CLAIMS

1. A nucleic acid construct which comprises:

(1) a polynucleotide encoding at least (i) the precursor of membrane (prM) protein of a Zika virus (ZIKV), and the envelope (E) protein of a ZIKV or a truncated version thereof of SEQ ID NO: 26, SEQ ID NO: 29 and SEQ ID NO: 32, or (ii) the E protein of a ZIKV or the truncated version thereof; wherein the polynucleotide encoding the E protein as defined in 1(i) or 1(ii) encodes either the full-length E protein or its soluble form lacking the two C-terminal transmembrane domains of the full-length E protein; and

(2) a cDNA molecule encoding a full-length, infectious antigenomic (+) RNA strand of a measles virus (MV);

wherein the polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof is operatively linked, in particular cloned into the cDNA molecule;

the nucleic acid construct comprising the following polynucleotides from 5' to 3':

(a) a polynucleotide encoding the N protein of the MV;

(b) a polynucleotide encoding the P protein of the MV;

(c) the polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof;

(d) a polynucleotide encoding the M protein of the MV;

(e) a polynucleotide encoding the F protein of the MV;

(f) a polynucleotide encoding the H protein of the MV; and

(g) a polynucleotide encoding the L protein of the MV;

wherein said polynucleotides are operably linked in the nucleic acid construct and under a control of viral replication and transcription regulatory sequences such as MV leader and trailer sequences.

2. The nucleic acid construct according to claim 1, characterized in that the polynucleotide of (1) and the cDNA molecule of (2) together consist of a number of nucleotides that is a multiple of six.

3. The nucleic acid construct according to claim 1 or 2, wherein said measles virus is an attenuated virus strain selected from the group consisting of the Schwarz strain, the Zagreb strain, the AIK-C strain and the Moraten strain.

4. The nucleic acid construct according to any one of claims 1 to 3, wherein said polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, has been optimized for a Macaca codon usage or has been optimized for a human codon usage.

5. The nucleic acid construct according to any one of claims 1 to 4, wherein *measles editing-like sequences* have been deleted from said polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof.

6. The nucleic acid construct according to any one of claims 1 to 5, wherein said ZIKV is from the African lineage, in particular from the African strain ArB1362 (GenBank: KF383115) or African isolate IbH_30656 (GenBank: HQ234500), or from the Asian strain, in particular from the Asian strain BeH818995 (GenBank: KU365777).

7. The nucleic acid construct according to any one of claims 1 to 6, wherein said polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, further encodes (iii) the signal peptide from the capsid of the ZIKV and the signal peptide from the membrane protein of the ZIKV, or

wherein said polynucleotide encoding at least (ii) the E protein of the ZIKV or the truncated version thereof, further encodes (iii) the signal peptide from the capsid of the ZIKV or the signal peptide from the membrane protein of the ZIKV.

8. The nucleic acid construct according to any one of claims 1 to 7, wherein the polynucleotide encoding the truncated version of the E protein as defined in claim 1(i) or 1(ii) is selected from the group consisting of (i) the polynucleotide encoding the E protein truncated at amino acid position 456 of the full-length E protein of the ZIKV of SEQ ID NO: 23, (ii) the polynucleotide encoding the E protein truncated at amino acid position 445 of the full-length E protein of the ZIKV of SEQ ID NO: 23 and (iii) the polynucleotide encoding the E protein truncated at amino acid position 404 of the full-length E protein of the ZIKV of SEQ ID NO: 23.

9. The nucleic acid construct according to any one of claims 1 to 8, wherein the polynucleotide encodes the prM protein of the ZIKV whose sequence is SEQ ID NO: 20, and the polynucleotide encodes the E protein of the ZIKV or the truncated version thereof whose sequence is selected from the group consisting of SEQ ID NO: 23, SEQ ID NO: 26, SEQ ID NO: 29 and SEQ ID NO: 32.

10. The nucleic acid construct according to any one of claims 1 to 9, wherein the polynucleotide encoding the prM protein of the ZIKV has the sequence of SEQ ID NO: 19, and the polynucleotide encoding the E protein of the ZIKV or the truncated version thereof has a sequence selected from the group consisting of SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 28 and SEQ ID NO: 31.

11. The nucleic acid construct according to any one of claims 1 to 10, wherein said nucleic acid construct comprises a sequence selected from the group consisting of SEQ ID NO: 46, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID

NO: 70, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 168 and SEQ ID NO: 170, preferably has the sequence of SEQ ID NO: 46, SEQ ID NO: 55 or SEQ ID NO: 76, more preferably has the sequence of SEQ ID NO: 46.

12. The nucleic acid construct according to any one of claims 1 to 11, which comprises the sequence from nucleotide at position 83 to nucleotide at position 18404 in the sequence of SEQ ID NO: 165, or the sequence from nucleotide at position 83 to nucleotide at position 18074 in the sequence of SEQ ID NO: 166, or the sequence from nucleotide at position 83 to nucleotide at position 17702 in the sequence of SEQ ID NO: 167.

13. A transfer vector plasmid, comprising the nucleic acid construct according to any one of claims 1 to 12.

14. The transfer vector plasmid according to claim 13, whose sequence is SEQ ID NO: 165, SEQ ID NO: 166 or SEQ ID NO: 167, preferably is SEQ ID NO: 165.

15. Transformed cells comprising inserted in their genome the nucleic acid construct according to any one of claims 1 to 12 or comprising the transfer vector plasmid according to claim 13 or 14, wherein said cells are in particular eukaryotic cells, such as avian cells, in particular CEF (Chicken Embryo Fibroblasts) cells, mammalian cells or yeast cells.

16. Recombinant infectious replicating measles virus-Zika virus (MV-ZIKV) particles, which comprise as their genome a nucleic acid construct according to any one of claims 1 to 12.

17. Recombinant infectious replicating MV-ZIKV particles according to claim 16, which are rescued from a helper cell line expressing an RNA polymerase recognized by said cell line, for example a T7 RNA polymerase, a nucleoprotein (N) of a MV, a phosphoprotein (P) of a MV, and optionally an

RNA polymerase large protein (L) of a MV, and which is further transfected with the transfer vector plasmid according to claim 13 or 14.

18. The recombinant infectious replicating MV-ZIKV particles according to claim 16 or 17, wherein said particles comprise in their genome a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO: 46, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 70, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 168 and SEQ ID NO: 170, preferably has the sequence of SEQ ID NO: 46, SEQ ID NO: 55 or SEQ ID NO: 76, more preferably has the sequence of SEQ ID NO: 46.

19. A composition or an assembly of active ingredients comprising both the recombinant infectious replicating MV-ZIKV particles according to any one of claims 16 to 18**,** and ZIKV-Virus Like Particles (VLPs) expressing the same ZIKV protein(s) as said MV-ZIKV particles, and a pharmaceutically acceptable vehicle.

20. The composition or the assembly of active ingredients according to claim 19 for use in the elicitation of a protective immune response against ZIKV by the elicitation of antibodies directed against said ZIKV protein(s), and/or of a cellular immune response, in a host, in particular a human host in need thereof.

21. The recombinant infectious replicating MV-ZIKV particles according to any one of claims 16 to 18 and ZIKV-VLPs expressing the same ZIKV protein(s), or the composition or the assembly of active ingredients according to claim 19, for use in the prevention of an infection by ZIKV in a subject or in the prevention of clinical outcomes of infection by ZIKV in a subject, in particular in a human.

22. A process to rescue recombinant infectious measles virus-Zika virus (MV-ZIKV) particles expressing at least (i) the precursor of membrane (prM)

protein of a ZIKV, and the envelope (E) protein of a ZIKV or a truncated version thereof of SEQ ID NO: 26, SEQ ID NO: 29 or SEQ ID NO: 32, or (ii) the E protein of a ZIKV or the truncated version thereof, and ZIKV Virus Like Particles (VLPs) expressing the same ZIKV protein(s), comprising:

1) co-transfecting helper cells, in particular HEK293 helper cells, that stably express T7 RNA polymerase, and measles N and P proteins with (i) the transfer vector plasmid according to claim 13 or 14 and with (ii) a vector, especially a plasmid, encoding the MV L polymerase;

2) cultivating said co-transfected helper cells in conditions enabling the production of recombinant MV-ZIKV particles;

3) propagating the thus produced recombinant MV-ZIKV particles by co-cultivating said helper cells of step 2) with cells enabling said propagation such as Vero cells;

4) recovering recombinant infectious replicating MV-ZIKV particles expressing at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, and ZIKV VLPs expressing the same ZIKV protein(s).

23. The process according to claim 22, wherein the transfer vector plasmid has the sequence of SEQ ID NO: 165, SEQ ID NO: 166 or SEQ ID NO: 167, preferably has the sequence of SEQ ID NO: 165.