Mycobacterial antigen vaccine

FIELD OF THE INVENTION

The present invention relates generally to novel immunogenic combinations comprising at least five antigens of a Mycobacterium species as well as fusion thereof and nucleic acid molecules encoding such combined antigens and fusion, where the antigens are from a Mycobacterium species, particularly a Mycobacterium of the tuberculosis complex such as *Mycobacterium tuberculosis (Mtb)*. The present invention also relates to vectors, host cells and compositions comprising or encoding said combinations of mycobacterial antigens and fusion polypeptides as well as to methods for expressing and producing them. The present invention also relates to methods of using said combinations of mycobacterial antigens, fusion polypeptides, vectors, host cells, compositions particularly for inducing or stimulating an immune response with the goal of providing a protective response against a Mycobacterium infection or any disease caused by or associated with a Mycobacterium infection. The present invention also concerns antibodies directed to the mycobacterial antigens and fusion polypeptides in use in this invention that can be used in the diagnosis of a Mycobacterium infection and diagnosis kits comprising said combinations of mycobacterial antigens, fusion polypeptides, vectors, host cells and compositions.

BACKGROUND OF THE INVENTION

With an estimated one third of the world's population infected with *Mycobacterium tuberculosis* (*Mtb*) (i.e. more than two billion individuals) and 9 to 10 million new cases and 2 million deaths every year, tuberculosis (TB) is a global and worldwide health problem. *Mycobacterium tuberculosis* (*Mtb*) bacillus, the causative agent of TB, possesses a circular genome of 4 411 529 base pairs (bp) which was fully sequenced in 1998 (Cole et al., 1998, Nature 393: 537-44). *Mtb* encodes approximately 4000 genes; however the function and role in *Mtb* life cycle and pathogenesis of the majority of these genes have not yet been elucidated yet. It has been hypothesized for a long time that separate sets of genes are expressed during distinct and sequential infection phases, namely the active phase followed by the latent state and, when conditions are gathered, the resuscitation phase leading to a novel active phase. Recent evidence has shaken this classical dogma and the field is now acknowledging that a certain "leakiness" is taking place, i.e. expression of genes can happen

in a phase-independent manner although to various thresholds. Moreover the latent nature of *Mtb* is also disputed: are bacteria mostly dormant, non-replicating, or do they continue to replicate and sometimes even escape from the infected cells into adjacent airways, thereby inducing recurring immune responses? (Ehlers et al., 2009, Infection 37: 87-95).

Generally, person-to-person transmission occurs by aerosolized droplets generated by a person suffering from pulmonary TB (active disease). Among those infected (an estimated 30% of exposed individuals), only 5–10% will develop active TB disease within 2 years post-exposure (known as primary TB). However, the majority of infected individuals develop latent infection (LTBI) which can last decades without clinical signs or symptoms of disease. LTBI represents a state of equilibrium in which the infected subject is able to control the infection but not completely eradicate the bacteria. Reactivation (active TB after remote infection) may occur at a later stage, particularly in the elderly or in immunocompromised individuals as in the case of HIV infection and treatment with TNF inhibitors. The risk of TB reactivation is estimated as 10% per lifetime and impaired immunity increases the risk to 10% per year.

There are several lines of evidence suggesting that stimulation of the cellular immune system plays a role in controlling TB disease (Rook et al. 2007, J Infect Dis 196:191-8). The central role of CD4 T lymphocytes to control the pathogen and prevent progression to disease (approximately 90% of *Mtb* infected subjects) is well established. For instance, HIV/AIDS patients with low $CD4^+$ T cells count are more susceptible to progression to TB disease while antiviral treatments that elevate $CD4^+$ T cells reduce progression to TB disease. However, CD4 T cells do not operate alone and are supported by CD8 T cells and other T cell subsets. In this respect, experience with tumor necrosis factor-alpha (TNFa) blockers and genetic polymorphisms such as interferon-gamma (IFNg) and other receptor deficiencies demonstrate the importance of specific cytokines and cytokine networks in controlling the disease, implicating the cellular immune nature of TB control in humans (Cooper et al., 2009, Annu Rev Immunol 27: 393-422).

The *Mtb*-caused million deaths every year are particularly dramatic considering that both vaccine (Bacille-Calmette-Guerin (BCG)) and antibiotics exist and are widely used. However, if BCG appears to be effective at preventing disease in newborns and toddlers, it does not protect adults and fails to prevent *Mtb* reactivation in latently infected persons. On the other hand, treatment of active TB with various antibiotic combinations appears efficacious but requires strong patient compliance with daily administrations of different drugs over several months. Moreover, while antibiotics are very efficient against wild type

Mtb strains when taken properly, there is an alarming rate of appearance of drug resistant *Mtb* strains (e.g."MultiDrug Resistant" (MDR), "eXtensively Drug-Resistant" (XDR) and "Totally Drug Resistant" (TDR) strains), mostly because of improper observance of this lengthy and costly drug regimen treatment. Development of effective TB vaccines is therefore a priority in this worrying context and two main approaches are being investigated for the last decade: replacement of BCG and BCG booster. More than a dozen vaccine candidates are now in clinical trials (for a review see Ottenhoff and Kaufmann, 2012, PLoS 8(5): e1002607). In addition, the field has also more recently considered using novel vaccine formulations to help in the treatment of *Mtb* infection, so called "therapeutic vaccines" to be used as novel stand-alone treatment or alternatively to adjunct to standard therapy, in particular for the treatment of drug resistant strains.

BCG replacement candidates aim at improving BCG efficacy and safety and are mainly based on live attenuated bacteria such as genetically modified BCG or *Mtb* strains engineered to express new sets of antigens that are absent from BCG or to overexpress *Mtb* antigens that BCG expresses but at a likely insufficient level or still to delete virulence genes and their regulators. Various recombinant BCG constructs have entered clinical trials to test their ability to substitute BCG. The most advanced VPM1002 currently in a Phase II trial is a urease-deficient rBCG that expresses the thiol-activated, cholesterol-binding listeriolysin (hly) from *Listeria monocytogenes* that has been shown to be safer than BCG in immunocompromised animals and to provide a superior protection in mice against challenge with *Mtb* (Grode et al., 2005, J Clin Invest 115: 2472-9). Two additional rBCG have recently entered clinical assessment, respectively rBCG30 expressing Ag85B and AERAS422 expressing Ag85A, Ag85B and Rv3407 together with perfringolysin.

BCG boosters aim at inducing cellular and/or humoral immune responses and generally rely on recombinant vaccines designed for providing TB antigens, either as protein composition generally admixed with potent Th1-activating adjuvants or through viral expressing vectors, (for a review see Thaissa et al., 2010, Yale J. of Biol. and Medicine 83: 209-15; Andersen, 2007, Nature 5: 484 and Kaufman, 2012, Trend in Immunology 241: 1-7). Among the 4000 potential TB antigens, a number of them proved immunogenic in preclinical models.

One of the most advanced protein-based candidates is the hybrid 1 (H1) protein which consists of Ag85B fused to ESAT-6 (Langermans et al., 2005, Vaccine 23: 2740-50; Dietrich et al., 2007, J. Immunol. 178: 3721-30). A strong CD4+ Th1 IFNg-mediated response was observed in humans when administered with IC31 adjuvant (Van Dissel et al.,

2010, Vaccine 28: 3571-81). More recently, this vaccine was found to boost immune responses previously induced by either BCG or latent *Mtb* infection (Van Dissel, 2011, Vaccine 29: 2100-9). Another fusion protein Hyvac 4 (H4), which consists of Ag85B fused to the TB10.4 (Aagaard et al., PLoS One 4: 1-8) is in a parallel development program. The GSK's M72 fusion protein made of Rv1196 inserted in the middle of the serine protease Rv0125 showed a favourable clinical profile in terms of safety and immunogenicity when administered with different synthetic adjuvants (Von Eschen et al., 2009, Hum Vaccine 5: 475-82). One may also cite the so-called ID fusion proteins (WO2008/124647) such as ID83 made of Rv1813, Rv3620 and Rv2608 (Baldwin et al., 2009, Vaccine 27: 3063-71) and ID93 including Rv3619 fused to the three ID83 antigens (Bertholet et al., 2010, Sci Transl Med 2(53): 53ra74).

Viral-vectored TB vaccines that are being tested in clinical trials include the modified vaccinia virus Ankara (MVA) expressing the Ag85A antigen (MVA85A/Aeras-485; WO2006/72787), and the replication-deficient adenovirus (Ad) 35 expressing Ag85A, Ag85B and TB10.4 antigens (Crucell Ad35/Aeras-402; WO2006/053871). MVA85A has proved immunogenic in both naïve as well as BCG primed individuals, inducing high CD4+ T cell response (Mc Shane et al., 2004, Nat Med 10: 1240-4; Scriba et al., 2010, Eur J Immunol 40: 279-90) whereas Aeras-402 seemed to favor CD8 T cell and IFNg responses (Radosevic et al., 2007, Infect Immunol 75: 4105-15; Magalhaes et al., 2008, PLoS One 3, e3790; Abel et al., 2010 Am J Respir Crit Care Med 181: 1407-17).

More recent studies now focuse on multi-phasic compositions (see e.g. WO2008/124647 and WO2011/144951). Some of these vaccine candidates have produced results in preclinical and clinical studies that demonstrate an ability to induce a robust cellular mediated immune response against *Mtb* (Thaissa et al., 2010, Yale J. of Biol. and Medicine 83: 209-15; Delogu et al., 2009, J Infect Developing Countries 3: 5-15). For example, the H56 fusion protein combining the latent *Mtb* Rv2660 together with the active Ag85B and ESAT-6 antigens showed potentially promising BCG booster activity although it has not yet reached clinical trials (Aagaard et al, 2011, Nature Med 17: 189-94; Lin et al., 2012, J Clin Invest 122: 303-14). However, these studies have highlighted the influence of various factors on the T cell response and protective efficacy such as the antigen doses (e.g. Aagaard et al., PLoS One 4: 1-8) and administration routes (Goonetilleke et al., 2003, J. Immunol. 171: 1602-9).

Tuberculosis is far from being controlled for different reasons: poor patient compliance with the prescribed standard-of-care in areas with limited resources, exacerbation of TB epidemics due to HIV coinfection, poor performance of BCG vaccination which is ineffective in protecting adults. In view of the increasing worldwide threat of TB and the inherent complexity of the *Mtb* infection and anti-mycobacterial immune response, there remains a need for improved vaccine strategies for diagnosing, preventing and treating tuberculosis, especially in endemic regions.

The present invention fulfils this and other needs by providing an immunogenic combination of *Mtb* antigens that is tailored for all phases of the natural course of infection.

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.

BRIEF SUMMARY OF THE INVENTION

The present invention relates generally to an immunogenic combination comprising at least 5 different antigens or nucleic acid molecules encoding the at least 5 antigens, wherein said antigens are independently obtained from a Mycobacterium species, particularly from a Mycobacterium species of the tuberculosis complex such as *Mycobacterium tuberculosis* (*Mtb*). A data mining scoring system was developed and used to classify a panel of *Mtb* antigens based on their immunogenicity and protection properties. Upon sequence alignment, biochemical and bioinformatics prediction studies, 14 *Mtb* antigens were selected and combined into antigen/vector combination and fusion polypeptides.

In one aspect of the invention, the antigen combination of the invention is multiphasic where the at least 5 mycobacterial antigens are from two or the three phases of the natural course of a Mycobacterium infection, namely the active, latent and resuscitation phases. The mycobacterial antigens can be employed/expressed in the form of mixture or in one or more fusion polypeptide(s) as described herein.

The present invention also concerns fusion polypeptides of specific mycobacterial antigens, nucleic acid molecules and vectors encoding/expressing such fusion polypeptides and compositions comprising or encoding said fusion polypeptides as well as methods of

preparing said fusions, vectors and compositions. The present invention also relates to antibodies against such mycobacterial antigens and fusion polypeptides. It further relates to the use of such immunogenic combinations, fusion polypeptides, nucleic acid molecules, vectors, compositions or antibodies for the purpose of the diagnosis, prevention, or treatment of a Mycobacterium infection or ameliorating a condition associated with a Mycobacterium infection.

A further aspect of the present invention includes a method of treating, preventing or inhibiting a Mycobacterium infection or ameliorating a condition associated with Mycobacterium infection in a subject in need thereof, comprising providing or administering this immunogenic combination, fusion polypeptide, nucleic acid molecule, vector or composition.

Still a further aspect of the present invention concerns a method of eliciting an immune response in a subject in need thereof, comprising providing or administering this immunogenic combination, fusion polypeptide, nucleic acid molecule, vector or composition, for the purpose of inducing or stimulating an immune response in this subject or for preventing or treating a Mycobacterium infection.

Still yet aspect of the present invention provides a kit of parts comprising a plurality of containers and instructions for providing or administering to a subject this immunogenic combination, fusion polypeptide, nucleic acid molecule, vector or composition.

Still yet more aspect of the present invention provides a kit of reagents for antibody assay for diagnosis of a Mycobacterium infection (e.g. tuberculosis) comprising this immunogenic combination, fusion polypeptide, nucleic acid molecule, vector or composition.

The antigen combination provided by the invention offers improved and unexpected immunogenic properties (e.g. level, quality and/or scope of the immunogenic response) as compared to the individual antigens.

The present invention is particularly useful in the context of immunotherapy as stand alone or as BCG booster for preventive or therapeutic purposes in the Mycobacterium infection field, e.g. preventing *Mtb* infection and/or prevention of primary TB and/or prevention of reactivation in latently infected subjects. It can also be used in association with standard (e.g. antibiotic-therapy) or any other novel treatment that is currently developed (e.g. small direct or indirect inhibitor molecules; antibodies or immunotherapeutics, etc). The present invention is also useful in the veterinary field, for example to reduce or abolish the

risk of Mycobacterium infection and/or active disease in animals, especially in bovine and goat breedings.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates generally to an immunogenic combination comprising at least 5 antigens of a Mycobacterium species or nucleic acid molecules encoding said at least 5 antigens.

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.

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.

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 term “polypeptide” refers to a polymer of amino acid residues which comprises at least nine or more amino acids bonded via covalent peptide bonds. The polypeptide can be linear, branched or cyclic and may comprise naturally occurring and/or amino acid analogs. It may be chemically modified by being glycosylated, lipidated, acetylated, cleaved, cross-linked by disulfide bridges and/or phosphorylated, or still by containing additional amino acids such as tag (his, myc, Flag, etc) or a targeting peptide (signal peptide, trans-membrane domain, etc). It will be understood that the term “polypeptide” encompasses proteins (usually employed for polypeptides comprising 50 or more amino acid residues), oligopeptides, and peptides (usually employed for polypeptides comprising less than 50 amino acid residues). Each polypeptide may thus be characterized by specific amino acids and be encoded by specific nucleic acid sequences.

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. Thus, a polypeptide "comprises" an amino acid sequence when the amino acid sequence might be part of the final amino acid sequence of the polypeptide. Such a polypeptide can have up to several hundred additional amino acids residues (e.g. tag and targeting peptides as mentioned herein). "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 carriers. 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. "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.

The term "identity" refers to an amino acid to amino acid or nucleotide to nucleotide correspondence between two polypeptide or nucleic acid sequences. The percentage of identity between two sequences 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 available at NCBI or ALIGN in Atlas of Protein Sequence and Structure (Dayhoffed, 1981, Suppl., 3: 482-9). Programs for determining identity between nucleotide sequences are also available in specialized data base (e.g. Genbank, the Wisconsin Sequence Analysis Package, BESTFIT, FASTA and GAP programs). For illustrative purposes, "at least 80% identity" means 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%.

As used herein, "operably linked" means that the elements being linked are arranged so that they function in concert for their intended purposes. For example a promoter is operably linked to a nucleic acid molecule if the promoter effects transcription from the transcription initiation to the terminator resulting in the expression of the coding sequence present in the nucleic acid molecule in a permissive host cell.

As used herein, the terms "Mycobacterium", "Mycobacterium species" and "mycobacterial" are used interchangeably to refer to any member of the genus of

Actinobacteria belonging to the *Mycobacteriaceae* family. The terms encompass laboratory strains as well as clinical isolates.

A "Mycobacterium infection" refers to the exposure of a subject to a Mycobacterium species followed by a colonization of the subject or the subject's tissue(s) by the bacterium. The colonization can cause serious diseases (e.g. tuberculosis, leprosy, Bureli ulcer etc, depending on the Mycobacterium), or can result in no adverse signs (asymptomatic or latent infection).

The term "combination" as used herein refers to any arrangement possible of various components (e.g. mycobacterial antigens and/or encoding nucleic acid molecules). Such an arrangement includes mixture of mycobacterial antigens (e.g. mixture of individual antigens and/or fusion of antigens) or mixture of nucleic acid molecules (e.g. carried by one or more vector) as well as mixture of polypeptide(s) and nucleic acid molecule(s). The present invention encompasses combinations comprising equal molar concentrations of each component as well as combinations with very different concentrations. It is appreciated that optimal concentration of each Mycobacterium component can be determined by the artisan skilled in the art.

The term "immunogenic" refers to the ability to induce or stimulate a measurable T and/or B cell-mediated immune response in a subject into which the component qualified as immunogenic has been introduced. For example, the antigenic combination of the invention is immunogenic in the sense as it is capable of inducing or stimulating an immune response in a subject which can be innate and/or specific (i.e. against at least one mycobacterial antigen/epitope comprised in or expressed by said immunogenic combination), humoral and/or cellular (e.g. 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, etc) and usually results in a protective response in the administered subject. A vast variety of direct or indirect biological assays are available in the art to evaluate the immunogenic nature of a component either *in vivo* (animal or human being), or *in vitro* (e.g. in a biological sample) as described herein.

As used herein, the term "mycobacterial antigen" refers to a polypeptide present in or obtained from a Mycobacterium species or fragment thereof (e.g. an epitope) capable of being bound by an antibody or a T cell receptor. Typically, such an antigen contains one or more B and/or T epitope(s), in particular CTL or T_H epitope(s) or both, involved in recognition by a particular antibody or T-cell receptor in the context of the Major Histocompatibility Complex (MHC). In the context of the invention, this term encompasses

native mycobacterial polypeptide as well as fragment and modified version thereof (i.e. variant) as described hereinafter.

An "epitope" corresponds to a minimal peptide motif (usually a set of 8-25 amino acid residues) that forms a site recognized by an antibody, a T-cell receptor or a HLA molecule. Those residues can be consecutive (linear epitope) or not (conformational epitope that includes residues that are not immediately adjacent to one another).

The term "treating" (and any form of treating such as "treatment", "treat") as used herein encompasses prophylaxis (e.g. prevention of a subject at risk of being infected with a Mycobacterium) and/or therapy (e.g. a subject diagnosed as being infected with a Mycobacterium). Treatment requires administer externally or internally to a subject an active agent (e.g. the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector and/or composition described herein), eventually in association with conventional therapeutic modalities, especially the one currently used in the treatment of active Mycobacterium disease (e.g. TB).

The term "subject" generally refers to a vertebrate that would benefit from induction or stimulation of an immune response against a Mycobacterium species and particularly a mammalian selected from the group consisting of domestic animals, farm animals, sport animals, and primates. Preferably, the subject is a human who has been diagnosed as being or at risk of being infected with a Mycobacterium and especially *Mtb* and thus is susceptible of having or at risk of having a disease or condition caused by or associated with a Mycobacterium infection (e.g. active or latent tuberculosis).

"Protective response" has its usual meaning, that the treatment provides a benefit to the treated subject as compared to the response in a non-treated subject; e.g. induction or stimulation of an immune response, protection from contracting a Mycobacterium infection, or increased resistance to an active disease or prevention against reactivation of a latent Mycobacterium infection or even curing after active disease development.

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

The term "obtained from", "originating" or "originate" is used to identify the original source of a component (e.g. polypeptide, nucleic acid molecule) but is not meant to limit the method by which the component is made which can be, for example, by chemical synthesis or recombinant means.

Mycobacterium species

As defined above, the mycobacterial antigens comprised/encoded by the immunogenic combination of the invention can independently be obtained from any member of a Mycobacterium (M.) species identified at present time. A vast number of Mycobacteria for use in the context of the invention are described in the art. Exemplary Mycobacterium species include without limitation *M. phlei, M. smegmatis, M. africanum, M. canetti, M. fortuitum, M. marinum, M. ulcerans, M. tuberculosis (Mtb), M. paratuberculosis, M. bovis, M. microti, M. celatum M. avium, M. leprae, M. lepraemurium, M. intracellulare, M. scrofulaceum, M. xenopi, M. genavense, M. kansasii, M. simiae, M. szulgai, M. haemophilum, M. asiaticum, M. malmoense, M. vaccae, M. caprae, M. pinnipedii and M. shimoidei*.

In a preferred embodiment, the mycobacterial antigens in use in this invention are obtained from a Mycobacterium species of the tuberculosis complex which includes those species traditionally considered as causing the disease tuberculosis, as well as Mycobacterium environmental and opportunistic species that cause tuberculosis and pulmonary disease in immune compromised subjects (e.g. HIV-infected patients). Exemplary species of the tuberculosis complex for use herein include without limitation M. tuberculosis (*Mtb*), *M. bovis*, *M. bovis* BCG, *M. africanum*, *M. canetti*, *M. caprae*, and *M. microti*. A preferred embodiment is directed to *Mtb* including the *Mtb* laboratory strains such as H37Rv and H37Ra and clinical isolates such as KZN4207, T85, CDC1551 (isolated in the US), F11 (isolated in South Africa), C, K85 (isolated in Netherland), CPHL-A, as well as the MDR or XDR isolates such as TN5904, Haarlem, KZN1435, Bejing and KZN605. Other preferred species for mycobacterial antigen sources are *M. bovis*, *M. bovis* BCG and *M. caprae*, especially for veterinary use. However, one would indeed expect cross-reactivity given the high percentage of homology existing between the M. species at the amino acid and nucleotide levels. For example, Rv1733 antigens of *Mtb* and *M. bovis* are 100% identical whereas *M. africanum* Rv1733 shares 209 amino acids in common out of 210 with that of *Mtb*. Thus, a combination of *Mtb* antigens is likely to be useful for treating both *Mtb*-infected (human use), *M. bovis*- and *M. caprae*- (veterinary use) infected subjects.

Amino acid sequences of the suitable mycobacterial antigens and the encoding nucleotide sequences are readily available in specialized data banks (and in the literature. For example, *Mtb* sequences can be found in Cole et al. (1998, Nature 393: 537) or at websites such as those maintained by the Wellcome Trust Sanger Institute, Institut Pasteur and others (e.g. TB database (@tbdb.org) and tuberculist (@tuberculist.epfl.ch)). However, the present

invention is not limited to these exemplary Mycobacterium species. Indeed the nucleotide and amino acid sequences can vary between different isolates and strains 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.

Immunogenic combination

As used herein, "at least five" is a number comprised within a range going from 5 to 50 (i.e. 5, 6, 7, 8, 9, 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, etc.), desirably from 5 to 33, preferably from 7 to 20, and more preferably from 8 to 18 with a specific preference for 10 to 15 (e.g. 12, 13 or 14). Preferably the combination of the present invention comprises approximately 10 to 15 *Mtb* antigens or corresponding nucleic acid molecules.

In the context of the present invention the "at least 5 mycobacterial antigens" are different from each other (e.g. multiple copies of the same mycobacterial antigen can be used provided that the combination comprises/encodes at least 5 different mycobacterial antigens).

Alternatively or in addition, each of the at least 5 mycobacterial antigens may be a native mycobacterial antigen (e.g. a full length antigen) or a modified version (fragment or variant) thereof.

A "native" mycobacterial antigen can be found, isolated, obtained from a source of Mycobacterium in nature. Such sources include biological samples (e.g. blood, plasma, sera, saliva, sputum, tissue sections, biopsy specimen etc.) collected from a subject infected or that has been exposed to a Mycobacterium, cultured cells as well as recombinant materials available in depositary institutions (e.g. ATCC or TB institutions), libraries or described in the literature (e.g. Mycobacterium isolates, Mycobacterium genomes, genomic fragments, genomic RNA or cDNA as well as any plasmid and vector known in the art to include such elements).

A modified mycobacterial antigen (e.g. a variant) typically differs from a polypeptide specifically disclosed herein or a native one in one or more position(s). Any modification(s) can be envisaged, including substitution, insertion, addition and/or deletion of one or more amino acid residue(s), non-natural arrangements and any combination of these possibilities. Amino acid substitution can be conservative or not. 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 synthetic techniques (e.g. resulting in a synthetic nucleic acid molecule encoding the desired polypeptide variant).

Whatever their origin (native or modified), it is preferred that each of the mycobacterial antigen comprised in or encoded by the immunogenic combination of the invention retains one or more immunogenic portions of the corresponding native antigen including B and/or T cell epitope(s). Methods to identify such relevant immunogenic portions are well known in the art. For example, T cell epitopes can be identified by implementing biological assays (e.g. IFNg assays using libraries of synthetic overlapping oligopeptides) or available prediction programs.

In one embodiment, the immunogenic combination of the present invention comprises or encodes mycobacterial antigens from at least 2 different infection phases selected from the group consisting of active, resuscitation and latent phases (e.g. active and resuscitation, active and latent or resuscitation and latent phases). A preferred combination is "multiphasic" comprising or encoding mycobacterial antigens, and particularly *Mtb* antigens, from the three infection phases, with at least one antigen from the active infection phase, at least one antigen from the resuscitation infection phase and at least one antigen from the latent infection phase.

"Antigens of the active phase" are typically the set of proteins that are mainly expressed when Mycobacterium is actively growing and replicating *in vivo*. A vast number of active mycobacterial antigens for use in this invention are described in the literature (e.g. Bertholet et al., 2008, J. Immunol. 181: 7948-57; Bertholet and al., 2010, Sci Transl Med 2: 53ra74). Particularly appropriate antigen(s) of the active phase is/are selected from the group consisting of ESAT-6 (Rv3875), CFP-10 (Rv3874), TB10.4 (Rv0288), Ag85A (Rv3804), Ag85B (Rv1886), Rv3619, Rv3620 and PPE family proteins Rv3478 and Rv2608 and any combination thereof. A preferred immunogenic combination comprises or encodes at least ESAT-6 (Rv3875), Ag85B (Rv1886) and TB10.4 (Rv0288).

"Antigens of the latent phase" are mainly expressed during the dormant (or latent) phase of the Mycobacterium infection, a reversible state of low metabolic activity in which the Mycobacterium can persist for extended periods. A vast number of latent mycobacterial antigens for use in the present invention are described in the literature. Exemplary *Mtb* latent antigens are those encoded by the DosR regulon which mediates the bacteria response to

hypoxia and starvation antigens that are up-regulated upon depletion of nutrients (Voskuil et al., 2003, J. Exp Med 198: 705-13; Leyten et al., 2006, Microbes Inf. 8: 2052-60; Roupie et al., 2007, Infection and Immunity 75: 941-9; Black et al., 2009, Clin Vaccine Immunol 16: 1203-12; Schuck et al., 2009, PLoS One 4: e5590; Vipond et al., 2006, Vaccine 24: 6340-50; Vipond et al., 2007, Tuberculosis 86: 218-24; Bertholet et al., 2008, J. Immunol. 181: 7948-57; Bertholet et al., 2010, Sci Transl Med 2: 53ra74, Mollenkopf et al., 2004, Infect Immun 72: 6471-9); WO03/000721; WO03/004520; WO03/035681; WO2004/006952 and WO2006/104389). Particularly appropriate antigen(s) of the latent phase is/are selected from the group consisting of Rv0081, Rv0111, Rv0198, Rv0569, Rv1733c, Rv1735, Rv1737, Rv1806, Rv1807, Rv1813, Rv2005c, Rv2029c, Rv2032, Rv2626, Rv2627, Rv2628, Rv2660c, Rv3407 and Rv3812 and Rv3478 and any combination thereof; and more preferably from the group consisting of Rv0111, Rv1733, Rv2029 and Rv2626 or from Rv0569, Rv1807, Rv1813, Rv3407 and Rv3478 or from both Rv0111, Rv1733, Rv2029, Rv2626, Rv0569, Rv1807, Rv1813, Rv3407 and Rv3478.

"Antigens of the resuscitation phase" refer to any antigen mainly expressed or involved into the transition between the dormancy state and active growth and replication (active state of Mycobacterium infection). The resuscitation antigens for use in this invention are described in the literature (e.g. Mukamolova et al., 2002, Mol Microbiol 46: 623-35; Yeremeev et al., 2003, Infection and Immunity 71: 4789-94; Mukamolova et al., 2006, Mol Microbiol 59: 84-98; Tufariello et al., 2006, Infect Immun 74: 2985-95; Biketov et al., 2007, MMC Infect Dis 7: 146; Kana et al., 2008, Mol Microbiol 67: 672-84; Kana et al., 2009, FEMS Immunol Med Microbiol 58: 39-50; Russel-Goldman et al., 2008, Infect Immun 76: 4269-81; Gupta et al., 2010, Microbiol 156: 2714-22 and Commandeur et al., 2011, Clin Vaccine Immunol. 18: 676-83). Particularly appropriate antigen(s) of the resuscitation phase is/are selected from the group consisting of RpfA, RpfB, RpfC, RpfD and RpfE and any combination thereof. A preferred immunogenic composition comprises or encodes at least RpfB and RpfD (e.g. immunogenic fragment thereof).

In a preferred embodiment, the immunogenic combination of the present invention comprises or encodes at least 5 mycobacterial antigens selected from the group consisting of ESAT-6 (Rv3875), CFP-10 (Rv3874), TB10.4 (Rv0288), Ag85A (Rv3804), Ag85B (Rv1886), Rv3619, Rv3620, RpfA, RpfB, RpfC, RpfD, RpfE, Rv0081, Rv0111, Rv0198, Rv0569, Rv1733c, Rv1735, Rv1737, Rv1806, Rv1807, Rv1813, Rv2005c, Rv2029c, Rv2032, Rv2626, Rv2627, Rv2628, Rv2660c, Rv3407 Rv3478, and Rv3812; preferably

from the group consisting of ESAT-6 (Rv3875), TB10.4 (Rv0288), Ag85B (Rv1886), RpfB, RpfD, Rv0111, Rv0569, Rv1733c, Rv1807, Rv1813, Rv2029c, Rv2626, Rv3407 and Rv3478; and more preferably from the group of polypeptides comprising the amino acid sequences shown in SEQ ID NO: 1-14 or any variant or fragment thereof.

For illustrative purposes, SEQ ID NO: 1 represents the amino acid sequence of Rv0111; SEQ ID NO: 2 the amino acid sequence of TB10.4; SEQ ID NO: 3 the amino acid sequence of Rv0569; SEQ ID NO: 4 the amino acid sequence of RpfB; SEQ ID NO: 5 the amino acid sequence of Rv1733; SEQ ID NO: 6 the amino acid sequence of Rv1807; SEQ ID NO: 7 the amino acid sequence of Rv1813; SEQ ID NO: 8 the amino acid sequence of Ag85B; SEQ ID NO: 9 the amino acid sequence of Rv2029; SEQ ID NO: 10 the amino acid sequence of Rv2626; SEQ ID NO: 11 the amino acid sequence of RV2839c; SEQ ID NO: 12 the amino acid sequence of Rv3407; SEQ ID NO: 13 the amino acid sequence of Rv3478 and SEQ ID NO: 14 the amino acid sequence of ESAT-6.

Each modified mycobacterial antigen that can be envisaged in the context of the invention comprises one or more modifications with respect to the native counterpart, and especially one or more modifications which are beneficial to the synthesis, processing, stability and/or solubility of the resulting polypeptide and/or to its immunogenicity. Representative examples of suitable modifications include without limitation (a) the deletion of internal highly hydrophobic region(s), (b) the deletion of N-terminal signal peptide (replacement with heterologous ones if needed) and/or (c) the deletion of unfolded region that may interfere negatively with stability, immunogenicity and recombinant expression and/or (d) the deletion or mutation of a catalytic domain to abolish biological activity.

A particularly appropriate immunogenic composition comprises or encodes mycobacterial antigens selected from the group of polypeptides comprising an amino acid sequence as set forth in SEQ ID NO: 15-24. More specifically, SEQ ID NO: 15 represents the Rv0111 antigen (Rv0111*) modified with respect to the native counterpart by deletion of the hydrophobic N-terminal part (from the first residue to about position 393). SEQ ID NO: 16 represents a RpfB antigen modified with respect to the native counterpart by deletion of the signal peptide (from the first residue to approximately residue in position 29, and by deletion of the catalytic domain, thus retaining RfpB from approximately position 30 to position 283). SEQ ID NO: 17 represents the Rv1733 antigen (Rv1733*) modified with respect to the native counterpart by deletion of the N-terminal predicted TM domain (from the first residue to about position 61). SEQ ID NO: 18 represents the Rv1807 antigen

(Rv1807*) modified with respect to the native counterpart by deletion of the unfolded C-terminal part (approximately the last 60 residues). SEQ ID NO: 19 represents the Rv1813 antigen (Rv1813*) modified with respect to the native counterpart by deletion of the N-terminal signal peptide (from the first residue to about position 34). SEQ ID NO: 20 represents the Ag85B (Ag85B*) modified with respect to the native counterpart by deletion of the N-terminal signal peptide (from the first residue to about position 39). SEQ ID NO: 21 represents the Rv2029 antigen (Rv2029*) modified with respect to the native counterpart by deletion of the C-terminal part (approximately the last 25 residue) and mutated at position 265 to abolish the Rv2029 enzymatic activity (e.g. D265N; Cabrera et al., 2010, Arch Biochem Biophys 502: 23-30). SEQ ID NO: 22 represents the RpfD antigen modified with respect to the native counterpart so as to retain the catalytic domain (also called LD for lysozyme domain) with three mutations aimed at abolishing the associated enzymatic activity (e.g. E292K, T315A and Q347A) and deletion of the last 7 residues. SEQ ID NO: 23 represents the Rv3407 antigen (Rv3407*) modified with respect to the native counterpart by deletion of the unfolded C-terminal part (approximately the last 33 residues). SEQ ID NO: 24 represents the Rv3478 antigen (Rv3478*) modified with respect to the native counterpart by deletion of the unfolded C-terminal part (approximately the last 40 residues).

In a preferred embodiment, the immunogenic combination of the invention comprises or encodes at least 5 mycobacterial antigens showing at least 80% identity (e.g. 80%, 85%, 90%, 92%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity) with an amino acid sequence set forth herein, in over the full length polypeptide or a fragment thereof (e.g. a fragment of 50 consecutive amino acid residues or more such as 60, 75, 80 or still 90 amino acid residues), and especially at least 5 *Mtb* antigens selected from the group of polypeptides comprising an amino acid sequence at least 80% homologous or identical to any of SEQ ID NO: 1-24 (with or without initiator Met).

In a more preferred embodiment, the immunogenic combination of the invention comprises or expresses at least Rv0111 with a specific preference for Rv0111* as illustrated in SEQ ID NO: 15.

In an even more preferred embodiment, the immunogenic combination of the invention comprises or expresses at least Rv0111, Rv2626, RpfB, RpfD, TB10.4 and Ag85B and with a specific preference for Rv0111* as illustrated in SEQ ID NO: 15, Rv2626 as illustrated in SEQ ID NO: 10, RpfB as illustrated in SEQ ID NO: 16, RpfD as illustrated in SEQ ID NO: 22, TB10.4 as illustrated in SEQ ID NO: 2 and Ag85B as illustrated in SEQ ID NO: 20.

As mentioned above, the immunogenic combination of the present invention encompasses any arrangement of its constitutive mycobacterial antigens and/or encoding nucleic acid molecules. Therefore the immunogenic combination of the invention may comprise or encode the mycobacterial antigens in the form of separate polypeptides (e.g. a mixture of recombinantly produced *Mtb* antigens) or in the form of one or more fusion polypeptides (covalent linkage of at least two of the mycobacterial antigens) or both separate antigen(s) and fusion(s).

On the same line, a combination of nucleic acid molecules encompasses either separate nucleic acid molecules or covalently linked nucleic acid molecules (e.g fusion-encoding nucleic acids) or both separate and fusionned nucleic acid molecules which can be carried by one or more vector(s). Given the number of mycobacterial antigens (from 5 up to 50), a preferred combination comprises one or more vector(s) encoding antigen fusions as described below. The vector combination may use the same type of vectors (e.g. two MVA) or different type of vectors (e.g. a plasmid DNA and a MVA) to express the various mycobacterial antigens or fusion as described herein.

Fusion polypeptide

According to another aspect, the present invention also provides isolated fusion polypeptides comprising two or more mycobacterial antigens comprised or encoded by the immunogenic combination of the invention as well as compositions comprising such fusion polypeptides.

The term “fusion” or “fusion polypeptide” as used herein refers to the covalent linkage in a single polypeptide chain of two or more polypeptides and is performed by genetic means, i.e. by fusing in frame the nucleic acid molecules encoding each of said polypeptides. By "fused in frame", it is meant that the expression of the fused coding sequences results in a single polypeptide 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 indirect (e.g. through a linker between the fused polypeptides) and can take place at the N or C terminus of a polypeptide or internally. The presence of a linker may facilitate correct folding and/or functioning of the fusion polypeptide. The present invention is not limited by the form, size or number of linker sequences employed. For illustrative purposes, typical linkers 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.

As before, the mycobacterial antigens that make up the fusion polypeptide of the invention may be native, and/or modified (variants) and/or fragment(s) thereof as described above. Such combination of mycobacterial antigens for use in the form of a fusion polypeptide may provide improved immunogenicity as compared to the same antigen combination used in a mixture of separate antigens (or expressing vectors).

Preferably, the fusion polypeptide of the invention comprises at least two (e.g., 2, 3, 4, 5, 6, etc) mycobacterial antigens as described herein, and preferably at least 2 polypeptides selected from the group of polypeptides comprising an amino acid sequence at least 80% (e.g. 98 or 100%) identical to any of SEQ ID NO: 1-24.

In one embodiment, the fusion polypeptide of the invention comprises mycobacterial antigens of the same infection phase. An exemplary fusion of latent *Mtb* antigens comprises Rv2029, Rv2626, Rv1733 and Rv0111; an exemplary fusion of active *Mtb* antigens comprises Ag85B, TB10.4 and ESAT6; and an exemplary fusion of resuscitation *Mtb* antigens comprises RpfB and RpfD antigens.

In another embodiment, the fusion polypeptide of the invention comprises mycobacterial antigens from 2 different infection phases or even from the active, resuscitation and latent phases. Exemplary fusions of this type include without limitation a fusion of latent and active *Mtb* antigens comprising Rv2029, TB10.4, ESAT-6 and Rv011; a fusion of resuscitation and active *Mtb* antigens comprising RpfB, RpfD, Ag85B, TB10.4 and ESAT-6 as well as a fusion of latent, resuscitation and active *Mtb* antigens comprising Ag85B, Rv2626, RpfB, -RpfD and Rv1733.

In a preferred embodiment, the fusion polypeptide of the invention is selected from the group consisting of:

- A fusion polypeptide comprising *Mtb* antigen Rv0111 (with a specific preference for Rv0111 as illustrated in SEQ ID NO: 15);
- A fusion polypeptide comprising the *Mtb* antigens Rv2029, Rv2626, Rv1733 and Rv0111;
- A fusion polypeptide comprising the *Mtb* antigens Rv0569, Rv1813, Rv3407, Rv3478 and Rv1807;
- A fusion polypeptide comprising the *Mtb* antigens Ag85B, TB10.4 and ESAT6;
- A fusion polypeptide comprising the *Mtb* antigens RpfB and RpfD (e.g. as illustrated by the so-called RPFB-Dhyb which is a fusion between a LD-deleted

RpfB antigen and the LD domain of RpfD with mutation abolishing enzymatic activity));

- A fusion polypeptide comprising the *Mtb* antigens RpfB, RpfD (e.g. RPFB-Dhyb), Ag85B, TB10.4 and ESAT6;
- A fusion polypeptide comprising the *Mtb* antigens Ag85B, Rv2626, RpfB, RpfD (e.g. RPFB-Dhyb) andRv1733;
- A fusion polypeptide comprising the *Mtb* antigens Rv2029, TB10.4, ESAT6 and Rv0111; and
- A fusion polypeptide comprising the *Mtb* antigens Ag85B, Rv2626 and Rv1733.

In the context of the invention the mycobacterial antigens identified in the exemplary fusion polypeptides can be in any order from the N to the C terminus and not necessary in the recited order. Thus, a fusion comprising the *Mtb* antigens Ag85B, Rv2626 and Rv1733 encompasses Ag85B-Rv1733-Rv2626; Rv1733-Rv2626-Ag85B; Rv1733-Ag85B-Rv2626; Rv2626-Ag85B-Rv1733; Rv2626-Rv1733-Ag85B and Ag85B-TB10.4-Rv2626-Ag85B, etc fusions further to the recited Ag85B-Rv2626-Rv1733 fusion.

Further to the mycobacterial antigens, the immunogenic combination and/or the fusion polypeptide of the invention may optionally comprise other components that may derive from a Mycobacterium species (e.g. additional mycobacterial antigen(s)) or be heterologous (i.e. from a source different of a Mycobacterium). Such additional component(s) may be immunogenic or not. Representative additional components include without any limitation tag peptide(s), targeting peptide(s), oligomerization domain(s), immunoactivator peptide(s)/polypeptide(s) and nucleic acid molecule(s) encoding such element(s), etc.

In one embodiment, any of the mycobacterial antigen(s) present or encoded by the immunogenic combination or the fusion polypeptide of the invention may be operably linked to targeting peptides such as signal and/or trans-membrane peptides. Such targeting peptides are well known in the art (see for example WO99/03885). Briefly, signal peptides (SS) 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 or more essentially hydrophobic amino acids which are then removed by a specific ER-located endopeptidase to give the mature polypeptide. Trans-membrane peptides (TM) are usually

highly hydrophobic in nature and serve to anchor the polypeptides in the cell membrane. 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 plasminogen activator (tPA), 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.

Alternatively or in addition, any of the mycobacterial antigen(s) present or encoded by the immunogenic combination or the fusion protein of the invention may be operably linked to tag peptides in order to facilitate its isolation and detection or to facilitate identification of host cells expressing such antigen or fusion. A vast variety of tag peptides can be used in the context of the invention including without limitation PK tag, FLAG tag (SEQ ID NO: 25), MYC tag (SEQ ID NO: 26), polyhistidine tag (usually a stretch of 5 to 10 histidine residues; e.g. SEQ ID NO: 27). Tag peptides can be detected by immunodetection assays using anti-tag antibodies as described in the appended examples. The tag peptide(s) may be independently positioned at the N-terminus of the mycobacterial antigen or fusion (tag-polypeptide) or alternatively at its C-terminus (polypeptide-tag) or alternatively internally or at any of these positions when several tags are employed.

Alternatively or in addition, any of the mycobacterial antigen(s) present or encoded by the immunogenic combination or the fusion polypeptide of the invention may be operably linked to one or more immunoactivator peptides/polypeptides capable of enhancing immunogenic properties. One may cite for example calreticulin (Cheng et al., 2001, J. Clin. Invest. 108: 669), *Mtb* heat shock protein 70 (HSP70) (Chen et al., 2000, Cancer Res. 60: 1035), ubiquitin (Rodriguez et al., 1997, J. Virol. 71: 8497), and 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), P30TT (Demotz et al., 1993, Eur. J. Immunol. 23: 425), hemaglutinin epitope (Rothbard et al., 1989, Int. Immunol. 1: 479) and C4bp oligomerization domain (Spencer et al., 2012, PLos One 7:e33555).

Depending of the mycobacterial antigen, the presence of such peptide(s) may be beneficial for enhancing expression and/or immunogenicity of the resulting combination or fusion polypeptide when compared with combination or fusion expressed without such

peptides. Enhanced expression may be determined by conventional techniques such as Western blotting. Enhanced immunogenicity may be determined using conventional assays such as ELISpot assay.

In a preferred embodiment, the fusion polypeptide of the invention is operably linked to targeting and/or tag peptides. For example, fusions n° 2, 3, 4 and 5, illustrated in the appended example section are operably linked to a signal peptide and a Flag tag positioned at the N-terminus immediately after the initiator Met and a myc tag, a trans-membrane peptide and a His tag at the C-terminus immediately before the STOP codon whereas fusions n° 9, 10, 11 and 12 are operably linked to a Flag tag positioned at the N-terminus immediately after the initiator Met and a myc tag followed by a His tag at the C-terminus immediately before the STOP codon. On the other hand, fusions n° 6, 8, 13 and 14 are operably linked to a signal peptide and a Flag tag positioned at the N-terminus immediately after the initiator Met and a myc tag and a His tag at the C-terminus immediately before the STOP codon.

Preferred examples of fusion polypeptides are selected from the group of polypeptides 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, desirably at least 90% of identity, preferably at least 95% of identity, and more preferably 98% identity and even more preferably 100% identity with any of the amino acid sequence shown in SEQ ID NO: 28-39. More specifically, SEQ ID NO: 28 and 29 comprise the fusion polypeptide comprising Ag85B, TB10.4 and ESAT6, with and without targeting peptides respectively (as illustrated by fusions n°2 and 10 in the appended examples). SEQ ID NO: 30 and 31 comprise the so-called RPFB-Dhyb fusion polypeptide comprising RpfB and RpfD, with and without targeting peptides respectively (as illustrated by fusions n°3 and 12 in the appended examples). SEQ ID NO: 32 and 33 comprise the fusion polypeptide comprising RPFB-Dhyb, Ag85B, TB10.4 and ESAT6, with and without targeting peptides respectively (as illustrated by fusions n°4 and 11 in the appended examples). SEQ ID NO: 34 and 35 comprise the fusion polypeptide comprising Rv0569 Rv1813, Rv3407, Rv3478 and Rv1807, with and without targeting peptides respectively (as illustrated by fusions n°5 and 9 in the appended examples). SEQ ID NO: 36 comprises the fusion polypeptide comprising Ag85B, Rv2626, RPFB-Dhyb and Rv1733, with a signal peptide (as illustrated by fusion n°6 in the appended examples). SEQ ID NO: 37 comprises the fusion polypeptide comprising Ag85B, Rv2626, and Rv1733, with a signal peptide (as illustrated by fusion n°8 in the appended examples).. SEQ ID NO: 38 comprises the fusion

polypeptide comprising Rv2029, Rv2626, Rv1733 and Rv0111, with a signal peptide (as illustrated by fusion n°13 in the appended examples).. SEQ ID NO: 39 comprises the fusion polypeptide comprising Rv2029, TB10.4, ESAT-6 and Rv0111, with a signal peptide (as illustrated by fusion n°14 in the appended examples).

More preferred examples of fusion polypeptides are selected from the group of polypeptides 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, desirably at least 90% of identity, preferably at least 95% of identity, and more preferably 98% identity and even more preferably 100% identity with any of the following amino acid sequences:

- the amino acid sequence shown in SEQ ID NO: 28 from approximately position 32 to approximately position 506 (fusion Ag85B*-TB10.4-ESAT-6 as illustrated by fusion n°2 or 10 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 29 from approximately position 10 to approximately position 484 (fusion Ag85B*-TB10.4-ESAT-6 as illustrated by fusion n°2 or 10 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 30 from approximately position 32 to approximately position 380 (fusion RPFB-Dhyb as illustrated by fusions n°3 and 12 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 31 from approximately position 10 to approximately position 358 (fusion RPFB-Dhyb as illustrated by fusions n°3 and 12 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 32 from approximately position 32 to approximately position 855 (fusion RPFB-Dhyb-Ag85B*-TB10.4-ESAT-6 as illustrated by fusions n°4 and 11 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 33 from approximately position 10 to approximately position 833 (fusion RPFB-Dhyb-Ag85B*-TB10.4-ESAT-6 as illustrated by fusions n°4 and 11 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 34 from approximately position 32 to approximately position 1115 (fusion Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807 as illustrated by fusions n°5 and 9 in the appended examples);

- the amino acid sequence shown in SEQ ID NO: 35 from approximately position 10 to approximately position 1093 (fusion Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807 as illustrated by fusions n°5 and 9 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 36 from approximately position 32 to approximately position 956 (fusion Ag85B*-Rv2626-RPFB-Dhyb-Rv1733* as illustrated by fusion n°6 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 37 from approximately position 32 to approximately position 607 (fusion Ag85B*-Rv2626-Rv1733* as illustrated by fusion n°8 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 38 from approximately position 37 to approximately position 932 (fusion Rv2029-Rv2626-Rv1733*-Rv0111* as illustrated by fusion n°13 in the appended examples); and
- the amino acid sequence shown in SEQ ID NO: 39 from approximately position 37 to approximately position 831 (fusion Rv2029*-TB10.4-ESAT-6-Rv0111*).

Of course, such amino acid sequences can be equipped with an initiator Met.

In a preferred embodiment, the fusion polypeptide of the invention further comprises appropriate targeting peptide(s) such as signal and/or trans-membrane peptides so as to allow its presentation at the cell membrane. Even more preferred fusion polypeptides are selected from the group of polypeptides 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, desirably at least 90% of identity, preferably at least 95% of identity, and more preferably 98% identity and even more preferably 100% identity with any of the following amino acid sequences:

- the amino acid sequence shown in SEQ ID NO: 28 from position 1 (initiator Met) to approximately position 23 and from approximately position 32 to approximately position 506 and from approximately position 517 to approximately position 583 (fusion SS-Ag85B*-TB10.4-ESAT-6-TM as illustrated by fusions n°2 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 30 from position 1 (initiator Met) to approximately position 23 and from approximately position 32 to approximately position 380 and from approximately position 391 to approximately position 457 (fusion SS- RPFB-Dhyb-TM as illustrated by fusion n°3 in the appended examples);

- the amino acid sequence shown in SEQ ID NO: 32 from position 1 (initiator Met) to approximately position 23 and from approximately position 32 to approximately position 855 and from approximately position 866 to approximately position 932 (fusion SS- RPFB-Dhyb-Ag85B*-TB10.4-ESAT-6-TM as illustrated by fusion n°4 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 34 from position 1 (initiator Met) to approximately position 23 and from approximately position 32 to approximately position 1115 and from approximately position 1126 to approximately position 1192 (fusion SS-Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807-TM as illustrated by fusion n°5 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 36 from position 1 (initiator Met) to approximately position 23 and from approximately position 32 to approximately position 956 (fusion SS-Ag85B*-Rv2626-RPFB-Dhyb-Rv1733*as illustrated by fusion n°6 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 37 from position 1 (initiator Met) to approximately position 23 and from approximately position 32 to approximately position 607 (fusion SS-Ag85B*-Rv2626-Rv1733*as illustrated by fusion n°8 in the appended examples);
- the amino acid sequence shown in SEQ ID NO: 38 from position 1 (initiator Met) to approximately position 28 and from approximately position 37 to approximately position 932 (fusion SS-Rv2029-Rv2626-Rv1733*-Rv0111*as illustrated by fusion n°13 in the appended examples); and
- the amino acid sequence shown in SEQ ID NO: 39 from position 1 (initiator Met) to approximately position 28 and from approximately position 37 to approximately position 831 (fusion SS-Rv2029*-TB10.4-ESAT-6-Rv0111* as illustrated by fusion n°14 in the appended examples).

Typically, the mycobacterial antigens and nucleic acid molecules encoding such antigens comprised in the immunogenic combination and fusion polypeptide of the invention can be isolated or prepared using standard techniques. They may be purified e.g. from bacteria culture or produced recombinantly in a host cell using any of the expression system available in the art or can be provided to the subject upon administration of suitable expression vector(s) such as those described herein.

Nucleic acid molecules and nucleic acid combinations

The present invention also provides isolated nucleic acid molecules encoding the at least 5 mycobacterial antigens comprised in the immunogenic combination and the fusion polypeptides of present invention as well as compositions comprising such nucleic acid molecules.

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) (e.g., mRNA, antisense RNA) or mixed polyribo-polydeoxyribonucleotides. They encompass single or double-stranded, linear or circular, natural or synthetic nucleic acids.

As defined before, the nucleic molecules of the invention may be native nucleic acids (e.g. isolated from a genome or genomic fragment of a Mycobacterium) or may be modified by man to include substitution, deletion, addition and/or insertion of one or more nucleotide(s). The present invention encompasses any modifications aimed to improve cloning, expression, stability (e.g. introduction of appropriate restriction sites, degeneration and/or optimisation of nucleotide sequence to optimize translation in a given host cell and/or suppression of potentially negative elements that may destabilize the nucleic acid molecule or its transcript). When several modifications are contemplated, they can concern consecutive and/or non-consecutive nucleotide residues. The modification(s) contemplated by the present invention encompass silent modifications that do not change the amino acid sequence of the encoded mycobacterial antigens and fusion polypeptides, as well as modifications that are translated into the encoded mycobacterial polypeptide. Preferably the modifications do not decrease the immunogenic potential of encoded mycobacterial antigens and fusion polypeptides with respect to the non-modified ones.

In one embodiment, the nucleic acid molecule of the invention can be degenerated over the full length nucleotide sequence or portion(s) thereof so as to reduce sequence homology between nucleic acid molecule(s) used in the context of the invention or in the host cell. It is indeed advisable to degenerate the portions of nucleic acid sequences that show a high degree of nucleotide sequence identity and the skilled person is capable of

identifying such portions by sequence alignment, to degenerate the nucleic acid molecules in the homologous portions so as to avoid stability problems during production process.

Alternatively or in addition, the nucleic acid molecule of the invention can be optimized for providing high level expression in a particular host cell or subject, e.g. avian (e.g. chicken embryonic fibroblast, *Cairina moschata* cell lines described in WO2010/130756 and WO2012/001075), mammalian, yeast (e.g. *Saccharomyces cerevisiae*, *Saccharomyces pombe* or *Pichia pastoris*) or bacteria (e.g. *E. coli*, *BCG* 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 and the utilisation of codons may be markedly different between different hosts. As the nucleotide sequences used in the invention are mostly of bacterial origin, they may have an inappropriate codon usage pattern for efficient expression in host cells such as higher eukaryotic cells. Typically, codon optimisation is performed by replacing one or more "native" (mycobacterial) 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 subject 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 "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.

The present invention encompasses a nucleic acid molecule encoding any mycobacterial antigen selected from the group of polypeptides set forth in any of SEQ ID NO: 1-24.

Of particular interest is a nucleic acid molecule which encodes a fusion polypeptide comprising an amino acid sequence which exhibits at least 80% of identity (e.g. 80%, 85%, 90%, 95%, 98%, 100%) with any of the amino acid sequences shown in SEQ ID NO: 28-39 or any variant and fragment thereof (e.g. a fragment encoding the exemplary portion(s) of such SEQ ID NO: 28-39 cited above).

A particularly preferred embodiment of the present invention is directed to a nucleic acid molecule comprising, alternatively essentially consisting of or alternatively consisting of a nucleotide sequence which exhibits at least 80% of identity (i.e. a nucleic acid molecule that hybridizes to the recited nucleic acid molecule under stringent conditions), 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 nucleotide sequence shown in any of SEQ ID NO: 40-51 or any variant and fragment thereof (e.g. encoding the exemplary portions of SEQ ID NO: 28-39 cited above).

The nucleic acid molecules of the present invention can be generated using sequence data accessible in the art and the sequence information provided herein. For example, they may be isolated using routine techniques well known in the art, e.g. by PCR isolation and/or cloning by conventional molecular biology from a Mycobacterium genome of a particular species or genomic fragment thereof, cDNA and genomic libraries or any prior art vector known to include it. Alternatively, the nucleic acid molecules of the invention can also be generated by chemical synthesis in automatised process (e.g. assembled from overlapping synthetic oligonucleotides).

Another embodiment of the invention pertains to fragments of the nucleic acid molecules of the invention, e.g. restriction endonuclease and PCR-generated fragments. Such fragments can be used as probes, primers or fragments encoding relevant immunogenic portion(s).

Vectors

The present invention also concerns vectors comprising one or more nucleic acid molecule(s) of the present invention as well as compositions comprising such vector(s).

The term “vector” as used herein refers to a vehicle, preferably a nucleic acid molecule or a viral particle that contains the elements necessary to allow delivery, propagation and/or expression of any of the nucleic acid molecule(s) described herein within a host cell or subject. This term encompasses vectors for maintenance (cloning vectors) or

vectors for expression in various host cells or subjects (expression vectors), extrachromosomal vectors (e.g. multicopy plasmids) or integration vectors (e.g. designed to integrate into the host cell genome and produce additional copies of the nucleic acid molecules when the host cell replicates) as well as shuttle vectors (e.g. functioning in both prokaryotic and/or eukaryotic hosts) and transfer vectors (e.g. for transferring nucleic acid molecule(s) in a viral genome). For the purpose of the invention, the vectors may be of naturally occurring genetic sources, synthetic or artificial, or some combination of natural and artificial genetic elements.

In the context of the invention, the term “vector” has to be understood broadly as including plasmid and viral vectors. A "plasmid vector" as used herein refers to a replicable DNA construct. Usually plasmid vectors contain selectable marker genes that allow host cells carrying the plasmid vector to be selected for or against in the presence of a corresponding selective drug. A variety of positive and negative selectable marker genes are known in the art. By way of illustration, an antibiotic resistance gene can be used as a positive selectable marker gene that allows a host cell to be selected in the presence of the corresponding antibiotic.

The term "viral vector" as used herein refers to a nucleic acid vector that includes at least one element of a virus genome and may be packaged into a viral particle or to a viral particle. The terms “virus”, “virions”, “viral particles” and “viral vector particle” are used interchangeably to refer to viral particles that are formed when the nucleic acid vector is transduced into an appropriate cell or cell line according to suitable conditions allowing the generation of viral particles. In the context of the present invention, the term “viral vector” has to be understood broadly as including nucleic acid vector (e.g. DNA viral vector) as well as viral particles generated thereof. The term “infectious” refers to the ability of a viral vector to infect and enter into a host cell or subject. Viral vectors can be replication-competent or -selective (e.g. engineered to replicate better or selectively in specific host cells), or can be genetically disabled so as to be replication-defective or replication-impaired.

Vectors which are appropriate in the context of the present invention, include, without limitation, bacteriophage, plasmid or cosmid vectors for expression in prokaryotic host cells such as bacteria (e.g. *E. coli, BCG or Listeria*); vectors for expression in yeast (e.g. *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*); baculovirus vectors for expression in insect cell systems (e.g. Sf 9 cells); viral and plasmid vectors for expression in plant cell systems (e.g. Ti plasmid, cauliflower mosaic virus CaMV; tobacco mosaic virus TMV); as well as plasmid and viral vectors for expression in higher eukaryotic

cells or subjects. Typically, such vectors are commercially available (e.g. in Invitrogen, Stratagene, Amersham Biosciences, Promega, etc.) or available from depositary institutions such as 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.

Representative examples of suitable plasmid vectors include, without limitation, pREP4, pCEP4 (Invitrogen), pCI (Promega), pVAX (Invitrogen) and pGWiz (Gene Therapy System Inc).

Representative examples of suitable viral vectors are generated from a variety of different viruses (e.g. retrovirus, adenovirus, adenovirus-associated virus (AAV), poxvirus, herpes virus, measles virus, foamy virus, alphavirus, vesicular stomatis virus, etc). As described above, the term "viral vector" encompasses vector DNA, genomic DNA as well as viral particles generated thereof, and especially infectious viral particles.

In one embodiment, the viral vector employed in this invention is replication-defective or replication-impaired which means that it cannot replicate to any significant extent in normal cells (eg. normal human cells) or in the subject to whom it is administered (the impairment or defectiveness of replication functions can be evaluated by conventional means - eg. via measuring DNA synthesis and/ or viral titre in non-permissive cells). Such replication-defective or impaired vectors typically require for propagation, permissive cell lines which bring up or complement the missing/impaired functions.

Examples of viral vectors that are useful in the context of the invention include adenoviral vectors which have a number of well-documented advantages for vaccination, immunotherapy, 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 of 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, Ad5, Ad6, and subgenus B such as Ad11, Ad34 and Ad35. It may also be advantageous to use animal Ad with a special preference for chimp Ad, such as chimp Ad3 and Ad63. The cited adenovirus are available from ATCC 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 6,136,594; US 6,133,028; WO00/50573; WO00/70071; WO2004/083418; WO2004/097016 and WO2005/071093).

Preferred replication-defective adenoviral vectors are E1-defective with an E1 deletion extending from approximately positions 459 to 3328 or from approximately positions 459 to 3510 (by reference to the sequence of Ad5 disclosed in the GeneBank under the accession number M 73260). 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 (e.g. deletion from approximately positions 27867 to 30743) or of other essential E2 and/or E4 regions as described in WO94/28152 and Lusky et al., 1998, J. Virol 72: 2022).

The nucleic acid molecules of the present invention can be independently inserted in any location of the adenoviral genome, with a specific preference for insertion in replacement of the E1 and/or E3 region. They may be positioned in sense or antisense orientation relative to the natural transcriptional direction of the region in question.

Other examples of viral vectors particularly appropriate in the context of the invention include poxvirus vectors such as fowlpox vectors (e.g. FP9), canarypox vectors (e.g. ALVAC) and vaccinia virus vectors, the latter being preferred. Suitable vaccinia viruses include without limitation the Copenhagen strain, the Wyeth strain, NYVAC (US 5,494,807) and the modified Ankara (MVA) strain (Antoine et al., 1998, Virol. 244: 365; WO02/42480). The general conditions for constructing and producing recombinant poxvirus are well known in the art (see for example WO2010/130753; WO03/008533; US 6,998,252; US 5,972,597 and US 6,440,422). The nucleic acid molecules of the present invention are preferably inserted within the poxviral genome in a non-essential locus. Thymidine kinase gene is particularly appropriate for insertion in Copenhagen vaccinia vectors and deletion II or III for insertion in MVA vector (WO97/02355).

Other viral vectors suitable in the context of the invention are morbillivirus which can be obtained from the paramyxoviridae family, with a specific preference for measles virus. Various attenuated strains are available in the art (Brandler et al, 2008, CIMID, 31: 271; Singh et al., 1999, J. virol. 73(6): 4823), such as and without limitation, the Edmonston A and B strains (Griffin et al., 2001, Field's in Virology, 1401-1441), the Schwarz strain (Schwarz A, 1962, Am J Dis Child, 103: 216), the S-191 or C-47 strains (Zhang et al., 2009, J Med Virol. 81 (8): 1477). Insertion between P and M genes or between H and L genes is particularly appropriate.

Suitable vector for use in the present invention also include bacterium cell which can be wild-type or mutant (e.g. avirulent). Well-known examples of such bacterium cells include without limitation avirulent Mycobacterium (e.g. Mycobacterium bovis BCG), Lactobacillus (e.g. *Lactococcus lactis*), Listeria (e.g. *Listeria monocytogenes*) and other microorganisms such as Salmonella and Pseudomona. A preferred embodiment is directed to a BCG vector into the genome of which has been incorporated nucleic acid molecule(s) encoding one or more mycobacterial antigen(s) or fusion polypeptide (s) as defined above in a manner allowing the BCG vector to express such element(s).

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.

In accordance with the present invention, the nucleic acid molecules comprised in the vector of the invention are in a form suitable for expression in a host cell or subject, which means that each of the nucleic acid molecules set forth herein is operably linked to appropriate regulatory sequences. As used herein, the term "regulatory elements" or "regulatory sequence" refers to any element that allows, contributes or modulates the expression of nucleic acid molecule(s) in a given host cell or subject, including replication, duplication, transcription, splicing, translation, stability and/or transport of the nucleic acid(s) or its derivative (i.e. mRNA).

It will be appreciated by those skilled in the art that the choice of the regulatory sequences can depend on such factors as the vector itself, the host cell or subject, the level of expression desired, etc. The promoter is of special importance. In the context of the invention, it can be constitutive directing expression of the nucleic acid molecule in many types of host cells or specific to certain host cells (e.g. lung-specific regulatory sequences) or regulated in response to specific events or exogenous factors (e.g. by temperature, nutrient additive, hormone, etc) or according to the phase of a viral cycle (e.g. late or early). One may also use promoters that are repressed during the production step in response to specific events or exogenous factors, in order to optimize vector production and circumvent potential toxicity of the expressed polypeptide(s).

Promoters suitable for constitutive expression in mammalian cells include but are not limited to the cytomegalovirus (CMV) immediate early promoter (US 5,168,062), the RSV promoter, the adenovirus major late promoter, the phosphoglycero kinase (PGK) promoter, the thymidine kinase (TK) promoter of herpes simplex virus (HSV)-1 and the T7 polymerase

promoter. Promoters such as the trp, lac, phage promoters, tRNA promoters and glycolytic enzyme promoters may be used in prokaryotic hosts. Useful yeast promoters include the promoter regions for metallothionein, 3-phosphoglycerate kinase or other glycolytic enzymes such as enolase or glyceraldehyde-3-phosphate dehydrogenase, enzymes responsible for maltose and galactose utilization. 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: 1094-7; Hammond et al., 1997, J. Virol Methods 66: 135-8; and Kumar and Boyle, 1990, Virology 179: 151-8) as well as early/late chimeric promoters. Promoters suitable for measles-mediated expression include without limitation any promoter directing expression of measles transcription units (Brandler and Tangy, 2008, CIMID 31: 271).

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, IRES ribosome binding sites, Shine-Dalgarno sequences, etc.) into the host cell or subject and purification steps (e.g. a tag as described herein).

In one embodiment, the nucleic acid molecules encoding the mycobacterial antigens present in or encoded by the immunogenic combination and/or the fusion polypeptides of the invention are carried out by a single vector.

In an alternative embodiment, the nucleic acid molecules encoding the mycobacterial antigens present in or encoded by the immunogenic combination and/or the fusion polypeptides of the invention are carried out by two or more vectors. Each vector encodes one or more mycobacterial antigens among those cited above or one or more fusion polypeptides. The two or more vectors can be administered to the subject substantially simultaneously, or sequentially.

Particularly preferred embodiments of the invention are directed to a single vector (or viral particles) selected from the group consisting of:

i. A vector encoding a fusion polypeptide comprising Rv2029, Rv2626, Rv1733 and Rv011 and a fusion polypeptide comprising RpfB, RpfD, Ag85B, TB10.4 and ESAT-6 (exemplary vectors encoding fusions 13 and 4 and fusions 13 and 11, respectively);

ii. A vector encoding a fusion polypeptide comprising Rv2029, Rv2626, Rv1733 and Rv0111, a fusion polypeptide comprising RpfB, RpfD, Ag85B, TB10.4 and ESAT-6 and a fusion polypeptide comprising Rv0569, Rv1813, Rv3407, Rv3478 and Rv1807 (exemplary vectors encoding fusions 13, 4 and 5 and fusions 13, 11 and 9, respectively);

iii. A vector encoding a fusion polypeptide comprising Rv2029, Rv2626, Rv1733 and Rv0111, a fusion polypeptide comprising RpfB, RpfD, Ag85B, TB10.4 and ESAT-6 and a fusion polypeptide comprising Rv0569, Rv1813, Rv3407, Rv3478 and Rv1807 (exemplary vectors encoding fusions 13, 4 and 9 and fusions 13, 11 and 5, respectively);

iv. A vector encoding a fusion polypeptide comprising Ag85B, Rv2626 RpfB, RpfD and Rv1733 and a fusion polypeptide comprising Rv2029 TB10.4, ESAT-6 and Rv0111 (exemplary vectors encoding fusions 6 and 14);

v. A vector encoding a fusion polypeptide comprising Ag85B, Rv2626 RpfB, RpfD and Rv1733, a fusion polypeptide comprising Rv2029 TB10.4, ESAT-6 and Rv0111 and a fusion polypeptide comprising Rv0569, Rv1813, Rv3407, Rv3478 and Rv1807 (exemplary vectors encoding fusions 6, 14 and 5 and fusions 6, 14 and 9, respectively);

vi. A vector encoding a fusion polypeptide comprising RpfB, RpfD, Ag85B, TB10.4 and ESAT-6 and a fusion polypeptide comprising Rv0569, Rv1813, Rv3407, Rv3478 and Rv1807 (exemplary vectors encoding fusions 9 and 11 and fusions 5 and 4, respectively).

More preferably, the vector described above is a MVA vector.

If needed, the immunogenic combination, fusion polypeptide or vector of the invention can further comprise additional copies of the selected mycobacterial antigens, or additional antigens from a different Mycobacterium species, such as *M. bovis* or *M caprae*, and/or additional polypeptides from other sources (i.e. heterologous polypeptide), aimed to improve therapeutic or protective activity against a Mycobacterium infection or any disease or condition caused by or associated with a Mycobacterium infection. Suitable additional

polypeptides include without limitation immunomodulators such as cytokines and any other antigen originating from a potentially co-infecting organism (e.g. HIV, HBV, etc).

According to a preferred embodiment, the vector of the invention is in the form of infectious viral particles. Typically, such viral particles are produced by a process comprising the steps of (i) introducing the viral vector of the invention into a suitable cell line, (ii) culturing said cell line under suitable conditions so as to allow the production of said infectious viral particle, (iii) recovering the produced viral particle from the culture of said cell line, and (iv) optionally purifying said recovered viral particle.

When the viral vector is replication-defective or replication-impaired, the particles are usually produced in a permissive cell line or via the use of a helper virus, which supplies *in trans* the missing/impaired functions. 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: 1909-17; WO97/00326) or any derivative of these cell lines. Avian cells are particularly suitable for propagating poxvirus vectors including without limitation primary chicken embryo fibroblasts (CEF) prepared from chicken embryos obtained from fertilized eggs, and duck cell lines (e.g. as described in WO03/076601, WO2009/004016, WO2010/130756 and US2011-008872).

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

The present invention also encompasses vectors or viral particles that have been modified to allow preferential targeting to a specific host cell. A characteristic feature of targeted vectors 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. a mycobacterium-infected cell), a tissue-specific marker (e.g. a lung-specific marker), etc. Examples of suitable ligands include antibodies or fragments thereof directed to a mycobacterial antigenic domain. 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).

Host cells and production methods

In another aspect, the invention also relates to host cells which comprise the immunogenic combinations, the fusion polypeptides, the nucleic acid molecules or vectors (e.g. viral particles) of the invention as well as compositions comprising such a host cell.

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 such as cultured cell lines, primary cells and proliferative cells. In the context of the invention, the term "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 cells capable of producing the vector of the invention (e.g. 293, HER96, PERC.6 cells, CEF, duck cell lines, etc). This term also includes cells which can be or has been the recipient of the vector described herein as well as progeny of such cells.

According to a specific embodiment of the invention, the host cell can be further encapsulated. Cell encapsulation technology is known in the art.

Still a further aspect of the present invention is a method for recombinant production of the mycobacterial antigens comprised in or encoded by the immunogenic combination or the fusion polypeptides of the invention, employing the vectors (or infectious viral particles) and/or host cells of the invention. Typically, the method comprises the steps of (i) introducing a vector into a suitable host cell to produce a transfected or infected host cell, (ii) culturing *in-vitro* said transfected or infected host cell under conditions suitable for growth of the host cell, (iii) recovering the cell culture, and (iv) optionally, purifying the mycobacterial antigen(s) or the fusion polypeptide from the recovered cell and/or culture supernatant.

It is expected that those skilled in the art are knowledgeable in the numerous expression systems available in the art for expressing polypeptides and of the methods for introducing a vector into a host cell. Such methods include, but are not limited to microinjection, $CaPO_4$- mediated transfection, DEAE-dextran-mediated transfection, electroporation, lipofection/liposome fusion, gene guns, transduction, viral infection as well as direct administration into a host organism via various means. The method may also be used in association with conventional transfection reagents that facilitate introduction of

nucleic acids in host cells, such as polycationic polymers (e.g. chitosan, polymethacrylate, PEI, etc) and cationic lipids (e.g.DC-Chol/DOPE, transfectam, lipofectin, etc).

Host cells 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 will be made here to describe in detail the various prokaryotic and eukaryotic expression systems available in the art for such purposes.

In a preferred embodiment, the method employs an *E coli* host cell and in particular a *E. coli* strain carrying the D13 prophage in its genome for allowing inducible expression of T7 polymerase by lactose or analogue of lactose (e.g. IPTG: IsoPropyl b-D-1-Thio Galactopyranoside). Such strains are available for various manufacturers (e.g. Lucigen, Merck, etc). After plasmid introduction, the transformed *E. coli* cell can be cultured at a temperature comprised between approximately 18°C to approximately 39°C (specific preference for approximately 30°C or approximately 37°C) for a time period varying from 6 to 48 hours (specific preference from approximately 8 to approximately 24h) in conventional medium adapted to the vector selection marker (e.g. presence of antibiotic) and to the host strain (e.g. in the presence of an inducer such as IPTG). The cell culture is recovered and can be lysed (e.g. chemical lysis with a detergent, sonication, etc). After centrifugation of the cell lysate, both the supernatant and the pellet can be collected for further analysis (e.g. by SDS PAGE) to evaluate the level of expression as well as the solubility of the expressed material (e.g. soluble material can be found in the cell lysate supernatant and insoluble material can be trapped in inclusion bodies).

The recovered mycobacterial antigen(s) or the fusion polypeptides can optionally 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, hydrophobic-interaction, hydroxyapatite, high performance liquid chromatography, etc). The conditions and techniques 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. For example protein concentration can be evaluated by Bransdford assay (Biorad), endotoxin levels can be evaluated by techniques such as the Portable Test System (Charles River Laboratories) and the mass of the purified polypeptides can be measured using MALDI (Matrix-Assisted Laser Desorption/Ionisation) or electrospray methods.

Compositions

In another aspect, this invention provides a composition comprising at least one of the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector (e.g. infectious viral particle), or host cell of the invention (also referred herein to "active agent") or any combination thereof (e.g. combination of different polypeptides or vectors/viral particles). Preferably, the composition is a pharmaceutical composition which comprises further to a therapeutically effective amount of the active agent(s), one or more pharmaceutically acceptable vehicle(s).

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 administration in a subject and in particular in a human.

As used herein a “therapeutically effective amount” is a dose sufficient for the intended use. When prophylactic use is concerned, this term means a dose sufficient to prevent or to delay the onset and/or establishment of a Mycobacterium infection (e.g. *Mtb* infection). For “therapeutic” use, the composition is administered to a subject already infected with a Mycobacterium species with the goal of treating active disease or preventing reactivation in latently infected individuals, eventually in combination with one or more conventional therapeutic modalities as described herein. In particular, a therapeutically effective amount of the composition of the invention could be that amount necessary to cause induction or stimulation of the immune system in the administered subject (e.g. resulting in the development of an innate and/or specific response).

The subject to be treated may be a newborn, an infant, a young adult or an adult. The subject may have been previously immunized with Bacillus Calmette-Guerin (BCG) or previously treated for a Mycobacterium infection before being treated with the active agent(s) described herein. It may or not be co-infected with another pathogenic organism (e.g. the human immunodeficiency virus HIV).

In particular, the subject to be treated is infected with a virulent Mycobacterium species (e.g. *Mtb*) which may be a drug resistant (e.g. MDR, XDR or TDR) strain. The infecting Mycobacterium can be the same strain or isolate as any of the Mycobacterium from which originate the antigens comprised or encoded by the active agent used in the present invention or it can be from a different strain or isolate.

The composition of the invention is suitably buffered in order to be appropriate for human or animal 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 of the invention can further comprise 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).

Additional pharmaceutically acceptable excipients may be used 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. lung).

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 (WO 98/56415), imidazo-quinoline compounds such as Imiquimod (WO2007/147529), cytosine phosphate guanosine oligodeoxynucleotides such as CpG and cationic peptides such as IC-31 (Kritsch et al., 2005, J. Chromatogr Anal. Technol Biomed Life Sci 822: 263) or any derivative thereof.

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 with a preference for at least one year) at freezing (e.g. -70°C, -20°C), refrigerated (e.g. 4°C), ambient temperatures. Such "long term" formulations are known in the art (e.g. WO98/02522; WO03/053463). One may cite (a) 1M saccharose, 150 mM NaCl, 1mM $MgCl_2$, 54 mg/l Tween 80, 10 mM Tris pH 8.5, (b) 10

mg/ml mannitol, 1 mg/ml HSA, 20 mM Tris, pH 7.2, and 150 mM NaCl and (c) physiological saline which are particularly adapted to the composition of the invention.

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. In a specific embodiment, the composition of the invention is formulated for delivery in the respiratory tract (e.g. by inhalation, intranasal or intrapulmonary route) in a spray-dried (see e.g. WO2010/135495) or droplet form (with a specific preference for droplets having an average diameter of 100-5000 μm).

The immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition of the present invention is suitable for a variety of modes of administration. Any of the conventional administration routes are applicable in the context of the invention including systemic, topical or mucosal routes.

Systemic administration includes for example subcutaneous, intradermal, intramuscular, intravenous, intraperitoneal, intravascular, intraarterial injection as well as scarification. Injections can be made with conventional syringes and needles, or any other appropriate devices available in the art (e.g. electroporation). Mucosal administration includes without limitation 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 appropriate dispenser. Topical administration can also be performed using transdermal means (e.g. patch and the like). Intramuscular, intradermal and subcutaneous routes are particularly preferred in the context of the invention as well as intranasal intratracheal and intrapulmonary administrations.

The appropriate dosage can be adapted as a function of various parameters, in particular the active agent(s) comprised in the composition, the mode of administration; the age, health, and weight of the subject; 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 viral vector-comprising composition varies from about 10^4 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 or HPLC, iu titers by quantitative DBP immunofluorescence 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. A preferred dose contains from about 10^5 to about 10^{12} vp of an adenoviral vector (e.g. about $5x10^8$, about 10^9, about $5x10^9$, about 10^{10}, about $5x10^{10}$ vp or about 10^{11} vp). A dose from about $5x10^5$ to about 10^9 pfu are preferred for vaccinia (e.g. MVA)-based composition with a specific preference for about $5x10^6$, about 10^7, about $5x10^7$, about 10^8 or about $5x10^8$ pfu. A dose from about $5x10^4$ to about 10^7 pfu are preferred for measles-based composition, with a specific preference for about 10^5, $5x10^5$, 10^6 or $5x10^6$ pfu. A composition based on plasmid vector 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 doses of between 10 µg and 20 mg, with a special preference for about 0.1 mg to about 2 mg per kg body weight for each of the mycobacterial antigens comprised in the composition. The administration may take place in a single dose or repeated doses after a certain time interval.

Repeated administrations (2, 3, 4, 5, 6, 7, 8, 9, 10, etc) can be separated from each other by an appropriate period of time and carried out by the same route or by different routes of administration, either at the same site or at different sites. Moreover, each administration can use the same active agent(s) or different ones. For illustrative purposes, two or three subcutaneous administrations separated from each other by approximately one week (e.g. from 3 to 10 days) are particularly suitable for MVA-based compositions whereas one or two intramuscular administration(s) are particularly suitable for Ad-, measles- and plasmid-based compositions. One or more "recall" administration(s) can be performed following the first series of priming administration(s) (e.g. after 6 months to several years) so as to recall the primed anti-Mycobacterium immune response. It is also possible to proceed via sequential cycles of administrations (e.g. a cycle of weekly administrations) that are repeated after a rest period.

In a specific embodiment, the administrations can be carried out according to a prime boost 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 active agents which comprise or encode at least a mycobacterial antigen, immunogenic domain or epitope in common. 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. by subcutaneous or intramuscular route. For illustrative purposes, one may contemplate priming the host's response with a live attenuated bacterium (such as BCG) and boosting with at least one of the "active agent" described herein (e.g. the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector (e.g. infectious viral particle), or host cell of the invention or any combination thereof).

Prophylactic and therapeutic use

The immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition of the invention is preferably for use for preventing or treating a Mycobacterium infection or any disease and pathologic condition caused by or associated with it. Such use aims at inducing or stimulating protective immune responses against a mycobacterial antigen/epitope.

In one embodiment, the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition of the invention is for use in methods for preventing infection or delaying the risk of infection with a Mycobacterium in a subject in need thereof, especially a subject who has been in close contact with an infected individual having developed an active disease and thus at risk of developing a Mycobacterium infection (e.g. transmission by inhalation of bacilli in moist droplets coughed out by the individual with TB).

In another embodiment, the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition of the invention is for use in methods for treating an active disease in a subject infected with a Mycobacterium species and especially *Mtb*, the method comprising the step of administering to the infected subject having developed an active disease, a therapeutically effective amount of at least one of the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition described herein, so as to induce an immune response against the infecting Mycobacterium species, thereby delaying or reducing the risk of development of active disease.

An "active disease" refers to a Mycobacterium infection with manifested serious disease symptoms. For example, in a human subject, TB is characterized by general clinical signs (such as weight loss, asthenia, fever, night sweats), clinical signs and/or symptoms (such as cough, hemoptysis, thoracic pain in case of pulmonary TB), and/or in some cases

extrapulmonary signs according to the sites of infection (such as lymph nodes, bone forms, meningitis, urologenital forms).

In still another embodiment, the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition of the invention is for use in methods for preventing or treating reactivation in a subject latently-infected with a Mycobacterium species and especially *M. tuberculosis*, the method comprising the step of administering to said latently-infected subject, a therapeutically effective amount of at least one of the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition described herein, so as to induce an immune response against the infecting Mycobacterium species, thereby preventing or delaying reactivation.

By "a latently infected subject" is understood an individual, who is already infected with a virulent Mycobacterium species (e.g. *Mtb*), but shows no manifested disease symptoms or clinical signs. Typically, the latently-infected subject retains the Mycobacterium within his bodies, is not clinically ill but retains a risk of subsequent progression to clinical disease (reactivation), particularly in the context of immunosuppression (e.g. co-infection with another pathogen such as HIV or under immunosuppressive treatment such as TNFa inhibitors). A *Mtb* latently-infected subject will be expected to be positive if tested by any test permitting the diagnosis of a *Mtb* infection (e.g. tuberculin test, Mantoux test for PPD reactivity, and/or IFNg release assays).

The term "reactivation" refers to the later manifestation of manifested disease symptoms of a Mycobacterium-associated disease in a subject who tests positive for a Mycobacterium infection but did not manifest apparent disease symptoms. For example reactivation may occur in an infected subject which may or may not have previously manifested active disease symptoms or who had been treated sufficiently to bring the infection into a latent state. For example, a *Mtb*-infected subject was previously immunized with BCG or previously treated for the *Mtb* infection (e.g. with one or more “front line” chemotherapeutic drug(s).

In a specific embodiment, the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition of the invention is for use as BCG booster to increase efficacy of BCG vaccination in a vaccinated subject.

Association with chemotherapy

The immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition of the invention may be employed in association with one or more

conventional therapy, e.g. one or more chemotherapeutic drug(s) effective against a Mycobacterium infection (e.g. *Mtb* infection).

The chemotherapy is typically determined by the treating physician using current practice. Examples of such chemotherapeutic drugs include without limitation antibiotic(s) as well as small direct and indirect inhibitor molecules, antibodies and immunotherapeutics as described in the art. Typically, "front-line" antibiotic chemotherapy currently used to treat a *Mtb* infection that is not drug resistant includes isoniazid, rifamycins (i.e., rifampin, rifapentine and rifabutin), ethambutol, streptomycin, pyrazinamide and fluoroquinolones. "Second-line" chemotherapy used to treat a *Mtb* infection that has demonstrated drug resistance to one or more "first-line" therapy includes ofloxacin, ciprofloxacin, ethionamide, aminosalicylic acid, cycloserine, amikacin, kanamycin and capreomycin. The one or more chemotherapeutic(s) is/are generally administered over an appropriate period of time, for example, for one or several months (e.g. 1, 2, 3, 4, 5, 6, 9 or 12 months) or longer. Daily administration of doses 200 to 600 mg (e.g. 300 or 400mg) over a period of time ranging from 6 to 12 months is appropriate.

In one embodiment, the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition of the invention is for use for reducing the time course of chemotherapy against a Mycobacterium (e.g. *Mtb*) infection. Usually, administration of the active agent(s) described herein will allow to enhance the efficacy of chemotherapy, (e.g. decrease the duration and/or severity of the clinical signs, improve the sputum conversion rate, etc.), reduce the length of the chemotherapy and/or the number of chemotherapeutic drugs to be employed, especially when the infecting mycobacteria is drug resistant.

In accordance with the present invention, the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition of the invention can be administered before, concurrently with, or after administration of the one or more chemotherapeutic drug(s). In one embodiment, the active agent described herein is administered at least 2 weeks after starting administration of the chemotherapy.

In a preferred embodiment, the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell and/or composition of the invention is for use for inducing or enhancing an immune response in the administered subject. Accordingly, the present invention also encompasses a method for inducing or stimulating an immune response against a mycobacterial antigen upon administration in a subject of the

immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell and/or composition of the invention.

The induced or stimulated immune response can be specific (i.e. directed to a mycobacterial epitopes/antigen) and/or non-specific (innate), humoral and/or cellular. In the context of the invention, the immune response is preferably a T cell response CD4+ or CD8+-mediated or both, directed to a mycobacterial antigen/epitope.

The ability of the active agents(s) described herein to induce or stimulate an immune response can be evaluated either *in vitro* or *in vivo* using a variety of direct or indirect assays which are standard in the art. Testing and validation are also illustrated in the appended Example section.

For example, induction of non-specific immunity can be performed by measurement of the NK/NKT-cells (e.g. representativity and level of activation), as well as IFN-related cytokine and/or chemokine producing cascades, activation of TLRs and other markers of innate immunity (e.g. Riano et al., 2012, Tuberculosis 92: 148-59).

The ability to stimulate a humoral response can be determined by an increase in antibody titer that is specific for at least one of the antigens comprised in or encoded by the immunogenic combination and fusion polypeptides described herein. Exemplary techniques include without limitation antibody binding, binding competition as well as ELISA and Western blot.

Evaluation of cellular immunity can be estimated for example by an increased frequency in immune cells such as T lymphocytes specific for at least one of the mycobacterial antigens comprised in or encoded by the immunogenic combination and fusion polypeptide described herein. One may also monitor cell proliferation upon radioactive labelling (e.g. T cell proliferation assays by [^{3}H] thymidine incorporation assay). Another and sensitive method for detecting the immune response is ELISpot in which the frequency of IFNg-producing cells is determined. Cytotoxic capacity for antigen-specific T lymphocytes can also be evaluated in a sensitized subject or by immunization of appropriate animal models. It is also possible to proceed by quantification of the release of relevant Th1 and/or Th2 cytokine(s) produced by activated T cells using routine bioassays (e.g. by multiparameters flow cytometry (ICS), by cytokine profile analysis using multiplex technologies or ELISA, etc.). PCR techniques can also be used to determine the presence of mRNA coding for the relevant cytokines. It will be appreciated by a skilled person that a significant increase or decrease in the amount of such relevant cytokines can be used to assess the immunogenic activity of one or more of the active agent(s) described herein.

Finally, the protective immune response can be evaluated *in vivo* in appropriate experimental animal, e.g. a mouse, a rat or a guinea pig (see Ashwin et al., 2008, Am J Resp, 39: 503-8; Acosta et al., 2011, Malays J Med, 18: 5-12), e.g. by measuring a reduction in mycobacterial colony-forming unit (cfu) from the spleen, lung or other tissue homogenates isolated from the animals which have received a challenge infection with a virulent strain of a Mycobacterium species (e.g. *Mtb*) after previously having been immunized with one or more of the active agent(s) described herein, as compared to the mycobacterial cfu in a control group of experimental animals infected with the same virulent strain of Mycobacterium, but which have not previously been immunized. The comparison between treated and non-treated groups can also be assessed on animal survival (an increased survival in the treated group will correlate with a protective immune response).

Such immunological read out are good correlate of protective immune response against a Mycobacterium infection provided by the active agent(s) described herein.

The protective response provided by the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition of the invention can also be estimated upon administration in a human subject according to the modalities described herein, over the baseline status or over the expected status if not treated. The protective response can be evidenced by any relevant clinical measurement typically used by physicians or other skilled healthcare staff, including, for instance:

- A diminishment of disease incidence and/or prevalence and/or frequency in a given population such as the Chinese population or a population of migrants in a given country (e.g. a lower proportion of new individuals who have been diagnosed with a Mycobacterium infection or at risk of developing a Mycobacterium infection or a disease associated with a Mycobacterium infection in the group having received the active agent(s) described herein);
- A higher percentage of sputum conversion rate in the group of treated subjects;
- A higher percentage of curing active disease in the group of treated subjects;
- A diminishment of extent of Mycobacterium transmission after close contact with an infected subject (e.g. reduction or delay the risk of being infected or the risk of developing active disease and/or reduction or delay the risk reactivation in latently infected subjects);
- An amelioration of a disease state (e.g. decrease of bacterial cfu in a target tissue or in a biological sample; diminishment of the disease symptoms or their severity (e.g.

number and/or severity of lesions in a target organ) or stabilized (not worsening) disease state); and

- An improved response of the treated subject to concurrent treatment (reduction of the need, number, duration and/or doses of conventional chemotherapeutic drugs).

In the context of the invention, the protective response can be transient (for a couple of weeks after cessation of administration) or sustained (for several months or years). As the natural course of clinical status which may vary considerably from a subject to another, it is not required that the protective response be observed in each subject treated but in a significant number of subjects (e.g. statistically significant differences between two groups can be determined by any statistical test known in the art, such as a Tukey parametric test, the Kruskal-Wallis test the U test according to Mann and Whitney, the Student's t-test, the Wilcoxon test, etc).

Such measurements can be performed before the administration of the active agent(s) described herein (baseline) and at various time points during treatment and at least for some (e.g. 12) weeks after cessation of the treatment.

For general guidance, a Mycobacterium-infection and associated disease can be detected by various means. For example, *Mtb* infection can also be oriented by a number of methods in clinical use today such as the Mantoux tuberculin skin test (TST), the Quantiferon test as well as *in vitro* detection of responses to HBHA (heparin binding haemagglutinin; Hougardy et al., 2007; PLos One 2(10): e926) or the detection of IP10 after stimulation *in vitro* with ESAT6, CFP10 and TB7.7 (Ruhwald et al., 2008; Microbes Infect 9: 806-12). Subjects developing an active disease may be diagnosed according to current practice. For illustrative purposes, TB diagnosis is based on detection of the causative bacterium in clinical specimens by microscopy, cultural techniques, polymerase chain reaction (PCR) and its various derivatives. DNA fingerprinting methods and spoligotyping can also be implemented. Mycobacterial culture is the gold standard method for identification of an isolate of the Mycobacterium tuberculosis complex and drug susceptibility testing. X ray techniques and clinical observations can also be implemented to support findings of active pulmonary and/or extrapulmonary disease. On the other hand, numerous serological assays have been developed for diagnosis of *Mtb* infection using a variety of antigens to detect circulating antibodies including complement fixation tests, haemagglutination tests, radio immunoassay and enzyme-linked immunosorbent assays (ELISA).

Antibody

In a further aspect, the present invention relates to an antibody which selectively binds to at least one of the mycobacterial antigens comprised in or encoded by the immunogenic combination or the fusion polypeptide of the present invention.

As used herein, an "antibody" encompasses any polypeptide that comprises an antigen binding fragment or an antigen binding domain and selectively binds a target protein when it binds the target protein and does not significantly bind to unrelated protein. In certain cases, it would be understood that antibody binding to the target protein is still selective despite some degree of cross-reactivity. Typically, binding between an antibody and an antigen is considered to be specific when the association constant K_A is higher than 10^{-6} M. The appropriate binding conditions, such as antibody concentration, ionic strength of the solution, temperature, time allowed for binding, concentration of a blocking agent (e.g., serum albumin, milk casein), etc., may be optimized by a skilled person using routine techniques.

The antibody of the present invention can be polyclonal, monoclonal, monospecific, polyspecific, human, humanized, single chain, chimeric, synthetic, recombinant antibodies, as well as any fragment of such antibodies that retain antigen binding, including, but not limited to, Fab, $F(ab')_2$, Fv and scFv fragments.

Antibodies of the present invention can be produced using conventional techniques in the art, e.g. following administering to an animal (e.g. rabbit, horse, etc.) an effective amount of any of the mycobacterial antigen, fusion protein described herein and/or a peptide fragment thereof, by display (e.g. phage, yeast or ribosome display) or hybridoma techniques. The general methodology for making monoclonal antibodies is well known in the art.

The antibody of the present invention may be provided in isolated form, in a solution (e.g. animal antisera) or in host cells (e.g. hybridomas). Moreover, it may be conjugated to appropriate labels (detectable or functional labels) including radioactive ($_{131}I$, or $_{99}Tc$, etc), enzymatic (horse radish peroxidase, alkaline phosphatase, etc.) and chemical (e.g. biotin, etc) labels.

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 a mycobacterial antigen in use in the present invention, (b) as reagents in assays to detect the presence of a Mycobacterium in a biological sample, and/or (c) as tools to detect and/or recover the recombinantly-produced mycobacterial antigens and fusion

polypeptide according to the method of the invention from a mixture of proteins and other contaminants (e.g. by permitting purification by affinity chromatography or immunoprecipitation from cultured host cells). They may also be used for therapeutic purposes, e.g. for treating a subject after exposure to a Mycobacterium (e.g. passive immunotherapy).

In one embodiment, the present invention relates to a method for the detection and/or quantification of a mycobacterial antigen in a biological sample (e.g. plasma, serum, sputum, etc) taken from a subject infected or susceptible to be infected by a Mycobacterium using the antibody of the invention which comprises the steps of bringing said biological sample into contact with the antibody of the invention as reagent under conditions allowing the formation of a complex between the mycobacterial antigen and the antibody reagent and detecting and/or quantifying the formation of said complex by any appropriate means. Detecting the presence of the target mycobacterial antigen is indicative of a Mycobacterium infection (e.g. *Mtb*).

In another embodiment, the present invention relates to a method for the detection and/or quantification of antibodies directed to a Mycobacterium in a biological sample (e.g. plasma, serum, etc taken from a subject infected or susceptible to be infected by a Mycobacterium), which comprises the steps of bringing said biological sample into contact with a reagent comprising any of the immunogenic combination, fusion polypeptide, nucleic acid molecules, vectors, infectious viral particles, host cells of the invention under conditions allowing the formation of a complex between the antibody and the mycobacterial antigen/epitope comprised or encoded by any of the above-cited reagents and detecting and/or quantifying the formation of said complex by any appropriate means. Detecting the presence of specific antibody is indicative of a Mycobacterium infection (e.g. *Mtb*).

A person skilled in the art will easily determine the quantity of reagent to be used in the methods of the invention. The means of detection and/or quantification of antigen/antibody complex 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 the above cited 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).

The present invention also concerns a kit of reagents for diagnosis a Mycobacterium (e.g. *Mtb*) infection for antigen assay comprising the antibody of the invention and for antibody assay comprising the immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell, composition of the invention.

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.

DESCRIPTION OF THE DRAWINGS

Figure 1 shows a schematic representation of the various fusion polypeptides of *Mtb* antigens that were generated and used as described in the appended Example section. "SS" means signal peptide, "TM" Transmembrane domain, "F" Flag tag, "M" Myc tag and "H" his tag. A * is indicative of a modification of the *Mtb* antigen with respect to the native counterpart. The Figure also mentions the n° of the fusion polypeptide and the reference of the expressing plasmid vector (pTGXXXXX) as used hereinafter.

Figure 2 illustrates expression of the individual *Mtb* genes by Western blot following immunodetection with specific antibodies. $2x10^6$ HEK293 cells were transfected with 5µg of DNA using Lipofectamine 2000. Proteasome inhibitor MG132 was added to the culture medium 18h after the transfection. Lysates of cells harvested after 48h of culture were analysed by electrophoresis on 10% gel criterion and immunodetection was performed with rabbit anti-sera diluted 1/1000 recognizing Rv2029* (Figure 2A), RPFB-Dhyb (Figure 2B), and commercial antibodies recognizing ESAT-6 (Figure 2C) and Rv2626 (Figure 2D).

Figure 3 illustrates Western blot analysis of *Mtb* fusions encompassing latent antigens (pTG18295 encoding fusion n°9), active antigens (pTG18296 encoding fusion n°10) resuscitation antigens (pTG18307 encoding fusion n°12) and both resuscitation and

active antigens (pTG18297 encoding fusion n°11) following anti Flag immunodetection. +/– represents with and without MG132.

Figure 4 illustrates Western blot analysis of *Mtb* fusions including TB10.4 (Figure 4A), Rv0569 (Figure 4B) and Rv2626 (Figure 4C) respectively, following immunodetection with commercial anti-TB10.4 antibody (ABIN361292), anti-Rv0569 rabbit antisera and anti-Rv2626 mouse monoclonal antibody 26A11.

Figure 5 illustrates IFNg-producing cells induced following immunization of animals with fusion-encoding plasmids pTG18266 (SS-Ag85B-TB10.4-ESAT6-TM; Figure 5A), pTG18296 (cytoplasmic Ag85B-TB10.4-ESAT6; Figure 5B), a mixture of pTG18310, pTG18315 and pTG18308 plasmids encoding the individual Ag85B, TB10.4 and ESAT6 antigens (Figure 5C) and pGWiz (Figure 5D). Cellular immune response was evaluated 2 weeks following the last DNA injection by ELISpot IFNγ assays after *ex vivo* re-stimulation with specific peptide pools.

Figure 6 illustrates IFNg-producing cells induced following immunization of animals with fusion-encoding plasmids pTG18268 (SS-RPFB-Dhyb-Ag85B-TB10.4-ESAT6-TM; Figure 6A), pTG18297 (cytoplasmic RPFB-Dhyb-Ag85B-TB10.4-ESAT6; Figure 6B), a mixture of pTG18307, pTG18310, pTG18315 and pTG18308 plasmids encoding the individual RPFB-Dhyb, Ag85B, TB10.4 and ESAT6 antigens (Figure 6C) and pGWiz (Figure 6D). Cellular immune response was evaluated 2 weeks following the last DNA injection by ELISpot IFNγ assays after *ex vivo* re-stimulation with specific peptide pools.

Figure 7 illustrates IFNg-producing cells induced following immunization of animals with fusion-encoding plasmids pTG18267 (SS-RPFB-TM; Figure 7A), pTG18307 (cytoplasmic RPFB-Dhyb; Figure 7B) and pGWiz (Figure 7C). Cellular immune response was evaluated 2 weeks following the last DNA injection by ELISpot IFNγ assays after *ex vivo* re-stimulation with specific peptide pools covering RpfB and RpfD antigens.

Figure 8 illustrates IFNg-producing cells induced following immunization of animals with fusion-encoding plasmids pTG18269 (SS-Rv0569-Rv1813-Rv3407-Rv3478-Rv1807-TM; Figure 8A), pTG18295 (cytoplasmic Rv0569-Rv1813-Rv3407-Rv3478-Rv1807; Figure 8B), a mixture of pTG18301, pTG18303, pTG18300, pTG18304 and pTG18302 plasmids

encoding the individual Rv0569, Rv1813, Rv3407, Rv3478 and Rv1807 antigens (Figure 8C) and pGWiz (Figure 8D). Cellular immune response was evaluated 2 weeks following the last DNA injection by ELISpot IFNγ assays after *ex vivo* re-stimulation with specific peptide pools.

Figure 9 illustrates SDS-PAGE analysis of the purified Rv2626 (Figure 9A), RPFB-Dhyb fusion (Figure 9B) and TB10.4 (Figure 9C).

Figure 10 illustrates the cellular immune response produced following immunization of animals with fusion-encoding plasmid pTG18323 (Rv2029 – Rv2626 – Rv1733 – Rv0111; Figure 10a) or pGWiz (Figure 10b). IFNγ-producing cells were evaluated 2 weeks following the last DNA injection by IFNγ ELISpot assays after *ex vivo* re-stimulation with specific peptide pools. Each bar represents response of one mouse (7 mice/group).

Figure 11 illustrates the cellular immune response induced following immunization of mice with (**a**) MVATG18365 (*Rv2029-Rv2626-Rv1733-Rv0111 + RpfB-Dhyb-Ag85B-TB10.4-ESAT6 W/O SS/TM*) or (**b**) MVATG18364 (*Rv2029-Rv2626-Rv1733-Rv0111 + RpfB-Dhyb-Ag85B-TB10.4-ESAT6*). IFNγ-producing cells were evaluated one week following the MVA injection by IFNγ ELISpot assays after *ex vivo* re-stimulation with specific peptide pools. Each bar represents response of individual mouse (5 mice/group).

Figure 12 summarizes levels of IFNγ response in BALB/c mice vaccinated with all MVA candidates, produced according to TB disease phase or biochemical rational. IFNγ-producing cells were evaluated one week following the MVA injection by IFNγ ELISpot assays after *ex vivo* re-stimulation with specific peptide pools of the 14 Mtb antigens. Intensity of the detected responses is ranked according to fold increase of median value (spots/10^6 splenocytes) for each re-stimulation with respect to the cut-off value, using a colour code (see legend ranging from -, +, ++, +++). Hatched boxes mean that the antigen is lacking in the given MVA vaccine.

Figure 13 illustrates the cellular immune response induced following immunization of transgenic HLA-A2 mice with (**a**) MVATG18376 (*Rv2029-Rv2626-Rv1733-Rv0111 + RpfB-Dhyb-Ag85B-TB10.4-ESAT6 + Rv0569-Rv1813-Rv3407-Rv3478-Rv1807*) or (**b**) the empty MVATGN33.1. IFNγ-producing cells were evaluated one week following the MVA

injection by IFNγ ELISpot assays after *ex vivo* re-stimulation with specific peptide pools. Each bar represents response of individual mouse (6 mice/group).

Figure 14 illustrates the cellular immune response induced following immunization of C3H/HeN mice with (**a**) MVATG18377 (*Rv2029-Rv2626-Rv1733-Rv0111 + RpfB-Dhyb-Ag85B-TB10.4-ESAT6 W/O SS/TM + Rv0569-Rv1813-Rv3407-Rv3478-Rv1807*) or (**b**) the empty MVATGN33.1. IFNγ-producing cells were evaluated one week following the MVA injection by IFNγ ELISpot assays after *ex vivo* re-stimulation with specific peptide pools. Each bar represents response of individual mouse (6 mice/group).

Figure 15 summarizes levels of IFNγ response in transgenic HLA-A2, C57BL/6 and C3H/HeN mice vaccinated with the indicated MVA candidates. IFNγ-producing cells were evaluated one week following the MVA injection by IFNγ ELISpot assays after *ex vivo* re-stimulation with specific peptide pools of the 14 Mtb antigens. Intensity of the detected responses is ranked according to fold increase of median value (spots/10^6 splenocytes) for each re-stimulation with respect to the cut-off value, using a colour code (see legend ranging from -, +, ++, +++). Hatched boxes mean that the antigen is lacking in the given MVA vaccine.

MATERIALS AND METHODS

Analytical methods

Existing data on *Mtb* antigens were investigated from the available literature and data bases with the goal of identifying a first selection of *Mtb* genes/antigens that may be useful in an immunotherapeutic vaccine capable of raising anti-TB immunity during all phases of the natural course of infection.

The selected antigens were then submitted to a data-mining scoring system that was developed to transcribe and compare data from different sources. An overall final "score" was generated reflecting the value of each antigen. This score takes into account the immunogenic potential of the antigen as well as its capacity to protect against an infectious challenge in animal models and in humans (for example protection data in humans will be better scored than inducing immunogenicity in animal models). Once all data for a particular

antigen were collected, a grade from 0 to 5 was attributed to each category, 0 being the worse possible grade while 5 being the best. The choice of the grade was also based on the quality of the data (e.g. right controls used in the experiments, rigorous interpretation) but also on the robustness of the data (e.g. number of times experiments were run, number of publications confirming/supporting the findings).

Antigen biochemical *in silico* analyses

Biochemical and biological data are also key data for optimizing expression and fusion design permitting to anticipate potential expression problems. For example, the biological functions of a protein may lead to a potential toxicity resulting in genetic unstability and/or safety profile upon vector-mediated expression. Moreover, protein unfolding may impact stability and expression levels due to a higher cellular degradation rate.

An extensive bibliographic search was carried out for all *Mtb* antigens in order to better understand and characterize the structure and the functions of these proteins.

Additionally, biochemical and bioinformatic predictions were also performed for characterization of *Mtb* antigens. Bioinformatic prediction tools (Nielsen et al., 2007 PLos One 2: e796; Nielsen et al., 2008, PLoS Comput Biol 4: e1000107) were used to look at predicted epitopes for class I and II HLA molecules. Identification of these epitopic regions may be useful for optimization of the selected *Mtb* antigens or to facilitate the development of immune based assays.

Moreover, extensive *in silico* structure prediction analyses were performed in order to predict biochemical properties and/or biological functions and thus allow *Mtb* antigens selection and design (e.g. whether a full length native form is likely to be expressed or whether modifications appear to be required).

More specifically

- Search for structural homologs in protein data bank (PDB). The program used was BLASTP with the default parameters and the selected database was NPS@ 3D SEQUENCES (from PDB). This search allows finding NMR or crystalline structures of the antigen or of proteins with sequence homologies higher than 25%. 3D structures were visualized using CN3D 4.1. or PDB viewer.
- Search in UNIPROT-SWISSPROT and TB databases. Protein homologs to the *Mtb* antigens of interest were searched on UNIPROT-SWISSPROT database using

primary structures as a query and BLAST search on NPS@. The program used was BLASTP with the default parameters and the selected database was UNIPROT-SWISSPROT; UNIPROT-SWISSPROT entries give access to general information on protein function, domains, potential signal peptide, posttranslational modifications as well as bibliographic references. General information (e.g. gene functions, genetic link between genes, phenotypes and mutations associated with genes, immunogenicity, as well as bibliographic references) about the selected *Mtb* antigens were retrieved using the Rv protein name as a query in the TB database.

- Prediction of signal peptides: these short N-terminus sequences are often predicted as transmembrane domains but are not present in native and mature proteins. The presence of signal peptide was notified in the UNIPROT-SWISSPROT database for certain antigens or using the hidden Markov model of signal v3.0 algorithm.

If no hit for homolog search, additional searches were undertaken:

- Prediction of potential transmembrane domains (TM) using three different programs (e.g. dense Alignment surface (DAS) method, Algorithm TMHMM and TopPred0.01). It is our observations that the presence of such hydrophobic TM domains with may impair genetic stability of the corresponding antigen when expressed in viral vectors such as MVA.
- Search for known protein motif associated with protein domains, families and functional sites using PROSITE SCAN
- Prediction of secondary structures using several prediction methods (namely: SOPM, MLRC, HNN, DSC, PHD, PREDATOR). A secondary structure was considered as highly probable if the 6 methods predicted it. A secondary structure was considered possible if 3 out of the 6 methods predicted it.
- Hydrophobic cluster analysis (HCA). The HCA method is based on essential features of protein folding: the hydrophilic/hydrophobic dichotomy and the hydrophobic compactness of protein globular domains. HCA plots were used to identify hydrophobic clusters along the protein sequence. These clusters are characteristic of folded proteins with a hydrophobic buried core. An antigen was considered as probably having a folded state if hydrophobic clusters were present at least at some part of the protein.
- Prediction of natively disordered regions that permit to identify unfolded regions (MetaPrDOS predictions). This analysis complements the HCA plot by predicting areas of the protein that are not folded. All areas above the threshold 0.5 (disordered

tendency) were considered as unfolded parts of the protein. To be noted that most of the time, N- and C-terminus parts of proteins are non-folded in their native state. If such stretches at the extremities were present and smaller than 10 residues, they were kept as potential linkers for fusion.

- Prediction of coiled coil (using the COILS program). Oligomerization state of the antigen could impact the antigen fusion design. A coiled coil domain was predicted if the output probability displayed a value of 1 for a part of the protein with at least 14 residues window analysis.

Further, sequence alignments were carried out to verify that the selected *Mtb* antigens are conserved among different *Mtb* strains and isolates. More precisely, multiple sequence alignments were performed using Clustal W2 (@.ebi.ac.uk/Tools/msa/clustalw2/) between the amino acid sequence of each selected antigen (the exemplified *Mtb* antigens originate from the H37Rv strain) and their equivalent of 11 other *Mtb* strains (clinical isolates) and M bovis that have been identified in protein databases (BLASTP search). As a result, the TB antigens showed high conservations among the 12 Mycobacteria strains analyzed with a percentage of identity ranging from 100% to 96% depending on the antigen and the Mycobacterium strain. The major exception was seen with Rv3478 for which only 88% identity was found between H37Rv and CDC1551 sequences.

Finally, another key criteria to reach final TB antigen selection was to ensure a balanced representativeness of antigens from the various phases of infection. For example, some latent antigens were selected despite lower final data mining score than most of the active phase antigens.

Construction of fusion of *Mtb* antigens

12 fusions of *Mtb* antigens were engineered as illustrated in Figure 1. Five fusions were designed based on biochemical rationales (fusions 3, 5, 6, 8 and 14) whereas fusions 2, 4 and 13 were designed relative to the TB phase of the disease, with fusion 2 containing active antigens, fusion 4 active and resuscitation antigens and fusion 13 being constituted by latent antigens. In order to facilitate detection of the various gene fusions and avoid the need of specific antibodies for each *Mtb* antigen, TAG sequences were added in each fusion, respectively Flag TAG (DYKDDDDK; SEQ ID NO: 25) at the N-terminus, and c-myc

(EQKLISEEDL; SEQ ID NO: 26) and His (HHHHHH; SEQ ID NO: 27) Tags at the C-terminus.

On the other hand, signal peptides (also called signal sequence or SS) and membrane-anchoring peptides (also called trans-membrane or TM peptide/domain) were added respectively at the N-terminus and C-terminus of the *Mtb* fusion proteins to ensure anchorage at the cell surface which is assumed to optimize immunogenic activity in certain cases. However, addition of TM domain was not necessary for fusions ending with Rv0111 or Rv1733, as these proteins already contain membrane-anchoring peptides. For comparative purposes, four fusions were also engineered without any signal sequence (SS) and TM domain so as to study the influence of cell location (membrane presentation in the presence of SS and TM peptides versus cytoplasmic location in the absence of such peptides) on expression level and immunogenic activity. For example, pTG18269 encodes the same *Mtb* antigens (Rv0569 - Rv1813* - Rv3407 - Rv3478 - Rv1807) as pTG18295 except that the pTG18269-encoded fusion is equipped with a SS at its N-terminus and a TM-at its C terminus between Myc and His tags whereas the pTG18295-encoded fusion is devoid of such SS and TM peptides.

Synthetic genes coding for the different *Mtb* antigens and fusions were synthesized by Geneart (Regensburg, Germany). The sequences were optimized for human codon usage and a Kozak sequence (ACC) was added before the ATG starting codon. Moreover some motives were excluded: TTTTTNT, GGGGG, CCCCC which are deleterious for expression in poxvirus vector and AAAGGG, AAAAGG, GGGAAA, GGGGAA, (and complementary sequences TTCCCC, TTTCCC, CCTTTT, CCCCTT) which can be deleterious for expression in some others vectors.

The fusions were cloned in pGWiz plasmid (Gelantis) digested by *Not*I and *BamH*. This plasmid contains a modified CMV promoter, followed by intron A from the CMV immediate early gene, and a high-efficiency artificial transcription terminator.

Construction of pTG18266 (fusion n°2)

The amino acid sequence of the fusion n°2 is shown in SEQ ID NO: 28. Amino acids 1 to 23 correspond to the signal peptide present at the N-terminus of the glycoprotein precursor of rabies virus ERA strain (described in Genbank n° M38452), amino acids 24 to 31 correspond to the Flag TAG, amino acids 32 to 317 correspond to Ag85B*, amino acids 318 to 412 correspond to TB10.4, amino acids 413 to 506 correspond to ESAT6, amino acids 507 to 516 correspond to the c-myc TAG, a Ser linker, amino acids 518 to 583

correspond to the membrane-anchoring peptide derived from the rabies glycoprotein of ERA strain and amino acids 584 to 589 correspond to the His TAG. The fusion n°2-encoding nucleotide sequence shown in SEQ ID NO: 40 was generated by synthetic way and the synthetic gene was cloned in pGWiz restricted by *Not*I and *BamH*1 to give pTG18266.

Construction of pTG18267 (fusion n°3)

The amino acid sequence of the fusion n°3 is shown in SEQ ID NO: 30. Amino acids 1 to 23 correspond to the signal peptide present at the N-terminus of the glycoprotein precursor of rabies virus PG strain (described in Genbank n° ay009097 and SEQ ID NO: 2 in WO2008/138649), amino acids 24 to 31 correspond to the Flag TAG, amino acids 32 to 380 correspond to RPFB-Dhyb*, amino acids 381 to 390 correspond to the c-myc TAG, a Ser linker, amino acids 392 to 457 correspond to the membrane-anchoring peptide derived from the rabies glycoprotein of PG strain (SEQ ID NO: 3 in WO2008/138649) and amino acids 458 to 463 correspond to the His TAG. The fusion n°3-encoding nucleotide sequence shown in SEQ ID NO: 42 was generated by synthetic way and the synthetic gene was cloned in pGWiz restricted by *Not*I and *BamH*1 to give pTG18267.

Construction of pTG18268 (fusion n°4)

The amino acid sequence of the fusion n°4 is shown in SEQ ID NO: 32. Amino acids 1 to 23 correspond to the signal peptide present at the N-terminus of the glycoprotein precursor of rabies virus PG strain (described in Genbank n° ay009097), amino acids 24 to 31 correspond to the Flag TAG, amino acids 32 to 380 correspond to RPFB-Dhyb*, amino acids 381 to 666 correspond to Ag85B*, amino acids 667 to 761 correspond to TB10.4, amino acids 762 to 855 correspond to ESAT6, amino acids 856 to 865 correspond to the c-myc TAG, a Ser linker, amino acids 867 to 932 correspond to the membrane-anchoring peptide derived from the rabies glycoprotein of PG strain and amino acids 933 to 938 correspond to the His TAG. The fusion n°4-encoding nucleotide sequence shown in SEQ ID NO: 44 was generated by synthetic way and the synthetic gene was cloned in pGWiz restricted by *Not*I and *BamH*1 to give pTG18268.

Construction of pTG18269 (fusion n°5)

The amino acid sequence of the fusion n°5 is shown in SEQ ID NO: 34. Amino acids 1 to 23 correspond to the signal peptide present at the N-terminus of the glycoprotein precursor of rabies virus ERA strain (described in Genbank n° M38452), amino acids 24 to 31 correspond to the Flag TAG, amino acids 32 to 118 correspond to Rv0569, amino acids 119 to 227 correspond to Rv1813*, amino acids 228 to 325 correspond to Rv3407, amino acids 326 to 717 correspond to Rv3478, amino acids 718 to 1115 correspond to Rv1807,

amino acids 1116 to 1125 correspond to the c-myc TAG, a Ser linker, amino acids 1127 to 1192 correspond to the membrane-anchoring peptide derived from the rabies glycoprotein of PG strain (SEQ ID N0: 3 in WO2008/138649) and amino acids 843 to 848 correspond to the His TAG. The fusion n°5-encoding nucleotide sequence shown in SEQ ID NO: 46 was generated by synthetic way and the synthetic gene was cloned in pGWiz restricted by *Not*I and *BamH*1 to give pTG18269.

Construction of pTG18270 (fusion n°6)

The amino acid sequence of the fusion n°6 is shown in SEQ ID NO: 36. Amino acids 1 to 23 correspond to the signal peptide present at the N-terminus of the glycoprotein precursor of rabies virus ERA strain (described in Genbank n° M38452), amino acids 24 to 31 correspond to the Flag TAG, amino acids 32 to 317 correspond to Ag85B*, amino acids 318 to 459 correspond to Rv2626, amino acids 460 to 808 correspond to RPFB-Dhyb*, amino acids 809 to 956 correspond to Rv1733*, amino acids 957 to 966 correspond to the c-myc TAG, a Ser linker, and amino acids 968 to 973 correspond to the His TAG. The fusion n°6-encoding nucleotide sequence shown in SEQ ID NO: 48 was generated by synthetic way and the synthetic gene was cloned in pGWiz restricted by *Not*I and *BamH*1 to give pTG18270.

Construction of pTG18272 (fusion n°8)

The amino acid sequence of the fusion n°8 is shown in SEQ ID NO: 37. Amino acids 1 to 23 correspond to the signal peptide present at the N-terminus of the glycoprotein precursor of rabies virus ERA strain (described in Genbank n° M38452), amino acids 24 to 31 correspond to the Flag TAG, amino acids 32 to 317 correspond to Ag85B*, amino acids 318 to 459 correspond to Rv2626, amino acids 460 to 607 correspond to Rv1733*, amino acids 608 to 617 correspond to the c-myc TAG, a Ser linker and amino acids 619 to 624 correspond to the His TAG. The fusion n°8-encoding nucleotide sequence shown in SEQ ID NO: 49 was generated by synthetic way and the synthetic gene was cloned in pGWiz restricted by *Not*I and *BamH*1 to give pTG18272.

Construction of pTG18323 (fusion n°13)

The amino acid sequence of the fusion n°13 is shown in SEQ ID NO: 38. Amino acids 1 to 28 correspond to the signal peptide present at the N-terminus of the F protein of measles virus (Hallé strain, described in Genbank n° X05597-1), amino acids 29 to 36 correspond to the Flag TAG, amino acids 37 to 349 correspond to Rv2029*, amino acids 350 to 491 correspond to Rv2626, amino acids 492 to 639 correspond to Rv1733*, amino acids 640 to 932 correspond to Rv0111*, amino acids 933 to 942 correspond to the c-myc TAG, a

Ser linker and amino acids 944 to 949 correspond to the His TAG. The fusion n°13-encoding nucleotide sequence shown in SEQ ID NO: 50 was generated by synthetic way and the synthetic gene was cloned in pGWiz restricted by *Not*I and *BamH*1 to give pTG18323.

Construction of pTG18324 (fusion n°14)

The amino acid sequence of the fusion n°14 is shown in SEQ ID NO: 39. Amino acids 1 to 28 correspond to the signal peptide present at the N-terminus of the F protein of measles virus (Hallé strain, described in Genbank n° X05597-1), amino acids 29 to 36 correspond to the Flag TAG, amino acids 37 to 349 correspond to Rv2029*, amino acids 350 to 444 correspond to TB10.4, amino acids 445 to 538 correspond to ESAT6, amino acids 539 to 831 correspond to Rv0111*, amino acids 832 to 841 correspond to the c-myc TAG, a Ser linker and amino acids 843 to 848 correspond to the His TAG. The fusion n°14-encoding nucleotide sequence shown in SEQ ID NO: 51 was generated by synthetic way and the synthetic gene was cloned in pGWiz restricted by *Not*I and *BamH*1 to give pTG18324.

Construction of fusions 9-12

The targeting sequences were deleted from plasmids pTG18267, pTG18269, pTG18266 and pTG18268 by directed mutagenesis (Quick Change Site-Directed mutagenesis kit, Stratagene) using appropriate pairs of primers, OTG20188 (CGCGGCCGCACCATGGATTACAAGGATGACGACG; SEQ ID NO: 52) and OTG20189 (CGTCGTCATCCTTGTAATCCATGGTGCGGCCGCG; SEQ ID NO: 53) for deleting signal peptide sequence and OTG20190 (CATCTCAGAAGAGGATCTG-CATCATCATCATCATTG; SEQ ID NO: 54) and OTG20191 (CAATGATGATGAT-GATGATGCAGATCCTCTTCTGAGATG; SEQ ID NO: 55) for deleting TM sequence. The resulting plasmids were respectively pTG18307 (fusion n° 12 = cytoplasmic fusion n°3), pTG18295 (fusion n° 9 = cytoplasmic fusion n°5), pTG18296 (fusion n° 10 = cytoplasmic fusion n°2) and pTG18297 (fusion n° 11 = cytoplasmic fusion n°4), corresponding to amino acid sequences SEQ ID NO: 31, 35, 29 and 33 encoded by the nucleotide sequences SEQ ID NO: 43, 47, 41 and 45.

Construction of individual *Mtb* gene expression plasmids

The Flag sequence and c-myc-His sequences separated by a *NheI* restriction site were introduced downstream the CMV promoter in pGWiz plasmid. A synthetic DNA fragment containing the end of CMV promoter, Flag and c-myc-His sequences was synthetized by Geneart and inserted into the plasmid FLAG_TAG_1. This plasmid was digested by *Pvu*II

and *BglII* and the resulting fragment was inserted in pGWiz restricted by the same enzyme, giving rise to pTG18282. The individual Rv3407, Rv0569, Rv1807, Rv1813*, Rv3478 and Rv2626 genes were then amplified by PCR from pTG18269 except Rv2626 for which the pTG18323 was used as template.

The amplification primer pairs used for isolation of each TB gene are illustrated in Table 1.

Table 1:

TB gene	Primer name	Primer sequence
Rv3407	OTG20232 SEQ ID NO: 56	GATGACGACGATAAGGCTAGCAGAGCCACCGTGGGACTGG
	OTG20233 SEQ ID NO 57	GATGAGTTTTTGTTCGCTAGCCTGTTCATCCCGCATCTCGT
Rv0569	OTG20234 SEQ ID NO: 58	GATGACGACGATAAGGCTAGCAAGGCCAAAGTCGGCG
	OTG20235 SEQ ID NO: 59	GATGAGTTTTTGTTCGCTAGCTGTTCCTCTGGCGTGC
Rv1807	OTG20236 SEQ ID NO: 60	GATGACGACGATAAGGCTAGCGATTTTGCCACCCTCCCACC
	OTG20237 SEQ ID NO: 61	GAGATGAGTTTTTGTTCGCTAGCGCCAGCTGCAGGAGGTCTGG
Rv1813*	OTG20238 SEQ ID NO: 62	GATGACGACGATAAGGCTAGCGCCAACGGCAGCATGAGCG
	OTG20239 SEQ ID NO: 63	GAGATGAGTTTTTGTTCGCTAGCGTTGCAGGCCCAGTTCACGA
Rv3478	OTG20240 SEQ ID NO: 64	GATGACGACGATAAGGCTAGCGTGGACTTCGGCGCCCTGC
	OTG20241 SEQ ID NO: 65	GAGATGAGTTTTTGTTCGCTAGCGCCAGCGGCTGGAGTTCTGG
Rv2626	OTG20242 SEQ ID NO: 66	GATGACGACGATAAGGCTAGCACAACCGCCAGAGACATCATG
	OTG20243 SEQ ID NO: 67	GATGAGTTTTTGTTCGCTAGCAGAGGCCAGGGCCATGGGG

The resulting amplicons were cloned by "In fusion Advantage" PCR cloning method (Clontech) in pTG18282 linearized by *NheI*. This allows the fusion of Tag sequences with *Mtb* genes. The generated plasmids were named respectively pTG18300 (Rv3407), pTG18301 (Rv0569), pTG18302 (Rv1807), pTG18303 (Rv1813*), pTG18304 (Rv3478) and pTG18305 (Rv2626).

Six plasmids containing expression cassettes for ESAT6, Rv1733*, Ag85B*, TB10-4, Rv0111* and Rv2029* fused to Flag in 5'and c-myc-His sequences in 3' were synthesized by Geneart and inserted in pGWiz. They were named respectively pTG18308 (ESAT6), pTG18309 (Rv1733*), pTG18310 (Ag85B*), pTG18315 (TB10.4), pTG18329 (Rv0111*), pTG18317 (Rv2029*). As Rv1733* and Rv0111* proteins contain a TM domain, the signal

peptide presents at the N-terminus of the glycoprotein precursor of rabies virus ERA strain was fused upstream to the Flag sequence to avoid expression issues.

Whether encoding individual or fused *Mtb* genes, plasmids used for immunization were produced in endotoxin-free conditions.

Construction of recombinant MVA

Deletion of TAG sequences

TAG sequences were removed from the *Mtb* antigen fusions to avoid their presence in the MVA vectors. TAG sequences located inside the *Mtb* fusion cassettes (i.e. Flag present between the signal peptide and the first amino acid of the *Mtb* fusion and cmyc TAG present between the last amino acid of the *Mtb* fusion and membrane-anchoring peptide) were deleted by directed mutagenesis using the QuikChange Site-directed Mutagenesis kit (Stratagene) and appropriate primers pairs as illustrated in the following Table 2. TAG sequences located outside the *Mtb* fusion cassettes (for cytoplasmic fusion and His TAG) were deleted by PCR using primers allowing the addition of an initiator Met and a terminator codon on both extremity of the fusions.

Table 2

Fusion	Primer pairs for deletion of Flag	Primer pairs for deletion of cmyc	Resulting plasmid
4	OTG20313 (SEQ ID NO:68) OTG20314 (SEQ ID NO: 69)	OTG20315 (SEQ ID NO: 70) OTG20316 (SEQ ID NO: 71)	pTG18339
5	OTG20317 (SEQ ID NO: 72) OTG20318 (SEQ ID NO: 73)	OTG20319 (SEQ ID NO: 74) OTG20320 (SEQ ID NO: 75)	pTG18340
6	OTG20321 (SEQ ID NO: 76) OTG20322 (SEQ ID NO: 77)	NA	pTG18341
13	OTG20333 (SEQ ID NO: 78) OTG20334 (SEQ ID NO: 79)	NA	pTG18342
14	OTG20333 (SEQ ID NO: 78) OTG20334 (SEQ ID NO: 79)	NA	pTG18343

Construction of MVATG18355 (fusion n°13)

The nucleotide sequence encoding fusion n°13 (SF-Rv2029*-Rv2626-Rv1733*-Rv0111* as illustrated by the portion of SEQ ID NO: 38 from 1 to 28 and 37 to 932) was placed under the control of the p7.5K promoter (SEQ ID NO: 80; CCACCCACTTTTTATAGTAAGTTTTTCACCCATAAATAATAAATACAATAATTAA TTTCTCGTAAAAGTAGAAAATATATTCTAATTTATTGCACGGTAAGGAAGTAGA

ATCATAAAGAACAGT). This latter was amplified by PCR from VV (Vaccinia virus) Copenhagen strain DNA using a pair of appropriate primers OTG20405 (SEQ ID NO: 81) and OTG20406 (SEQ ID NO: 82) while the fusion n°13 sequence was amplified from plasmid pTG18342 by PCR with OTG20407 (SEQ ID NO:83) and OTG20408 (SEQ ID NO: 84). Then p7.5K and fusion n°13-encoding sequence were reassembled by double PCR using the primers OTG20405 (SEQ ID NO: 81) and OTG20408 (SEQ ID NO: 84). The resulting fragment was inserted into the *Bgl*II and *Not*I restriction sites of a vaccinia transfer plasmid, pTG17960, resulting in pTG18355.

The MVA transfer plasmid, pTG17960, 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 the 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 grow 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. After clonal selection, the selection marker can be easily eliminated by several passages without selection allowing the growth of *eGFP-GPT*$^-$ recombinant MVA.

Generation of MVATG18355 was performed by homologous recombination in primary chicken embryos fibroblasts (CEF) infected with MVA and transfected by nucleofection with pTG18355 (according to Amaxa Nucleofector technology). Viral selection was performed by plaque purification after growth 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.

Construction of MVATG18364 (fusion n° 13 + fusion n°4)

The nucleotide sequence encoding fusion n°4 (SR-RPFB-Dhyb*-Ag85B*-TB10.4-ESAT6-TMR as illustrated by the portion of SEQ ID NO: 32 from 1 to 23 followed by 32 to 855 and 866 to 932) was placed under the control of pH5R promoter (SEQ ID NO: 85, TTTATTCTATACTTAAAAAATGAAAATAAATACAAAGGTTCTTGAGGGTTGTGTT AAATTGAAAGCGAGAAATAATCATAAATTATTTCATTATCGCGATATCCGTTAA GTTTG) cloned from genomic DNA of wild type MVA by PCR with primer pair OTG20445 (SEQ ID NO: 86) and OTG20446 (SEQ ID NO: 87). The amplified product was digested by *Not*I and *Pac*I. The fusion n°4-encoding sequence was amplified from pTG18339 by PCR using OTG20447 (SEQ ID NO: 88) and OTG20380 (SEQ ID NO: 89) primers. The amplified product was digested by *Pac*I and *Xho*I. Both fragments were cloned together into pTG18355 restricted by *Not*I and *Xho*I, resulting in pTG18364.

Generation of MVATG18364 virus was performed in CEF by homologous recombination as described above.

Construction of MVATG18365 (fusion n°13 + fusion n°11)

The nucleotide sequence encoding fusion n°11 (RPFB-Dhyb*-Ag85B*-TB10.4-ESAT6 as illustrated by the portion of SEQ ID NO: 33 from position 10 to position 833 preceded with the Met initiator in position 1) was placed under the control of pH5R promoter. The promoter was obtained from pTG18364 by PCR with OTG20445 (SEQ ID NO: 86) and OTG20446 (SEQ ID NO: 87) primers and the amplified fragment digested by *Not*I and *Pac*I. The fusion n°11-encoding sequence was cloned from pTG18297 by PCR using primer pair OTG20448 (SEQ ID NO: 90) and OTG20382 (SEQ ID NO: 91) and the amplified product digested by *Pac*I and *Xho*I. Both fragments were cloned together into pTG18355 restricted by *Not*I and *Xho*I to give pTG18365.

Generation of MVATG18365 virus was performed in CEF by homologous recombination as described above.

Construction of MVATG18376 (fusion n°13 + fusion n° 4 + fusion n°5)

The nucleotide sequence encoding the fusion n°5 (SR-Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807-TMR as illustrated by the portion of SEQ ID NO: 34 from positions 1 to 23 followed by 32 to 1115 and 1126 to 1192) was placed under the control of the B2R promoter (SEQ ID NO: 92, TATATTATTAAGTGTGGTGTTTGGTCGATGTAAAATTT-TTGTCGATAAAAATTAAAAAATAACTTAATTTATTATTGATCTCGTGTGTACAAC

CGAAATC). The promoter was amplified from VV Western Reserve strain DNA by PCR using primer pair OTG20469 (SEQ ID NO: 93) and OTG20470 (SEQ ID NO: 94) and the amplified fragment was digested by *Xho*I and *Nhe*I. The fusion n°5-encoding sequence was amplified from pTG18340 using primer pair OTG20472 (SEQ ID NO: 95) and OTG20473 (SEQ ID NO: 96) before being restricted by *Nhe*I and *Bam*HI. Both digested fragments were cloned together into pTG18364 linearized by *Xho*I and *Bam*HI to generate pTG18376.

Generation of MVATG18376 virus was performed in CEF by homologous recombination as described above.

Construction of MVATG18377 (Fusion n°13+ fusion n°11 + fusion n°5)

The B2R promoter was amplified from pTG18376 using primer pair OTG20469 and OTG20470 described above and digested by *Xho*I and *Nhe*I. The nucleotide sequence encoding the fusion n°5 (SR-Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807-TMR) was amplified as described above and cloned under the control of the B2R promoter into pTG18364 linearized by *Xho*I and *Bam*HI to generate pTG18377.

Generation of MVATG18377 virus was performed in CEF by homologous recombination as described above.

Construction of MVATG18378 (Fusion n°13+ fusion n°4 + fusion n°9)

The nucleotide sequence encoding the fusion n°9 (Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807 as illustrated by the portion of SEQ ID NO: 35 from positions 10 to 1093 preceded with the Met initiator in position 1) was amplified from pTG18295 by PCR using primer pair OTG20483 (SEQ ID NO: 97) and OTG20474 (SEQ ID NO: 98). The amplified product was digested by *Nhe*I and *Bam*HI and cloned with the *Xho*I and *Nhe*I-restricted B2R promoter (amplified from pTG18376 as described above) into pTG18364 linearized by *Xho*I and *Bam*HI, resulting in pTG18378.

Generation of MVATG18378 virus was performed in CEF by homologous recombination as described above.

Construction of MVATG18379 (Fusion n°13+ fusion n°11 +fusion n°9)

The nucleotide sequence encoding the fusion n°9 (Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807) and the B2R promoter were both amplified as described above and cloned together into pTG18365 linearized by *Xho*I and *Bam*HI, resulting in pTG18378.

Generation of MVATG18379 virus was performed in CEF by homologous recombination as described above.

Construction of MVATG18404 (Fusion n°14 + fusion n°6)

The nucleotide sequence encoding the fusion n°14 (SF-Rv2029*-TB10.4-ESAT6-Rv0111* as illustrated by the portion of SEQ ID NO: 39 from positions 1 to 28 and 37 to 831) was amplified from pTG18343 by PCR using primer pair OTG20407 (SEQ ID NO: 83) and OTG20525 (SEQ ID NO: 99). The p7.5K promoter was obtained from pTG18355 by PCR with OTG20524 (SEQ ID NO: 100) and OTG20406 (SEQ ID NO: 82) primers. The fusion n°14-encoding sequence was then cloned under the control of the p7.5K promoter by double PCR using OTG20524 (SEQ ID NO: 100) and OTG20525 (SEQ ID NO: 99). The resulting fragment was restricted with *BamH*I and *Not*I and inserted into the *Bgl*II and *Not*I restriction sites of the vaccinia transfer plasmid, pTG17960, resulting in pTG18395.

The nucleotide sequence encoding the fusion n°6 (SS-Ag85B*-Rv2626-RPFB-Dhyb*-Rv1733* as illustrated by the portion of SEQ ID NO: 36 from positions 1 to 23 and 32 to 956) was amplified from pTG18341 by PCR using primer pair OTG20527 (SEQ ID NO. 101) and OTG20376 (SEQ ID NO : 102) and the amplification product was digested with *Pac*I and XhoI. The pH5R promoter was amplified from pTG18355 as described above and digested by *Not*I and *Pac*I. Both digested fragments were cloned together into pTG18395 linearized by *Not*I and *Xho*I, resulting in plasmid pTG18404.

Generation of MVATG18404 virus was performed in CEF by homologous recombination as described above.

Construction of MVATG18417 (Fusion n°14 + fusion n°6 + fusion n°5)

The nucleotide sequence encoding the fusion n°5 (SR-Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807-TMR) placed under the control of B2R promoter was obtained by digestion of pTG18376 with *Xho*I and *Bam*HI. The resulting fragment was inserted in pTG18404 restricted by the same enzymes, giving rise to pTG18417.

Generation of MVATG18417 virus was performed in CEF by homologous recombination as described above.

Construction of MVATG18418 (Fusion n°14 + fusion n°6 + fusion n°9)

The nucleotide sequence encoding the fusion n°9 (Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807) placed under the control of B2R promoter was obtained by digestion of

pTG18379 with *Xho*I and *Bam*HI. The resulting fragment was inserted in pTG18404 restricted by the same enzymes, giving rise to pTG18418.

Generation of MVATG18418 virus was performed in CEF by homologous recombination as described above.

Production and protein purification

Four *E. coli* strains have been tested for the expression of the individual *Mtb* antigens. All the strains carry the DE3 prophage in their genome that allows the induction of expression of T7 polymerase by lactose or analogue of lactose (*i.e.* IPTG). The four strains were Bl21(DE3) (Lucigen) as a classic strain for protein expression, C41(DE3) (Lucigen) for the expression of toxic protein, Bl21(DE3) Rosetta (Merck Chemical) for expression of protein with a codon usage that is different of the *E. coli* one, and C43(DE3) (Lucigen) for the expression of protein with trans-membrane peptides (e.g. Rv1733). Moreover, three different temperatures and production time were tested for optimizing antigen production.

Expression assays for determining optimal conditions

Each *E. coli* strain was transformed with the plasmid encoding the *Mtb* antigen to be produced. Five colonies were isolated from a freshly transformed plate, inoculated in 50 ml of LB (Luria Broth) medium in the presence of ampicillin and allowed to grow overnight at 37°C under shaking. A flask of autoinducible medium (AI medium containing glucose/lactose and antibiotic; Studier, 2005, Protein Expr Purif. 41: 207-34) was inoculated with preculture specimen and was then cultured at either 18°C, 30°C and 37°C for 24, 8 and 8 hours, respectively. At the end of incubation, the absorbance at 600nm was measured and the cells were harvested by centrifugation. The cell pellet was resuspended in PBS and the OD 600 nm adjusted around 50 for each culture condition tested before lysing the cells by sonication. The cell lysate was then centrifuged at 10,000 g for 10 minutes at 4°C and a specimen (typically 10 µL) of the supernatant and the pellet were then loaded on a SDS-PAGE to estimate optimal conditions.

Production and purification of Mtb antigens

Purification of His tag-containing *Mtb* antigens was undertaken from 500mL culture grown in 2L flasks applying the optimal conditions determined previously. The cells were harvested by centrifugation and pellets corresponding to 250 mL of culture were kept at -20°C until use. The harvested bacteria were resuspended in PBS or in guanidine depending

of the solubility of the antigen, submitted to sonication for cell lysis and purified by IMAC affinity chromatography on Ni sepharose 6 fast Flow resin (GE Healthcare; reference 17-5318) either in native or denaturing conditions according to the provider's recommendations. Proteins were eluted by applying increasing concentrations of Imidazole (50 mM, 100 mM and 250mM). Fractions containing the pure protein were pooled and dialysed against PBS or Urea depending of the solubility of the antigen.

Protein characterization

A variety of tests can be performed to estimate the quantity and quality of the purified *Mtb* antigens present in the eluted fractions.

Endotoxin levels were measured using Portable Test System (PTS) from Charles River Laboratories. Cartridges with a range of detection of 0.005 to 0.5 EU/mL were used according to the manufacturer's recommendations.

Protein concentrations were determined by Bradford assay (Bioroad) according to the manufacturer's recommendations. Bovine serum albumin (BSA) diluted in the sample buffer was used as a standard.

Purity of the eluted fractions and dialysed solution can be evaluated by electrophoresis on SDS-PAGE (4-12% Invitrogen).

Mass of the purified proteins was measured using MALDI (Matrix-Assisted Laser Desorption/ionization) or electrospray methods. Measured and calculated masses were compared in order to determine if the protein is intact or not. Identity of the protein either in solution or in a band of gel was checked by mass measurement of peptides generated after trypsin digestion. Masses of peptides were determined by MALDI and/or liquid chromatography coupled to tandem mass Spectrometry (LC/MS/MS). Measured and calculated masses of peptides were compared in order to verify the identity of the protein.

Production of antibodies against *Mtb* antigens

Antibodies directed against the various *Mtb* antigens were produced following immunization of rabbits with a mixture of two different antigen-specific peptides (Eurogentec; Seraing, Belgium). Such peptides of 15 or 16 amino acid residues were selected after running epitope B prediction programs. Antisera against Rv1733*, Rv2029*, Rv0569, Rv1807, Rv0111, RPFB-Dhyb*, Rv1813* and Rv3407 antigens were generated

following rabbits immunization with the two specific peptides at day 0 and three boosts at day 7, 10 and 18. Blood samples were taken before first peptide injection and at day 21. Final bleeding of rabbits was done at day 29. For Rv3478, the rabbits were injected at day 0, 22, 49 and 77 with the two specific 16 mer peptides. Blood samples were taken before first peptide injection and at day 31 and 59. Final bleeding of rabbits was done at day 87.

The final sera were evaluated by ELISA using the specific peptides and by Western-blot analysis using the individual *Mtb* gene expression plasmids.

***In vitro* testing of the *Mtb* fusion proteins**

Western Blot on DNA-mediated expression products

$2x10^6$ HEK293 cells were transfected with 5µg of the various plasmids encoding *Mtb* antigen fusions or individual genes using Lipofectamine 2000 (Invitrogen; #11668-019) in presence of proteasome inhibitor MG132 (10µM) added to growth medium 18h after transfection. pGWIZ plasmid was used as negative control After 48 hours medium was discarded and cells were lysed with 450 µL/dish of Tris-Glycin-SDS 2 X buffer (ref: LC2676; Novex) supplemented with β-mercaptoethanol (5 % v:v). The lysate was then sonicated and boiled for 5 min at 95 °C. Thirty microliters of cell lysates were submitted to electrophoresis onto precasted 10% Criterion gel using the Criterion Precast gel system (Biorad). Following electrophoresis, proteins were transferred onto a PVDF membrane (Macherey Nagel, 741260). Immunodetection was performed with 1/500 diluted monoclonal anti-Flag M2 peroxydase (HRP) antibody (Sigma; #A8592) or with 1/5000 diluted monoclonal anti-His peroxydase antibody (Invitrogen; #R931-25). Immune-complexes were revealed using the ImmunStar WesternC kit (Biorad, ref 170.5070).

Sera (diluted 1/1000) obtained after immunization of rabbit, as described above, were also used for Western Blot detection of Rv1733*, Rv2029*, Rv0569, Rv1807, Rv0111*, Rpf-B-D, Rv1813*, Rv3407 and Rv3478. Commercial antibodies were used for detecting ESAT6, Ag85B *, TB10.4 and Rv2626, respectively, mouse monoclonal antibody HYB076-08 (Santa-Cruz; #sc-57730, diluted 1/500) for ESAT6, rabbit polyclonal anti-serum NR-13800 (BEI, diluted 1/5000) for Ag85B*, mouse monoclonal antibody 26A11 (Lifespan-Biosciences;#LS-C91052 diluted 1/1000) for Rv2626 and polyclonal rabbit antibody ABIN361292 (Antibodies–online, diluted 1/1000) for TB10.4.

Western Blot on MVA-mediated expression products

10^6 A549 cells were infected at MOI 1 with the various MVA producing *Mtb* antigen fusions in presence of proteasome inhibitor MG132 (10μM) added to growth medium 30 min after infection. MVATGN33.1 empty vector was used as negative control. After 24 hours, medium was discarded and cells were lysed with 300 μL/dish of Tris-Glycin-SDS 2 X buffer (ref: LC2676; Novex) supplemented with β-mercaptoethanol (5 % v:v). The lysate was then sonicated and heated for 5 min at 95 °C. Twenty microliters of cell lysates were submitted to electrophoresis onto precasted 4-15 % Criterion gel using the Criterion Precast gel system (Biorad). Following electrophoresis, proteins were transferred onto a PVDF membrane (Trans-blot® Turbo™ Transfer System (#170-4155, Biorad)). Immunodetection was performed with *Mtb* specific antibodies, as described above in connection with expression products of DNA plasmids. Immune-complexes were revealed using the ImmunStar WesternC kit (Biorad, ref 170.5070).

Immunogenicity evaluation in a mouse model

DNA Immunization protocols

Mice were immunized three times at 2 or 3-week interval either with the fusion encoding plasmid or with a mix of plasmids encoding the individual *Mtb* antigens included in the fusion. 100μg of DNA in 100 μL of sterile PBS were injected via intramuscular route in the tibialis anterior muscle. Cellular immune response was evaluated 2 weeks following the last DNA injection by ELISpot IFNγ assays.

MVA Immunization protocols

Immunogenicity of MVA TB candidates was evaluated in BALB/c, transgenic HLA-A2, C57BL/6 and C3H/HeN mice. Each MVA vector was administered subcutaneously at the base of the tail once at a dose of $1x10^7$ pfu in 100μL of a Tris-HCl-buffered and sucrose-containing buffer. Cellular immune responses were evaluated 7 days after MVA injection by ELISpot IFNγ assay.

Peptide libraries

A peptide library was used to restimulate *ex-vivo* the splenocytes from immunized mice. More precisely, 679 peptides (15mers overlapping by 11 amino acids) covering all 14

Mtb antigens contained in the fusions described above were synthetized (ProImmune). Pools of peptides were prepared in DMSO with a final concentration of 1μmol/L. One to 4 pools were needed so as to cover the full length of each *Mtb* antigen.

Rv1733 was covered by 2 pools of 18 and 17 peptides. Pool 1: 18 peptides covering Rv1733 residues 62 to 144; Pool 2: 17 peptides covering Rv1733 residues 134 to 210.

Rv2029 was covered by 4 pools of 19 peptides. Pool 1: 19 peptides covering Rv2029 residues 1 to 87; Pool 2: 19 peptides covering Rv2029 residues 77 to 163; Pool 3: 19 peptides covering Rv2029 residues 153 to 239; Pool 4: 19 peptides covering Rv2029 residues 229 to 314.

Rv0569 was covered by 1 pool of 20 peptides covering Rv0569 from residues 1 to 88.

Rv1807 was covered by 4 pools of 25 peptides for the first 3 pools and 22 peptides for the fourth pool. Pool 1: 25 peptides covering Rv1807 residues 1 to 111; Pool 2: 25 peptides covering Rv1807 residues 101 to 211; Pool 3: 25 peptides covering Rv1807 residues 201 to 311; Pool 4: 22 peptides covering Rv1807 residues 301 to 399.

Rv0111 was covered by 4 pools of 20 peptides for the first 3 pools and 19 peptides for the fourth pool. Pool 1: 20 peptides covering Rv0111 residues 361 to 451; Pool 2: 20 peptides covering Rv0111 residues 441 to 531; Pool 3: 20 peptides covering Rv0111 residues 521 to 611; Pool 4: 19 peptides covering Rv0111 residues 601 to 685.

RpfB-Dhyb was covered by 4 pools of 22 peptides for the first 3 pools and 19 peptides for the fourth pool. Pool 1: 22 peptides covering RpfB residues 30 to 127; Pool 2: 22 peptides covering RpfB residues 117 to 215; Pool 3: 22 peptides covering RpfB residues 205 to 284 and RpfD residues 53 to 71; Pool 4: 19 peptides covering RpfD residues 61 to 146.

Rv1813 was covered by 1 pool of 25 peptides covering Rv1813 residues 34 to 143.

Rv3407 was covered by 1 pool of 22 peptides covering Rv3407 residues 1 to 99.

Rv3478 was covered by 4 pools of 24 peptides. Pool 1: 24 peptides covering Rv3478 residues 1 to 107; Pool 2: 24 peptides covering Rv3478 residues 97 to 203; Pool 3: 24 peptides covering Rv3478 residues 193 to 299; Pool 4: 24 peptides covering Rv3478 residues 289 to 393.

Rv2626 was covered by 2 pools of 17 and 16 peptides. Pool 1: 17 peptides covering Rv2626 residues 1 to 79; Pool 2: 16 peptides covering Rv2626 residues 69 to 143.

Ag85B was covered by 3 pools of 23 peptides. Pool 1: 23 peptides covering Ag85B residues 39 to 141; Pool 2: 23 peptides covering Ag85B residues 131 to 233; Pool 3: 23 peptides covering Ag85B residues 223 to 325.

ESAT-6 was covered by 1 pool of 21 peptides covering ESAT-6 from residues 1 to 95.

TB10.4 was covered by 1 pool of 21 peptides covering TB10.4 from residues 1 to 95.

IFNγ ELISpot assays

Splenocytes from immunized mice were collected and red blood cells were lysed (Sigma, R7757). $2x10^5$ 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 αMEM culture medium (Gibco, 22571) supplemented with 10 % FCS (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:

- The above-described pool of peptides at a final concentration of 1µmol/L
- 5 µg/ml of Concanavalin A (Sigma, C5275) for positive control.
- Irrelevant peptide

IFNγ-producing T cells were quantified by ELISpot (cytokine-specific enzyme linked immunospot) assay as previously described (Himoudi et al., 2002, J. Virol. 76: 12735-46). Results are shown as the mean value obtained for triplicate wells. An experimental threshold of positivity for observed responses (or cut-off) was 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 (coefficient of variation) of the reader was systematically less than 20%). Statistical analyses of ELISpot responses were conducted by using a Kruskal-Wallis test followed, when a significant difference was obtained, by a Mann-Whitney test. P value equal or inferior to 0.05 will be considered as significant.

Evaluation of therapeutic efficacy of Mtb antigens-containing vaccines against Mycobacterium tuberculosis infection in mice

Female C57BL/6 mice (6 to 8 weeks old) were aerosol challenged at week 0 using a contained Henderson apparatus in conjunction with an Aero control unit (Hartings et al., 2004, J Pharmacol Toxicol Methods 49: 39-55). *Mycobacterium tuberculosis* challenge strain H37Rv (NCTC 7416) was cultured in a chemostat (James et al., 2000, J Appl Microbiol 88: 669-77) and fine particles of a mean diameter of 2µm were generated in a Collison nebulizer and delivered directly to the animal snout. The suspension in the Collison nebulizer was adjusted to deliver an estimated inhaled dose of approximately 100 CFU/lung to each group of mice.

Mice were immunized at 10 and 14 weeks post-infection with MVATG18364, MVATG18376 or MVATG18377 given subcutaneously at the base of tail in one site (10^7 pfu/100 µL/mouse). A group of mice was injected with MVATGN33.1 as negative control (10^7 pfu/100 µL/mouse).

Mice were treated with isoniazid (INH, 25 mg per kg body weight) and rifapentine (RIF, 10 mg per kg body weight) once a week by oral gavage for 10 weeks, from week 6 to week 15 (protocol adapted from Aagaard *et al.*, 2011, Nat Med, 17: 189-194). 5 mice were sacrificed at week 6 before drug treatment.

Mice from each of group were sacrificed, five at the end of the antibiotic treatment (15 weeks post-infection) to determine clearance at the end of the treatment phase and the others at week 21. Organs (e.g. spleen) were aseptically removed, frozen on the day of necropsy and processed for bacterial load analysis. Serial dilutions of samples of organ homogenates were plated onto 7H11 Middlebrook OADC selective agar and incubated for up to 3 weeks for enumeration of viable mycobacteria (CFU). Bacterial load data was expressed as Log10 total Colony Forming Unit (CFU).

The therapeutic efficacies of the MVA candidates were compared and ranked using the Mann-Whitney test. A *p* value inferior to 0.05 was considered significant.

RESULTS

EXAMPLE 1: Selection of suitable *Mtb* antigens for immunogenic combination:

The *Mtb* genome expresses approximately 4000 genes but the function and role in *Mtb* life cycle of the great majority of the gene products have not yet been characterized. As described in Materials and Methods, existing data on *Mtb* antigens were investigated from the available literature and data bases with the goal of identifying the most appropriate set of genes/antigens from *Mtb* genome for providing an immunotherapeutic vaccine capable of raising anti-TB immunity during all phases of the natural course of infection.

These bibliographic analyses permit to "pre-select" a set of 33 *Mtb* antigens belonging to all three phases of infection, namely seven antigens of the active phase, five resuscitation (Rpf) antigens and 19 latent antigens as well as two PE/PPE antigens.

- Antigens of the active phase: ESAT-6 (Rv3875), CFP-10 (Rv3874), TB10.4 (Rv0288), Ag85A (Rv3804), Ag85B, (Rv1886) and two "ESAT-6 like antigens" (Rv3620 and Rv3619);
- Two PE/PPE antigens (Rv2608 and Rv3478) which appear to be associated with virulence.
- Antigens of the resuscitation phase: the five existing Rpfs genes (RpfA (Rv0867c), RpfB (Rv1009), RpfC (Rv1884c), RpfD (Rv2389), RpfE (Rv2450c)) were preselected. Rpfs are secreted or membrane bound muralytic enzymes which expression is required for the resuscitation of the dormant cells.
- Nineteen latent antigens were preselected from the more than 150 existing latent genes described. More precisely, twelve belong to the DosR regulon, a set of 45 genes which expression is increased during latency period and five were selected among genes which expression was modulated during culture condition thought to mimic the latency condition that *Mtb* encounters in *vivo*. Three latent antigens were also selected based on preclinical and early clinical phases recently described (Bertholet et al., 2008, J. Immunol. 181: 7948-57; Bertholet et al., 2010, Sci Transl Med 2: 53ra74, Mollenkopf et al., 2004, Infect Immun 72: 6471-9). In summary, the 19 latent antigens preselected were Rv1733c, Rv2029c, Rv1735, Rv1737, Rv2628, Rv0569, Rv2032, Rv2627c, Rv0111, Rv3812, Rv1806, Rv1807, Rv0198, Rv2626, Rv0081, Rv2005c, Rv2660, Rv3407 and Rv1813.

Then, a second selection was undertaken in order to rank the 33 preselected *Mtb* antigens. The second selection of *Mtb* antigens was based on a data mining-based selection process (see Materials and Methods) reflecting their immunological and protective potential (highest score retained) as well as biochemical prediction.

The following antigens were chosen:

- Latent phase antigens: Rv1733, Rv2029, Rv0569, Rv0111, Rv1807 and Rv3407. Rv2626 and Rv1813 were also chosen due to their very good data mining score and biochemical prediction score.
- Active phase antigens: ESAT-6 (Rv3875), TB10.4 (Rv0288), Ag85B (Rv1886) and Rv3478. It has to be noted that the pre-selected active phase Rv3619 antigen had a good data mining score, but being an ESAT-6 like protein while not showing better score than ESAT-6 itself, it was not retained in the selected list. As another example, active Rv2608 and Rv3478 antigens had the same data mining score but Rv3478 was selected on the basis of its capacity of inducing a stronger percentage of responders in human cohort studies.
- Resuscitation phase antigens: RpfB and RpfD. Among the 5 resuscitation gene products, three Rpfs stood out (RpfB, D and E) with very similar score after the running data mining scoring process but only RpfB and D were selected for 2 main reasons. Firstly, the reported cross-reactivity in term of cellular and humoral responses between 4 out of 5 Rpfs (Yeremeev et al., 2003, Infect Immun 71: 4789-94), except for RpfB justified in our view the selection of the latter. Secondly, RpfD was chosen instead of RpfE after sequence analysis based on a lower sequence homology in the lysozyme domain (LD) between RpfB and D than between RpfB and E. It is thus assumed that keeping Rpfs B and D would be sufficient to generate immune response toward the 5 Rpfs.

EXAMPLE 2: Fusion design

Extensive *in silico* structure prediction and bibliographical analyses were performed in order to predict biochemical properties and/or biological functions of the selected *Mtb* antigens as described in Materials and Methods.

The selected 14 antigen candidates were classified into three groups that required different types of analysis.

- Antigens with available data concerning their expression in various viral vectors

namely Ag85B ESAT-6 and TB10-4 in MVA (Kolilab *et al.* 2010, Clin Vaccine Immunol 17: 793-801); vaccinia virus (Malin *et al.* 2000, Microbes Infect 2: 1677-85) and adenovirus (Mu et al., 2009, Mol Ther 17: 1093-100; Dietrich *et al.* 2005, J Immunol 174: 6332-9; and Havenga *et al.* 2006; J Gen Virol 87: 2135-43). In these cases, analysis of the bibliography was the main source of information to design the sequence to insert in vector constructions.

- Antigens with no data reported on viral vectorization but identical or homologous to a protein with a known structure. In these cases, structural data were the main source of information to design the *Mtb* sequence to insert in vector constructions (Rv2626, Rv2029, RpfB, RpfD and Rv0569).
- Antigens with no data reported on viral vectorization and with no homology with any protein with a known structure. In these cases, *in silico* biochemical analyses and predictions were used to characterize the antigens, and to design the *Mtb* sequence to insert in vector constructions (Rv0111, Rv3407, Rv3478, Rv1807 and Rv1813).

Design of Ag85B antigen

Ag85B displays a 40 residues long peptide signal that was conserved in the Kolilab's MVA vector but not in the Malin's vaccinia virus and the adenovirus constructs. As Ag85B signal peptide was predicted as a TM domain, the inventors recommended not to keep the Ag85B peptide signal in the vector constructions of this invention. The recommended primary structure of Ag85B* to be used in vector constructions described herein corresponds to the amino acid sequence shown in SEQ ID NO: 20.

Design of ESAT-6 antigen

ESAT-6 forms a heterodimeric complex with CFP-10 and this heterodimeric interaction is expected to induce the folding of both proteins. Alone ESAT-6 adopts a molten globule-like state and a helix-turn-helix when complexed with CFP10. Thus, ESAT-6 bound to its partner could be more stable than ESAT-6 expressed alone. However, the recommended primary structure of ESAT-6 to be used in vector constructions described herein corresponds to the full length protein, (amino acid sequence shown in SEQ ID NO: 14) eventually without its initiator Met (e.g. if internal position in the fusion).

Design of TB10-4 (Rv0288)

TB10-4 belongs to the same family of protein as ESAT-6. NMR structure of TB10-4 showed that it forms a heterodimeric complex with Rv0287 that is expected to stabilize the structure. There is no publication reporting TB10-4 expression by poxviruses whereas

expression of the full length TB10-4 was reported in adenovirus vectors in a form fused to the C-terminus part of either Ag85A or Ag85B. On this basis, the recommended primary structure of TB10.4 to be used in vector constructions described herein corresponds to the full length protein (amino acid sequence shown in SEQ ID NO: 2), eventually without its initiator Met.

Design of Rv2626

Crystalization of Rv2626 (Sharpe et al., 2008, J Mol Biol 383: 822-36) showed that it is expressed as a homodimer with an intra and an inter subunit disulfide bonds. No signal peptide was predicted for Rv2626. Since Rv2626 has a very well defined fold, the recommended primary structure of Rv2626 to be used in vector constructions described herein corresponds to the full length protein (amino acid sequence shown in SEQ ID NO: 10), eventually without its initiator Met.

Design of Rv0569

Rv0569 structure is not known but this protein displays a 62 % identity (81 % similarity) with Rv2302 in a 76 amino acid overlap region (out of 88 residues). The structure of this latter has been solved by NMR (Buchko et al., 2006, Bacteriol 188: 5993-6001) and showed a very well folded structure in solution with antiparallel β-sheet core and a C-terminal α-helix. No coiled coil prediction is associated with this protein. No known function is associated with Rv0569 protein. Due to the potential very well defined fold, the recommended primary structure of the *Mtb* Rv0569 to be used in vector constructions described herein corresponds to the full length protein (amino acid sequence shown in SEQ ID NO: 3, eventually without its initiator Met.

Design of Rv2029

Rv2029 structure is not known, but this protein displays a 35% identity with phosphofructokinase-2 (pfk2) of *Escherichia coli* in a 310 aa overlap region (out of 339). Moreover, PROSCAN search yielded to the identification of a fully conserved carbohydrate kinases signature. Therefore, Rv2029 has probably a phosphofructokinase activity in *Mtb*. Phosphofructokinase catalyzes the phosphorylation of fructose-6-phosphate during glycolysis. *E. coli* pfk2 structure is tetrameric when ATP is bound and dimeric when ATP is not present in the medium (allosteric regulation of the enzyme activity). In the *E. coli* enzyme, deletion of the last C-terminal 4 residues completely inhibits ATP induced tetramerization. Thus, in order to avoid oligomerization heterogeneity of Rv2029 (mix of dimeric and tetrameric forms), the deletion of the C-terminus part is recommended (*i.e.* deletion of the last 25 residues). Moreover, in order to abolish enzymatic activity of Rv2029,

the mutation D265N (position 265 starting from the Met initiator or 264 without Met) is recommended since it abolishes almost totally the enzymatic activity in *E. coli* pfk-2 (Cabrera *et al.*, 2010, Arch Biochem Biophys 502: 23-30). On this basis, the recommended primary structure of the Rv2029 antigen (Rv2029*) to be used in vector constructions described herein corresponds to the amino acid sequence shown in SEQ ID NO: 21.

Design of RpfB and RpfD

The Resuscitation Promoting Factors (Rpf) are secreted proteins that are produced during the reactivation phase of the bacteria (transition from dormancy to growth). *M. tuberculosis* has five different Rpf (A to E) that all contain a conserved catalytic domain (lysozyme like domain). Apart from this domain, there is no significant similarity among these five proteins. RpfB structure has been obtained for about half of the molecule (residues 194-362) and a signal peptide was predicted (residues 1-29; Ruggiero *et al.* 2009, J Mol Biol 385: 153-62). The full length protein (without its signal peptide) behaves as a monomer when expressed in *E. coli.*

In silico predictions and analyses were performed on RpfB to analyse the part of the protein (30-193) for which no structure was available. Except for the signal peptide, no transmembrane domain was predicted. HCA plots, secondary structure prediction and natively disordered regions predictions are in agreement with a well-defined fold of the 30-193 region. Coiled coils predictions and search for known motifs using PROSCAN did not yield any significant result.

Activity of the catalytic domain has been shown to depend on a conserved residue essential in the resuscitation activity of *Micrococcus luteus* Rpf in a *Mycobacterium smegmatis* resuscitation assay (mutation E292K; Mukamolova *et al.* 2006, Mol Microbiol 59: 84-98). Furthermore, the two residues T315 and Q347 are involved in substrate binding in lysozyme, and conserved in RpfB (Cohen-Gonsaud, *et al.* 2005, Nat Struct Mol Biol 12, 270-3).

In addition, it has been chosen to design a RPFB-D hybrid that corresponds to the RpfB molecule with its catalytic domain replaced by the most divergent catalytic domain among Rpfs (*i.e.* RpfD catalytic domain). Therefore, the RPFB-D hybrid to be expressed in viral vectors is a hybrid protein with a neutralized catalytic activity by three mutations (E292K, T315A and Q347A) and without signal peptide. The recommended primary structure for this RPFB-D hybrid protein used in fusions corresponds to the amino acid sequence shown in SEQ ID NO: 31 from residue 10 to residue 283 of RpfB fused to residue 51 to residue 147 of RpfD, eventually with a initiator Met.

Design of Rv1807

Rv1807 structure is not publicly available, but a BLAST search against the PDB database yielded a match with only the first 150 residues of a *Mtb* PPE protein (Rv2430). PE/PPE is a large family of *Mtb* proteins (around 100 PE and 60 PPE members) that have in common a PE (Proline, Glutamic acid) or PPE (Proline, Proline, Glutamic acid) motif, at their N-terminus parts. PE proteins are expressed as heterodimers with PPE, and their function is not known yet. BLAST search against UNIPROT-SWISSPROT yielded several matches but all of them were additional *Mtb* PPE that did not allow to gain additional information.

In *E. coli*, expression of a soluble PPE (Rv2430) or PE (Rv2431) is apparently possible only when expressed as a heterodimer (Strong *et al.* 2006, Proc Natl Acad Sci 103: 8060-5). These authors reported that Rv1807 expressed alone in *E. coli* forms inclusion bodies. PROSCAN search did not yield any significant match with a known motif. No signal peptide or transmembrane domain were reported or predicted for this protein. HCA plots, as well as secondary structure predictions were in agreement with a well-defined fold of the whole protein except the last 60-70 residues region. Moreover, the last 60 residues are predicted to be unfolded using natively disordered regions predictions whereas coiled coils predictions on Rv1807 did not yield any significant result.

As for ESAT6 and TB10-4, the coexpression of Rv1807 with its partner (*i.e.* Rv1806) would probably favourably impact the protein stability and therefore potentially its immunogenicity. The expression of a misfolded protein (a monomeric one) could impair the recombinant vector stability (protein toxicity). Moreover, the unfolded C-terminus part of Rv1807 could also have an unfavourable impact on either immunogenicity and/or on the recombinant virus stability. The recommended primary structure for Rv1807 used in fusions corresponds to the full length protein (SEQ ID NO: 6). In case of problem encountered with the full length antigen, one may use a C-terminus truncated antigen deleted of the last 60 residues (as shown in SEQ ID NO: 18).

Design of Rv3478

Rv3478 is another PPE protein. Its PPE domain is 57% identical to the PPE domain of Rv1807 (41% identity between the two whole proteins). BLAST search against UNIPROT-SWISSPROT yielded several matches that were all other *Mtb* PPE. HCA plot demonstrated the presence of hydrophobic patches all along the protein sequence. In other words, HCA plot does not indicate unfolded hydrophilic region in Rv3478. But, as for Rv1807, the last 40 to 50 residues of Rv3478 are predicted to be unfolded (based on both

secondary structure and natively disordered predictions). No signal peptide or transmembrane domain were reported or predicted for this protein. Coiled coils predictions on Rv3478 did not yield any significant result. As for Rv1807, the recommended primary structure is the full length protein (SEQ ID NO: 13) or, if problem are encountered, a C-terminus truncated antigen deleted of the last 40 residues (as shown in SEQ ID NO: 24).

Design of Rv0111

Rv0111 is predicted to be a membrane protein with a possible acyltransferase activity. Ten transmembrane domains are predicted by DAS, TMHMM and TopPred spanning from residues 58 to 427. No signal peptide was predicted. Secondary structures are predicted all along the primary structure, with a gap at 449-469 that corresponds to a predicted natively disordered region. Coiled coils predictions on Rv0111 did not yield any significant result.

Proscan analysis yielded four hits with ≥ 80% similarity : Aldo/keto reductase enzyme site, acyltransferase lipoyl binding site, sugar transport protein signature and the eukaryote lipocalin proteins. As the three first signatures are in the first 300 residues of the protein, it is thus recommended to remove at least this part of the protein in order to avoid any potential biological activity. This would also allow to get rid of the majority of the transmembrane domains of the protein. Therefore the recommended primary structure of Rv0111 to be used in viral vectors is the C terminus part of the protein (e.g. residues 393-685 of the native antigen as shown in SEQ ID NO: 15) with only one TM for plasmatic membrane anchorage in case of secreted construction. If expression problems are encountered, one may use an even more truncated antigen without any TM domain (residues 429-685 of the native Rv0111 starting at residue 37 of SEQ ID NO: 15).

Design of Rv1813

Rv1813 structure is not publicly available and BLAST search against PDB yielded no match. Rv1813 is a small protein (143 residues), that is predicted to contain a signal peptide (1-32) and no transmembrane domain. It displays no significant homology with other proteins in the Uniprot-Swissprot database. HCA plots, secondary structure prediction and natively disordered regions predictions are all in agreement with a well-defined fold of the whole protein. Coiled coils predictions did not yield any significant result. No function is reported in the TB base and a PROSCAN search yielded no significant match with a known motif. Therefore the recommended primary structure of Rv1813 to be used in viral vectors is the full-length protein without its signal peptide (residues 1 to 34) which amino acid sequence is shown in SEQ ID NO: 19.

Design of Rv3407

Rv3407 structure is not publicly available and a BLAST search against PDB did not yield any match. Rv3407 is a small protein (99 residues) with no significant homology with other protein in Uniprot-Swissprot database. No signal peptide or transmembrane domain was reported or predicted for this protein. HCA plot and secondary structure predictions were in agreement with a well-defined fold of the whole protein. However, natively disordered regions predictions indicated that the last 33 residues may not be folded in a defined structure. This last result that is not in agreement with HCA and secondary structure predictions could be the signature of a MORE ("Molecular Recognition Element") that folds upon binding to a partner protein. In the case of Rv3407 a C-terminal alpha helix could be present only when Rv3407 is bound to its partner. Coiled coils predictions did not yield any significant result. No function is reported in TB base for this protein and PROSCAN search did not yield any significant match with a known motif. The recommended primary structure of Rv3407 is the full length protein (SEQ ID NO: 12). If stability issue are encountered, one may use a C-terminus truncated antigen deleted of the last 33 residues (as shown in SEQ ID NO: 23).

Design of Rv1733

Rv1733 is predicted to be a membrane protein according to UNIPROT-SWISSPROT and TB base, with two transmembrane domains (that are also predicted using DAS, TMHMM and TopPred). The first TM domain was predicted as a signal peptide. Apart from these transmembrane domains, few secondary structures are predicted for this protein. HCA plot demonstrates the presence of few hydrophobic patches between the two transmembrane helices. Finally, a natively disordered region (about 20 residues long) was predicted between the two transmembrane helices. All together, theses results indicate a probably loose fold beside the transmembrane domains. PROSCAN search on Rv1733 without its signal peptide did not yield any significant match with a known motif. Coiled coil prediction on Rv1733 did not yield any significant result. Therefore the recommended primary structure of Rv1733 to be used in viral vectors is the whole protein minus its signal peptide (62 first residues) as shown in SEQ ID NO: 17. Alternatively, one may also use the full length Rv1733 (SEQ ID NO: 5).

EXAMPLE 3: Construction of *Mtb* gene fusions

Twelve different fusion proteins were engineered as illustrated in Figure 1 and Table 3. More specifically, 5 fusions were designed based on biochemical rationales as described

below, respectively:

- Fusion n°3 (RPFB-Dhyb*);
- Fusion n°5 (Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807);
- Fusion n°6 (Ag85B*-Rv2626-RPFB-Dhyb*-Rv1733*);
- Fusion n°8 (Ag85B*-Rv2626- Rv1733*); and
- Fusion n°14 (Rv2029*-TB10.4-ESAT6-Rv0111*).

The following biochemical rationales have been followed to design the fusions

- Two dimeric proteins (*i.e.* Rv2626 and Rv2929*) should not be fused in the same fusion to avoid any steric clashes.
- Two membrane proteins should not be used in the same fusion (*i.e.* Rv1733* and Rv0111*) to avoid potential toxicity issue.
- Proteins with TM (Rv1733* and Rv0111*) should be inserted at the end of the fusion to allow plasmatic membrane anchorage for secreted constructions.
- If possible, the fusion protein should start with a well folded protein (*i.e.* Ag85B*, Rv2029*, Rv2626, Rv0569, RPFB-D hybrid*) to have a « chaperone » effect on the rest of the fusion.
- Make three fusions, two of which with the minimal set of antigens (*i.e.* Ag85B*, Rv2029*, Rv2626, Rv0111*, Rv1733*, TB10-4, ESAT-6, RPFB-D hybrid*) and the last fusion with the rest (optional) of the antigens (*i.e.* Rv0569, Rv1813*, Rv3407, Rv1807, Rv3478).

On the other hand, fusions were also designed relative to the phase of TB disease. Fusion n°2 contains active antigens (Ag85B*-TB10.4-ESAT6) while fusion n°4 contains active and resuscitation antigens (RPFB-Dhyb*-Ag85B*-TB10.4-ESAT6). The fusion n°13 is constituted by latent antigens (Rv2029*-Rv2626-Rv1733*-Rv0111*).

As described in Materials and Methods, a series of peptides were added to the *Mtb* antigen fusion, respectively a N-terminal Flag Tag and C-terminal c-myc and His Tag peptides aimed to facilitate detection of the encoded gene products as well as N-terminal signal and C-terminal membrane-anchoring peptides to enhance immunogenic activity (to be noted that addition of a TM domain was not necessary for fusions ending with Rv0111* or Rv1733*, as these proteins already contain such domains).

For comparative purposes, fusions were also constructed without any SS and TM peptides in order to evaluate cytoplasmic expression of the encoded *Mtb* antigens. The fusions n°3 (pTG18267), n°5 (pTG18269), n°2 (pTG18266) and n°4 (pTG18268) were

deleted from the SS and TM peptides, giving fusions n°12 (pTG18307), n°9 (pTG18295), n°10 (pTG18296) and n°11 (pTG18297). The N-terminus Flag TAG and the C-terminus c-myc and His TAG were kept in these constructions.

Table 3 provides a summary of the various fusions constructed in this study

	Fusion #	TB antigens	plasmids
Fusion by phase	13	Rv2029*-Rv2626-Rv1733*-Rv0111*	pTG18323
	2	Ag85B*-TB10.4-ESAT6	pTG18266
	4	RPFB-Dhyb-Ag85B*-TB10.4-ESAT6	pTG18268
Max list	5	Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807	pTG18269
Fusion by biochemistry rules	6	Ag85B*-Rv2626-RPFB-Dhyb-Rv1733*	pTG18270
	14	Rv2029-TB10.4-ESAT6-Rv0111*	pTG18324
	8	Ag85B*-Rv2626-Rv1733*	pTG18272
	3	RPFB-Dhyb	pTG18267
Fusion without SS and TM	9	Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807	pTG18295
	10	Ag85B*-TB10.4-ESAT6	pTG18296
	11	RPFB-Dhyb-Ag85B*-TB10.4-ESAT6	pTG18297
	12	RPFB-Dhyb	pTG18307

For comparative purposes, plasmids encoding the individual *Mtb* genes used in the above-described fusions were amplified by PCR or gene sequence synthetized by Geneart. More precisely, pTG18269 was used as template to amplify Rv3407, Rv0569, Rv1807, Rv1813* and Rv3478 whereas pTG18323 was used to amplify Rv2626. ESAT6, Rv1733*, Ag85B*, TB10-4, Rv0111* and Rv2029* were produced as synthetic genes.

The individual genes were placed in the same context as the fusions, i.e. inserted in pGWiz downstream the CMV promoter and fused to Flag in 5'and c-myc-His sequences in 3'. As Rv1733* and Rv0111* proteins contain a TM domain, the signal peptide presents at the N-terminus of the glycoprotein precursor of rabies virus ERA strain was fused upstream to the Flag sequence to avoid expression issues. The generated plasmids were named respectively pTG18300 (Rv3407), pTG18301 (Rv0569), pTG18302 (Rv1807), pTG18303 (Rv1813*), pTG18304 (Rv3478), pTG18305 (Rv2626), pTG18308 (ESAT6), pTG18309

(Rv1733*), pTG18310 (Ag85B*), pTG18315 (TB10.4), pTG18329 (Rv0111*), pTG18317 (Rv2029*).

The various fusion proteins was assessed in eukaryotic expression system after introduction of the corresponding expression plasmids. Expression was assessed by Western Blot whereas immunogenic activity was evaluated by ELISpot IFNγ assays after DNA immunization of mice. When possible, expression and immunogenicity of the cytoplasmic (without SS and TM) and membrane-anchored versions were compared as well as immunogenicity provided by the fusions with that obtained with a mix of plasmids expressing the individual *Mtb* antigens.

EXAMPLE 4: Analysis of expression of *Mtb* antigens and fusions

Whether expressed individual or in fusion, expression of *Mtb* genes was analyzed by Western Blot from cell lysates obtained from transfected HEK293 cells.

4.1 Western blot analysis of cell lysate transfected with plasmids encoding individual Mtb antigens.

Immunodetection of the individual *Mtb* antigens was performed with either antibodies directed to the tag peptides included in the expression cassettes (e.g. anti-Flag M2 peroxydase (HRP) antibody, monoclonal anti-c-myc peroxidase antibody and monoclonal anti-His peroxydase antibody) or antibodies specific for *Mtb* antigens. Specifically, the sera obtained after immunization of rabbits (see Materials and Methods) were used for detection of Rv1733*, Rv2029*, Rv0569, Rv1807, Rv0111*, Rpf-B-D, Rv1813*, Rv3407, and Rv3478 whereas commercial antibodies were used for the detection of ESAT6, Ag85B *, TB10.4 and Rv2626.

The results are summarized in Table 4. More specifically, a band corresponding to the expected size was detected for all individual proteins, whatever the immunodetection system used (anti-Flag, anti-His antibodies, specific rabbit sera and commercial antibodies). Additional products were also detected for some proteins and depending on the immunodetection system used. Moreover, high levels of expression were detected, except for Rv3407 and, to a lesser extend TB10.4 and ESAT6. Examples of expression detection are shown in Figure 2 for a panel of representative *Mtb* antigens, namely Rv2029* (Figure 2A), RPFB-Dhyb (Figure 2B), ESAT6 (Figure 2C) and Rv2626 (Figure 2D).

Table 4:

TB antigen (plasmid)	Expected size (level expr.)	Additional products with anti Flag and anti-His antibodies	Additional products with anti *Mtb* antibodies
Rv3407 (pTG18300)	14.4 kDa (+)		
Rv0569 (pTG18301)	12.9 kDa (+++)		1 weak band ≈10 kDa
Rv1807 (pTG18302)	43.3kDa (++)		
Rv1813* (pTG18303)	15.1 kDa (+++)		
Rv3478 (pTG18304)	42.8 kDa (+++)	2 N-terminal clived products (recognized by anti-Flag antibody) of about 16 and 26 kDA	1 band ≈ 30 kDa
Rv2626 (pTG18305)	18.9 kDa (+++)	Additional band corresponding to Rv2626 dimers	Dimer ≈43 kDa
ESAT6 (pTG18308)	13.0 kDa (++)		
Rv1733* (pTG18309)	21.2 kDa (+++)	One N-terminal clived product of about 20 kDa and 3 C-terminal products comprised between 8 and 10 kDa	2 bands ≈10 and 20 kDa
Ag85B* (pTG18310)	33.9 kDa (+++)	5 minor N-terminal clived products of about 26, 24, 20, 17 and 12 kDa as well as a C-terminal clived product (detected with anti-His antibody) of about 34 kDa.	3 weak bands ≈26, 28 and 34 kDa
TB10.4 (pTG18315)	13.5 kDa (++)		
Rv0111* (pTG18329)	37.6 kDa (+++)	one N-terminal clived product of about 8 kDa and one C-terminal products of about 34 kDa	1 band ≈34 kDa and 2 very weak bands ≈18 and 20 kDa
Rv2029* (pTG18317)	35.8 kDa (+++)		
RfpB-Dhyb* (pTG18307)	39.4kDa (+++)		2 weak bands ≈40 kDa

4.2 Western blot analysis of cell lysate transfected with plasmids encoding Mtb antigen fusions.

HEK293 cells were transfected with the plasmids expressing the different *Mtb* gene fusions and expression products were analysed by Western blot in the same conditions as

above. Transfections were done in the presence, but also in the absence of proteasome inhibitor MG132. Here again, immunodetection was performed with anti-Flag M2 peroxydase (HRP) antibody, monoclonal anti-c-myc peroxidase antibody and monoclonal anti-His peroxydase antibody as well as anti-*Mtb* specific antibodies.

The expected sizes of the tagged fusions are indicated below:

- fusion n°2 (pTG18266) : 63.6 kDa
- fusion n°3 (pTG18267) : 49.0 kDa
- fusion n°4 (pTG18268) : 99.7 kDa
- fusion n°5 (pTG18269) : 122.0 kDa
- fusion n°6 (pTG18270): 103.5 kDa
- fusion n°8 (pTG18272) : 67.3 kDa
- fusion n°9 (pTG18295) : 112.9 kDa
- fusion n°10 (pTG18296) : 53.8 kDa
- fusion n°11 (pTG18297) : 90.0 kDa
- fusion n°12 (pTG18307) : 39.3 kDa
- fusion n°13 (pTG18323) : 101.5 kDa
- fusion n°14 (pTG18324) : 90.6 kDA

All the *Mtb* antigen fusions were detected with the anti-Flag and anti-His monoclonal antibodies. *Mtb* fusion products were also detected with the anti-c myc monoclonal antibody except for pTG18266, pTG18267, pTG18268 and pTG18269. The c-myc epitope might be inaccessible in these fusions due to adjacent TM domains since the cytoplasmic counterparts (pTG18296, pTG18307, pTG18297 and pTG18295) are well detected with the anti-myc antibody. Figure 3 illustrates Western blot analysis of *Mtb* fusions encompassing latent antigens (pTG18295 encoding fusion n°9), active antigens (pTG18296 encoding fusion n°10), resuscitation antigens (pTG18307 encoding fusion n°12) and both resuscitation and active antigens (pTG18297 encoding fusion n°11) following anti Flag immunodetection. Immunodetection with anti-His antibodies gave the same expression pattern.

Figure 4 illustrates Western blot analysis of *Mtb* fusions including TB10.4 (Figure 4A), Rv0569 (Figure 4B) and Rv2626 (Figure 4C) following immunodetection with the corresponding specific sera, respectively TB10.4-containing fusions n°2 (pTG18266), n°10 (pTG18296), n°4 (pTG18268), n°11 (pTG18297), n°14 (pTG18324); Rv0569-containing fusions n°5 (pTG18269) and n°9 (pTG18295) and Rv2626-containing fusions n°13 (pTG18323), n°6 (pTG18270) and n°8 (pTG18272). pGWiz is shown as negative control and TB10.4-encoding pTG18315 as positive control.

Whatever the immunodetection system, a band corresponding to the expected size was highlighted for all fusions and, in some cases, additional fusion products were also observed. In particular, dimers were detected for pTG18270, pTG18272 and pTG18323. These three fusions contain Rv2626 which has the ability to form dimers resistant to reducing conditions. Immunodetection with anti-Flag and anti-His antibodies highlighted some additional minor proteolytic products for pTG18323 and pTG18269. Moreover, additional products higher than the expected size were detected for pTG18266, pTG18268, pTG18269, pTG18270, pTG18272, pTG18323 and pTG18324 with anti-Flag and anti-His antobodies. These bands correspond to N-glycosylated products as it was demonstrated by *in vitro* treatment with N-Glycosidase F (i.e. expression products at the expected size were obtained after N-glycosidase treatment of cellular extracts). All fusions containing a signal peptide lead to N-glycosylated products, except fusion n°4 (pTG18267, RpfB-D*). N-glycosylated products were also detected with antigen-specific antibodies as well as dimers for Rv2626-containing fusions pTG18270, pTG18272 and pTG18323. Proteolytic products were also evidenced for some fusions with specific sera (data not shown) depending on the fusions and the sera. For example, additional bands of ≈40 kDa for pTG18269 and ≈36 and 38 kDa for pTG18295 were detected with Rv3407 specific serum but are not seen with Rv0569 specific serum.

Similar and high levels of expression were obtained for all fusions and higher amounts of products were detected in the presence of MG132. The expression levels of membrane-anchored fusions (pTG18269, pTG18268) were comparable to those detected with their cytoplasmic counterparts (pTG18295, pTG18297), except for pTG18266 which was better expressed than the cytoplasmic fusion (pTG18296). Fusion n°5 (pTG18269) was very weakly detected with Rv1807 specific antibody while it is not the case for the cytoplasmic fusion (pTG18295). Rv1807 specific epitopes might be inaccessible in this fusion due to adjacent TM sequence.

EXAMPLE 5: DNA immunization evaluation

Immunogenic activity of the various *Mtb* antigen fusions was evaluated in various mouse models following DNA immunization.

5.1. Evaluation of the immunogenicity induced by fusions based on Mtb antigens of the active phase.

BALB/c mice were immunized three times at 3-week interval via intramuscular route with the plasmid expressing the fusion *"Ag85B – TB10.4 – ESAT6"* either in an anchored form at the cell membrane (SS/TM: pTG18266*)* or cytoplasmic form (pTG18296). For comparative purposes, mice were also immunized with a mix of plasmids encoding the individual *Mtb* antigens included in the fusion (pTG18310 *(Ag85B)* + pTG18315 *(TB10.4)* + pTG18308 *(ESAT6)*) and with empty pGWiz as negative control. Cellular immune response was evaluated 2 weeks following the last DNA injection by ELISpot IFNγ assays after ex vivo re-stimulation with the various peptide pools described in Materials and Methods.

As illustrated in Figure 5, a strong cellular response against Ag85B and TB10.4 antigens was induced in all the mice immunized with pTG18266 (expressing the anchored version of the Ag85B-TB10.4-ESAT fusion) whereas IFNγ producing cells against ESAT-6 were generated in 6 out of 8 animals (Figure 5a). In mice immunized with pTG18296 (expressing the cytoplasmic version of the Ag85B-TB10.4-ESAT fusion), activation of IFNγ producing cells against Ag85B and TB10.4 antigens was also detected but to a lesser level compared to that induced by the anchored fusion whereas very weak responses were detected against ESAT-6 (Figure 5b). Very interestingly, when comparing Figures 5a/5b and Figure 5c, strongest responses against all three antigens were detected when Ag85B, TB10.4 and ESAT-6 are expressed as a fusion protein (pTG18266 and pTG18296) rather than being independently expressed from individual plasmids (mix of pTG18310, pTG18315 and pTG18308). As expected, immunization with the empty plasmid did not induce any specific immune response (Figure 5d).

Thus, at least for *Mtb* antigens of the active phase, these results highlight the benefit of designing antigen fusions expressed at the cell surface (with SS and TM peptides) to optimize the immunogenic activity of the resulting *Mtb* antigen fusions.

5.2. Evaluation of the immunogenicity induced by fusions based on Mtb antigens of the active and resuscitation phases.

BALB/c mice were immunized three times at 3-week interval via intramuscular route with the plasmid expressing the fusion *"RpfB-Dhyb – Ag85B – TB10.4 – ESAT6"* either in an anchored form at the cell membrane (SS/TM: pTG18268*)* or cytoplasmic form (pTG18297). For comparative purposes, mice were also immunized with a mix of plasmids encoding the individual TB antigens included in the fusion (pTG18307 *(RpfB-Dhyb)* + pTG18310 *(Ag85B)* + pTG18315 *(TB10.4)* + pTG18308 *(ESAT6)*) and with empty pGWiz as negative control. Cellular immune response was evaluated 2 weeks following the last DNA

injection by ELISpot IFNγ assays after *ex vivo* re-stimulation with the various peptide pools described in Materials and Methods.

As illustrated in Figure 6, immunization with pTG18268 plasmid (expressing the anchored version of the RpfB-DHyb-Ag85B-TB10.4-ESAT-6 fusion) resulted in a strong response specific of RpfB-DHyb, Ag85B and TB10.4 antigens characterized by detection of high levels of IFNγ producing cells after *ex vivo* re-stimulation with the corresponding peptide pools whereas IFNγ producing cells against ESAT-6 were induced in fewer animals and at lower levels (Figure 6a). In mice immunized with pTG18297 (expressing the cytoplasmic version of the RpfB-DHyb-Ag85B-TB10.4-ESAT-6 fusion), activation of IFNγ producing cells against RpfB-DHyb, Ag85B and TB10.4 antigens was also detected but to a lesser level compared to that induced by the anchored fusion whereas very weak responses were generated against ESAT-6 (Figure 6b). With the exception of ESAT-6, as illustrated in Figure 6c, strongest anti *Mtb* responses were obtained against RpfB-DHyb, Ag85B and TB10.4 when expressed as a fusion protein (pTG18268 and pTG18297 Figures 6a and 6b) rather than being independently expressed from individual plasmids (mix of pTG18307 + pTG18310 + pTG18315 + pTG18308). As expected, immunization with the empty plasmid did not rise any specific immune response (Figure 6d).

5.3. Evaluation of the immunogenicity induced by fusions based on Mtb antigens of the resuscitation phase.

BALB/c mice were immunized three times at 3-week interval via intramuscular route with the plasmid expressing the fusion *"RpfB-Dhyb"* either in an anchored form at the cell membrane (SS/TM: pTG18267*)* or cytoplasmic form (pTG18307). Empty pGWiz was used as a negative control. Cellular immune response was evaluated 2 weeks following the last DNA injection by ELISpot IFNγ assays after *ex vivo* re-stimulation with the four peptide pools described in Materials and Methods.

As illustrated in Figure 7, high levels of IFNγ producing cells were observed in mice vaccinated with pTG18267 (expressing the anchored version of the RpfB-DHyb fusion with SS/TM peptides), indicating that these mice mounted a strong specific cellular response (Figure 7a). Immunization with pTG18307 (expressing the cytoplasmic version of the RpfB-DHyb fusion), also resulted in activation of IFNγ producing cells but to a slightly lesser extend (Figure 7b). Moreover, the response seemed more homogeneous within the group of

animals treated with pTG18267 than within the group treated with pTG18307. As expected, immunization with the empty plasmid did not rise any specific immune response (Figure 7c).

5.4. Evaluation of the immunogenicity induced by fusions based on Mtb antigens of the latent phase.

BALB/c mice were immunized three times at 3-week interval via intramuscular route with the plasmid expressing the fusion "Rv0569 - Rv1813 - Rv3407 - Rv3478 -Rv1807" either in an anchored form at the cell membrane (pTG18269) or cytoplasmic form (pTG18295). For comparative purposes, mice were also immunized with a mix of plasmids encoding the individual *Mtb* antigens included in the fusion (pTG18300 *(Rv3407)* + pTG18301 *(Rv0569)* + pTG18302 *(Rv1807)* + pTG18303 *(Rv1813)* + pTG18304 *(Rv3478)*) and with empty pGWiz as a negative control. Cellular immune response was evaluated 2 weeks following the last DNA injection by ELISpot IFNγ assays after *ex vivo* re-stimulation with the various peptide pools described in Materials and Methods.

As illustrated in Figure 8, immunization with pTG18269 plasmid (expressing the anchored version of the Rv0569 - Rv1813 - Rv3407 - Rv3478 -Rv1807 fusion) resulted in a strong response specific for Rv3407 and Rv3478 antigens and to a lower extend for Rv1807 (Figure 8a). Similar levels of IFNγ producing cells against these three antigens were obtained in mice immunized with pTG18295 (expressing the cytoplasmic version of the Rv0569 - Rv1813 - Rv3407 - Rv3478 -Rv1807 fusion) (Figure 8b). The responses were within the same order in mice injected with the plasmid mix (Figure 8c). On the other hand, no significant responses could be detected against Rv1813 and Rv0569 in all cases (Figures 8a, b and c). As expected, immunization with the empty plasmid did not rise any specific immune response (Figure 8d).

Other strains of mice were also used for investigation of the anti *Mtb* antigen responses in order to cover different MHC haplotypes: BALB/c mice are H-2^d, C57BL/6 mice are H-2^b, CBA/J and C3H/HeN mice are H-2^k.

Mice were immunized three times at 2-week interval via intramuscular route with pTG18323 expressing the antigens from the latent phase "Rv2029 – Rv2626 – Rv1733 – Rv0111" or with empty pGWiz as a negative control. Cellular immune response was evaluated 2 weeks following the last DNA injection by ELISpot IFNγ assays after *ex vivo* re-stimulation with the various peptide pools described in Materials and Methods section. As illustrated in Figure 10, immunization of C3H/HeN mice with pTG18323 plasmid resulted in

a strong immune response specific for Rv2029 (positive pool of peptides n°1), Rv2626 (positive pool n°2) and Rv1733 antigens (positive pool n°2) (Figure 10a). Unspecific background response was detected following immunization with pGWiz and *ex vivo* re-stimulation with Rv0111 peptide pools (Figure 10b), thus complicating the detection of anti-Rv0111 specific response following vaccination with pTG18323.

Immune responses specific for Rv2029, Rv2626 and Rv1733 antigens were also detected to similar levels as seen in H-2^k CBA/J mice immunized with pTG18323. In contrast, in BALB/c mice, IFNγ producing cells were specifically detected only after re-stimulation with Rv2626 peptides while in C57BL/6 mice no signal was detected.

Overall, these results highlight the fact that the tested *Mtb* antigen fusion sequences are able to induce robust cell-based immune responses in different haplotype of mice.

5.5. Evaluation of the immunogenicity induced by fusions based on biochemistry rules.

BALB/c mice or C57BL/6 mice were immunized three times at 2-week interval via intramuscular route with plasmids coding for the fusion number 6, 8 or 14, designed according to biochemistry properties of *Mtb* antigens, i.e. pTG18270 (*Ag85B – Rv2626 – RpfB-Dhyb – Rv1733),* pTG18272 (*Ag85B – Rv2626 – Rv1733)* and pTG18324 *(Rv2029 – TB10.4 – ESAT-6 – Rv0111)*. For comparative purposes, mice were also immunized with empty pGWiz as negative control. Cellular immune response was evaluated 2 weeks following the last DNA injection by ELISpot IFNγ assays after *ex vivo* re-stimulation with the various peptide pools described in Materials and Methods section.

A strong cellular response specific of Ag85B and RpfB-Dhyb antigens was induced in both BALB/c and C57BL/6 mice immunized with pTG18270, whereas high level of IFNγ producing cells specific of Rv2626 were detected only in BALB/c mice. Immunization with pTG18272 resulted in activation of IFNγ producing cells specific of Ag85B in BALB/c mice and specific of Ag85B and Rv2626 antigens in C57BL/6 mice, but to a lower level compared to response induced by pTG18270. In mice immunized with pTG18324, high levels of IFNγ producing cells specific of TB10.4 and ESAT-6 antigens was detected, whereas IFNγ producing cells specific of Rv2029 and Rv0111 were also induced but to lower levels. As expected, immunization with the empty plasmid did not induce any specific immune response.

Overall, the tested fusions, designed according a biochemical-based rationale in order to increase stability and production of the fusions, display a good immunogenic response specific of the *Mtb* antigens from the different phases of infection.

5.6. Evaluation of the anti-Rv1733 humoral response induced by Mtb antigen fusions.

BALB/c mice were immunized three times at 3-week interval via intramuscular route with the plasmids expressing the fusion *"Ag85B* – Rv2626 – Rv1733*"* (pTG18270) and the fusion *"Ag85B* – Rv2626 – RPFB-Dhyb*- Rv1733** (pTG18272). For comparative purposes, mice were also immunized with a mix of plasmids encoding the individual *Mtb* antigens included in the fusion (pTG18310 *(Ag85B*)* + pTG18305 *(Rv2626)* + pTG18309 *(Rv1733*)*) and with empty pGWIZ as negative control. Humoral immune response was evaluated 2 weeks following the last DNA injection. Sera of immunized-mice were pooled and analysed by Western-blot. More specifically, 100 ng / lane of recombinant protein Rv1733 (produced in *E.coli*, see example n°8) were loaded on an acrylamide gel and immunodetection was performed with 1/200 diluted sera. As a result, specific detection on Rv1733 protein was observed with the sera of mice immunised with pTG18270, pTG18272 and the mix of plasmids encoding the individual *Mtb* antigens.

5.7. Evaluation of the anti-Rv1813 humoral response induced by Mtb antigen fusions.

BALB/c mice were immunized three times at 3-week interval via intramuscular route with the plasmid expressing the fusion *"*Rv0569 - Rv1813 - Rv3407 - Rv3478 -Rv1807*"* either in an anchored form at the cell membrane (SS/TM: pTG18269*)* or cytoplasmic form (pTG18295). For comparative purposes, mice were also immunized with a mix of plasmids encoding the individual *Mtb* antigens included in the fusion (pTG18300 *(Rv3407)* + pTG18301 *(Rv0569)* + pTG18302 *(Rv1807)* + pTG18303 *(Rv1813)* + pTG18304 *(Rv3478)*) and with empty pGWiz as a negative control. Humoral immune response was evaluated 2 weeks following the last DNA injection. Sera of immunized mice were pooled and analysed by Western-blot with 100 ng / lane of recombinant protein Rv1813 (produced in *E.coli*, see example n°8) loaded on an acrylamide gel. Immunodetection was performed with 1/200 diluted sera. As a result, Rv1813 protein was specifically detected with the sera of mice immunised with pTG18269 (encoding fusion in an anchored form at the cell membrane).

EXAMPLE 6: Generation of recombinant MVA expressing *Mtb* antigens

A total of 10 MVA vaccine candidates were engineered for expression of one or up to three *Mtb* fusions and expression of the various *Mtb* antigens was analyzed by Western Blot from cell lysates obtained from infected A549 cells.

6.1 Generation of recombinant MVA by phase of the TB disease

Seven recombinant MVA candidates were engineered so as to contain one, two or three cassettes for expression of *Mtb* fusions representative of the various phases of TB disease. Fusion n°4 and fusion n°11 both contain active and resuscitation antigens (RPFB-Dhyb*-Ag85B*-TB10.4-ESAT6) either expressed anchored in the cell membrane (fusion n°4 equiped with N-terminal signal and C-terminal membrane anchoring peptides) or in the cytoplasm (fusion n°11 corresponds to the cytoplasmic version of fusion n°4). Fusion n°13 contains latent antigens (Rv2029*-Rv2626-Rv1733*-Rv0111*). Fusion n°5 and fusion n°9 both contain additional latent antigens (Rv056-Rv1813*-Rv3407-Rv3478-Rv1807) expressed at different cell location either anchored in the cell membrane (fusion n°5 contains N-terminal signal and C-terminal membrane anchoring peptides) or in the cytoplasm (fusion n°9).

All together, the seven MVA candidates are the followings:

- **MVATG18355** contains the fusion n°13 under the control of p7.5K promoter.
- **MVATG18364** contains the fusion n°13 under the control of p7.5K promoter and the fusion n°4 under the control of pH5R promoter.
- **MVATG18365** contains the fusion n°13 under the control of p7.5K promoter and the fusion n°11 under the control of pH5R promoter.
- **MVATG18376** contains the fusion n°13 under the control of p7.5K promoter, the fusion n°4 under the control of pH5R promoter and the fusion n°5 under the control of B2R promoter.
- **MVATG18377** contains the fusion n°13 under the control of p7.5K promoter, the fusion n°11 under the control of pH5R promoter and the fusion n°5 under the control of B2R promoter
- **MVATG18378** contains the fusion n°13 under the control of p7.5K promoter, the fusion n°4 under the control of pH5R promoter and the fusion n°9 under the control of B2R promoter.

- **MVATG18379** contains the fusion n°13 under the control of p7.5K promoter, the fusion n°11 under the control of pH5R promoter and the fusion n°9 under the control of B2R promoter.

6.2 Generation of recombinant MVA on biochemical rational

Three recombinant MVA candidates were engineered so as to contain two or three cassettes for expression of *Mtb* fusions designed relative to biochemical rationales. Fusion n°6 contains the following antigens Ag85B*-Rv2626-RPFB-Dhyb*-Rv1733* while fusion n°14 contains Rv2029*-TB10.4-ESAT6-Rv0111*. N-terminal signal peptides were added for both fusions while no TM domain were added since these fusions end with Rv0111 or Rv1733 which already contain membrane-anchoring peptides.

- **MVATG18404** contains the fusion n°14 under the control of p7.5K promoter and the fusion n°6 under the control of pH5R promoter.
- **MVATG18417** contains the fusion n°14 under the control of p7.5K promoter, the fusion n°6 under the control of pH5R promoter and the fusion n°5 under the control of B2R promoter.
- **MVATG18418** contains the fusion n°14 under the control of p7.5K promoter, the fusion n°6 under the control of pH5R promoter and the fusion n°9 under the control of B2R promoter.

6.3 Western Blot analysis of MVA-expressed Mtb antigens and fusions

A549 cells were infected (MOI 1) with the various MVA candidates described above and expression products were analyzed by Western blot under the conditions described in Materials and Methods. Immunodetection was performed with antibodies specific of the various *Mtb* antigens described herein. Specifically, the sera obtained after immunization of rabbits (see Materials and Methods) were used for detection of Rv1733*, Rv2029*, Rv0569, Rv1807, Rv0111*, RPFB-Dhyb*, Rv1813*, Rv3407, and Rv3478 whereas commercial antibodies were used for the detection of ESAT6, Ag85B *, TB10.4 and Rv2626.

As a result, a band corresponding to the expected size was highlighted for all fusions whatever the recombinant MVA tested. More specifically, a band of approximately 98.4 kDa (expected size for fusion n°13) was detected following anti-Rv2626 and anti-Rv0111 immunodetection in the cell lysates originating from cells infected with MVATG18355,

MVATG18364, MVATG18365, MVATG18376, MVATG18377, MVATG18378 and MVATG18379. A band of approximately 96.7 kDa (expected size for fusion n°4) and a band of approximately 87 kDa (expected size for fusion n°11) were detected following anti-ESAT6 immunodetection in the cell lysates originating from cells infected respectively with fusion n°4-containing MVATG18364, MVATG18376 and MVATG18378 and fusion n°11-containing MVATG18365, MVATG18377 and MVATG18379. Moreover a band of approximately 119.7 kDa (expected size for fusion n°5) and a band of approximately 109.9 kDa (expected size for fusion n°9) were detected following anti-Rv3407 immunodetection in the cell lysates originating from cells infected respectively with fusion n°5-containing MVATG18376 and MVATG18377 and fusion n°9-containing MVATG18378 and MVATG18379. Finally, a band of approximately 100.4 kDa (expected size for fusion n° 6) and a band of approximately 87.5 kDa (expected size for fusion n°14) were detected in the cell lysates originating from cells infected with MVATG18404 following anti-Rv2626 and anti-Rv0111 immunodetection, respectively.

Moreover, in some case, additional fusion products were also observed. In particular, dimers were detected for fusion n°13 and fusion n°6 likely resulting of the ability of Rv2626 to form dimers resistant to reducing conditions. Concerning fusion n°13, expression of the entire fusion n°13 (expected size 98.4 kDa) was indeed detected but at low level. Major proteolytic products were observed with anti-Rv2626 (around 70 kDa) and with anti-Rv0111 (around 30kDa), suggesting a proteolytic cleavage of the fusion n°13.

Similar level of expression was detected for fusions n° 4 and n°11 which contain the same antigens (RPFB-Dhyb*-Ag85B*-TB10.4-ESAT6) but either membrane-anchored (fusion n°4) or cytoplasmic (fusion n°11). A higher band than the expected size (115 kDa instead of 96.7 kDa) was observed for fusion n° 4, corresponding probably to N-glycosylated products. Minor proteolytic products were also detected for both fusions.

Similar level of expression was also revealed with anti-Rv3407 in cell lysates of MVA expressing fusions n°5 and n°9 (both corresponding to the fusion of Rv0569-Rv1813*-Rv3407-Rv3478-Rv1807 antigens but expressed in membrane anchored form (fusion n°5) or in cytoplasmic (fusion n°9)). A higher band than the expected size (120 kDa instead of 98.4 kDa) was present in fusion n° 5-expressing cell lysates, corresponding probably to N-glycosylated products. On the other hand, fusion n°5 was very weakly detected with anti-Rv1807 antibody while it is not the case for the cytoplasmic version. It is

assumed that Rv1807 specific epitopes might be inaccessible in the membrane-anchored fusion due to the adjacent TMR sequence.

EXAMPLE 7: Evaluation of the immunogenicity of MVA candidate vaccines expressing *Mtb* antigens

7.1 Evaluation of immunogenicity of MVA candidate vaccines expressing Mtb antigens in BALB/c mice

BALB/c mice were immunised with MVATG18365 and MVATG18364 both expressing « *Rv2029-Rv2626-Rv1733-Rv0111* » (corresponding to fusion n°13) as well as « *RpfB-Dhyb-Ag85B-TB10.4-ESAT6* » (corresponding to fusion n° 4 or n°11). In the fusion n°13, a SS domain is present at the N-terminus and Rv1733 and Rv0111 are expressed with a TM domain which should direct expression of the fusion to the cell surface. Fusion n°4 expressed by MVATG18364 contains both a SS and a TM domain whereas fusion n°11 (MVATG18365) does not and should theoretically retain a bcytoplasmic expression. Specific-cellular immune responses were evaluated one week after injection by IFNγ ELISpot assays following restimulation with peptide pools described herein. Mice were also immunized with empty MVA vector (MVATGN33.1) as a negative control.

As illustrated in Figure 11a and b respectively, both vectors MVATG18365 and MVATG18364 induced IFNγ positive responses specific of Rv2626, Rv0111, RpfB-Dhyb, Ag85B and TB10.4 in BALB/c mice when compared with MVATGN33.1 vector. These responses were systematically stronger with the MVATG18364 (anchored fusion) as compared with MVATG18365 (cytoplasmic fusion) except for Rv2626 showing similar responses. Weaker and sporadic responses specific of Rv2029, Rv1733 and ESAT6 were detected.

In addition, all recombinant MVA candidate vaccines described in "Example 6" section were injected in BALB/c mice and cellular immune responses specific of all Mtb antigens were assessed by IFNγ ELISpot assays as described in Materials and Methods section. A summary of the scope and intensity of responses induced by each MVA candidate in BALB/c mice is described in Figure 12. All MVA vaccines, with Mtb antigens fusions designed according to phase of TB disease or biochemical rationale, were able to

induce an IFNγ response specific of 12 out of 14 antigens in BALB/c mice. No positive cellular response specific of the two latent antigens, Rv1733 and Rv0569, was detected.

7.2 Evaluation of immunogenicity of MVA candidate vaccines expressing Mtb antigens in transgenic HLA-A2 mice

As we have observed in the DNA-based studies, the mice haplotype has an influence on immunogenicity of the selected Mtb antigens (see section 5). In order to further analyze immunogenicity of Rv1733 and Rv0569 antigens induced by MVA candidates, transgenic mice expressing human MHC class I molecule, HLA-A2, were injected with recombinant MVAs expressing both antigens. Cellular immune response was evaluated one week after injection by IFNγ ELISpot assay after restimulation with the peptide pools described herein. Mice were also immunized with empty MVA vector (MVATGN33.1) as a negative control. Specifically, HLA-A2 mice were immunized with MVATG18376 or MVATG18378 vaccines expressing « *Rv2029-Rv2626-Rv1733-Rv0111* » (corresponding to fusion n°13), « *RpfB-Dhyb-Ag85B-TB10.4-ESAT6* » (corresponding to fusion n° 4) as well as « *Rv0569-Rv1813-Rv3407-Rv3478-Rv1807* » (corresponding to fusion n° 5 or n° 9). In the fusion n° 5 expressed by MVATG18376, SS and TM domains were expressed at the N-terminus and C-terminus part, respectively. Figure 13 illustrates IFNγ response induced in HLA-A2 mice immunized with MVATG18376 vaccine. Immune response specific of 7 out of 14 antigens was detected (Figure 13a). High levels of IFNγ-producing cells were detected when splenocytes were restimulated with peptides specific of RpfB-Dhyb and Ag85B antigens (1397 spots/10^6 cells and 1160 spots/10^6 cells, respectively). In contrast, lower levels of cellular responses specific of Rv1807, Rv1813, Rv3407 and ESAT6 were induced by the MVATG18376 vaccine. In addition, a low (1x cut-off < median < 2x cut-off, 186 spots/10^6 cells, Figure 13a) but significant level of IFNγ-producing cells was detected when cells were restimulated with Rv0569-specific peptides as compared with signal detected with the MVATGN33.1 empty vaccine (36 spots/10^6 cells, Figure 13b). Similar results were also induced in HLA-A2 mice vaccinated with the MVATG18378 candidate which induced additional weak responses specific of Rv0111 and TB10.4 antigens. IFNγ responses induced by both MVATG18376 and MVATG18378 vaccines are summarized in Figure 15. Whatever the MVA candidate injected, no detectable response specific of Rv1733, Rv2029, Rv2626 and Rv3478 could be observed in HLA-A2 transgenic mice.

7.3 Evaluation of immunogenicity of MVA candidate vaccines expressing Mtb antigens in C57Bl/6 mice

H-2^b haplotype C57BL/6 mice were immunized with MVATG18377 or MVATG18379 vaccines expressing « *Rv2029-Rv2626-Rv1733-Rv0111* » (corresponding to fusion n°13), « *RpfB-Dhyb-Ag85B-TB10.4-ESAT6* » (corresponding to fusion n° 11) as well as « *Rv0569-Rv1813-Rv3407-Rv3478-Rv1807* » (corresponding to fusion n° 5 or n° 9) in order to demonstrate immunogenicity of Rv0569 and Rv1733 antigens. Cellular immune response was evaluated one week after injection by IFNγ ELISpot assays after restimulation with the peptide pools described herein. Mice were also immunized with empty MVA vector (MVATGN33.1) as a negative control. Cellular IFNγ responses are summarized in Figure 15. Both MVA vaccines were able to trigger strong immune response specific of Rv1807, RpfB-Dhyb, Rv3478, Ag85B and ESAT6 antigens (ranging from 92 to 861 spots/10^6 cells) while a positive IFNγ response specific of TB10.4 and Rv0569 antigens was only detected in mice immunized with MVATG18379 candidate (78 and 58 spots/10^6 cells, respectively). No positive response specific of Rv1733, Rv2029, Rv2626, Rv0111, Rv1813 and Rv3407 was detected in immunized C57BL/6 mice.

7.4 Evaluation of immunogenicity of MVA candidate vaccines expressing Mtb antigens in C3H/HeN mice

As immunogenicity specific of Rv1733 has been demonstrated in H-2^k haplotype C3H/HeN mice vaccinated with plasmids (see section 5.4), MVATG18376, MVATG18378, MVATG18377 and MVATG18379 expressing fusions containing the Rv1733 protein were injected to this mouse strain. Cellular immune response was evaluated one week after injection by IFNγ ELISpot assays after restimulation with the peptide pools described herein. Mice were also immunized with empty MVATGN33.1 vector as a negative control. As illustrated in Figure 14, MVATG18377 vaccine induced IFNγ responses in C3H/HeN mice as compared with MVATGN33.1. High levels of IFNγ-producing cells were detected upon splenocytes restimulation with Rv2029 and Rv2626 peptides (660 and 353 spots/10^6 cells, respectively). A low cellular immune response specific of RpfB-Dhyb, Rv1813, Rv3407 and Rv3478 antigens, ranging from 78 to 250 spots/10^6 cells, was also induced in immunized C3H/HeN mice. As demonstrated in DNA-vaccinated C3H/HeN mice, Rv1733-specific IFNγ response (183 spots/10^6 cells) was triggered in this mouse strain as compared with

signals resulting from mice injected with empty MVATGN33.1 vaccine (9 spots/10^6 cells, Figure 14b). Unspecific background response was detected following immunization with MVATGN33.1 and *ex vivo* restimulation with Rv0111, Ag85B and Rv1807 peptide pools (Figure 14b), rendering difficult the detection of response specific of these antigens following vaccination with MVATG18377.

In addition to MVATG18377, immune responses induced by MVATG18376, MVATG18378 and MVATG18379 in C3H/HeN mice are illustrated in Figure 15. Among the four MVA candidates tested, MVATG18377 was the most immunogenic (7 out of 14 antigens). MVATG18376 and MVATG18378 induced cellular immune responses specific of only 2 (Rv2029 and Rv2626) out of 14 antigens, while MVATG18379 was able to trigger response to not only both antigens but also Rv1733. MVATG18377 and MVATG18379 express the same fusion proteins except the fusion « *Rv0569-Rv1813-Rv3407-Rv3478-Rv1807* ». In MVATG18377, SS and TM domains are expressed at the N-terminus and C-terminus part respectively of fusion n° 5 while in MVATG18379 both domains are not present. 3 out of 5 antigens present in this fusion were immunogenic in MVATG18377, while none was in MVATG18379. These results show that addressing fusion protein to cell membrane improve their immunogenicity.

Overall, immunization with MVA vectors as well as with DNA plasmids leads to induction of strong and specific cellular responses targeting all *Mtb* antigens included in the fusions described in the present application. Humoral immune responses specific of two tested antigens were also detected in DNA-immunized mice. As with DNA plasmids, membrane-anchorage of the MVA-expressed *Mtb* fusions improves to some extent the level of induction of specific immune responses.

EXAMPLE 8: Production and purification of the *Mtb* antigens

8.1 Optimal conditions for biomass production of the selected Mtb antigens

Four *E. coli* strains have been tested for the expression of the individual *Mtb* antigens as well as different culture conditions (e.g. temperature).

These assays highlight that all the 14 selected antigens could be expressed at least in one bacterial strain at one defined temperature but significant differences were observed from one *Mtb* antigen to another. Indeed, some *Mtb* antigens could be easily produced in

various *E. coli* strains and whatever the culture conditions (e.g. Rv0111, Rv0569, Rv1807, Rv2029, Rv2626, RpfB-D fusion) while other antigens require very specific host cells and conditions (e.g. Rv1733, Rv1813, TB10-4). On the other hand, high expression levels could be obtained for most of *Mtb* antigens in the different *E. coli* strains except Rv3407, Ag85B and Rv1813 expressed at lower but detectable levels. Moreover, certain *Mtb* antigens are produced as soluble material (e.g. Rv2626, Rv3407 and Ag85B that could be collected directly from cell lysate supernatants) while others are in insoluble material (e.g. RPFB-D, Rv0111, Rv1733, Rv2029, Rv3478, Rv1807, ESAT6 and TB10.4 that are collected from the pellet after cell lysis). Interestingly, Rv0569 is soluble when produced from transformed Bl21 cells cultured at 18°C and both in soluble and insoluble material (in supernatant and pellet after lysis) when the Bl21 cells are cultured at 37°C.

8.2 Purification of the Mtb antigens

As described in Materials and Methods, *Mtb* antigens were purified by IMAC chromatography on nickel columns, eventually followed by gel filtration columns.

Representative purification assays are shown for Rv2626 (purified from soluble material produced in C41 (DE3) cells at 37°C), RPFB-D fusion (denatured RpfB-D purified from solubilized inclusion bodies produced in Bl21 (DE3) at 37°C) and for TB10.4 (purified from soluble and insoluble material produced in C41 (DE3) cells at 37°C . The eluted fractions were assayed on SDS-PAGE as shown in Figures 9 a, b and c, respectively.

As illustrated in Figure 9A, the Rv2626 purified pool did not show any visible contaminant. A major band was seen at the expected Rv2626 molecular weight as well as a minor band (the so-called band B) which has been identified by MS as Rv2626. Rv2626 is known to form dimers that are partially resistant to denaturation and reduction. Therefore, it is assumed that minor band B corresponds to the dimeric form of Rv2626.

When visualized on SDS-PAGE (lanes 1 to 8 represent intermediate purification fractions and lanes 9 to 11 5, 10 and 15µL of purified pool), the RPFB-Dhyb purified pool did not show any visible contaminant (see Figure 9B).

TB10-4 was purified in denaturing conditions followed by a final step in native conditions. As illustrated in Figure 9C, the gel analysis of the purified pool did not show any visible contaminant (lanes 2 to 6 represent intermediate purification fractions and lanes 7 to 9 1, 3 and 6µL of purified pool).

In the three cases, endotoxin levels were measured in the purified pools and showed to be at a maximum level of 10EU/mg protein.

Therefore, the three proteins have been purified with acceptable amount, purity and endotoxin level.

As a summary, the present invention provides an optimized combination of *Mtb* antigens. 14 *Mtb* antigens were selected after extensive bibliographic, data mining scoring and biochemical *in silico* analyses and cloned in plasmid vectors either individually or in the form of fusions. As demonstrated by Western blotting, all fusions were expressed at high levels and detected at the correct expected size following immunodetection with a series of antibodies directed against tags present at the N and C termini or against each *Mtb* antigen present in the fusion. Immunization assays in BALB/c mice support the immunogenic potential of the selected *Mtb* antigen combinations and fusions for inducing T cell responses.

Moreover, the selected *Mtb* antigens (RpfB and RpfD in fusion) were individually produced in bacteria by recombinant means. Conditions for expression in *E. coli* were optimized by studying criteria such as bacterial strains and culture conditions (e.g. growth temperature). All proteins have been successfully expressed and produced at a litter scale.

EXAMPLE 9: Evaluation of therapeutic efficacy of Mtb antigen-containing vaccines against *Mycobacterium tuberculosis* infection in mice

Therapeutic efficacies of three Mtb-expressing MVA candidates, MVATG18364, MVATG18376 and MVATG18377 were investigated in a therapeutic setting co-administered with antibiotics in mice that were previously infected with Mtb strain H37Rv. As negative control, MVATGN33.1 was also injected in one group. Bacterial load was evaluated in spleens collected from the treated mice at the end of antibiotic treatment (at week 15 post-infection) and 6 weeks after (at week 21 post-infection). Groups of mice, drug regimen and immunization schedule are described in Table 5.

Table 5:

Group	N mice	Treatment	Week 0 Aerosol challenge	Pre-treat CFU (day1, Week 6)	INH/RIF Treatment (week 6 to week 15)			CFU (relapse) Week 21
					MVA Week 10	MVA Week 14	CFU Week 15	
1	5	None	5	5				
2	20	INH/RIF	20	-			5	15
3	20	INH/RIF + MVATG18376	20	-	20	20	5	15
4	20	INH/RIF + MVATG18377	20	-	20	20	5	15
5	20	INH/RIF + MVATG18364	20	-	20	20	5	15
6	20	INH/RIF + MVATGN33.1	20		20	20	5	15

Six weeks post-Mtb infection and before starting chemotherapy and MVA immunization, the mycobacteria developed in the spleen of all mice groups (2.64 $\log_{10}$ total cfu). As expected, mycobacterial load decreased during chemotherapy treatment. In group 2 treated only with chemotherapy, the Mtb level decreased progressively to reach 1.18 $\log_{10}$ total cfu at week 15 and 0.70 $\log_{10}$ total cfu at week 21. Interestingly, at week 15, the mycobacterial loads were lower in mice co-treated with antibiotics and Mtb antigens-expressing MVA (0.70 $\log_{10}$ total CFU at week 15 in groups 3-5) than in mice treated with antibiotics only (group 2) and with the control empty MVA in combination with antibiotics (group 6), suggesting that Mtb-expressing MVA contributed to a stronger antibacterial effect. It is noteworthy that 6 weeks after the end of treatment (week 21), mycobacteria did not proliferate and loads were controlled in MVA-vaccinated mice (ranging from 0.70 to 0.85 $\log_{10}$ total cfu) at a level similar to the one observed in antibiotics therapy alone-treated mice. As control, the empty MVATGN33.1 vector combined with drugs therapy did not induce any anti-mycobacterial effect better than antibiotic regimen only at week 15 and week 21.

Claims

1. An immunogenic combination comprising at least 5 different antigens or nucleic acid molecules encoding the at least 5 antigens, wherein said antigens are independently obtained from a Mycobacterium species.

2. The immunogenic combination according to claim 1, wherein the mycobacterial antigens are obtained from a Mycobacterium species of the tuberculosis complex selected from the group consisting of *M. tuberculosis* (*Mtb*), *M. bovis*, *M. bovis* BCG, *M. africanum*, *M. canetti*, *M. caprae*, and *M. microti*.

3. The immunogenic combination according to claim 1 or 2, wherein said immunogenic composition comprises or encodes mycobacterial antigens from at least 2 different infection phases selected from the group consisting of active, resuscitation and latent phases.

4. The immunogenic combination according to claim 3, wherein said immunogenic composition is multiphasic comprising or encoding at least one antigen from the active infection phase, at least one antigen from the resuscitation infection phase and at least one antigen from the latent infection phase.

5. The immunogenic combination according to claim 3 or 4, wherein said antigen(s) of the active phase is/are selected from the group consisting of ESAT-6 (Rv3875), CFP-10 (Rv3874), TB10.4 (Rv0288), Ag85A (Rv3804), Ag85B (Rv1886), Rv3619, Rv3620 and PPE family proteins Rv3478 and Rv2608.

6. The immunogenic combination according to claim 5, wherein said immunogenic composition comprises or expresses at least ESAT-6 (Rv3875), Ag85B (Rv1886) and TB10.4 (Rv0288).

7. The immunogenic combination according to claim 3 or 4, wherein said antigen(s) of the latent phase is/are selected from the group consisting of Rv0081, Rv0111, Rv0198, Rv0569,

Rv1733c, Rv1735, Rv1737, Rv1806, Rv1807, Rv1813, Rv2005c, Rv2029c, Rv2032, Rv2626, Rv2627, Rv2628, Rv2660c, Rv3407 and Rv3812.

8. The immunogenic combination according to claim 7, wherein said antigen(s) of the latent phase is/are selected from the group consisting of Rv0111, Rv0569, Rv1733, Rv1807, Rv1813, Rv2029, Rv2626, Rv3407 and Rv3478.

9. The immunogenic combination according to claim 3 or 4, wherein said antigen(s) of the resuscitation phase is/are selected from the group consisting of RpfA, RpfB, RpfC, RpfD and RpfE.

10. The immunogenic combination according to claim 9, wherein said immunogenic composition comprises or expresses at least RpfB and RpfD.

11. The immunogenic combination according to anyone of claims 1 to 10, wherein said immunogenic combination comprises or encodes at least 5 mycobacterial antigens selected from the group consisting of ESAT-6 (Rv3875), CFP-10 (Rv3874), TB10.4 (Rv0288), Ag85A (Rv3804), Ag85B (Rv1886), Rv3619, Rv3620, RpfA, RpfB, RpfC, RpfD, RpfE, Rv0081, Rv0111, Rv0198, Rv0569, Rv1733c, Rv1735, Rv1737, Rv1806, Rv1807, Rv1813, Rv2005c, Rv2029c, Rv2032, Rv2626, Rv2627, Rv2628, Rv2660c, Rv3407 Rv3478, and Rv3812.

12. The immunogenic combination according to claim 11, wherein the at least 5 mycobacterial antigens are selected from the group consisting of from the group consisting of ESAT-6 (Rv3875), TB10.4 (Rv0288), Ag85B (Rv1886), RpfB, RpfD, Rv0111, Rv0569, Rv1733c, Rv1807, Rv1813, Rv2029c, Rv2626, Rv3407 and Rv3478; and preferably from the group of polypeptides comprising an amino acid sequence at least 80% homologous or identical to any of SEQ ID NO: 1-24.

13. The immunogenic combination according to anyone of claims 1 to 12, wherein said immunogenic combination comprises or encodes the mycobacterial antigens in the form of

separate polypeptides or in the form of one or more fusion polypeptides or both in the form of separate antigen(s) and fusion(s).

14. A fusion polypeptide comprising two or more mycobacterial antigens comprised or encoded by the immunogenic combination according to anyone of claims 5 to 12.

15. The fusion polypeptide according to claim 14 comprising at least 2 polypeptides selected from the group of polypeptides comprising an amino acid sequence at least 80% identical to any of SEQ ID NO: 1-24.

16. The fusion polypeptide according to claim 14 or 15, wherein said fusion polypeptide comprises mycobacterial antigens of the same infection phase.

17. The fusion polypeptide according to claim 14 or 15, wherein said fusion polypeptide comprises mycobacterial antigens from two different infection phases or even from the active, resuscitation and latent phases.

18. The fusion polypeptide according to claim 16 or 17, wherein said fusion polypeptide is selected from the group consisting of:

(i) A fusion polypeptide comprising *M. tuberculosis* antigens Rv2029, Rv2626, Rv1733 and Rv0111;

(ii) A fusion polypeptide comprising *M. tuberculosis* antigens Rv0569, Rv1813, Rv3407, Rv3478 and Rv1807;

(iii) A fusion polypeptide comprising *M. tuberculosis* antigens Ag85B, TB10.4 and ESAT6;

(iv) A fusion polypeptide comprising *M. tuberculosis* antigens RpfB and RpfD;

(v) A fusion polypeptide comprising *M. tuberculosis* antigens RpfB, RpfD, Ag85B, TB10.4 and ESAT6;

(vi) A fusion polypeptide comprising *M. tuberculosis* antigens Ag85B, Rv2626, RpfB, RpfD andRv1733;

(vii) A fusion polypeptide comprising *M. tuberculosis* antigens Rv2029, TB10.4, ESAT6 and Rv0111; and

(viii) A fusion polypeptide comprising *M. tuberculosis* antigens Ag85B, Rv2626 and Rv1733.

19. The fusion polypeptide according to claim 18, wherein said fusion polypeptide is selected from the group of polypeptides comprising an amino acid sequence which exhibits at least 80% identity with anyone of the following amino acid sequences

- the amino acid sequence shown in SEQ ID NO: 28 from approximately position 32 to approximately position 506;
- the amino acid sequence shown in SEQ ID NO: 29 from approximately position 10 to approximately position 484;
- the amino acid sequence shown in SEQ ID NO: 30 from approximately position 32 to approximately position 380;
- the amino acid sequence shown in SEQ ID NO: 31 from approximately position 10 to approximately position 358;
- the amino acid sequence shown in SEQ ID NO: 32 from approximately position 32 to approximately position 855;
- the amino acid sequence shown in SEQ ID NO: 33 from approximately position 10 to approximately position 833;
- the amino acid sequence shown in SEQ ID NO: 34 from approximately position 32 to approximately position 1115;
- the amino acid sequence shown in SEQ ID NO: 35 from approximately position 10 to approximately position 1093;
- the amino acid sequence shown in SEQ ID NO: 36 from approximately position 32 to approximately position 956;
- the amino acid sequence shown in SEQ ID NO: 37 from approximately position 32 to approximately position 607;
- the amino acid sequence shown in SEQ ID NO: 38 from approximately position 37 to approximately position 932; or
- the amino acid sequence shown in SEQ ID NO: 39 from approximately position 37 to approximately position 831; and

wherein said amino acid sequence further comprises an initiator Met.

20. The fusion polypeptide according to claim 18 or 19, wherein said fusion polypeptide further comprises appropriate targeting peptide(s) such as signal and/or trans-membrane peptides.

21. A nucleic acid molecule encoding said at least 5 mycobacterial antigens comprised in the immunogenic combination according to anyone of claims 5 to 13 or the fusion polypeptide according to anyone of claims 14 to 20.

22. The nucleic acid molecule according to claim 21, which exhibits at least 80% identity, with the nucleotide sequence shown in any of SEQ ID NO: 40-51 or a fragment thereof.

23. A vector comprising one or more nucleic acid molecule(s) according to claim 21 or 22.

24. The vector of claim 23, wherein said vector is a plasmid or a viral vector selected from the group consisting of retrovirus, adenovirus, adenovirus-associated virus (AAV), poxvirus, herpes virus, measles virus, foamy virus, alphavirus, vesicular stomatis virus.

25. The vector of claim 24, wherein said vector is a E1-defective adenoviral vector.

26. The vector of claim 25, wherein said vector is a poxvirus vector selected from the group consisting of fowlpox, canarypox and vaccinia virus vector.

27. The vector of claim 26, wherein said vaccinia virus vector is Copenhagen, Wyeth, NYVAC and modified Ankara (MVA) strains.

28. The vector of claim 23, wherein said vector is a bacterium cell selected from the group consisting of *M. bovis* BCG, Lactobacillus, Listeria, Salmonella and Pseudomonas.

29. The vector according to anyone of claims 23 to 28 which is selected from the group consisting of:

i. A vector encoding a fusion polypeptide comprising Rv2029, Rv2626, Rv1733 and Rv0111 and a fusion polypeptide comprising RpfB, RpfD, Ag85B, TB10.4 and ESAT-6;

ii. A vector encoding a fusion polypeptide comprising Rv2029, Rv2626, Rv1733 and Rv0111, a fusion polypeptide comprising RpfB, RpfD, Ag85B, TB10.4 and ESAT-6 and a fusion polypeptide comprising Rv0569, Rv1813, Rv3407, Rv3478 and Rv1807;

iii. A vector encoding a fusion polypeptide comprising Rv2029, Rv2626, Rv1733 and Rv0111, a fusion polypeptide comprising RpfB, RpfD, Ag85B, TB10.4 and ESAT-6 and a fusion polypeptide comprising Rv0569, Rv1813, Rv3407, Rv3478 and Rv1807;

iv. A vector encoding a fusion polypeptide comprising Ag85B, Rv2626 RpfB, RpfD and Rv1733 and a fusion polypeptide comprising Rv2029 TB10.4, ESAT-6 and Rv0111;

v. A vector encoding a fusion polypeptide comprising Ag85B, Rv2626 RpfB, RpfD and Rv1733, a fusion polypeptide comprising Rv2029 TB10.4, ESAT-6 and Rv0111 and a fusion polypeptide comprising Rv0569, Rv1813, Rv3407, Rv3478 and Rv1807; and

vi. A vector encoding a fusion polypeptide comprising RpfB, RpfD, Ag85B, TB10.4 and ESAT-6 and a fusion polypeptide comprising Rv0569, Rv1813, Rv3407, Rv3478 and Rv1807.

30. The vector according to anyone of claims 23 to 29 which is in the form of infectious virus particles.

31. A process of producing an infectious virus particle comprising the steps of (i) introducing the viral vector of anyone of claims 24 to 27 and 29 to 30 into a suitable cell line, (ii) culturing said cell line under suitable conditions so as to allow the production of said infectious viral particle, (iii) recovering the produced viral particle from the culture of said cell line, and (iv) optionally purifying said recovered viral particle.

32. A host cell comprising the immunogenic combination of anyone of claims 1 to 13, the fusion polypeptide of anyone of claims 14 to 20, the nucleic acid molecule of anyone of claims 21 to 22 or the vector of anyone of claims 23 to 30.

33. A method for recombinant production of the mycobacterial antigens comprised or encoded by the immunogenic combination of anyone of claims 1 to 13 or in the fusion polypeptide of anyone of claims 14 to 20, which comprises the steps of (i) introducing a vector into a suitable host cell to produce a transfected or infected host cell, (ii) culturing *in-vitro* said transfected or infected host cell under conditions suitable for growth of the host cell, (iii) recovering the cell culture, and (iv) optionally, purifying the mycobacterial antigen(s) or the fusion polypeptide from the recovered cell and/or culture supernatant.

34. The method of claim 33, wherein said suitable host cell is an *E coli* host cell and in particular a *E. coli* strain carrying the D13 prophage in its genome.

35. A composition comprising at least one of the immunogenic combination of anyone of claims 1 to 13, the fusion polypeptide of anyone of claims 14 to 20, the nucleic acid molecule of anyone of claims 21 to 22, the vector of anyone of claims 23 to 30 or the host cell of claim 32 or any combination thereof.

36. The composition of claim 35 which further comprises a pharmaceutically acceptable vehicle.

37. The immunogenic combination of anyone of claims 1 to 13, the fusion polypeptide of anyone of claims 14 to 20, the nucleic acid molecule of anyone of claims 21 to 22, the vector of anyone of claims 23 to 30, the host cell of claim 32 or the composition of anyone of claims 35 or 36 for use for preventing or treating a Mycobacterium infection or any disease and pathologic condition caused by or associated with such a Mycobacterium infection.

38. The immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition according to claim 37, for use for preventing infection or delaying the

risk of infection with a Mycobacterium in a subject in need thereof, especially a subject who has been in close contact with an infected individual having developed an active disease.

39. The immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition according to claim 37, for use for treating an active disease in a subject infected with a Mycobacterium species and especially *M. tuberculosis*.

40. The immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition according to claim 37, for use for preventing or treating reactivation in a subject latently infected with a Mycobacterium species and especially *M. tuberculosis*.

41. The immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition according to claim 37, for use as a BCG booster.

42. The immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition according to anyone of claims 37 to 41 for use in association with one or more chemotherapeutic drug(s) effective against a Mycobacterium infection, and especially one or more antibiotic chemotherapy.

43. The immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition according to anyone of claims 37 to 42, for use for inducing or enhancing an immune response in the administered subject.

44. The immunogenic combination, fusion polypeptide, nucleic acid molecule, vector, host cell or composition according to claim 43, wherein said induced or stimulated immune response is a CD4+ and/or CD8+-mediated T cell response directed to a mycobacterial antigen/epitope.

45. An antibody which selectively binds to at least one of the mycobacterial antigens comprised in or encoded by the immunogenic combination of anyone of claims 1 to 13 or the fusion polypeptide of anyone of claims 14 to 20, the nucleic acid molecule of anyone of

claims 21 to 22, the vector of anyone of claims 23 to 30, the host cell of claim 32 or the composition of anyone of claims 35 or 36.

46. A method for the detection and/or quantification a mycobacterial antigen in a biological sample taken from a subject infected or susceptible to be infected by a Mycobacterium which comprises the steps of bringing said biological sample into contact with the antibody of claim 45 as reagent under conditions allowing the formation of a complex between the mycobacterial antigen and the antibody reagent and detecting and/or quantifying the formation of said complex by any appropriate means.

47. A kit of reagents for diagnosis a Mycobacterium infection for antigen assay comprising the antibody of claim 45 and for antibody assay comprising the immunogenic combination of anyone of claims 1 to 13 or the fusion polypeptide of anyone of claims 14 to 20, the nucleic acid molecule of anyone of claims 21 to 22, the vector of anyone of claims 23 to 30, the host cell of claim 32 or the composition of anyone of claims 35 or 36.