosis/fibrosis conditions typically associated with HBV infection or by an improved response of the individual to conventional therapies.

Accordingly, the present invention also encompasses the use of at least one of the HBV moieties, nucleic acid molecules, vectors, infectious viral particles, host cells or compositions of the invention for the preparation of a drug intended for treating or preventing HBV infections, HBV-associated diseases and pathologic conditions, according to the modalities described herein.

The present invention also provides a method for the treatment or prevention of HBV infections, in particular chronic HBV infection, HBV-associated diseases and pathologic conditions, comprising administering to a human or animal organism in need thereof a therapeutically effective amount of at least one of the HBV moieties, nucleic acid molecules, vectors, infectious viral particles, host cells or compositions of the invention.

The method or use of the invention comprises one or more administrations (1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc) of a therapeutically effective amount of said active agent(s), said administrations being separated from each other by an appropriate period of time and being carried out by the same route of administration or by different routes of administrations (e.g. intramuscular and

subcutaneous routes), at the same site or at different sites. Three administrations separated from each other by 3 to 10 days (e.g. 3 weekly administrations) are particularly suitable for MVA-based compositions and vector(s). This first series of administration can be followed by one or more subsequent administration(s) using the same active agent(s) which can take place one or several months so as to recall the anti-HBV immune response primed by the 3 sequential administrations. With respect to Ad-based compositions and vector(s), a preferred method or use includes one administration, eventually followed by one or two subsequent administration(s) one and 6 months later.

If desired, the method or use of the invention can be carried out in combination with one or more conventional therapeutic modalities (e.g. radiation, chemotherapy and/or surgery). The use of multiple therapeutic approaches provides the patient with a broader based intervention. In one embodiment, the method of the invention can be preceded or followed by a surgical intervention. In another embodiment, it can be preceded or followed by radiotherapy (e.g. gamma radiation). Those skilled in the art can readily formulate appropriate radiation therapy protocols and parameters which can be used (see for example Perez and Brady, 1992, Principles and Practice of Radiation Oncology, 2nd Ed. JB Lippincott Co; using appropriate adaptations and modifications as will be readily apparent to those skilled in the field).

In still another embodiment, the method or use of the invention is associated to chemotherapy with one or more HBV drugs which are conventionally used for treating or preventing HBV infections, HBV-associated diseases and pathologic conditions. Their administration may precede, be concomitant, or subsequent to the administration of the active agent in use in the invention. Representative examples of HBV drugs include without limitation polymerase inhibitors, RNase H inhibitors, nucleoside analogs, nucleotide analogs, TLR agonists, N-glycosylation inhibitors, siRNA, antisense oligonucleotides, anti-HBV antibodies, immune modulators, therapeutic vaccines and antitumor agents usually used in the treatment of HBV-associated liver cancers (e.g. adriamycin, adriamicin with lipiodol or sorasenib). Examples of suitable therapeutic vaccines include without limitation recombinant antigens, VLPs, vectors or synthetic peptides based on or encoding HBV proteins (Core, preS1, PreS2, S and/or polymerase) which are particularly suited to trigger an anti-HBV humoral response. Such HBV drugs can be provided in a single dose or, alternatively, in multiple doses according to standard protocols, dosages and regimens over several hours, days and/or weeks. A particularly suitable method or use according to the invention is used in combination with

standard of care which can be before, in parallel or subsequently to the method or use of the invention. Although such standard of care may vary from patient to patient, it generally comprises treatment with cytokines (e.g. IFNa, pegylated IFNa2) and/or with,nucleotide or nucleoside analogs such as lamivudine, entecavir, telbivudine, adefovir, dipivoxil or tenofovir.

In another embodiment, the method or use of the invention is carried out according to prime boost therapeutic modality which comprises sequential administrations of one or more priming composition(s) and one or more boosting composition(s). Typically, the priming and the boosting compositions use different vehicles which comprise or encode at least an antigenic domain in common. Moreover, the priming and boosting compositions can be administered at the same site or at alternative sites by the same route or by different routes of administration. For example, compositions based on polypeptide can be administered by a mucosal route whereas compositions based on vectors are preferably injected, e.g. subcutaneous injection for a MVA vector, intramuscular injection for a DNA plasmid and subcutaneous or intramuscular injection for an adenoviral vector.

The present invention also provides a method of inducing or stimulating an immune response against HBV in a host organism comprising administering to said organism at least one of the HBV moieties, nucleic acid molecules, vectors, infectious viral particles, host cells or compositions of the invention so as to induce or stimulate said immune response. The immune response can be a specific and/or a nonspecific, humoral and/or cellular and, in this context, it can be CD4+ or CD8+-mediated or both. The immune response is preferably a T cell response directed to an HBV antigen.

The ability of the method of the invention to induce or stimulate an anti-HBV immune response upon administration in an animal or human organism can be evaluated either *in vitro* or *in vivo* using a variety of assays which are standard in the art. For a general description of techniques available to evaluate the onset and activation of an immune response, see for example Coligan et al. (1992 and 1994, Current Protocols in Immunology ; ed J Wiley & Sons Inc, National Institute of Health). Measurement of cellular immunity can be performed by measurement of cytokine profiles secreted by activated effector cells including those derived from CD4+ and CD8+ T-cells (e.g. quantification of IL-10 or IFNg-producing cells by ELIspot), by determination of the activation status of immune effector cells (e.g. T cell

proliferation assays by a classical [^{3}H] thymidine uptake), by assaying for antigen-specific T lymphocytes in a sensitized subject (e.g. peptide-specific lysis in a cytotoxicity assay). The ability to stimulate a humoral response may be determined by antibody binding and/or competition in binding (see for example Harlow, 1989, Antibodies, Cold Spring Harbor Press). The method of the invention can also be further validated in animal models challenged with an appropriate infectious or tumor-inducing agent (e.g. a vaccinia virus or a Listeria Monocytogenes bacteria expressing HBV gene products) to determine neutralization of the infectious or tumor-inducing agent and eventually partial resistance to the associated symptoms, reflecting an induction or an enhancement of an anti-HBV immune response. Testing and validation of the compositions of the invention are also illustrated in the appended Example section.

In another aspect, the invention provides a kit of parts for use in the treatment or prevention of HBV infections, including chronic HBV infection, HBV-associated diseases and pathologic conditions according to the modalities described herein, and more particularly for inducing or generating an immune response in a subject infected with HBV, wherein said kit comprises a plurality of active agents selected from the group consisting of the HBV moieties, nucleic acid molecules, vectors, infectious viral particles, host cells and compositions described herein. Desirably, said plurality of active agents is provided in the form of separate polypeptides or separate vectors and administration of each of the active agents can take place simultaneously (at the same time) or separately (one following the other(s) after a certain time interval), by the same route or different routes of administration and at the same site (or close vicinity) or different sites and using the same dose or different doses.

Of particular interest in the present invention is a kit of parts which comprises a first vector comprising a nucleic acid molecule encoding the polymerase moiety as defined herein and a second vector comprising a nucleic acid molecule encoding the core moiety and/or the env moiety as defined herein.

According to a preferred embodiment, said first vector is a MVA vector comprising a nucleic acid molecule placed under the control of a vaccinia promoter such as the 7.5K promoter and encoding a polymerase moiety comprising an amino acid sequence as shown in SEQ ID NO: 7, 8 or 9 or in SEQ ID NO:7 with the substitution of the Asp residue in position 494 to an His residue and the substitution of the Glu residue in position 672 to an His residue ; and said second vector is a MVA vector comprising a nucleic acid molecule placed under the control

of a vaccinia promoter such as the pH5r promoter and encoding a core moiety and an env moiety comprising an amino acid sequence as shown in SEQ ID NO: 18 or 19.

According to another preferred embodiment, said first vector is an adenovirus vector comprising a nucleic acid molecule placed under the control of a suitable promoter such as the CMV promoter and encoding a polymerase moiety comprising an amino acid sequence as shown in SEQ ID NO: 7 or SEQ ID NO: 8 or SEQ ID NO: 7 with the substitution of the Asp residue in position 494 to an His residue and the substitution of the Glu residue in position 672 to an His residue ; and said second vector is an adenovirus vector comprising a nucleic acid molecule placed under the control of a suitable promoter such as the CMV promoter and encoding a core moiety and an env moiety comprising an amino acid sequence as shown in SEQ ID NO: 18, 19 or 20 or the portion of SEQ ID NO: 20 starting at residue 1 and ending at residue 251 (core-env1-env2) or the portion of SEQ ID NO: 20 starting at residue 1 and ending at residue 221 (core-env1).

The kit of parts of the present invention may further comprise a third vector expressing an immunomodulator as defined above. For illustrative purposes, preferred doses of each active ingredient comprised in the kit of parts is of the same order as that described above in connection with the composition of the invention, with a specific preference for a dose from $5x10^5$ to 10^9 pfu for each poxviral or MVA vector and from about 10^6 to about 10^{12} vp for each adenoviral vector.

The invention also provides antibodies that selectively bind to the HBV moieties in use in the present invention or peptide fragments thereof. As used herein, an antibody selectively binds a target peptide when it binds the target peptide and does not significantly bind to unrelated proteins. In certain cases, it would be understood that antibody binding to the peptide is still selective despite some degree of cross-reactivity. It is nonetheless preferred that the antibody of the invention does not bind with high affinity or high selectivity to HBV native protein.

As used herein, an antibody is defined in terms consistent with that recognized within the art. The antibodies of the present invention include polyclonal antibodies and monoclonal antibodies, as well as fragments of such antibodies, including, but not limited to, Fab or F(ab').sub.2, and Fv fragments. Antibodies of the present invention can be produced using conventional techniques in the art, e.g. following administering to an animal an effective amount of any of the HBV moieties described herein and/or a peptide fragment thereof. Antibodies are preferably prepared from regions or discrete fragments of the HBV moieties

comprising unique sequences, such as the ones directed to the modifications described herein introduced into the native HBV proteins.

Antibodies of the present invention have a variety of potential uses that are within the scope of the present invention. For example, such antibodies can be used (a) as reagents in assays to detect the first or second polypeptides of the present invention, (b) as reagents in assays to detect the presence of a HBV virus in a biological sample, and/or (c) as tools to recover the recombinantly-produced HBV moieties from a mixture of proteins and other contaminants (e.g. by permitting purification by affinity chromatography or immunoprecipitation from cultured host cells).

The present invention also relates to a method for the detection and/or quantification an HBV virus or an anti-HBV antibody in a biological sample (e.g. plasma, serum, tissue) taken from an individual susceptible to be infected by said HBV virus using at least one of the HBV moieties nucleic acid molecules, vectors, infectious viral particles, host cells, compositions or antibodies of the invention.

In one embodiment, the method is more particularly suited for the detection and/or quantification an HBV virus in a biological sample and comprises at least the steps of bringing said biological sample into contact with at least one of the antibodies of the invention under conditions allowing the formation of a complex between the virus and the antibody and detecting and/or quantifying the formation of said complex by any appropriate means.

In another embodiment, the method is more particularly suited for the detection and/or quantification an anti-HBV antibody in a biological sample and comprises at least the steps of bringing said biological sample into contact with at least one of the HBV moieties, nucleic acid molecules, vectors, infectious viral particles, host cells, compositions of the invention under conditions allowing the formation of a complex between the anti-HBV antibody and the HBV moiety, nucleic acid molecule, vector, infectious viral particle, host cell, composition of the invention and detecting and/or quantifying the formation of said complex by any appropriate means.

A person skilled in the art will easily determine the quantity of antibody, HBV moiety, nucleic acid molecule, vector, infectious viral particle, host cell, composition to be used in the methods of the invention. The means of detection and/or quantification of the virus are routine and well known to a person skilled in the art. By way of illustration, one may mention blots, ELISA, so-called sandwich techniques, competition techniques, and PCR techniques, in particular so called "real-time" techniques. The use of an antibody, HBV moiety, nucleic acid molecule, vector, infectious viral particle, host cell, or composition of the present invention as reagent can be facilitated by coupling (i.e., physically linking) to a detectable substance. Examples of detectable substances include various enzymes (e.g. horseradish peroxidase, alkaline phosphatase, beta-galactosidase or acetylcholinesterase), prosthetic groups (e.g. streptavidin/biotin, or avidin/biotin), fluorescent materials (e.g. umbelliferone, fluorescein, or fluorescein derivatives), luminescent materials, bioluminescent materials (e.g. luciferase, luciferin, or aequorin), and radioactive materials (e.g. ^{125}I, ^{131}I, ^{35}S or ^{3}H).

Finally, the invention relates to the use of at least one of the HBV moieties, nucleic acid molecules, vectors, infectious viral particles, host cells, compositions, or antibodies of the invention for the *in vitro* diagnosis of an HBV infection in a biological sample.

The invention has been described in an illustrative manner, and it is to be understood that the terminology which has been used is intended to be in the nature of words of description rather than of limitation. Obviously, many modifications and variations of the present invention are possible in light of the above teachings. It is therefore to be understood that within the scope of the appended claims, the invention may be practiced in a different way from what is specifically described herein.

All of the above cited disclosures of patents, publications and database entries are specifically incorporated herein by reference in their entirety to the same extent as if each such individual patent, publication or entry were specifically and individually indicated to be incorporated by reference.

Legends of Figures

Figure 1 illustrates HBV polypeptide expression from adenovirus and MVA infected cells. A549 cells or chicken embryo fibroblasts were infected at MOI 10 or 50 for adenovirus or MOI 0.2 or 1 for MVA and cells were lysed 48h after infection. Western blot were then performed with cell lysates obtained from cells infected with the various Ad (Figure 1A) and MVA (Figure 1B) constructs to detect specific HBV proteins. Core-containing polypeptides were detected using an anti-Core antibody (C1-5 or 13A9, dilution 1/200) and polymerase-containing polypeptides with an anti-Pol antibody (8D5, dilution 1/200) as primary antibodies and the secondary antibody was coupled to HRP. Expected sizes for the proteins expressed by Ad TG17909 and Ad TG17910 are respectively 31.6kDa and 88.5kDa. Expected sizes for proteins expressed by MVA TG17971, MVA TG17972, MVA TG17993 and MVA TG17994 are respectively 20.2kDa, 15.8kDa, 20kDa and 23.5 kDa. Expected sizes for proteins expressed by MVA TG17842 and MVA TG17843 are 88.5kDa and 98.2 kDa respectively.

Figure 2 illustrates the immunogenicity of HBV polypeptides encoded by adenovirus in Elispots IFNγ assays. Five individual mice (HLA-A2 transgenic mice) were immunised once with either Ad TG17909 alone (black bars), Ad TG17910 alone (white bars) or in combination (Ad TG17909 + Ad TG17910) (grey bars). Figure 2A illustrates specific T cell responses targeting Polymerase protein using the HLA-A2 restricted peptide SLY (SEQ ID NO: 55) or an irrelevant one (not shown). Figure 2B illustrates specific T cell responses targeting Core protein using the HLA-A2 restricted peptides FLP (SEQ ID NO: 56) or ILC (SEQ ID NO: 57). Figure 2C illustrates specific T cell responses targeting Env domains using the HLA-A2 restricted peptides VLQ (SEQ ID NO: 58), FLG (SEQ ID NO: 59) or GLS (SEQ ID NO: 60). Each bar represents an individual vaccinated mouse and the hatched bars represent the median of each group. Results are shown as the mean value of the number of spots observed for 10^6 spleen cells, obtained from triplicate wells. A response was considered positive if the number of spots was higher than 50 spots per 10^6 cells (this cut-off is represented by a thick black line).

Figure 3 illustrates the immunogenicity of HBV polypeptides encoded by adenovirus vector in intracellular cytokine staining assays. Five individual mice (HLA-A2 transgenic mice) were immunised once with either AdTG17909 (Figure 3B), AdTG17910 (Figure 3A) or a combination of AdTG17909 and AdTG17910 (Figure 3C). Splenocytes were cultured for 5h with Golgi-Plug and in presence of each HLA-A2 restricted peptide (SLY for Pol, FLP, ILC

for Core, VLQ, FLG and GLS for Env) or an irrelevant one. The percentage of CD8+ cells producing cytokines (IFNg and/or TNFa) specific of each HLA-A2 restricted epitopes, was assessed by ICS assays. Each bar represents an individual vaccinated mouse, with IFNg producing cells represented by a black bar, TNFa producing cells by a white bar and IFNg + TNFa producing cells by a hatched bar and all these cell populations are piled for each mouse.

Figure 4 illustrates the ability of HBV polypeptides encoded by adenovirus vector to induce CD8 and CD4 T cell responses, detected by intracellular cytokine staining assays. Five individual mice (HLA-A2 transgenic mice) were immunised once with a mixture of AdTG17909 and AdTG17910. Splenocytes were cultured for 5h with Golgi-Plug and in presence of each HLA-A2 restricted peptide (SLY for Pol, FLP, ILC for Core, VLQ, FLG and GLS for Env) or pools of overlapping peptides (15aa overlapping by 11amino acids, 2 pools of peptides for Core and 2 pools of peptides for Env) covering the whole antigenic domains or an irrelevant peptide. Induced specific CD8 T cells producing IFNgamma and/or TNFalpha (Figure 4A) and induced specific CD4 T cells producing IFNgamma and/or TNFalpha (Figure 4B) or producing IFNgamma and/or IL2 (Figure 4C) were monitored by ICS assays. Each bar represents an individual vaccinated mouse, with IFNg producing cells represented by a grey bar, TNFa or IL2 producing cells by a white bar and IFNg + TNFa or IFNg + IL2 producing cells by a hatched bar and all these cell populations are piled for each mouse. The median of each group is also showed.

Figure 5 illustrates the ability of adenovirus vector encoding HBV polypeptides to induce in vivo functional cytolysis against target cells loaded with HBV HLA-A2 restricted epitopes. Three individual mice (HLA-A2 transgenic mice) were immunised once with a combination of AdTG17909 and AdTG17910 (M1 to M3) and one mouse was immunized once with an empty adenovirus vector as negative control (M0). CFSE stained splenocytes from syngenic mice, loaded with HBV HLA-A2 epitopes or not (negative control) were injected intraveinously to vaccinated mice. The *in vivo* lysis of stained cells was assessed for each mouse 24h later by flow cytometry and calculated as indicated in Material and methods. The mean of specific lysis observed for each peptide for the 3 mice vaccinated with AdHBV was calculated and showed (Mean M1-M3).

Figure 6 illustrates the immunogenicity of HBV polypeptides encoded by MVA vector as determined by Elispots IFNgamma assays. Individual mice (HLA-A2 transgenic mice)

were immunised three times at one week interval with either MVATG17842 or MVATG17843 (Figure 6A) or MVATG17971 (Figure 6B) or MVA TG17972 or the negative control MVA TGN33.1 (data not shown). Figure 6A illustrates specific T cell responses targeting Polymerase protein following immunization with MVA TG17842 (dark grey bars) or MVATG17843 (light grey bars) using the HLA-A2 restricted peptide SLY (SEQ ID NO: 55), pool 8 of peptides covering the C-terminal part of the polymerase protein (25 peptides of 15 amino acids overlapping by 11amino acids /pool), an irrelevant peptide or medium (negative controls). Figure 6B illustrates specific T cell responses targeting Core protein following immunization with MVA TG17971 using the HLA-A2 restricted peptides FLP (SEQ ID NO: 56), ILC (SEQ ID NO: 57), peptides pools "core 1 and core 2" (21 to 22 peptides of 15 amino acids overlapping by 11amino acids /pool), an irrelevant peptide or medium (negative controls). Each bar represents an individual vaccinated mouse and the hatched bars represent the mean of each group. Results are shown as the mean value of the number of spots observed for 10^6 spleen cells, obtained from triplicate wells. A response was considered positive if the number of spots was higher than 50 spots per 10^6 cells (this cut-off is represented by a dotted black line).

Figure 7 illustrates the immunogenicity of HBV polypeptides encoded by MVA vectors co-injected in mouse, as determined by Elispots IFNgamma assays. Individual mice (HLA-A2 transgenic mice) were immunised three times at one week interval with a mix of MVATG17843 and either MVATG17972 (Figure 7A) or MVATG17993 (Figure 7B) or MVATG17994 (Figure 7C) or with MVA TG N33.1 alone as negative control (data not shown). Specific T cell responses targeting Polymerase protein were determined using the HLA-A2 restricted peptide SLY (SEQ ID NO: 55) and specific T cell responses targeting Env domains using the HLA-A2 restricted peptide GLS (SEQ ID NO: 60) or a pool of peptides covering the Env2 domain (pool of 15 amino acid-long peptides overlapping by 11amino acids). An irrelevant peptide and medium were used as negative controls. Each bar represents an individual vaccinated mouse and the hatched bars represent the mean of each group. Results are shown as the mean value of the number of spots observed for 10^6 spleen cells, obtained from triplicate wells. A response was considered positive if the number of spots was higher than 92 spots per 10^6 cells (this cut-off is represented by a dotted black line).

EXAMPLES

1. Material and Methods

The constructions described below are carried out according to the general genetic engineered and molecular cloning techniques detailed in Maniatis et al. (1989, Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor NY) or according to the manufacturer's recommendations when a commercial kit is used. PCR amplification techniques are known to the person skilled in the art (see for example PCR protocols --A guide to methods and applications, 1990, published by Innis, Gelfand, Sninsky andWhite, Academic Press). The recombinant plasmids carrying the ampicillin resistance gene are replicated in the *E. coli* C600 (Stratagene) on agar or liquid medium supplemented with 100µg/ml of antibiotic. The constructions of the recombinant vaccinia viruses are performed according to the conventional technology in the field in the documents above cited and in Mackett et al. (1982, Proc. Natl. Acad. Sci. USA 79, 7415-7419) and Mackett et al. (1984, J. Virol. 49, 857-864). The selection gene *gpt* (xanthine guanine phosphoribosyltransferase) of *E. coli* (Falkner and Moss, 1988, J. Virol. 62, 1849-1854) is used to facilitate the selection of the recombinant vaccinia viruses.

1.1. Vectors constructions and production

1.1.1. Selected antigens and HBV sequence strain

The vectors exemplified hereinafter have been engineered to express the polymerase, core polypeptides and immunogenic domains of the envelope protein. They all originate from HBV strain Y07587 which sequence is described in international databases (Genbank Y07587) and in different publications. It is a genotype D virus of serotype ayw.

The Core polypeptide is either wild-type (aa 1-183) or a Core polypeptide deleted of amino acids 77 to 84 (i.e. Core containing amino acid 1 to 76 and 85 to 183 designated core*) or a C-terminally truncated polypeptide (1-148) or a C-terminally truncated core (1-148) further deleted of amino acids 77 to 84 (i.e. Core containing amino acid 1 to 76 and 85 to 148 designated core*t).

The polymerase polypeptide is either wild type or a N-terminally truncated polypeptide lacking the first 47 amino acids (48-832) or a N-truncated polymerase (48-832) further

mutated at posititon 540 (D in H) and 718 (E in H) (positions 450 and 718 being given with respect to the wild-type polymerase) or the truncated (48-832) and mutated polymerase (D540H and E718H) which is fused to the peptide signal and transmembrane domain of the rabies virus glycoprotein (Pol*TMR).

The selected Env domains are : domain from amino acids 14 to 51 of the S protein (Env 1) and domain from amino acids 165 to 194 of the HBs protein (Env 2) and domain from amino acid 202 to 226 of the HBs protein (Env 4).

1.1.2. Construction and production of a MVATG17842 expressing a truncated and mutated HBV polymerase (Pol*)

The nucleotide sequences encoding a modified HBV polymerase polypeptide were synthesized by Geneart company using synthetic oligonucleotides and PCR products. The modified HBV polymerase corresponds to the polymerase protein of HBV Y07587 (SEQ ID NO:1) mutated at position 540 (D in H) and 718 (E in H) in order to eliminate Rnase H and RTase activities exhibited by the native HBV polymerase (resulting in amino acid sequence shown in SEQ ID NO: 8 and nucleotide sequence shown in SEQ ID NO: 22). The reassembled Pol sequence was then cloned in a plasmid vector resulting in PGA15-pol (SEQ ID NO: 27). A truncated version deleted of the first 47 amino acids present at the N-terminus of the native HBV polymerase was amplified by PCR from pGA15-Pol plasmid using the following primers OTG19037 (GAGCGATATCCACCATGAATGTTAGTATTCCTTGGAC) (SEQ ID NO: 28) and OTG19038 (GATCGCTAGCTCACGGTGGTCTCCATGCGAC) (SEQ ID NO: 29). The resulting fragment was inserted into the *NheI* and *EcoRV* restriction sites of a MVA transfer plasmid downstream the p7.5K promoter (Cochran *et al*, 1985, J. Virol. 54:30), resulting in pTG17842. The mutated and truncated polymerase is designated hereinafter pol*.

The MVA transfer plasmid is designed to permit insertion of the nucleotide sequence to be transferred by homologous recombination in deletion III of the MVA genome. It originates from plasmid pTG1E (described in Braun *et al.*, 2000, Gene Ther. 7:1447) into which were cloned the flanking sequences (BRG3 and BRD3) surrounding the MVA deletion III (Sutter and Moss, 1992, Proc. Natl. Acad. Sci. USA 89:10847). The transfer plasmid also contains a fusion between the *Aequorea victoria* enhanced Green Fluorescent protein (*eGFP* gene,

isolated from pEGP-C1, Clontech) and the *Escherichia coli* xanthine-guanine phosphoribosyltransferase gene (*gpt* gene) under the control of the early late vaccinia virus synthetic promoter p11K7.5 (kindly provided by R. Wittek, University of Lausanne). Synthesis of xanthine-guanine phosphoribosyltransferase enables GPT^+ recombinant MVA to form plaques in a selective medium containing mycophenolic acid, xanthine, and hypoxanthine (Falkner *et al*, 1988, J. Virol. 62, 1849-54) and *eGFP* enables the visualisation of recombinant MVA plaques. The selection marker *eGFP-GPT* is placed between two homologous sequences in the same orientation. When the clonal selection is achieved, the selection marker is easily eliminated by several passages without selection allowing the growth of eGFP-*GPT* recombinant MVA.

Generation of MVATG17842 virus was performed by homologous recombination in primary chicken embryos fibroblasts (CEF) infected with MVA and transfected with pTG17842 (according to the standard calcium phosphate DNA precipitation). Viral selection was performed by three round of plaque purification in the presence of a selective medium containing mycophenolic acid, xanthine and hypoxanthine. As mentioned above, the selection marker was then eliminated by passage in a non-selective medium. Absence of contamination by parental MVA was verified by PCR.

Analysis of expression of HBV polymerase was performed by Western-blot. A549 cells (ATCC CCL-185) were infected at MOI of 1 with MVATG17842 (Pol*) in presence or in absence of proteasome inhibitor MG-132 (10µM) added to growth medium. After 24 hours, cells were harvested. Western-blot analysis was performed using commercial monoclonal anti-Pol antibody Hep B Pol (8D5, Santa Cruz, # sc-81591).

1.1.3. Construction and production of MVATG17843 expressing a truncated and mutated HBV polymerase fused to the membrane-anchoring domain of rabies envelop glycoprotein (Pol*TMR)

The HBV Pol* sequence was then modified by fusion at its N-terminus to a peptide signal (SS) and at its C-terminus to a membrane-anchoring sequences (TMR) derived from the glycoprotein of the rabies virus (ERA isolate; described in Genbank N° M38452). The SS and TMR sequences were amplified from plasmid pTG8042 (described in WO99/03885) by PCR using respectively primer pairs OTG19045 (SEQ ID NO: 30)

(GAGTGATATCCACCATGGTTCCTCAGGCTCTCCTG) / OTG19047 (SEQ ID NO: 31) (GTCCAAGGAATACTAACATTAATAGGGAATTTCCCAAAACACAATG) and OTG19049 (SEQ ID NO: 32) (GTCGCATGGAGACCACCGTATGTATTACTGAGTGCAGGG / OTG19050 (SEQ ID NO: 33) (GAGTGCTAGCTCACAGTCTGGTCTCACCC). Pol* sequence was amplified from plasmid pGA15-Pol by PCR using primer pair OTG19046 (SEQ ID NO: 34) (GTTTTGGGAAATTCCCTATTAATGTTAGTATTCCTTGGACTC) / OTG19048 (SEQ ID NO: 35) (CTGCACTCAGTAATACATACGGTGGTCTCCATGCGACGTGC). Then, SS-Pol*-TMR sequence was reassembled by triple PCR using the following primers OTG19045 (SEQ ID NO: 30) and OTG19050 (SEQ ID NO: 33). The resulting fragment was inserted into the *NheI* and *EcoRV* restriction sites of a vaccinia transfer plasmid downstream the p7.5K promoter (Cochran *et al,* 1985, J. Virol. 54:30), resulting in pTG17843.

Generation of MVATG17843 virus was performed in CEF by homologous recombination as described above.

Analysis of Pol*-TMR expression was performed by Western-blot. A549 cells were infected at MOI 1 with MVATG17843 in presence or in absence of proteasome inhibitor MG-132 (10µM) added to growth medium. After 24 hours, cells were harvested. Western-blot analysis was performed using commercial monoclonal anti-Pol antibody Hep B Pol (8D5, Santa Cruz, # sc-81591).

1.1.4 Construction and production of MVATG17971 expressing a deleted Core polypeptide (Core*)

Core* corresponds to the Core sequence of HBV Y07587 (SEQ ID NO: 2) deleted of amino acids 77 to 84.

The Core* encoding sequences were reconstituted by double PCR from pGA4-Core plasmid. This plasmid was made by Geneart company. It contains a full length coding sequence of modified HBV Core gene which was assembled from synthetic oligonucleotides and/or PCR products. The last two codons CAA TGT of the coding sequence were modified in CAG TGC to avoid sequence homology with Pol (SEQ ID NO: 36).

Core sequence from positions 1 to 76 was amplified by PCR using the following primers OTG19290 (SEQ ID NO: 37) (GACTGTTAACCACCATGGACATTGATCCTTA-TAAAGAATTTG) and OTG19292 (SEQ ID NO: 38) (GTTGACATAACTGACTA-CCAAATTACCACCCACCCAGGTAG). Core sequence from positions 85 to 183 was amplified by PCR with the following primers OTG19291 (SEQ ID NO: 39) (GTGGGTGGTAATTTGGTAGTCAGTTATGTCAACACTAATATG) and OTG19080 (SEQ ID NO: 61) (GACTCTCGAGTTAGCACTGAGATTCCCGAGATTG). A double PCR was performed using OTG19290 (SEQ ID NO: 37) and OTG19080 (SEQ ID NO: 61) and both latter generated amplicons. The resulting fragment was inserted into the XhoI and HpaI restriction sites of a vaccinia transfer plasmid downstream the pH5R promoter (Rosel et al, 1986, J Virol. 60:436), resulting in pTG17971.

Generation of MVATG17971 virus was performed in CEF by homologous recombination as described above.

Analysis of Core* expression was performed by Western-blot. Chicken embryo fibroblasts were infected at MOI 0.2 with MVATG17971. After 24 hours, cells were harvested. Western-blot analysis was performed using a commercial monoclonal anti-core antibody Hep B cAg (13A9) (Santa Cruz, # sc-23946).

1.1. 5 Construction and production of MVATG17972 expressing a deleted and truncated Core polypeptide (Core*t)

Core*t corresponds to the Core sequence of HBV Y07587 (SEQ ID NO: 2) truncated after amino acid 148 and deleted of amino acids 77 to 84.

The Core*t-encoding sequences were reconstituted by double PCR from pGA4-Core plasmid which contains the sequence encoding the full length HBV Core gene which was assembled from synthetic oligonucleotides and PCR products except that the last two codons CAA TGT of the coding sequence were modified in CAG TGC to avoid sequence homology with Pol (SEQ ID NO: 36).

Core sequence from positions 1 to 76 was amplified by PCR using the following primers OTG19290 (SEQ ID NO: 37) (GACTGTTAACCACCATGGACATTGATCCTTA-TAAAGAATTTG) and OTG19292 (SEQ ID NO: 38) (GTTGACATAACTGACTA-

CCAAATTACCACCCACCCAGGTAG). Core sequence from positions 85 to 148 was amplified by PCR from pGA4-core with the following primers OTG19291 (SEQ ID NO: 39) (GTGGGTGGTAATTTGGTAGTCAGTTATGTCAACACTAATATG) and OTG19299 (SEQ ID NO: 40) (GACTCTCGAGTTAAACAGTAGTCTCCGGAAGTG). The double PCR was performed using OTG19290 (SEQ ID NO: 37) and OTG19299 (SEQ ID NO: 40). The resulting fragment was inserted into the *XhoI* and *HpaI* restriction sites of a vaccinia transfer plasmid downstream the pH5R promoter (Rosel *et al*, 1986, J Virol. 60:436), resulting in pTG17972.

Generation of MVATG17972 virus was performed in CEF by homologous recombination as described above.

Analysis of Core*t expression was performed by Western-blot. Chicken embryo fibroblasts were infected at MOI 0.2 with MVATG17972. After 24 hours, cells were harvested. Western-blot analysis was performed using a commercial monoclonal anti-core antibody Hep B cAg (13A9) (Santa Cruz, # sc-23946).

1.1. 6 Construction and production of MVATG17993 expressing a deleted and truncated Core polypeptide fused to the Env1 immunogenic domain (Core*t-env1)

The Core-t* moiety was fused to Env1 domain extending from amino acids 14 to 51 of the HBs protein.

The Core*t -Env1 sequence was reconstituted by double PCR. Core*t sequence was amplified by PCR from pTG17972 using the following primers OTG19317 (SEQ ID NO: 41) (GACGGGATCCACCATGGACATTGATCCTTATAAAGAATTTGG) and OTG19319 (SEQ ID NO: 42) (GCCTGCTTGCAGGACAACAGTAGTCTCCGGAAGTGTTG). Env1 sequence was amplified by PCR from plasmid pMK-C/E (SEQ ID NO: 43) using the following primers OTG19318 (SEQ ID NO: 44) (CCGGAGACTACTGTTGTCC-TGCAAGCAGGCTTCTTC) and OTG19320 (SEQ ID NO: 45) (GAGTCATTCTCGAC-TTGCGGCCGCTTACTGACCCAGGCAAACCGTGG). The double PCR was performed using OTG19317 (SEQ ID NO: 41) and OTG19320 (SEQ ID NO: 45). The resulting fragment was inserted into the *BamHI* and *NotI* restriction sites of a vaccinia transfer plasmid downstream the pH5R promoter (Rosel *et al*, 1986, J Virol. 60:436), resulting in pTG17993.

For illustrative purposes, the plasmid pMK-C/E was made by Geneart and contains a chimeric sequence consisting of an insertion of three HBV env domain sequences into core sequence (SEQ ID NO: 43). The native core and env nucleotide sequences were degenerated to avoid sequence homology with HBV Pol sequence and also sequence instability due to polyT or polyGC stretches. In addition, the core sequence was deleted of amino acids 77 to 84 and truncated at aa148. The selected Env domains are : domain from amino acids 14 to 51 of the S protein (Env 1) and domain from amino acids 165 to 194 of the S protein (Env 2) and domain from amino acid 202 to 226 of the S protein (Env 4). The three domains were inserted respectively at positions nt 127, at nt 222 and at nt 416 of core sequence. It has to be noted that insertion of this sequence in a MVA vector results in cytotoxicity in the expressing cells, emphasizing the fact that the design of the env-core fusion is not straightforward.

Generation of MVATG17993 virus was performed in CEF by homologous recombination as described above.

Analysis of Core*t-env1 expression was performed by Western-blot. Chicken embryo fibroblasts were infected at MOI 0.2 with MVATG17993. After 24 hours, cells were harvested. Western-blot analysis was performed using a commercial monoclonal anti-core antibody Hep B cAg (13A9)(Santa Cruz, # sc-23946).

1.1. 7. Construction and production of MVATG17994 expressing a deleted and truncated Core polypeptide fused to Env1 and Env2 immunogenic domains (Core*t-env1-env2)

The Core*t polypeptide described in 1.1.5 was then fused to two immunogenic domains extending from amino acids 14 to 51 (Env 1) and from amino acid 165 to 194 (Env2) of the HBs protein

The nucleotide sequences encoding the Core*t-Env1-Env2 were reassembled by triple PCR. Core*t sequence was amplified by PCR from pTG17972 using the following primers OTG19317 (SEQ ID NO: 41) and OTG19319 (SEQ ID NO: 42). Env1 was amplified from pMK-C/E plasmid using the following primers OTG19318 (SEQ ID NO: 44) and OTG19322 (SEQ ID NO: 46 (GCGTGCGCTTGCCCACTGACCCAGGCAAACCGTGG). Env2 was

amplified from pMK-C/E plasmid using the following primers OTG19321 (SEQ ID NO: 47 (CGGTTTGCCTGGGTCAGTGGGCAAGCGCACGCTTTAGC) and OTG19323 (SEQ ID NO: 48) (GAGTCATTCTCGACTTGCGGCCGCTTACACGCTCAGCCACACGGTTGG). The triple PCR was performed using OTG19317 (SEQ ID NO: 41) and OTG19323 (SEQ ID NO: 48). The resulting fragment was inserted into the *BamHI* and *NotI* restriction sites of a vaccinia transfer plasmid downstream the pH5R promoter (Rosel *et al*, 1986, J Virol. 60:436), resulting in pTG17994.

Generation of MVATG17994 virus was performed in CEF by homologous recombination as described above.

Analysis of Core*t-env1-env2 expression was performed by Western-blot. Chicken embryo fibroblasts were infected at MOI 0.2 with MVATG17994. After 24 hours, cells were harvested. Western-blot analysis was performed using a commercial monoclonal anti-core antibody Hep B cAg (13A9, Santa Cruz, # sc-23946).

1.1.8. Construction and production of an adenoviral vector AdTG17909 expressing CORE-Env1-Env2-Env4 :

A synthetic gene (831 nucleotides) encoding a CORE-Env1-Env2-Env4 fusion was reconstituted by double PCR. CORE was amplified by PCR from pGA4-Core (described in 1.1.4.) using the following primers OTG19152 (SEQ ID NO: 49) (GGGGGGCTAGCAAGCTTCCACCATGGACATTGATCCTTATAAAGAATTTG) and OTG19154 (SEQ ID NO: 50) (GAAAGAATCCAGCTTGCAGGACGCACT-GAGATTCCCGAGATTGAG). Env1-Env2-Env4 were amplified by PCR from pGA4-Env using the following primers OTG19153 (SEQ ID NO: 51) (CTCAATCTCGGGAATCT-CAGTGCGTCCTGCAAGCTGGATTCTTTC) and OTG19159 (SEQ ID NO: 52) (GAGTCATTCTCGACTTGCGGCCGCTTAGATATAAACCCACAAGC).The double PCR was performed using OTG19152 (SEQ ID NO: 49) and OTG19159 (SEQ ID NO: 52). The resulting fragment was inserted into the *Nhe*I and *Not*I restriction sites of an adenoviral shuttle plasmid containing a CMV-driven expression cassette surrounded by adenoviral sequences (adenoviral nucleotides 1-454 and nucleotides 3513-5781 respectively) to allow generation of the vector genome by homologous recombination (Chartier et al., 1996, J. Virol. 70:4805). The resulting adenoviral vector pTG17909 is E3 (nucleotides 28593-30464) and E1

(nucleotides 455-3512) deleted, with the E1 region replaced by the expression cassette containing, from 5' to 3', the CMV immediate-early enhancer/promoter, a chimeric human β-globin/IgG intron (as found in pCI vector available in Promega), the sequence encoding the CORE-Env1-Env2-Env4 and the SV40 late polyadenylation signal. The recombinant adenovirus was generated by transfecting the *PacI* linearized viral genomes into an E1 complementation cell line. Virus propagation, purification and titration were made as described previously (Erbs et al., 2000, Cancer Res. 60:3813)

Expression of the fusion protein was evaluated by Western-blot. 10^6 A549 cells (ATCC CCL-185) were infected at MOI of 10 or 50 for 48 hours with AdTG17909 or with an empty adenovirus as negative control. The cell pellets were collected and probed with an anti CORE mouse monoclonal antibody (C1-5, sc-23945, Santa Cruz).

1.1.9. Construction and production of adenoviral vector AdTG17910 expressing Pol*:

The gene encoding Pol*, a polymerase protein truncated of the 47 first amino acids except the Met initiator (48 to 832) and mutated at posititon 540 (D in H) and 718 (E in H) (with respect to the wild type polymerase) was inserted in an adenovirus vector. The Pol gene (2364 nucleotides) was amplified by PCR from pGA15-Pol (described in 1.1.2) using primers OTG19155 (SEQ ID NO: 53) (GGGGGGCTAGCAAGCTTCCACCATGAA-TGTTAGTATTCCTTGGACTCATAAG) and OTG19156 (SEQ ID NO: 54) (GAGTCATTCTCGACTTGCGGCCGCTCACGGTGGTCTCCATGCGACGTGC). The resulting fragment was inserted into the *Nhe*I and *Not*I restriction sites of an adenoviral shuttle plasmid containing a CMV-driven expression cassette surrounded by adenoviral sequences (adenoviral nucleotides 1-454 and nucleotides 3513-5781 respectively) to allow generation of the vector genome by homologous recombination (Chartier et al., 1996, J. Virol. 70:4805). The resulting adenoviral vector pTG17910 is E3 (nucleotides 28593-30464) and E1 (nucleotides 455-3512) deleted, with the E1 region replaced by the expression cassette containing, from 5' to 3', the CMV immediate-early enhancer/promoter, a chimeric human β-globin/IgG intron (as found in pCI vector available in Promega), the sequence encoding the truncated and mutated Pol and the SV40 late polyadenylation signal. The recombinant adenovirus was generated by transfecting the *PacI* linearized viral genomes into an E1 complementation cell line. Virus propagation, purification and titration were made as described previously (Erbs et al., 2000, Cancer Res. 60:3813).

Expression of the fusion protein was evaluated in adenovirus infected cells by Western-blot. A549 cells (10^6 cells) (ATCC CCL-185) were infected at MOI of 10 or 50 for 48 hours with the adenovirus AdTG17910, as well as an empty adenovirus as negative control. The cell pellets were collected and probed with an anti Pol mouse monoclonal antibody (8D5, sc-81591, Santa Cruz).

1.2. Evaluation of antigen immunogenicity

Antigen immunogenicity was evaluated *in vivo* by Elispot IFNγ and intracellular cytokine staining (ICS) assays following immunization of HLA transgenic mice.

1.2.1 Mouse model

The HLA-A2.1 transgenic mice used in the study were described by Pascolo et al. (1997, J. Exp. Med. 185:2043). These mice have the H-$2D^b$ and murine β_2-microglobulin genes knocked-out and express a transgenic monochain histocompatibility class I molecule (HHD molecule) in which the C-terminus of the human β2m is covalently linked to the N-terminus of a chimeric heavy chain (HLA-A*0201 α1-α2, H-$2D^b$ α3 transmembrane and intracytoplasmic domains). Seven to 10 weeks-old mice (male and female) were immunized. Average weight of the mice was around 25-30 g.

1.2.2. Immunization protocols

Mice were divided in 4 groups; group 1 immunized by AdTG17909 (encoding HBV Core fused to env1, env2 and env4 immunogenic domains), group 2 immunized AdTG17910 (encoding the truncated and mutated Pol*), group 3 immunized with both vectors and group 4 immunized with an empty adenovirus (AdTG15149) as negative control. All animals were immunized by subcutaneous injection at the base of the tail, groups 1 and 2 animals received one subcutaneous injection of 10^8 IU of each Adenovirus (TG17909 or TG17910), group 3 one subcutaneous injection of a mix containing 10^8 IU of each adenovirus (total of 2.10^8 IU: 10^8 IU of AdTG17909 + 10^8 IU of AdTG17910) and negative controls received one subcutaneous injection of 2.10^8 IU of AdTG15149. Cellular immune responses were assessed by IFNg Elispot and intracellular cytokine staining (ICS) assays 2 weeks after the immunization.

1.2.3 Peptides

Peptides used for cells stimulation *in vitro* were either short peptides of 9 to 10 amino acids which are described or predicted as HLA-A2 restricted epitopes or long peptides of 15 amino acids included in peptide libraries covering all the antigens of interest.

Short peptides corresponding to described or predicted HLA-A2 restricted epitopes of Polymerase protein, Core protein or Env domains were synthesized by Eurogentec (Belgium) and were dissolved in 100% DMSO (sigma, D2650) at a concentration of 10mM.

Peptides libraries covering the whole Polymerase, Core and Envelope proteins were synthesized by ProImmune (Oxford, United Kingdom). The Pol, Core and Env libraries were composed of 15 mer peptides overlapping by 11 amino acids. Each crude peptide was dissolved in 100% DMSO (sigma, D2650) at a concentration of 50mg/ml. For each library, peptides were pooled to a concentration of 2mg/ml per peptide:

HBV Pol protein is covered by 8 pools of 24 to 25 peptides from Pol library (Pool 1: 24 peptides covering residues 45 to 151; Pool 2: 24 peptides covering residues 140 to 251; Pool 3: 24 peptides covering residues 241 to 347; Pool 4: 24 peptides covering residues 337 to 447; Pool 5: 24 peptides covering residues 437 to 543; Pool 6: 24 peptides covering residues 533 to 639; Pool 7: 24 peptides covering residues 629 to 735; Pool 8 : 25 peptides covering residues 725 to 832);

HBV Core protein is covered by 2 pools of 21-22 peptides from Core library (Pool 1: 22 peptides covering residues 1 to 100; Pool 2: 21 peptides covering residues 89 to 183);

HBV Env protein is covered by 3 pools of 6 to 10 peptides from Env library (Pool 1: 10 peptides covering HBs residues 9 to 59; Pool 2: 9 peptides covering HBs residues 157 to 194; Pool 4: 6 peptides covering HBs residues 193 to 226).

1.2. 4. IFNg Elispot assays

Splenocytes from immunized mice were collected and red blood cells were lysed (Sigma, R7757). 2.10^5 cells per well were cultured in triplicate for 40 h in Multiscreen plates (Millipore, MSHA S4510) coated with an anti-mouse IFNγ monoclonal antibody (BD Biosciences; 10 µg/ml, 551216) in (MEM culture medium (Gibco, 22571) supplemented with 10 % FCS (Sigma, F7524 or JRH, 12003-100M), 80 U/mL penicillin / 80 µg/mL streptomycin (PAN, P06-07-100), 2 mM L-glutamine (Gibco, 25030), 1X non-essential amino acids (Gibco, 11140), 10 mM Hepes (Gibco, 15630), 1 mM sodium pyruvate (Gibco,

31350) and 50 µM β-mercaptoethanol (Gibco, 31350) and in presence of 10 units/ml of recombinant murine IL2 (Peprotech, 212-12), alone as negative control, or with:

- 10 µM of one HLA-A2 restricted peptide present in HBV antigens encoded by Ad vectors (SLY in Pol, FLP, ILC for Core, VLQ, FLG and GLS for Env) or an irrelevant one;
-a pool of peptides at a final concentration of 5µg/ml per peptide
- 5 µg/ml of Concanavalin A (Sigma, C5275) for positive control.

IFNg-producing T cells were quantified by Elispot (cytokine-specific enzyme linked immunospot) assay as previously described (Himoudi et al., 2002, J. Virol. 76:12735). The number of spots (corresponding to the IFNg-producing T cells) in negative control wells was substracted from the number of spots detected in experimental wells containing HBV peptides. Results are shown as the mean value obtained for triplicate wells. An experimental threshold of positivity for observed responses (or cut-off) is determined by calculating a threshold value which corresponds to the mean value of spots observed with medium alone + 2 standard deviations, reported to 10^6 cells. A technical cut-off linked to the CTL Elispot reader was also defined as being 50 spots/10^6 cells (which is the value above which the CV of the reader was systematically less than 20%). The highest value between the technical cut-off and the experimental threshold calculated for each experiment is taken into account to define the cut-off value of each experiment. Statistical analyses of Elispot responses were conducted by using a Mann-Whitney test. P value equal or inferior to 0.05 was considered as significant.

1.2. 5. Intracellular cytokine staining (ICS) assays

ICS was performed on splenocytes from each animal of each group. Following red blood cells lysis with lysis buffer (Sigma, R7757), $2x10^6$ cells per well in flat-bottom 96-well plate were incubated in complete alpha (MEM culture medium (Gibco BRL, 22571) in presence of 10 units/ml of murine recombinant IL-2 (Peprotech, 212-12) alone as negative control or with 10µM of specific HBV peptide or with a pool of peptides at a final concentration of 5µg/ml per peptide or with 10µM of an irrelevant peptide. The GolgiPlug (BD Biosciences, 555029) was immediately added at a 1µl/ml final concentration for 5 h. Then, cells were harvested in V-bottom 96-well plates and washed with 1 % FCS-PBS. Staining was performed using monoclonal antibodies against CD3 (hamster MAb anti-CD3e-PE, dilution 1/200), CD8 (rat MAb anti CD8a-APC, dilution 1/600) and CD4 (rat MAb anti-CD4-PerCP, dilution 1/600) (all from BD Biosciences, 553063, 553035 and 553052 respectively) in 50 µl of 1 % FCS-

PBS for 15 min at room temperature. After washing, cells were fixed and permeabilized with Cytofix/Cytoperm and washed with Perm/Wash solution (BD Biosciences, 554714). Then, the anti-mouse IFNg-PE antibodies (BD Biosciences, 554412557724) and anti-mouse TNFa - Alexa488 antibodies (BD Biosciences, 557719) or the anti-mouse IFNg-PE antibodies (BD Biosciences, 554412557724) and anti-mouse IL2-Alexa488 antibodies (BD Biosciences, 557719) were added for 15 min at room temperature and after washing with Perm/Wash, cells were resuspended in 1% FCS-PBS and analysed by flow cytometry using a FacsCalibur (Becton Dickinson). CD3e+, CD8a+ cells or CD3e+, CD4+ cells were gated to determine percentages of IFNg+ CD8+ or IFNg+ CD4+ T or TNFa+ CD8+ or TNFa+ CD4+ T or IL2+ CD8+ or IL2 CD4+ T or IFNg+ TNFa+ CD8+ or IFNg+ TNFa+ CD4+ or IFNg+ IL2+ CD8+ or IFNg+ IL2+ CD4+ T cell population. The percentage obtained in medium only was considered as background.

1.2. 6. In vivo CTL assays

In vivo CTL assays were performed as described (Fournillier et al., 2007). Splenocyte suspensions were obtained from syngenic mouse spleens and adjusted to $20x10^6$ cells/ml after lysis of red blood cells. One third of the cells was incubated with one of the HBV specific peptide, the second third of the cells was incubated with another HBV peptide, all at 10 µM final concentration for 1 hour at 37°C, whereas the last fraction was left unpulsed. 5(6)-carboxyfluorescein diacetate succinimidyl ester (CFSE) (Molecular probes, C1157) was added at 16 µM (CFSE-high) to unpulsed cells, at 4 µM (CFSE-medium) to ILC or VLQ peptide pulsed cells and at 1 µM (CFSE-low) to SLY or FLP peptide pulsed cells, for 10 min. After washing with PBS, the three populations (unpulsed, ILC and SLY peptide pulsed cells or unpulsed, FLP and ILC peptide pulsed cells) were mixed and 30.10^6 total cells were injected to anaesthetized mice via the retro-orbital vein (using ketamine-xylazine-PBS mix (Kétamine Virbac, Centravet KET204, final concentration 25 mg/ml; Xylazine hydrochloride Rompun Bayer, Centravet, final concentration 5 mg/ml)). Thus, CFSE-low and medium population represented specific targets supposed to be lysed by cytotoxic T cells and CFSE-high population was an internal reference allowing assay normalisation. Splenocytes from recipient mice were analyzed 24 h later by flow cytometry to detect the CFSE-labeled cells. Following gating on lymphocytes (SSC/FSC), a second gating was performed based on the number of events/CFSE fluorescence (FL1) which reveals 3 peaks, a 1rst one corresponding to CFSE-low cells, the 2nd one to CFSE-medium cells and the 3rd one to CFSE-high cells. For each animal, ratio between CFSE+ peptide-pulsed targets and CFSE+ unpulsed targets

was calculated (R=Number CFSE-low cells/Number CFSE-high cells). Two naive mice were used to determine R reference. The percentage of specific lysis for each animal was determined by the following formula: % lysis = $(1-R_{mouse}/R_{reference}) \times 100$. A response was considered positive if the percentage of specific lysis was higher than 10% (cut-off).

2. Results

2.1 Antigen expression by viral vectors

2.1.1 Expression of antigens from adenovirus constructs AdTG17909 and AdTG17910

Expression of the core-env1-env2-env4 fusion protein was evaluated by Western-blot. A549 cells (10^6 cells) were infected at MOI of 10 or 50 for 48 hours with AdTG17909 or an empty adenovirus as negative control. The cell pellets were collected and p robed with an anti-Core mouse monoclonal antibody (C1-5, sc-23945, Santa Cruz). As illustrated in Figure 1A, a major band having the expected molecular weight (31.6 kDa) was revealed in the sample collected from cells infected with AdTG17909.

Expression of the Pol* polypeptide was evaluated by Western--blot following AdTG17910 infection of A549 cells. The cell pellets were then collected and probed with an anti-Pol mouse monoclonal antibody (8D5, sc-81591, Santa Cruz). As illustrated in Figure 1A, a band having the expected molecular weight (88.5 kDa) was revealed in the sample collected from cells infected with AdTG17910 together with some sub-products (partial polymerase proteins).

2.1.2 Expression of antigens from MVA constructs

Analysis of Pol*, Pol*TMR, Core*t, Core*tEnv1, Core*t-Env1-Env2 expression was performed by Western-blot. A549 cells or CEF were infected at MOI of 1 or 0.2 respectively with MVATG17842, MVATG17843, MVATG17971, MVATG17972, MVATG17993, and MVATG17994 respectively in presence or in absence of proteasome inhibitor MG-132 (10µM) added to growth medium for MVATG17842 and MVATG17843. After 24 hours, cells were harvested.

For MVATG17842, Western-blot analysis was performed using commercial monoclonal anti-Pol antibody Hep B Pol (8D5, Santa Cruz, # sc-81591). As shown in Figure 1B, expression of a protein with an apparent molecular weight of 88.5 kDa was detected only in presence of MG-132. This band has the expected molecular weight for the Pol* protein.

For MVATG17843, Western-blot analysis was performed using commercial monoclonal anti-Pol antibody Hep B Pol (8D5, Santa Cruz, # sc-81591). As shown in Figure 1B, expression of a protein with an apparent molecular weight of 98.2 kDa was detected in presence or in absence of MG-132. This band has the expected molecular weight for the Pol*-TMR protein. It should be noticed that in presence of MG132 more product and an additional product of high molecular weight, over 200 KDa, were detected.

For MVATG17971, Western-blot analysis was performed using a commercial monoclonal anti-core antibody Hep B cAg (13A9) (Santa Cruz, # sc-23946). As shown in Figure 1B, expression of Core* was detected with an apparent molecular weight of 21 kDa which corresponds to the expected molecular weight.

For MVATG17972, Western-blot analysis was performed using a commercial monoclonal anti-core antibody Hep B cAg (13A9) (Santa Cruz, # sc-23946). As shown in Figure 1B, expression of Core*t was detected with an apparent molecular weight of 15.8 kDa which corresponds to the expected molecular weight.

For MVATG17993 and MVATG17994, Western-blot analysis was performed using a commercial monoclonal anti-core antibody Hep B cAg (13A9, Santa Cruz, # sc-23946). As shown in Figure 1B, expression of a protein with an apparent molecular weight of 19.9 and 23.4 kDa respectively was detected. This band has the expected molecular weight for the Core*t-Env1 protein and Core*t-Env1-Env2

2.2. Immunogenicity of antigens expressed from adenovirus vectors AdTG17909 and AdTG17910

The immunogenicity of the HBV polypeptides expressed by adenovirus vectors was assessed in HLA-A2 transgenic mice immunized with either AdTG17909 or AdTG17910 alone or with a mixture of the 2 adenoviruses. Specific T cell responses induced following one subcutaneous injection were evaluated by Elispot IFNg, ICS and *in vivo* cytolysis assays

using known (described as being the target of specific T cell responses in patients) HLA-A2 epitopes present in Polymerase, Core or the envelope domains or/and pools of overlapping peptides covering the HBV antigens of interest.

2.2.1. HBV specific IFNγ producing cell evaluation by Elispot assays

Elispot IFNg assays showed that AdTG17910 is able to induce IFNg producing cells specific of an HLA-A2 restricted epitope (SLYADSPSV) (SEQ ID NO: 55 located within the HBV polymerase at positions 816-824) (Figure 2A). Immunization with AdTG17909 also resulted in high frequency induction of IFNg producing cells specific for 2 Core HLA-A2 restricted epitopes (FLPSDFFPSV at position 18-27 (SEQ ID NO: 56) and ILCWGELMTL at position 99-108 (SEQ ID NO: 57) as well as for 3 envelope HLA-A2 restricted epitopes (VLQAGFFLL (SEQ ID NO: 58) at positions 14-22 and FLGGTTVCL (SEQ ID NO: 59) at positions 41-49 both present in Env1, and GLSPTVWLSV (SEQ ID NO: 60) at positions 185-194 present in Env2) (Figure 2B and C). Immunization with the mixture of AdTG17909 and AdTG17910 also induced a comparable level of specific IFNg producing cells targeting the same epitopes in the 3 antigens, ie the SLY epitope present in Pol, the FLP and ILC epitopes in the Core protein, and the 3 epitopes of the envelope domains (VLQ, FLG and GLS) (Figure 2A, B and C). Frequency of T cell responses detected following immunization with a single Ad or the mixture of the two was comparable, showing that there is no major immunodominance between the 3 antigens expressed from the described vectors.

2.2.2. HBV specific IFNg/TNFa producing cell evaluation by intracellular staining assays

The number of CD8 T cells able to produce either IFNg alone or IFNg + TNFa targeting HLA-A2 restricted epitopes present in polymerase (SLY) in Core (FLP and ILC) and in envelope domains (VLQ, FLG and GLS) were evaluated by ICS assay. All these epitopes were the target of double and simple secreting cells. The results are shown in Figure 3. Animals immunized with AdTG17909 alone or in combination with AdTG17910 mounted roughly equivalent Core- and Env-specific CD8 T cell responses (same percentages of specific CD8 T cells producing IFNg or IFNg + TNFa following restimulation with FLP, ILC, VLQ, FLG and GLS peptides as shown in Figures 3B and 3C). On the other hand, concerning the polymerase specific CD8 T cell response (SLY epitope), a very high percentage of CD8+ cells producing IFNg or IFNg + TNFa was detected in mice treated with AdTG1710 expressing Pol* (Figure 3A) as well as in those immunized with the mixture of AdTG17910 and AdTG17909 although at a lower level (Figure 3C).

2.2.3. HBV specific IFNg/TNFa producing CD8 and CD4 T cell evaluation following immunization with a mix of Adenovirus vectors, by intracellular staining assays

The percentages of CD8 and CD4 T cells able to produce either IFNg alone or IFNg + TNFa or IFNg + IL2 targeting HLA-A2 restricted epitopes present in polymerase (SLY) in Core (FLP and ILC) and in envelope domains (VLQ, FLG and GLS) or pools of overlapping peptides covering Core protein and Env domains were evaluated by ICS assay. All the tested HLA-A2 restricted epitopes were the target of single and double secreting cells (IFNg and IFNg + TNFa) and some pools of overlapping peptides were the target of single and double producing cells too (IFNg and IFNg+TNF and IFNg + IL2). The results are shown in Figure 4. Five HLA-A2 transgenic mice were immunized with a mix of AdTG17909 and AdTG17910 and 3 HLA-A2 transgenic mice were immunized with AdTG15149 (negative control). Animals immunized with AdTG15149 displayed no HBV-specific T cell responses (data not shown). Animals immunized with AdTG17909 combined with AdTG17910 displayed a strong CD8 T cell response specific of HBV targeted antigens (Figure 4A), with high percentage of single (IFNg) and double (IFNg + TNFa) producing cells specific of the HLA-A2 epitopes present in Polymerase, Core and Env domains and specific of the "core 1" pool of peptides and the pools of peptides covering Env1 and Env2 domains. As illustrated in Figures 4B and 4C, these vaccinated mice also displayed CD4 T cell responses specific of HBV antigens, in particular single (IFNg) and double (IFNg + TNFa and IFNg + IL2) producing cells specific of the "core 2" pool of peptides and the Env2-covering pool of peptides.

2.2.4. Induction of in vivo cytolysis measured by in vivo CTL assays

The ability of adenovirus vectors AdTG17909 and AdTG17910 to induce *in vivo* cytolysis against cells presenting HBV HLA-A2 epitopes was assessed by *in vivo* CTL assays. Four HLA-A2 epitopes were tested, respectively SLY (Pol), FLP and ILC (Core) and VLQ (Env 1 domain). Six animals were immunized with a mix of AdTG17909 + AdTG17910 and 2 animals were immunized with AdTG15149 (negative control). The half of each group (three AdTG17909+AdTG17910 immunized mice and one AdTG15149 immunized mouse) was tested for its ability to lyse *in vivo* cells pulsed with SLY peptide and cells pulsed with ILC peptide. The other half was tested for the ability of the vaccinated animals to lyse *in vivo* cells pulsed with FLP peptide and cells pulsed with VLQ peptide. The results are shown in Figure 5. As expected, no HBV-specific *in vivo* cytolysis could be detected with AdTG15149

immunized mice (data not shown). I*n vivo* cytolysis against the 2 core epitopes FLP and ILC was weak in AdTG17909+AdTG17910 immunized mice. However, in contrast, animals immunized with the mixture of AdTG17909 and AdTG17910 displayed a strong *in vivo* cytolysis against the polymerase epitope SLY (Figure 5A) and Env1 epitope VLQ (Figure 5B), reaching more than 50% of specific lysis in both cases.

Interestingly, the combination of Ad vectors expressing pol, core and env moieties allows the induction of specific T cell responses targeting the 3 HBV antigens when co-injected. Induced T cells are able to produce one or 2 cytokines and to lyse *in vivo* cells loaded with some HBV peptides. All together these data demonstrate the immunogenic activity of the compositions described and their ability to induce CD8 and CD4 T cell responses when vectorised by Ad.

2.3. Immunogenicity of antigens expressed from MVA vectors MVATG17842, MVATG17843, MVATG17971, MVA TG17972, MVA TG17993 and MVA TG17994

The immunogenicity activity of the MVA-based compositions was assessed in HLA-A2 transgenic mice immunized with one of the MVA vectors described in Examples 1.1.2 to 1.1.7 (MVATG17842, MVATG17843, MVATG17971 or MVATG17972 alone) or with a mixture of 2 MVA (MVATG17843 + MVATG17972, MVATG17843 + MVATG17993 or MVATG17843 + MVATG17994). Mice were immunized with three subcutaneous injections at one week interval and specific T cell responses were evaluated by Elispot IFNg and ICS using the above-described HLA-A2 epitopes present in Polymerase, Core or the envelope domains or/and pools of overlapping peptides covering the HBV antigens of interest.

2.3.1. HBV specific IFNγ producing cell evaluation by Elispot assays following immunization with polymerase expressing MVA.

Three mice were immunized with either MVATG17842 expressing a truncated and mutated polymerase antigen or MVATG17843 expressing a membrane-targeted version of the same truncated and mutated polymerase or MVA N33.1 (negative control). Polymerase-specific T cell responses were evaluated by IFNg Elispot assays using the SLY HLA-A2 restricted epitope and pools of peptides covering the polymerase. No HBV-specific T cell response was detected for mice immunized with MVA N33.1 and with MVATG17842 (data not shown). However, as shown in Figure 6A, IFNg producing cells were induced following immunization with MVATG17843 which are specific of the HLA-A2 restricted epitope SLY and of the peptide pool 8 covering the C-terminal portion of the polymerase (No specific response could

be detected against the other peptide pools 1-7 under the tested experimental conditions). These data highlight the benefit of expressing polymerase as a membrane-anchored antigen at least in MVA-based compositions.

2.3.2. HBV specific IFNγ producing cell evaluation by Elispot assays following immunization with core expressing MVA.

Eigth mice were immunized with either MVATG17971 expressing a core moiety deleted of residues 77-84 or MVATG17972 expressing a truncated version thereof (C-terminal truncation from residue 149) or MVA N33.1 (negative control). Core specific T cell responses were determined by IFNg Elispot assays using HLA-A2 restricted epitopes (FLP and ILC peptides) and the above-described core 1 and core 2 pools of peptides. As illustrated in Figure 6B, immunization with MVA TG17971 is able to induce sporadic T cell responses specific against HLA-A2-restricted FLP and ILC peptides and the two peptide pool covering core antigen (Figure 6B). No core specific T cell responses could be detected in mice immunized with MVATG17972 using the tested peptides and under the tested experimental conditions (data not shown).

2.3.3. HBV specific IFNγ producing cell evaluation by Elispot assays following immunization with combination of MVA vectors.

Three mice were immunized with a mixture of MVA TG17843 and either MVA TG17972, MVA TG17993 and MVA TG17994 and HBV specific T cell responses were evaluated by Elispot IFNg assay using the above-described peptides.

- Polymerase specific T cell responses were detected in the vast majority of animals vaccinated with the combination MVATG17843 + MVATG17972 (positive responses in 2/3 animals as shown in Figure 7A), MVATG17843 + MVATG17993 (positive responses in 3/3 animals as shown in Figure 7B) and MVATG17843 + MVATG17994 (positive responses in 2/3 animals as shown in Figure 7C). Frequency of IFNg producing cells seems to be comparable with the one observed when MVA TG17843 was injected alone (Figure 6A) which demonstrates that vector combination is not detrimental to the induced immune response.
-no core-specific response could be detected under the experimental conditions tested in any of the vaccinated animals using HLA-A2 or pools of peptides (data not shown).

- no env-specific response could be detected under the experimental conditions tested in any of the animals vaccinated with the MVATG17993-comprising combination using Env1 HLA-A2 or pools of peptides (data not shown).

- Env 2-specific T cell responses were detected in 2 out of 3 animals immunized with the MVATG17994-comprising combination as illustrated in Figure 7C which were directed against both the HLA-A2-restricted GLS epitope and the Env2-covering pool of peptides (no detection of T cell response against Env1 domain could be observed under these experimental conditions; data not shown).

ICS assays performed in the same conditions confirmed the results observed in Elispot assays (data not shown).

Interestingly, the combination of MVA vectors expressing pol, core and env moieties allows the induction of specific T cell responses targeting the pol and env2 antigens when co-injected.

All together, these data demonstrate the immunogenic activity of the compositions described and their ability to induce T cell responses against the major HBVantigens.

Claims

1. An immunogenic composition comprising at least one polypeptide or a nucleic acid molecule encoding said at least one polypeptide, wherein said at least one polypeptide is selected from the group consisting of:

(i) A polymerase moiety comprising at least 450 amino acid residues of a polymerase protein originating from a first HBV virus;

(ii) A core moiety comprising at least 100 amino acid residues of a core protein originating from a second HBV virus; and

(iii) An env moiety comprising one or more immunogenic domain(s) of 15 to 100 consecutive amino acid residues of a HBsAg protein originating from a third HBV virus; or

Any combination of said polymerase moiety, core moiety, env moiety, said nucleic acid molecule encoding said polymerase moiety, said nucleic acid molecule encoding said core moiety and/or said nucleic acid molecule encoding said env moiety.

2. The immunogenic composition according to claim 1, wherein said the immunogenic composition of the invention comprises a combination of at least two of said polymerase moiety, core moiety, env moiety or of at least two of said nucleic acid molecules encoding said polymerase moiety, said nucleic acid molecule encoding said core moiety and/or said nucleic acid molecule encoding said env moiety.

3. The immunogenic composition according to claim 2, wherein said composition is selected from the group consisting of (i) a composition comprising a combination of said polymerase moiety and said core moiety or a combination of nucleic acid molecules encoding said polymerase moiety and said core moiety; (ii) a composition comprising a combination of said core moiety and said env moiety or a combination of nucleic acid molecules encoding said core moiety and said env moiety; and (iii) a composition comprising a combination of said polymerase moiety, said core moiety and said env moiety or a combination of nucleic acid molecules encoding said polymerase moiety, said core moiety and said env moiety.

4. The immunogenic composition according to anyone of claims 1 to 3, wherein said first, second and third HBV virus are from different genotypes.

5. The immunogenic composition according to anyone of claims 1 to 3, wherein at least two of said first, second and third HBV viruses are from the same HBV genotype and preferably said first, second and third HBV viruses are from the same genotype.

6. The immunogenic composition according to claim 5, wherein said first, second and third HBV viruses are from genotype D and preferably from HBV isolate Y07587.

7. The immunogenic composition according to claim 5, wherein said first, second and third HBV viruses are from genotype B or C

8. The immunogenic composition according to anyone of claims 1 to 7, wherein said polymerase moiety is modified by truncation of at least 20 amino acid residues and at most 335 amino acid residues normally present at the N-terminus of a native HBV polymerase.

9. The immunogenic composition according to claim 8, wherein said truncation includes at least 45 and at most 50 amino acid residues, and preferably the first 47 or 46 amino acid residues following the initiator Met residue located at the N-terminus of a native HBV polymerase.

10. The immunogenic composition according to claim 9, wherein said polymerase moiety comprises an amino acid sequence which exhibits at least 80% of identity with the amino acid sequence shown in SEQ ID NO: 7.

11. The immunogenic composition according to anyone of claims 1 to 10, wherein said polymerase moiety is modified so as to exhibit a reduced reverse-transcriptase (RTase) enzymatic activity with respect to a native HBV polymerase.

12. The immunogenic composition according to claim 11, wherein said polymerase moiety comprises the substitution of the Asp residue corresponding to position 540 in SEQ ID NO: 1 and to position 494 in SEQ ID NO: 7 to any amino acid residue other than Asp, and preferably to a His residue.

13. The immunogenic composition according to anyone of claims 1 to 12, wherein said polymerase moiety is modified so as to exhibit a reduced RNase H enzymatic activity with respect to a native HBV polymerase.

14. The immunogenic composition according to claim 13, wherein said polymerase moiety comprises the substitution of the Glu residue corresponding to position 718 in SEQ ID NO: 1 and to position 672 in SEQ ID NO: 7 to any amino acid residue other than Glu, and preferably to a His residue.

15. The immunogenic composition according to claim 14, wherein said polymerase moiety comprises an amino acid sequence which exhibits at least 80% of identity with the amino acid sequence shown in SEQ ID NO: 8 or with the amino acid sequence shown in SEQ ID NO: 7 with the substitution of the Asp residue in position 494 to an His residue and the substitution of the Glu residue in position 672 to an His residue.

16. The immunogenic composition according to anyone of claims 1 to 15, wherein said polymerase moiety is fused in frame to a heterologous hydrophobic sequence.

17. The immunogenic composition according to claim 16, wherein the polymerase moiety is fused in frame to the signal and trans-membrane peptides of the rabies glycoprotein and wherein said rabies signal sequence is fused in frame at the N terminus and said rabies transmembrane sequence is fused in frame at the C-terminus of said polymerase moiety.

18. The immunogenic composition according to claim 17, wherein said polymerase moiety comprises an amino acid sequence which exhibits at least 80% of identity with the amino acid sequence shown in SEQ ID NO: 9.

19. The immunogenic composition according to anyone of claims 1 to 18, wherein said core moiety is modified by truncation of at least 10 amino acid residues and at most 40 amino acid residues normally present at the C-terminus of a native HBV core.

20. The immunogenic composition according to claim 19, wherein said truncation includes the last 35 amino acid residues of a native HBV core.

21. The immunogenic composition according to claim 20, wherein said core moiety comprises an amino acid sequence which exhibits at least 80% of identity with the amino acid sequence shown in SEQ ID NO: 10.

22. The immunogenic composition according to anyone of claims 1 to 21, wherein said core moiety is modified so as to exhibit a reduced recognition of and/or interaction with an HBV envelope protein with respect to a native HBV core.

23. The immunogenic composition according to claim 22, wherein said core moiety comprises an amino acid sequence which exhibits at least 80% of identity with the amino acid sequence shown in SEQ ID NO: 11.

24. The immunogenic composition according to anyone of claims 1 to 23, wherein said one or more immunogenic domain(s) in use in the present invention are selected from the group consisting of:

- The portion of an env protein (HBsAg) extending from position 14-51 (env 1 domain);
- The portion of an env protein (HBsAg) extending from position 165-194 (env 2 domain);
- The portion of an env protein (HBsAg) extending from position 81-106 (env 3 domain);
- The portion of an env protein (HBsAg) extending from position 202-226 (env 4 domain); and
- Any combination thereof.

25. The immunogenic composition according to claim 24, wherein said immunogenic domain(s) comprises an amino acid sequence which exhibits at least 80% of identity with any of the amino acid sequence shown in SEQ ID NO: 12-15.

26. The immunogenic composition according to claim 25, wherein said env moiety comprises an amino acid sequence which exhibits at least 80% of identity with the amino acid sequence shown in SEQ ID NO: 16 or in SEQ ID NO: 17.

27. The immunogenic composition according to anyone of claims 1 to 26, wherein said polymerase, core and/or env moieties are fused in frame in a single polypeptide chain by pairs or all together.

28. The immunogenic composition according to claim 27, wherein said env moiety is fused in frame to the C-terminus of said core moiety.

29. The immunogenic composition according to claim 28, wherein said fusion polypeptide of the core moiety with the env moiety is selected from the group consisting of:

- A polypeptide comprising an amino acid sequence which exhibits at least 80% of identity with the amino acid sequence shown in SEQ ID NO: 18;
- A polypeptide comprising an amino acid sequence which exhibits at least 80% of identity with the amino acid sequence shown in SEQ ID NO: 19; and
- A polypeptide comprising an amino acid sequence which exhibits at least 80% of identity with the amino acid sequence shown in SEQ ID NO: 20 or with the portion of the amino acid sequence shown in SEQ ID NO: 20 starting at residue 1 and ending at residue 251 or alternatively with the portion of the amino acid sequence shown in SEQ ID NO: 20 starting at residue 1 and ending at residue 221; or deleted versions thereof lacking residues 77-84 in SEQ ID NO: 20.

30. A nucleic acid molecule encoding the polymerase moiety as defined in anyone of claims 1 and 8 to 18, the core moiety as defined in anyone of claims 1 and 19 to 23 and the env moiety as defined in anyone of claims 1 and 24 to 29 or any combination thereof.

31. The nucleic acid molecule according to claim 30, wherein said nucleic acid molecule is selected from the group consisting of:

- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 21;
- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 22;
- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 21 with the substitution of the G nucleotide in position 1480 to a C, the G nucleotide in position 2014 to a C and the A nucleotide in position 2016 to a T;

- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 23;
- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 24;
- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 25; and
- A nucleic acid molecule comprising a nucleotide sequence which exhibits at least 80% of identity with the nucleotide sequence shown in SEQ ID NO: 26 or with the portion of the nucleotide sequence shown in SEQ ID NO: 26 starting at nucleotide 1 and ending at nucleotide 753 or with the portion of the nucleotide sequence shown in SEQ ID NO: 26 starting at nucleotide 1 and ending at nucleotide 663 or deleted versions thereof lacking the portion extending from the G in position 229 to the A in position 252 of SEQ ID NO: 26.

32. A vector comprising one or more nucleic acid molecule(s) as defined in claim 30 or 31.

33. The vector according to claim 32, wherein said vector is a plasmid or a viral vector.

34. The vector according to claim 33, wherein said viral vector is a replication-defective adenoviral vector.

35. The vector according to claim 34, wherein said nucleic acid molecule(s) is/are inserted in replacement of the E1 region.

36. The vector according to claim 33, wherein said viral vector is a poxviral vector and more particularly obtained from canarypox, fowlpox or vaccinia virus.

37. The vector according to claim 36, wherein said vaccinia virus is the modified Ankara (MVA) strain.

38. The vector according to any one of claims 32 to 37, wherein said vector carries the nucleic acid molecules encoding said polymerase moiety, said core moiety and said env moiety.

39. The vector according to any one of claims 32 to 37, wherein said vector carries only one or two of the nucleic acid molecules encoding said polymerase moiety, said core moiety and said env moiety.

40. The vector according to claim 39, wherein said vector is selected from the group consisting of:

(i) A MVA vector comprising a nucleic acid molecule placed under the control of a vaccinia promoter such as the 7.5K promoter and encoding a polymerase moiety comprising an amino acid sequence as shown in SEQ ID NO: 7, 8 or 9 or in SEQ ID NO: 7 with the substitution of the Asp residue in position 494 to an His residue and the substitution of the Glu residue in position 672 to an His residue;

(ii) A MVA vector comprising a nucleic acid molecule placed under the control of a vaccinia promoter such as the pH5r promoter and encoding a core moiety and an env moiety comprising an amino acid sequence as shown in SEQ ID NO: 18 or 19;

(iii) An E1-defective Ad vector comprising inserted in place of the E1 region a nucleic acid molecule placed under the control of the CMV promoter and encoding a polymerase moiety comprising an amino acid sequence as shown in SEQ ID NO: 7, 8 or 9 or in SEQ ID NO: 7 with the substitution of the Asp residue in position 494 to an His residue and the substitution of the Glu residue in position 672 to an His residue; and

(iv) An E1-defective Ad vector comprising inserted in place of the E1 region a nucleic acid molecule placed under the control of the CMV promoter and encoding a core moiety and an env moiety comprising an amino acid sequence as shown in SEQ ID NO: 18, 19 or 20 or the portion of SEQ ID NO: 20 starting at residue 1 and ending at residue 251 or the portion of SEQ ID NO: 20 starting at residue 1 and ending at residue 221.

41. An infectious viral particle comprising the nucleic acid molecule according to anyone of claims 30 to 31 or the vector according to anyone of claims 32 to 40.

42. The infectious viral particle according to claim 41, wherein said infectious viral particles is produced by a process comprising the steps of:

(e) introducing the viral vector of the invention into a suitable cell line,

(f) culturing said cell line under suitable conditions so as to allow the production of said infectious viral particle,

(g) recovering the produced infectious viral particle from the culture of said cell line, and

(h) optionally purifying said recovered infectious viral particle.

43. A host cell comprising the nucleic acid molecule according to anyone of claims 30 to 31, the vector according to anyone of claims 32 to 40 or the infectious viral particle according to claim 42 or 43.

44. A composition comprising the nucleic acid molecule according to anyone of claims 30 to 31, the vector according to anyone of claims 32 to 40 or the infectious viral particle according to claim 42 or 43 or the host cell according to claim 43 and a pharmaceutically acceptable vehicle.

45. The composition according to claim 44 which further comprises one or more adjuvant(s) suitable for systemic or mucosal application in humans.

46. The composition according to claim 44 or 45 which is formulated for intramuscular or subcutaneous administration.

47. The composition according to anyone of claims 44 to 46, which comprises from about 10^5 to about 10^{13} infection units of a viral vector or of an infectious viral particle.

48. Use of at least one of the HBV moieties as defined in any one of claims 1 and 8 to 29, of the immunogenic composition according to anyone of claims 1 to 29, of the nucleic acid molecule according to anyone of claims 30 to 31, of the vector according to anyone of claims 32 to 40, of the infectious viral particle according to claim 41 or 42, of the host cell according to claim 43 or of the composition according to anyone of claims 44 to 47 for the preparation of a drug intended for treating or preventing an HBV infection or an HBV-associated disease or pathologic condition.

49. A method for the treatment or prevention of an HBV infection, or an HBV-associated disease or pathologic condition, comprising administering to a human or animal organism in need thereof a therapeutically effective amount of at least one of the HBV moieties as defined in any one of claims 1 and 7 to 29, of the immunogenic composition according to anyone of

claims 1 to 29, of the nucleic acid molecule according to anyone of claims 30 to 31, of the vector according to anyone of claims 32 to 40, of the infectious viral particle according to claim 41 or 42, of the host cell according to claim 43 or of the composition according to anyone of claims 44 to 47.

50. The use according to claim 48 or the method according to claim 49, for treating a patient having a chronic hepatitis B viral infection.

51. The method or use according to anyone of claims 48-50, wherein said method or use is used in combination with standard of care.

52. The method or use according to claim 51, wherein said standard of care comprises cytokines and/or nucleotide or nucleoside analogs selected from the group consisting of lamivudine, entecavir, telbivudine, adefovir, dipivoxil and tenofovir.

53. A method of inducing or stimulating an immune response against HBV in a host organism comprising administering to said organism at least one of the HBV moieties as defined in any one of claims 1 and 7 to 29, of the immunogenic composition according to anyone of claims 1 to 29, of the nucleic acid molecule according to anyone of claims 30 to 31, of the vector according to anyone of claims 32 to 40, of the infectious viral particle according to claim 41 or 42, of the host cell according to claim 43 or of the composition according to anyone of claims 44 to 47, so as to induce or stimulate said immune response.

54. The method of claim 53, wherein said immune response is cellular and CD4+ and/or CD8+-mediated.

55. A kit of parts for use in the treatment of an HBV infection, wherein said kit comprises a plurality of active agents selected from the group consisting of the HBV moieties as defined in any one of claims 1 and 7 to 29, of the immunogenic composition according to anyone of claims 1 to 29, of the nucleic acid molecule according to anyone of claims 30 to 31, of the vector according to anyone of claims 32 to 40, of the infectious viral particle according to claim 41 or 42, of the host cell according to claim 43 or of the composition according to anyone of claims 44 to 47.

56. The kit of parts of claim 55, which comprises a first vector comprising a nucleic acid molecule encoding the polymerase moiety as defined in anyone of claims 1 and 7 to 18 and a second vector comprising a nucleic acid molecule encoding the core moiety and/or the env moiety as defined in anyone of claims 1 and 19 to 29.

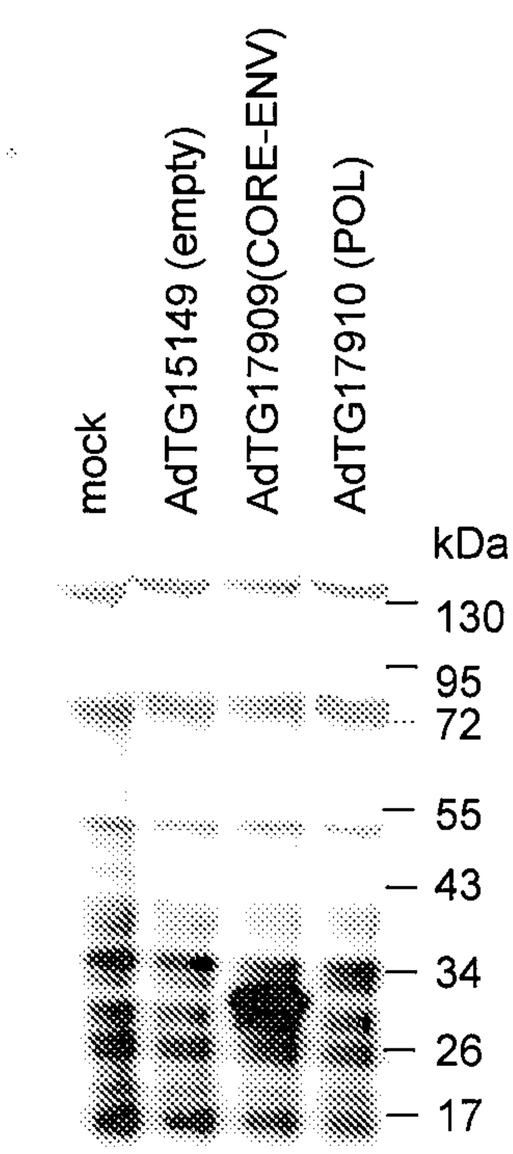
57. The kit of part according to claim 56, wherein said first vector is a MVA vector as defined in claim 40(i) and said second vector is a MVA vector as defined in claim 40(ii).

58. The kit of part according to claim 56, wherein said first vector is an Ad vector as defined in claim 40(iii) and said second vector is an Ad vector as defined in claim 40(iv).

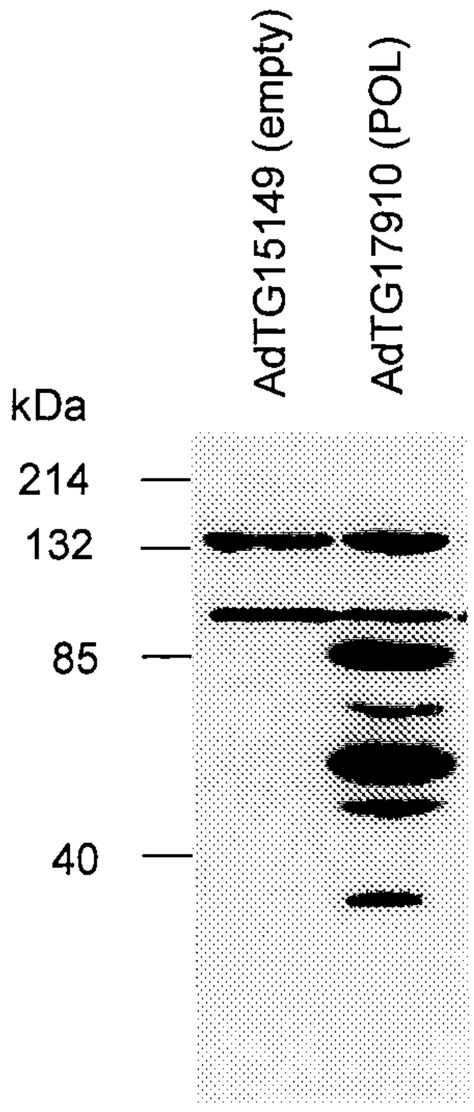
59. The kit of part according to anyone of claims 56 to 58, further comprising a third vector expressing an immunomodulator.

Figure 1

Fig. 1A

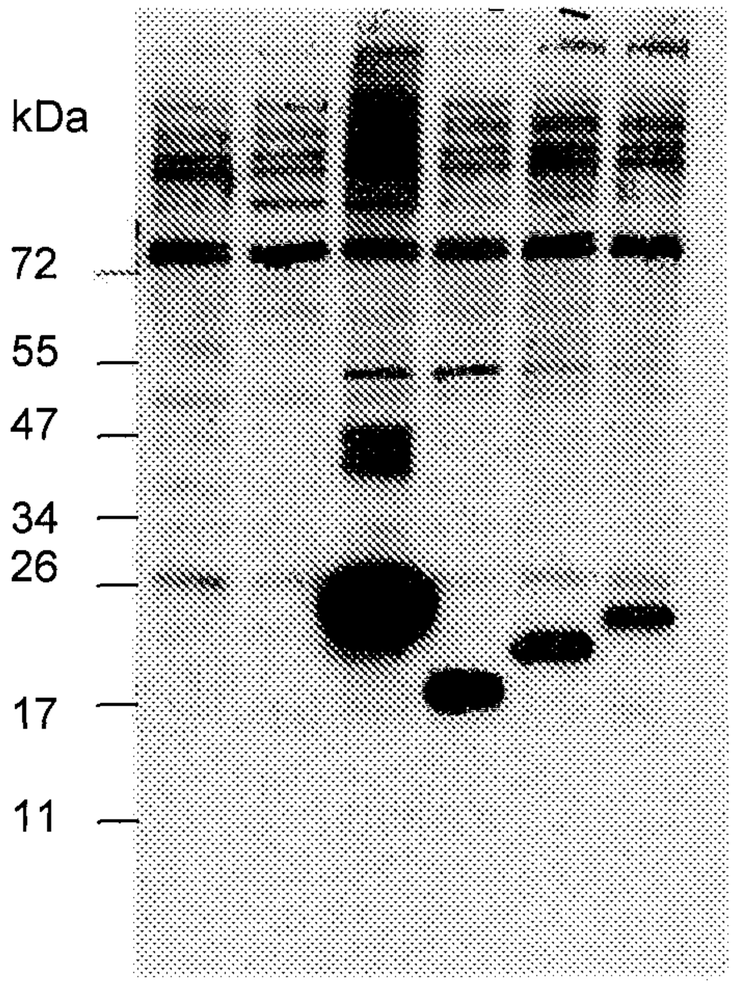


α-CORE C1-5 antibody

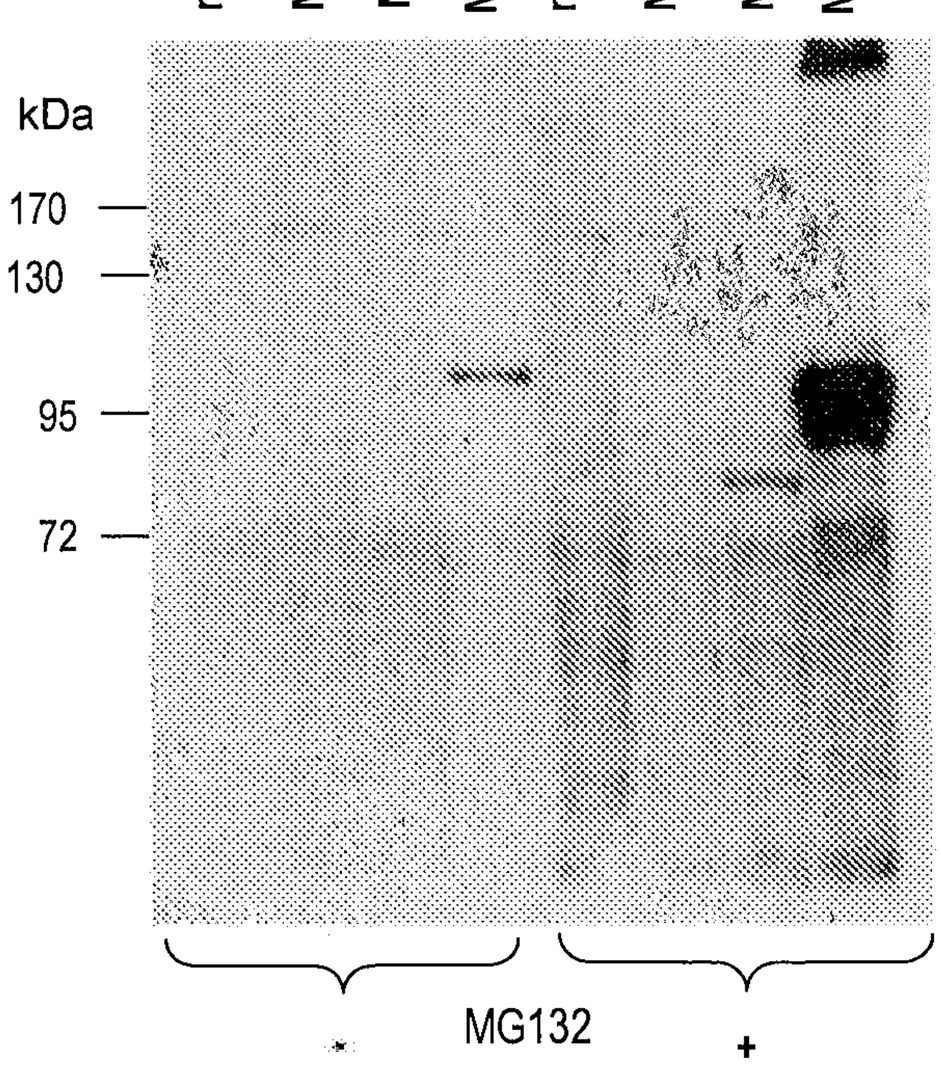


α-POL 8D5 antibody

Fig. 1B



α-CORE 13A9 antibody



α-POL 8D5 antibody

Figure 2

Fig. 2A -Specific T cell responses targeting Pol protein

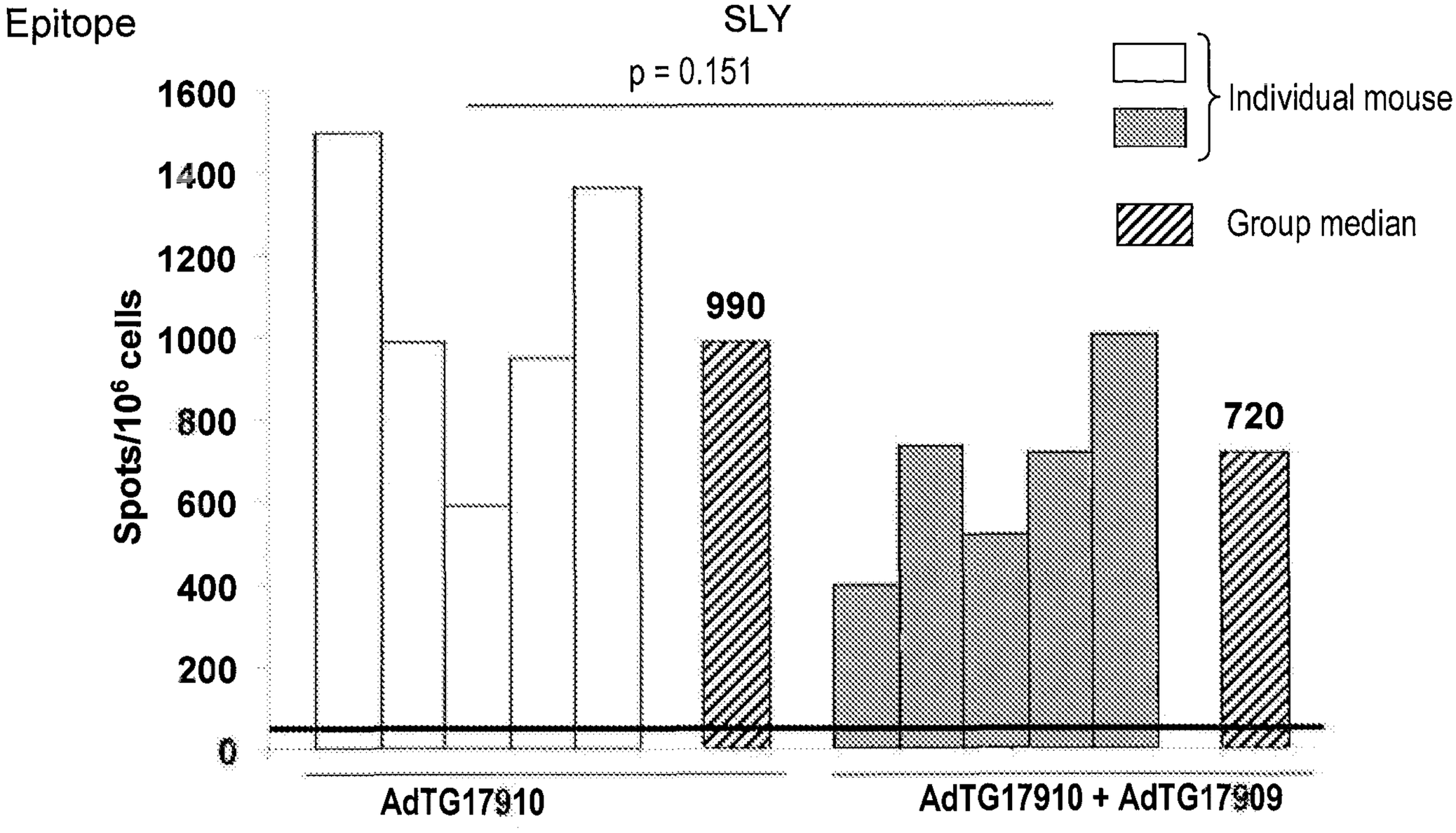


Fig. 2B -Specific T cell responses targeting Core protein

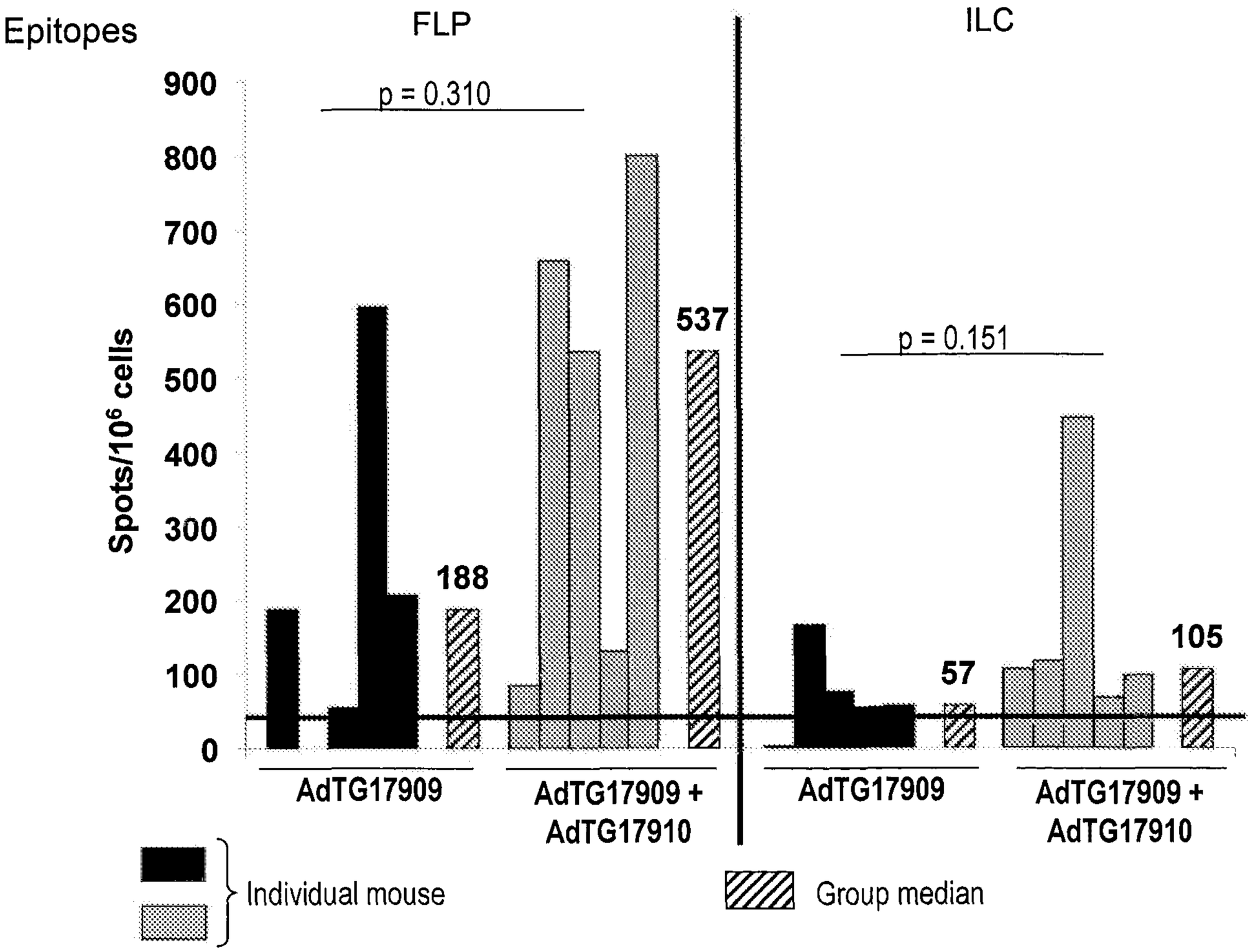


Figure 2

Fig. 2C - Specific T cell responses targeting Env domains

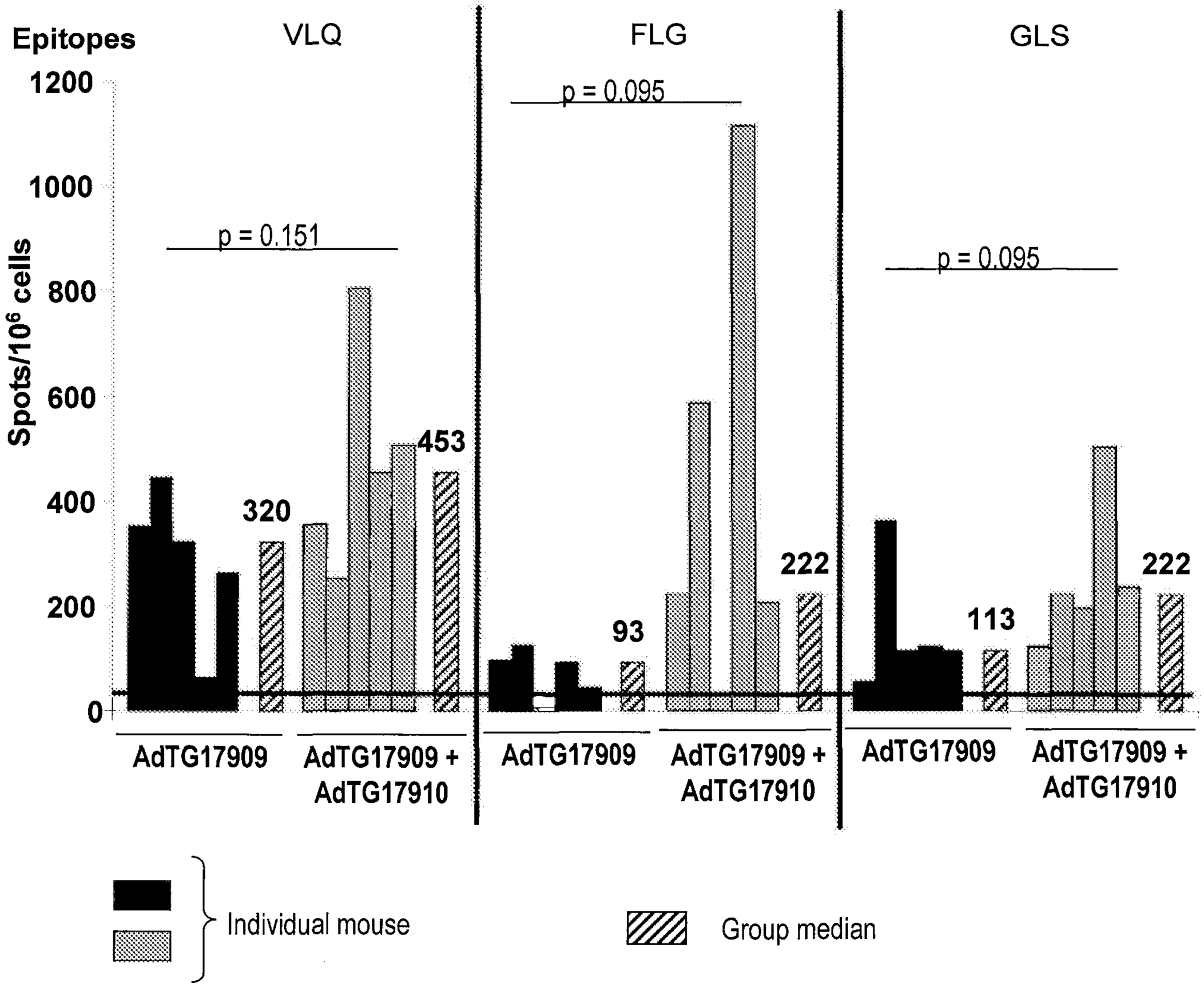


Figure 3

IFN γ CD8+ producing cells IFNγ + TNFα CD8+ producing cells TNF α CD8+ producing cells

Fig. 3A -AdTG17910 (Pol) alone



Fig. 3B -AdTG17909 (Core-env) alone

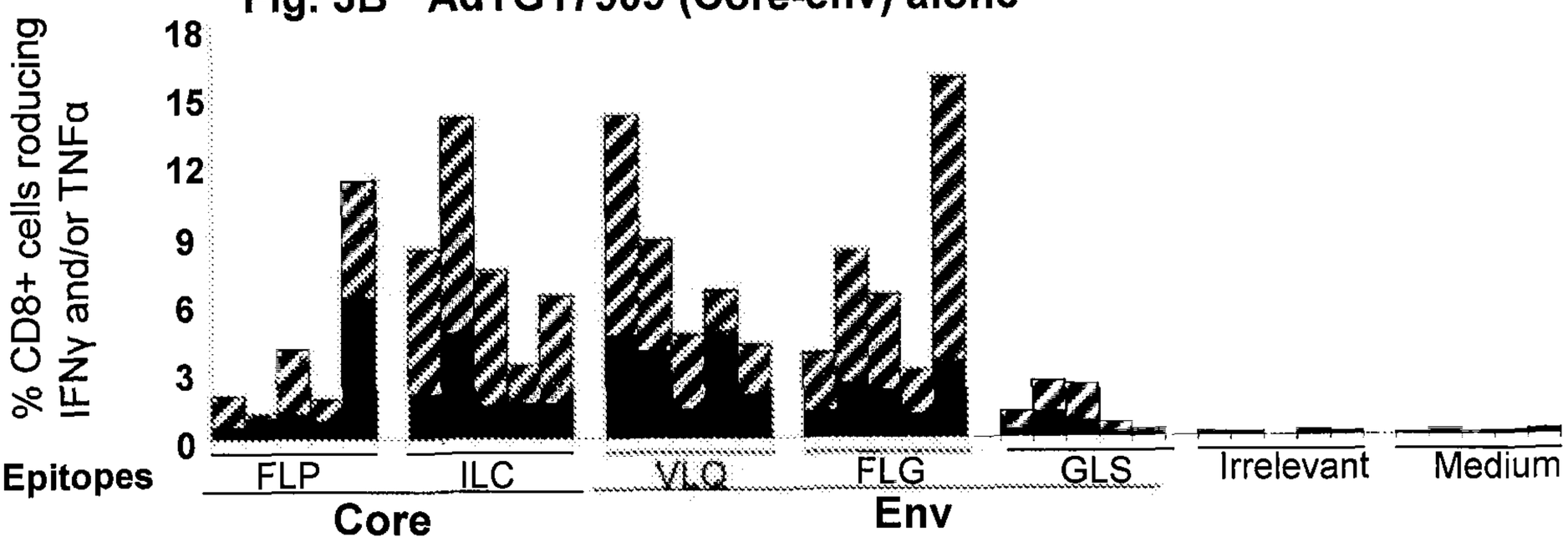


Fig. 3C -AdTG17910 (Pol) + AdTG17909 (Core-env)

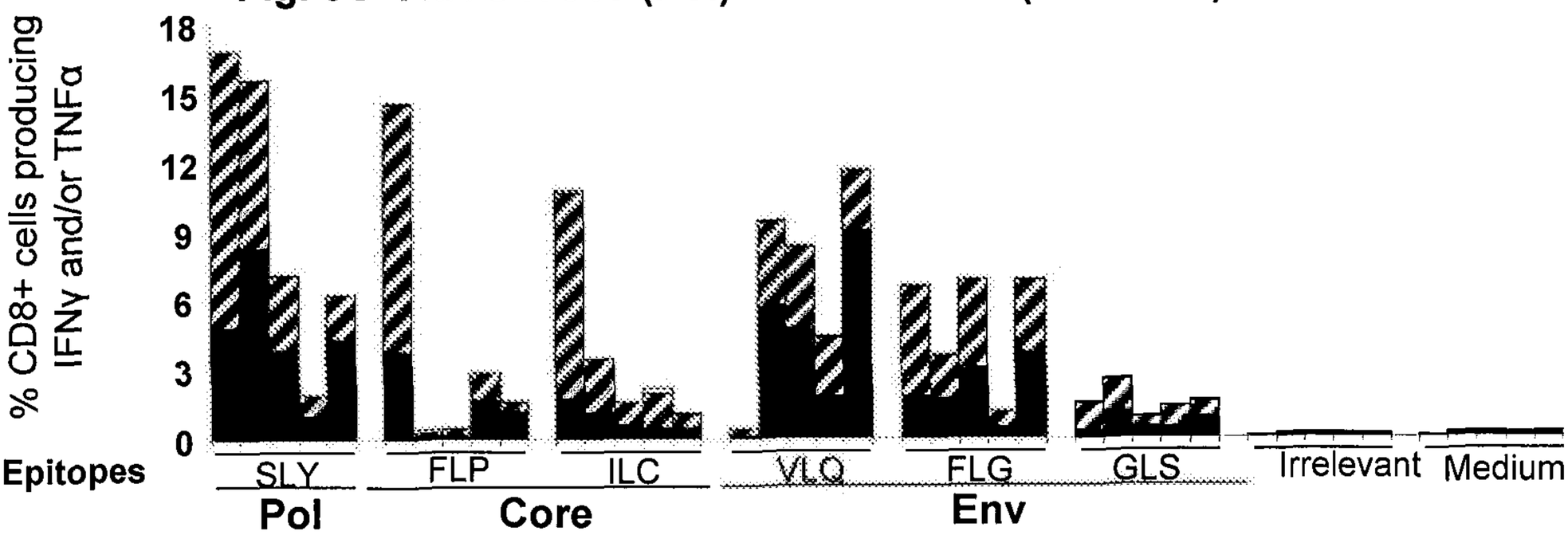


Figure 4

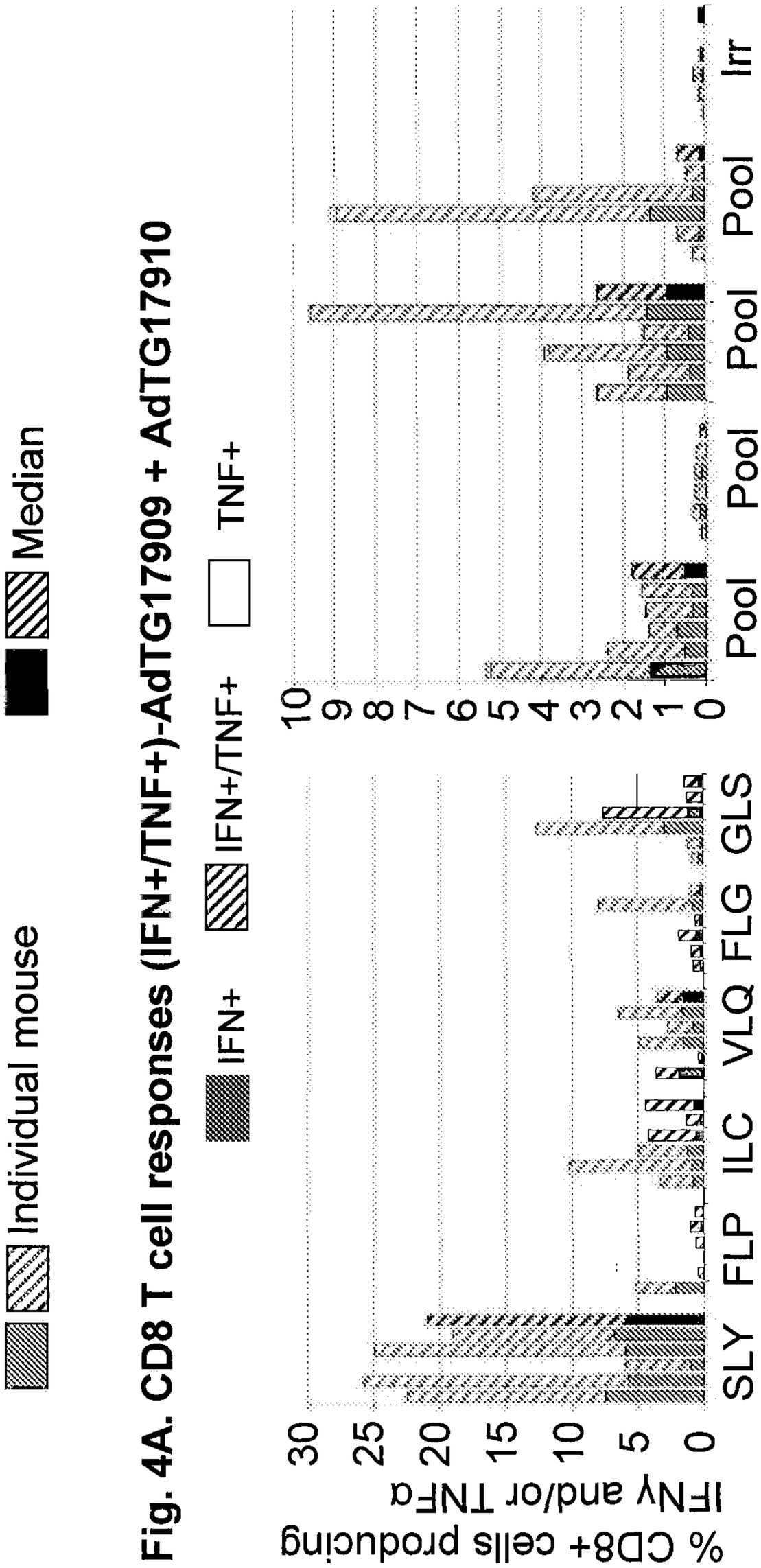


Fig. 4A.

Figure 4

Individual mouse Median

Fig.4B. CD4 T cell responses (IFN+/TNF+)-AdTG17909+ AdTG17910

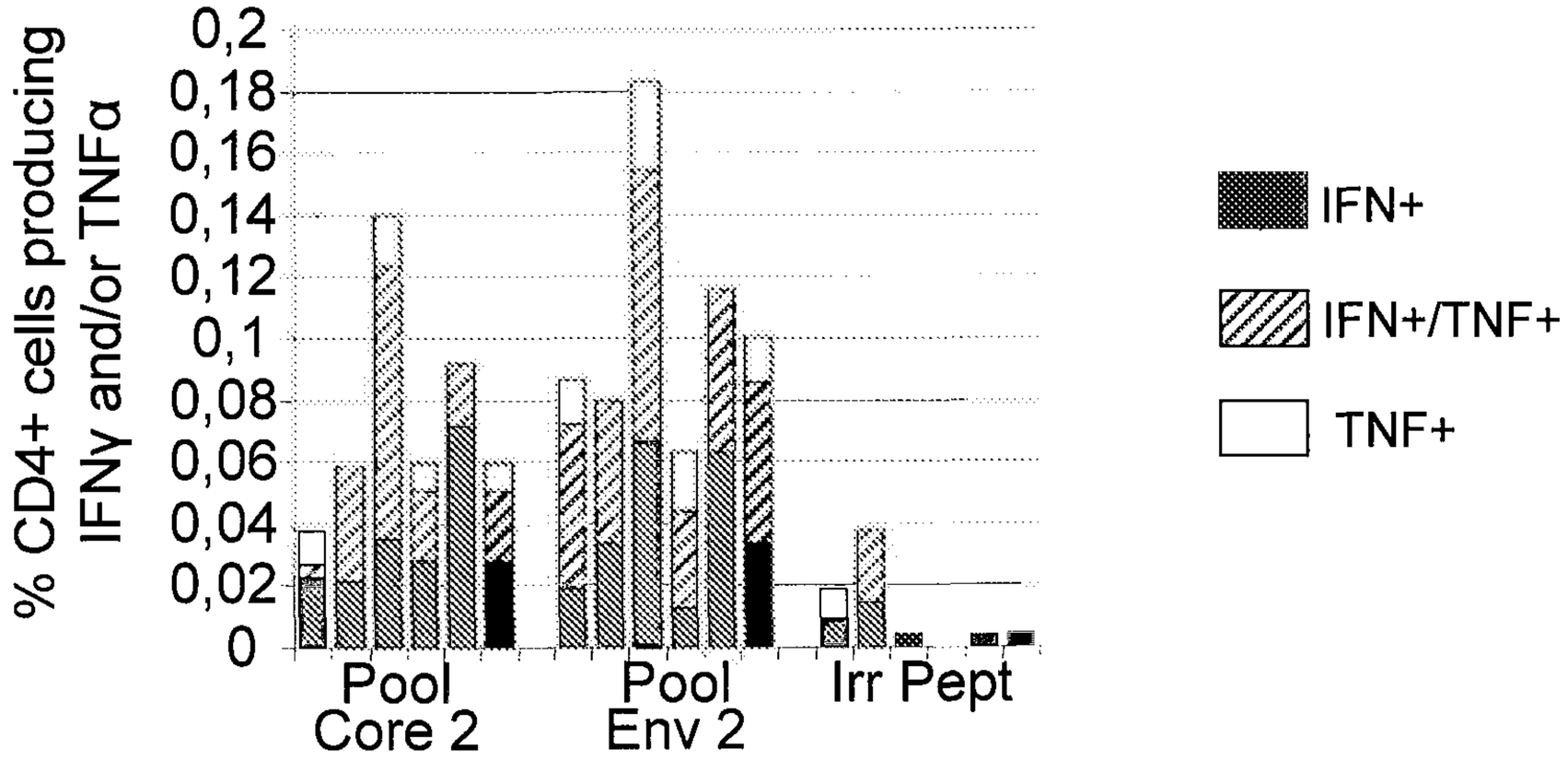


Fig. 4C. CD4 T cell responses (IFN+/IL2+)-AdTG17909+ AdTG17910

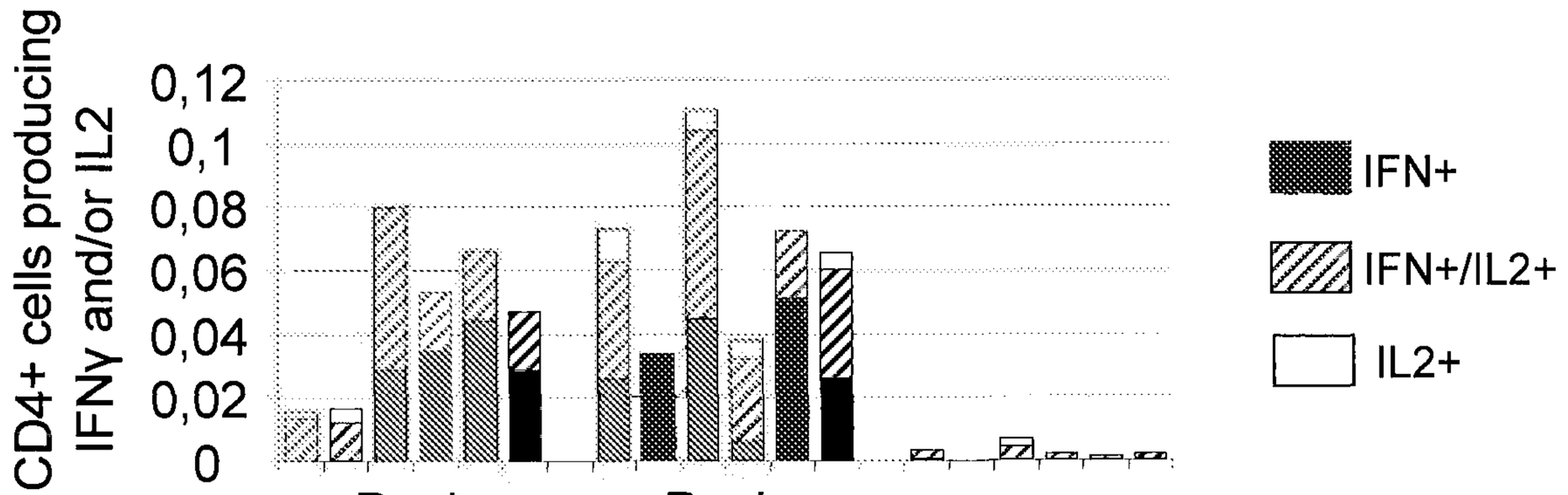


Figure 5

Fig5A. AdTG17909 + AdTG17910. *In vivo* lysis against SLY and ILC peptides

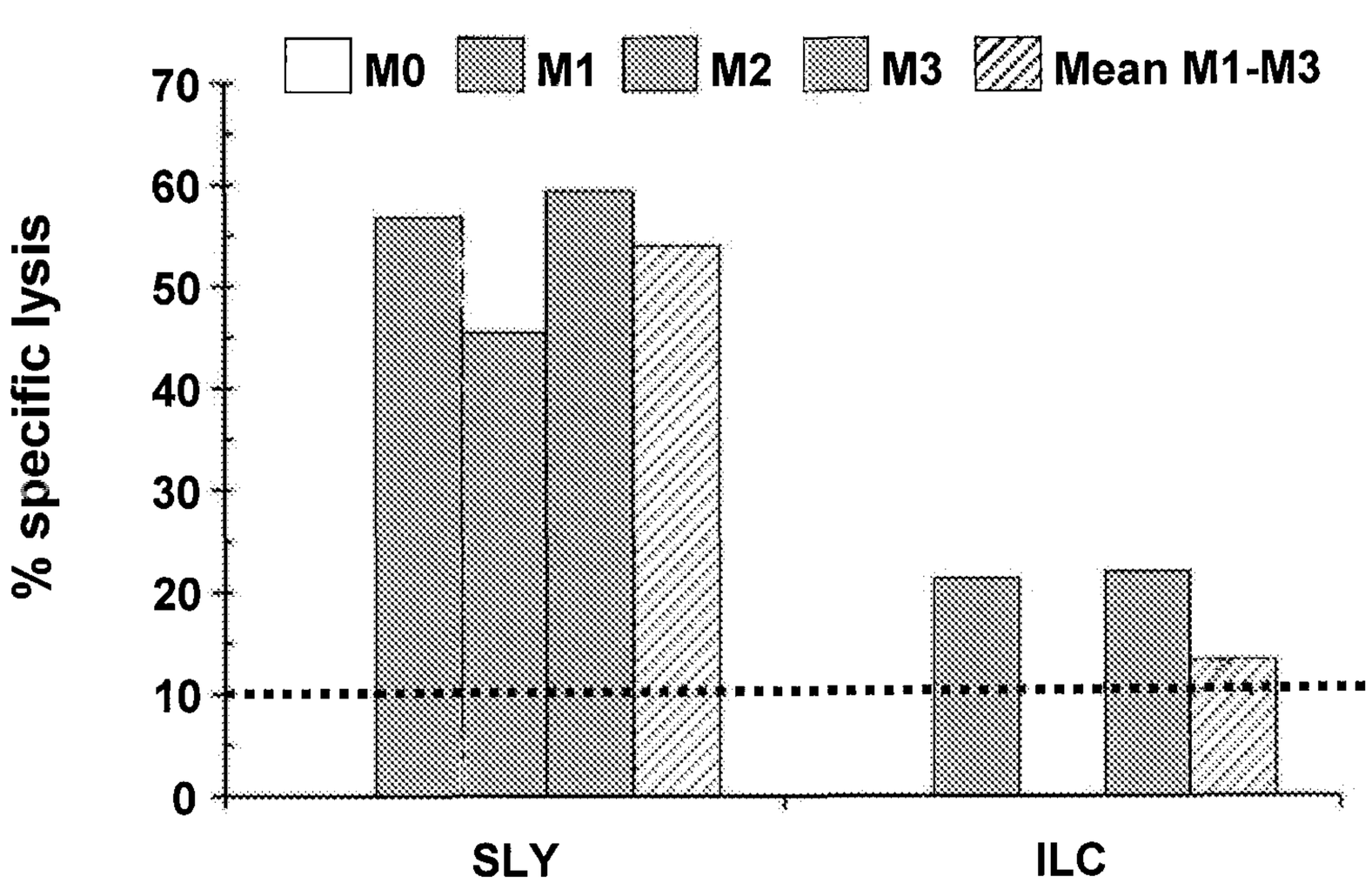


Fig.5B. AdTG17909 + AdTG17910. *In vivo* lysis against FLP and VLQ peptides

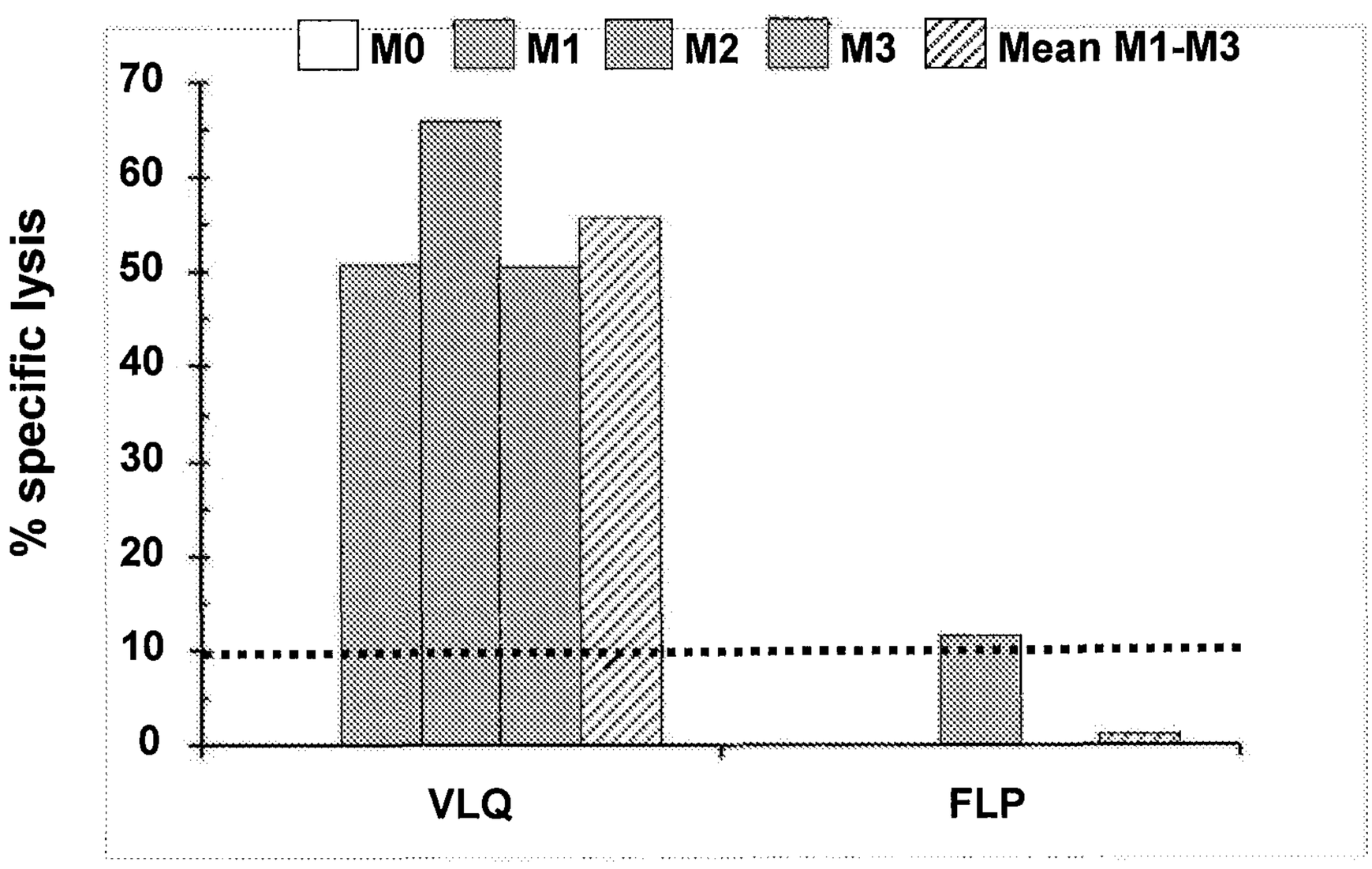


Figure 6

Figure 6A. MVA TG17842 or MVA TG17843

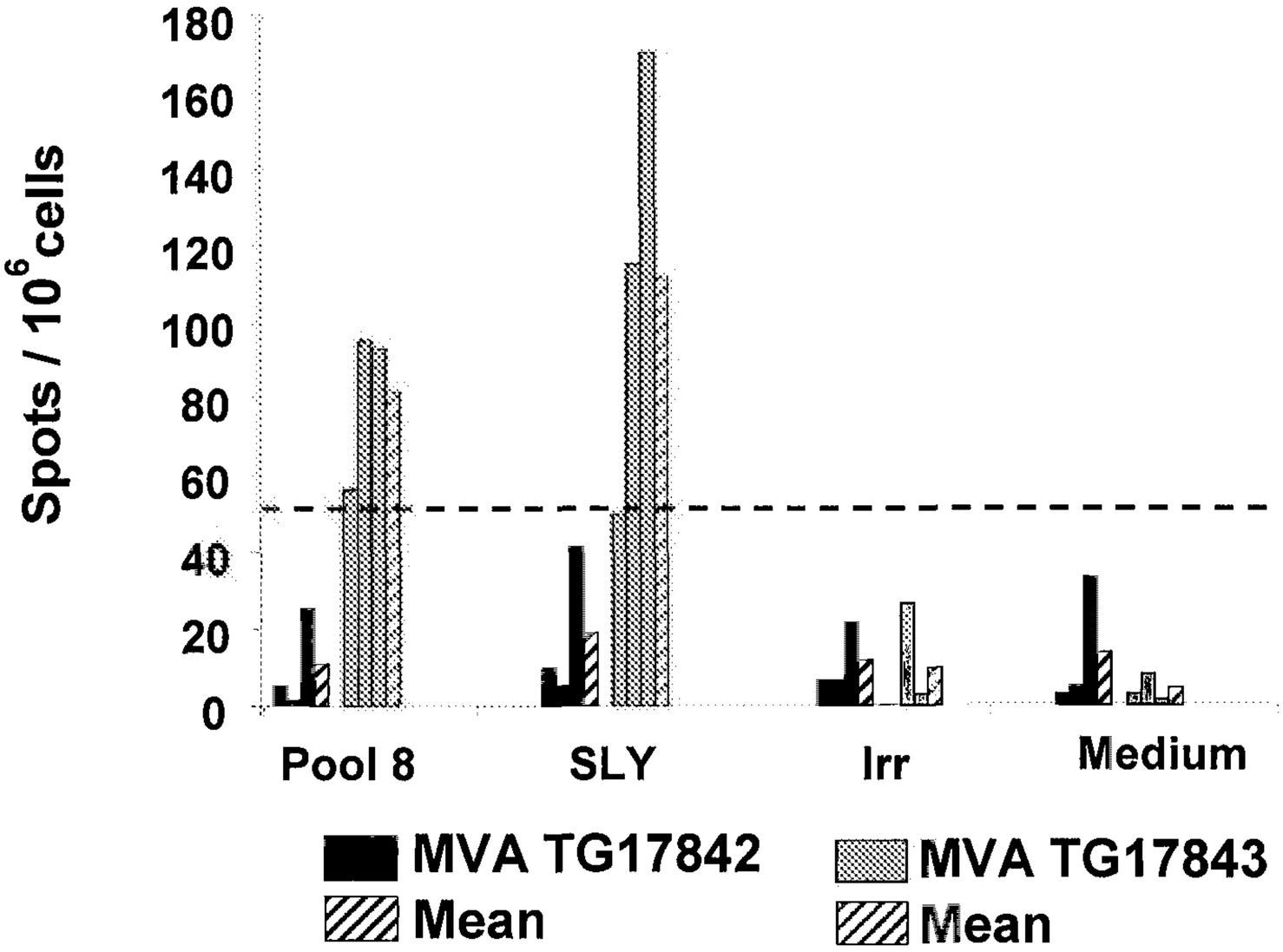


Figure 6B. MVA TG17971

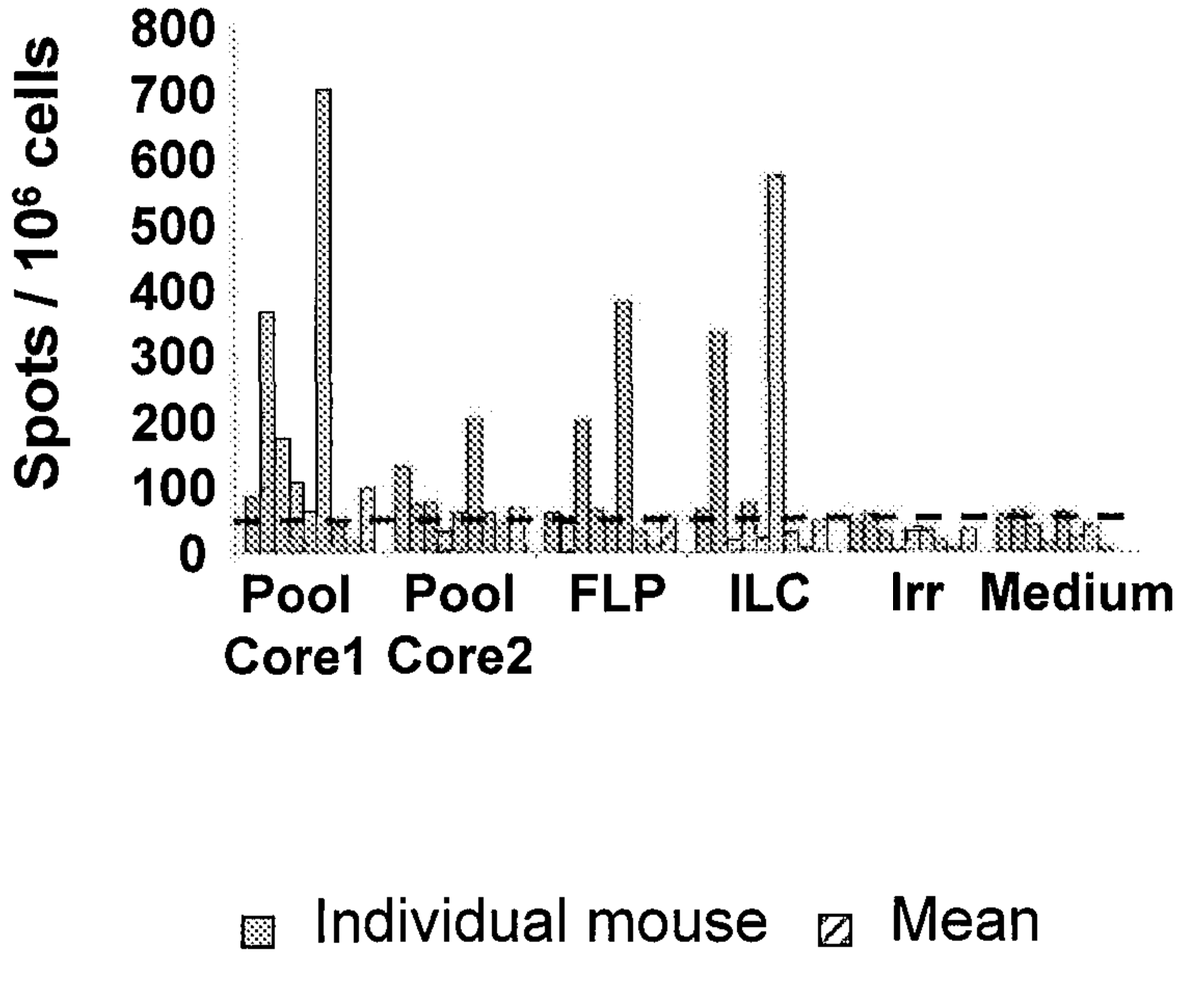


Figure 7

Figure 7A. MVA TG17972 + MVA TG17843

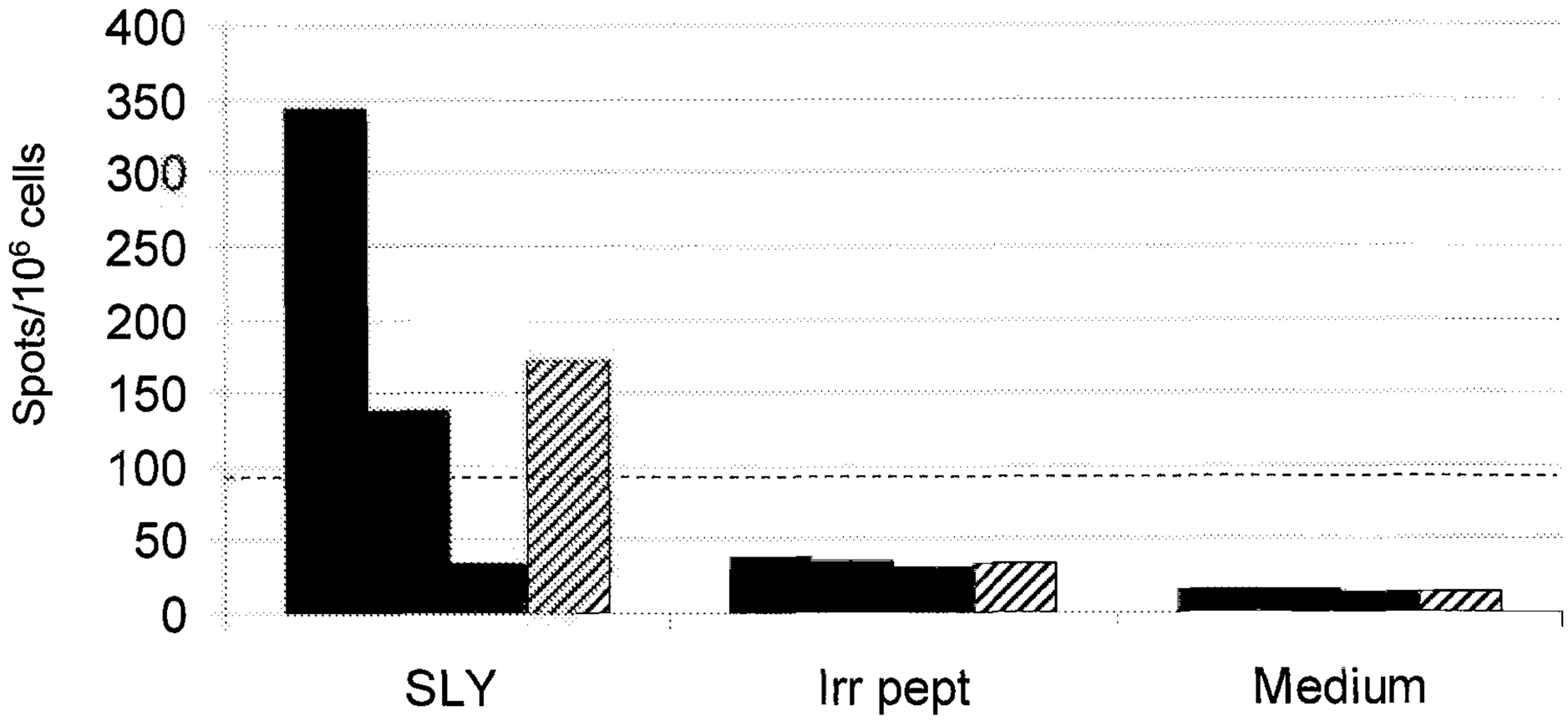


Figure 7B. MVA TG17993 + MVA TG17843

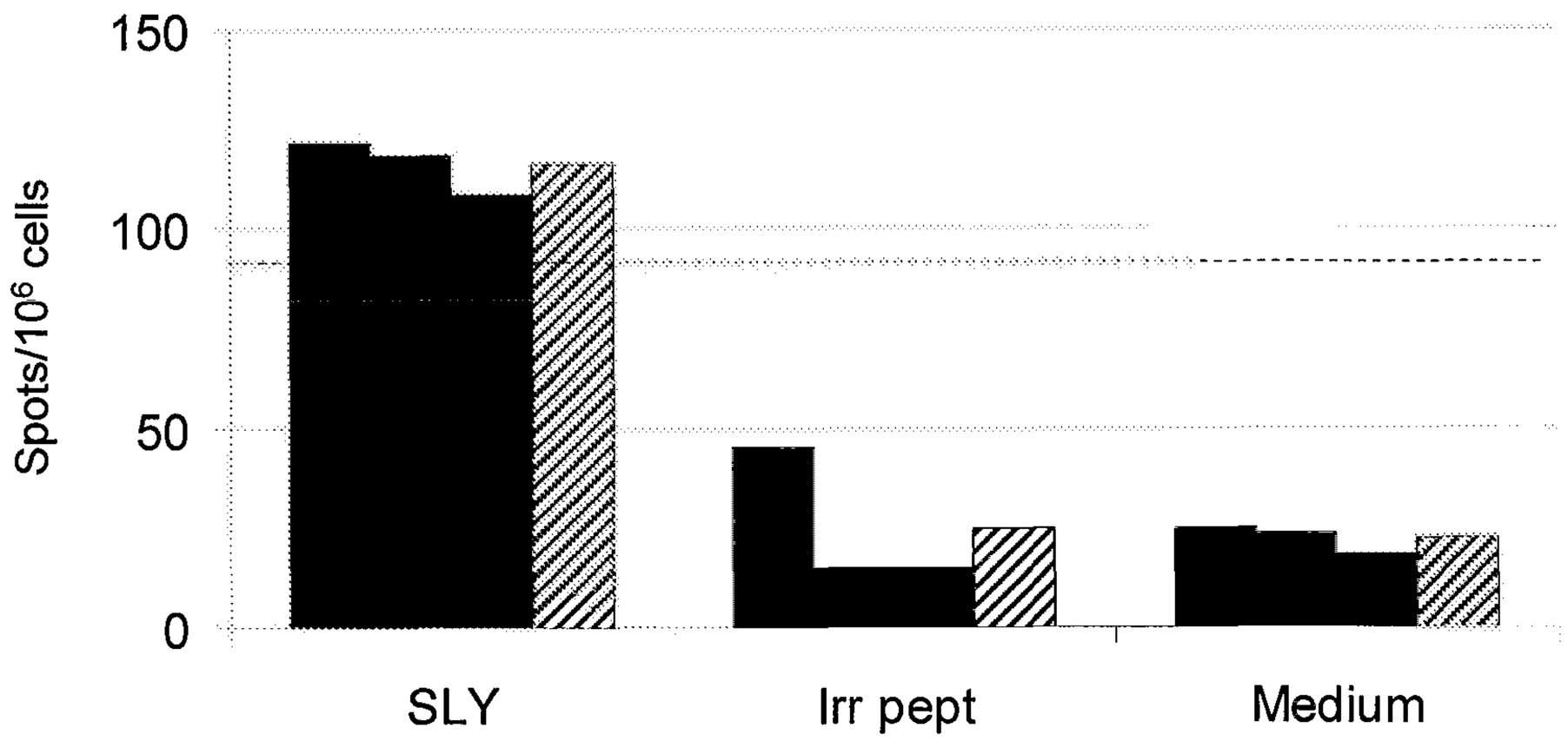


Figure 7C. MVA TG17994 + MVA TG17843

