#### **DECLARATION**

I hereby declare that "Molecular Epidemiology of Group A Rotaviruses (RVA) in Children of the State of Imphal, Manipur, India" has been submitted to Tezpur University in the Department of Molecular Biology and Biotechnology under the School of Sciences for partial fulfilment for the award of the degree of Doctor of Philosophy in Molecular Biology and Biotechnology. This is an original work carried out by me. Further, I declare that no part of this work has been reproduced elsewhere for award of any degree.

Date:

2/8/2023

Place: Tezpur University, Tezpur

(Yengkhom Damayanti Devi)

Registration no. TZ189793 of 2018

# DEPARTMENT OF MOLECULAR BIOLOGY AND BIOTECHNOLOGY



(DBT, DST-FIST, UGC-SAP DRS-II SUPPORTED)

तेजपुरविश्वविद्यालय/ TEZPUR UNIVERSITY (संसदकेअधिनियमद्वारास्थापितकेंद्रीयविश्वविद्यालय) (A Central University established by an Act of Parliament) तेजपुर-784028 :: असम/ TEZPUR-784028 :: ASSAM

(सर्वोत्तमविश्वविद्यालयकेलिएकुलाध्यक्षपुरस्कार,2016 औरभारतके 100श्रेष्ठउच्चशिक्षणसंस्थानोंमेंपंचमस्थानप्राप्तविश्वविद्यालय) (Awardee of Visitor's Best University Award, 2016 and 5<sup>th</sup> among India's Top 100 Universities, MHRD-NIRF Ranking, 2016)

## CERTIFICATE OF THE SUPERVISOR

This is to certify that the thesis entitled "Molecular epidemiology of group A rotaviruses in children of the State of Imphal, Manipur, India" submitted to the School of Sciences, Tezpur University in partial fulfillment for the award of the degree of Doctor of Philosophy in Molecular Biology and Biotechnology is a record of research work carried out by Ms. Yengkhom Damayanti Devi under my supervision and guidance.

All help received by her from various sources have been duly acknowledged. No part of this thesis has been submitted elsewhere for award of any other degree.

Date: 09 08222

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LIST OF FIGURES		
Figure No.	Figure title	Page No.
Figure 2.1	Rotavirus genome and structure organization: (A) Migration pattern on on polyacrylamide gel stained with silver nitrate showing the separation of 11 dsRNA segments of group A rotavirus (RVA) genome. The gene segments are numbered on the left and the corresponding encoded proteins are indicated on the right, (B) Electron microscopy image of the rotavirus triple- layered particle (TLP) (Crawford et al. 2017) and (C) Diagrammatic representation of RV structure and its organization.	10
Figure 2.2	Life cycle of rotavirus: RVs attach to glycan receptors and co- receptors on the host cell surface, through interaction VP8* domain of VP4. Initial attachment of some animal strains of RV involves sialic acid receptors (SA sensitive RVs) while human RV strains like Wa and DS-1, often attach to and enter cells in a sialic acid-independent manner (SA insensitive RVs) (Yang Liu 2012) where they interact with potential host receptors like histo blood group antigens (HBGA) (Hu et al., 2012; Huang et al., 2012; Ramani et al., 2013). Cell entry starts with RVs interaction with co-receptors, cellular surface molecules, such as heat shock protein (Hsc70), gangliosides (Martínez, M. A., 2013) and integrins (Graham et al.,2003; Zárate et al., 2004; Gutiérrez et al., 2010, Hussain 2015). Depending on the strain, RVs are internalized into cells by clathrin-dependent or clathrin- independent and caveolin-independent endocytic pathways (Arias CF 2015, Diaz-Salinas MA 2013). Gradient in calcium levels triggers the removal of the outer capsid layer (VP7 and VP4), which releases the transcriptionally active double-layered particle (DLP) into the cytoplasm. Viral (+)RNA is used for translation of the viral proteins and also as a template for RNA synthesis during genome replication. The new virions are assembled and RNA is then packaged into new DLPs within the electron dense structures called viroplasms which are mainly composed of NSP2 and NSP5. Triple-layered particles (TLPs) assembly takes place by the coordinated action of NSP4 and VP6. DLPs buds into the endoplasmic reticulum (ER) forming transiently enveloped particle and the outer capsid proteins VP4 and VP7 are added onto the DLPs. The envelope is lost when RV particles acquire the outer layer consisting of VP4 and VP7 (Estes and Greenberg, 2013). Virions are then released from the cells through cell lysis or Golgi-independent non-classical	16-17

	vesicular transport mechanism in polarized epithelial cells.	
Figure 3.1	Schematic flowchart showing G-P typing of rotavirus positive stool specimens.	55
Figure 3.2	Schematic flowchart showing enrolment criteria for collection of stool specimens from RIMS, Imphal, Manipur.	57
Figure 3.3	Bar graph showing seasonal distribution of rotaviral gastroenteritis from December 2015-March 2019.	63
Figure 3.4	Rotavirus infection trends among hospitalized children <5 years from Imphal, Manipur, India visited RIMS, Imphal during December 2015 to March 2019.	64
Figure 3.5	Amplification of the VP7 and VP4 genes by RT-PCR followed by G and P genotyping. A.i. Amplification products corresponding to VP7 (881bp), A.ii. Amplification products corresponding to VP4 (867bp), B.i. G genotyping by semi-nested multiplex PCR, and B.ii. P genotyping by semi-nested multiplex PCR. lane 1 in all the gel images are DNA ladder (Thermo Scientific-SM0333, SM1163 & SM1333).	67-68
Figure 3.6	Frequency of rotavirus G and P genotype distribution isolated from stool specimens positive for rotavirus from children <5 years hospitalized for acute watery diarrhoea (AWD) during December 2015 – March 2019. A.i. Distribution of rotavirus G types strains in the region, A.ii. Distribution of rotavirus mix G type strains, B.i. Distribution of rotavirus P types in the region, and B.ii. Distribution of rotavirus mix P type strains.	70
Figure 3.7	Frequency of rotavirus G and P genotype distribution isolated from stool specimens positive for rotavirus from children <5 years hospitalized for acute watery diarrhoea (AWD) during December 2015 – March 2019. A.i. Distribution of rotavirus G types strains in the region, A.ii. Distribution of rotavirus mix G type strains, B.i. Distribution of rotavirus P types in the region, and B.ii. Distribution of rotavirus mix P type strains.	71
Figure 3.8	Year-wise distribution of rotavirus genotypes in $< 5$ years children admitted with acute gastroenteritis, December 2015 – March 2019.	73
Figure 3.9	Phylogenetic tree based on the VP7 nucleotide sequence of human rotavirus A strains. The evolutionary history was inferred by using the Maximum Likelihood method and General Time Reversible model. The bootstrap consensus tree inferred from 1000 replicates were taken to represent the evolutionary history of the taxa analyzed. The percentage of trees in which the associated taxa clustered together is shown next to the branches. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA X. The strains	74-76

	in this study are shown in red triangles, the vaccine strains in	
	green triangles and genotypes on the right side. A. G1 strains, B.	
	G2 strains, C. G3 strains and D. G9 strains.	
	Phylogenetic tree based on the VP4 and VP6 nucleotide	
	sequence of human rotavirus A strains. The evolutionary history	
	was inferred by using the Maximum Likelihood method and	
	General Time Reversible model. The bootstrap consensus tree	
	inferred from 1000 replicates were taken to represent the	
Figure 3.10	evolutionary history of the taxa analyzed. The percentage of	77-78
	trees in which the associated taxa clustered together is shown	
	next to the branches. All positions containing gaps and missing	
	data were eliminated. Evolutionary analyses were conducted in	
	MEGA X. The strains in this study are shown in red triangles,	
	the vaccine strains in green triangles and genotypes on the right	
	side. A. P[6] strains, B. P[8] strains and C. VP6.	
	A representative photograph showing the detection of rotavirus,	
	adenovirus, astrovirus and norovirus using CerTest Combo card	
	test (CerTestBiotec). Top green line represents control line and	
Figure 3.11	bottom red line indicates presence of the virus under test. (b) Bar	80
	graph showing no. of hospitalized individuals infected with	
	rotavirus and co-infection of rotavirus with other three viruses	
	Adenovirus, Astrovirus and Norovirus.	
5 0 10	Seasonal prevalence of rotavirus and other common enteric virus	0.1
Figure 3.12	(Adenovirus, astrovirus and norovirus) gastroenteritis from	81
	December 2015-March 2019.	
	Detection of rotavirus, adenovirus, astrovirus and norovirus. A.	
	Detection of other enteric viruses by Rota+Adeno+Astro+Noro	
	EIA Combo Card (Cat No. RG862001V) where the green line	
Figure 3.13	shows control line and red line shows test line; Agarose gel	82-83
8	image for B. adenovirus fibre partial gene (540 bp), C. norovirus	
	genogroup II capsid gene, and D. astrovirus capsid gene PCR	
	product (449 bp). lane 1 in all the gel images are DNA ladder	
	(Thermo Scientific-SM0333 & Axygen® M-DNA-100BP).	
Figure 3.14	Phylogenetic tree based on the Adenovirus fiber gene sequence.	
	The evolutionary history was inferred by using the Maximum	
	Likelihood method and General Time Reversible model. The	
	bootstrap consensus tree inferred from 1000 replicates were	
	taken to represent the evolutionary history of the taxa analyzed.	84
	The percentage of trees in which the associated taxa clustered	
	together is shown next to the branches. All positions containing	
	gaps and missing data were eliminated. Evolutionary analyses	
	were conducted in MEGA X.	
Figure 4.1	Mutation effect analysis of three amino acid substitutions by	106

	PROVEAN tool. A. Mutation sites, B. Superimpostion image of VP7 protein modelled structure of Rotavac strain and circulating G9 strain. Inset table is mutation effect analysis result; postion 87 where it changes from Isoleucine (I) to Threonine (T), position 100 Ghycine (G) substituted by Aspartate (D) and postion 145 where it changes from Asparagine (N) to Asparatate (D).	
Figure 4.2	Schematic diagram of interactions between VP7 protein of Rotavac strain and Fab region of IgG and interacting residues. Interacting chains (A; VP7, H; Heavy chain, L; Light chain) are joined by coloured lines, each representing a different type of interaction, as per the key above. The area of each circle is proportional to the surface area of the corresponding protein chain. The extent of the interface region on each chain is represented by a coloured wedge whose colour corresponds to the colour of the other chain and whose size signifies the interface surface area. Statistics for all the interfaces are given as inset table. B. Residue interactions across interface Coloured by residue type. The number of H-bond lines between any two residues indicates the number of potential hydrogen bonds between them. For non-bonded contacts, which can be plentiful, the width of the striped line is proportional to the number of atomic contacts.	107
Figure 4.3	Schematic diagram of interactions between VP7 protein of circulating G9 strain and Fab region of IgG and interacting residues. Interacting chains (A; VP7, H; Heavy chain, L; Light chain) are joined by coloured lines, each representing a different type of interaction, as per the key above. The area of each circle is proportional to the surface area of the corresponding protein chain. The extent of the interface region on each chain is represented by a coloured wedge whose colour corresponds to the colour of the other chain and whose size signifies the interface surface area. Statistics for all the interfaces are given as inset table. B. Residue interactions across interface Coloured by residue type. The number of H-bond lines between any two residues indicates the number of potential hydrogen bonds between them. For non-bonded contacts, which can be plentiful, the width of the striped line is proportional to the number of atomic contacts.	108
Figure 5.1	Laboratory stretagy to identify unusual and untypable rotavirus strains.	121
Figure 5.2	Workflow for preparation of samples for WGS by Illumina.	122
Figure 5.3	Workflow for analysis of raw sequence reads from Illumina	125

Characterization   of   dsRNA   by   RNA-PAGE   A.     Figure 5.4   Electropherotypic of 11 segments of RV dsRNA for Group A rotaviruses, B. Electropherotypic of 11 segments of RV dsRNA for Group B rotaviruses, B. Electropherotypic of 11 segments of RV dsRNA for Group B rotaviruses, B. Electropherotypic of 11 segments of RV dsRNA for Group B rotavirus, Betection of Group B and C rotaviruses in VP6-ELISA negative specimens by PCR. Inset table; Primer for Group B rotavirus genes (VP7, VP4 and NSP2) and Group C rotavirus genes (VP7, VP6 and VP4).   129     Figure 5.5   A. Patient clinical details of rotavirus isolate RM251122016 dsRNA qualified for WGS. B. Analysis of RVA RM251122016 dsRNA by RNA-PAGE.   130     Figure 5.7   Circos plot of Rotavirus Whole Genome data of RM251122016. Outermost circle represents contigs with their corresponding length in base pair and identified genes. From outer to innermost circles depict GC percentage, query coverage, identity, no. of mapped reads and coverage(X) respectively. Values for each of the features are plotted as ranges from red (high values) to blue (lower values).   131     Phylogenetic analysis of 11 sene segments of rotavirus isolate Figure 5.8   Schematic representation of an in-silico strategy followed for prediction of S elected linear B-cell epitope in native rotavirus protein. A.VP2; 189-AVENKNSRDAGK-200, B. VP3; 238-TIKLKQERWLGK-249, C. VP4; 208-IPRSEESKCTEYI-220, D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262-WKEMQYNRDI-271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDRIVEG-21, H. VP6; 139-WNLQNRQRTG-149, I.VP6; 373-NYSPSREDNLQR-384, J.   168     Figure 6.2   VP7; 308-QVMSKRSRSLNAA- 320, K. NSP2; 267-QNW		Novaseq 6000.	
Figure 5.4   rotaviruses, B. Electropherotypic of 11 segments of RV dsRNA for Group B rotaviruses.   128     Figure 5.5   Detection of Group B and C rotaviruses in VP6-ELISA negative specimens by PCR. Inset table; Primer for Group B rotavirus genes (VP7, VP4 and NSP2) and Group C rotavirus genes (VP7, VP6 and VP4).   129     Figure 5.6   A. Patient clinical details of rotavirus isolate RM251122016 qualified for WGS. B. Analysis of RVA RM251122016 dsRNA by RNA-PAGE.   130     Figure 5.7   Circos plot of Rotavirus Whole Genome data of RM251122016. Outermost circle represents contigs with their corresponding length in base pair and identified genes. From outer to innermost circles depict GC percentage, query coverage, identity, no. of mapped reads and coverage(X) respectively. Values for each of the features are plotted as ranges from red (high values) to blue (lower values).   131     Figure 5.8   RM251122016. A. VP7, B.VP4, C.VP6, D.VP1, E.VP2, F.VP3, G.NSP1, H. NSP2, I. NSP3, J. NSP4 and K. NSP5.   136-142     Figure 6.1   Schematic representation of an in-silico strategy followed for prediction of selected linear B-cell epitope in native rotavirus protein. A.VP2; 189-AVENKNSRDAGK-200, B. VP3; 238-TIKLKQERWLGK-249, C. VP4; 208-IPRSEESKCTEY1-220, D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262-WKEMQYNRD1-271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139-WNLQNRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J. VP7; 308-QVMSKRSRLNSA- 320, K. NSP2; 267-QNWYAFTSSMKQGNT-281, L. NSP3; 108-LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK-128, N.NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group D); 93-EAVCDDEIVREA-104, R. VP6 (Group C); 93-EAVCDDEIVREA-104, R. VP		5	
Figure 5.5specimens by PCR. Inset table; Primer for Group B rotavirus genes (VP7, VP4 and NSP2) and Group C rotavirus genes (VP7, VP6 and VP4).129Figure 5.6A. Patient clinical details of rotavirus isolate RM251122016 qualified for WGS. B. Analysis of RVA RM251122016 dsRNA by RNA-PAGE.130Figure 5.7Circos plot of Rotavirus Whole Genome data of RM251122016. Outermost circle represents contigs with their corresponding length in base pair and identified genes. From outer to innermost circles depict GC percentage, query coverage, identity, no. of mapped reads and coverage(X) respectively. Values for each of the features are plotted as ranges from red (high values) to blue (lower values).131Phylogenetic analysis of 11 sene segments of rotavirus isolate Figure 5.8RM251122016. A. VP7, B. VP4, C.VP6, D.VP1, E.VP2, F.VP3, G. NSP1, H. NSP2, I. NSP3, J. NSP4 and K. NSP5.136-142Figure 6.1Schematic representation of an in-silico strategy followed for prediction of B- and T-cell epitope using proteome of rotavirus protein. A. VP2; 189-AVENKNSRDAGK-200, B. VP3; 238- TIKLKQERWLGK-249, C. VP4; 208-IPRSEESKCTEY1-220, D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262- WKEMQYNRDI- 271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139- WNLQNRRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J.168GNWYAFTSSMKQGNT-281, L. NSP3; 108- LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK- 128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group D); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 93- EAVCDDEIVREA-104	Figure 5.4	rotaviruses, B. Electropherotypic of 11 segments of RV dsRNA	128
Figure 5.5   genes (VP7, VP4 and NSP2) and Group C rotavirus genes (VP7, VP6 and VP4).   129     A. Patient clinical details of rotavirus isolate RM251122016   qualified for WGS. B. Analysis of RVA RM251122016 dsRNA by RNA-PAGE.   130     Figure 5.6   Circos plot of Rotavirus Whole Genome data of RM251122016. Outermost circle represents contigs with their corresponding length in base pair and identified genes. From outer to innermost circles depict GC percentage, query coverage, identity, no. of mapped reads and coverage(X) respectively. Values for each of the features are plotted as ranges from red (high values) to blue (lower values).   131     Phylogenetic analysis of 11 sene segments of rotavirus isolate   Figure 5.8   RM251122016. A. VP7, B.VP4, C.VP6, D.VP1, E.VP2, F.VP3, 136-142     G. NSP1, H. NSP2, I. NSP3, J. NSP4 and K. NSP5.   136-142     Figure 6.1   Schematic representation of an in-silico strategy followed for prediction of B- and T-cell epitope using proteome of rotavirus protein. A.VP2, 189-AVENKNRDAGK-200, B. VP3; 238-TIKLKQERWLGK-249, C. VP4; 208-IPRSEESKCTEX1-220, D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262-WKEMQYNRDI- 271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139-WNLQNRRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J.   168     GNWYAFTSSMKQGNT-281, L. NSP3; 108-LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK-128, N.NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197-GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93-EAVCDDEIVREA-104, R. VP6 (G			
genes (VP,, VP4 and NSP2) and Group C rotavirus genes (VP7, VP6 and VP4).     A. Patient clinical details of rotavirus isolate RM251122016     Figure 5.6   qualified for WGS. B. Analysis of RVA RM251122016 dsRNA     by RNA-PAGE.   130     Eigure 5.7   Circos plot of Rotavirus Whole Genome data of RM251122016.     Outermost circle represents contigs with their corresponding length in base pair and identified genes. From outer to innermost circles depict GC percentage, query coverage, identity, no. of the features are plotted as ranges from red (high values) to blue (lower values).     Phylogenetic analysis of 11 sene segments of rotavirus isolate RM251122016. A. VP7, B.VP4, C.VP6, D.VP1, E.VP2, F.VP3, G.NSP1, H. NSP2, I. NSP3, J. NSP4 and K. NSP5.     Figure 6.1   Schematic representation of an in-silico strategy followed for prediction of B- and T-cell epitope using proteome of rotavirus protein. A.VP2; 189-AVENKNSRDAGK-200, B. VP3; 238-TIKLKQERWLGK-249, C. VP4; 208-IPRSEESKCTEY1-220, D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262-WKEMQYNRDI- 271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139-WNLQNRRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J. VP7; 308-QVMSKRSRSLNSA- 320, K. NSP2; 267-QNWYAFTSSMKQGNT-281, L. NSP3; 108-LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK-128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197-GMDSEHRFTVELKTR-211, Q. VP6 (Group B); 197-GMDSEHRFTVELKTR-211, Q. VP6 (Group B); 197-GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93-EAVCDDEIVREA-104, R. VP6 (Group	Figure 5.5		129
Figure 5.6 by RNA-PAGE.130Circos plot of Rotavirus Whole Genome data of RM251122016 Outermost circle represents contigs with their corresponding length in base pair and identified genes. From outer to innermost rapped reads and coverage(X) respectively. Values for each of the features are plotted as ranges from red (high values) to blue (lower values).131Figure 5.8RM251122016. A. VP7, B.VP4, C.VP6, D.VP1, E.VP2, F.VP3, G.NSP1, H. NSP2, I. NSP3, J. NSP4 and K. NSP5.136-142Figure 6.1Schematic representation of an in-silico strategy followed for prediction of B- and T-cell epitope using proteome of rotavirus protein. A.VP2; 189-AVENKNSRDAGK-200, B. VP3; 238- TIKLKQERWLGK-249, C. VP4; 208-IPRSEESKCTEYI-220, D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262- WKEMQYNRDI- 271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139- WNLQNRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J.168Figure 6.2VP7; 308-QVMSKRSRSLNSA- 320, K. NSP2; 267- QNWYAFTSSMKQGNT-281, L. NSP3; 108- LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK- 128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156.169	C		
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Figure 5.7length in base pair and identified genes. From outer to innermost circles depict GC percentage, query coverage, identity, no. of mapped reads and coverage(X) respectively. Values for each of the features are plotted as ranges from red (high values) to blue (lower values).131Phylogenetic analysis of 11 sene segments of rotavirus isolate RM251122016. A. VP7, B.VP4, C.VP6, D.VP1, E.VP2, F.VP3, G. NSP1, H. NSP2, I. NSP3, J. NSP4 and K. NSP5.136-142G.NSP1, H. NSP2, I. NSP3, J. NSP4 and K. NSP5.Figure 6.1Schematic representation of an in-silico strategy followed for prediction of B- and T-cell epitope using proteome of rotavirus.Localization of selected linear B-cell epitope in native rotavirus protein. A.VP2; 189-AVENKNSRDAGK-200, B. VP3; 238- TIKLKQERWLGK-249, C. VP4; 208-IPRSEESKCTEYI-220, D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262- WKEMQYNRDI- 271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139- WNLQNRRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J.Figure 6.2VP7; 308-QVMSKRSRSLNSA- 320, K. NSP2; 267- QNWYAFTSSMKQGNT-281, L. NSP3; 108- LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK- 128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156.Structure modeling of rotavirus proteins using I-TASSER. A. Figure 6.3YP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.			
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Figure 5.8RM251122016. A. VP7, B.VP4, C.VP6, D.VP1, E.VP2, F.VP3, G. NSP1, H. NSP2, I. NSP3, J. NSP4 and K. NSP5.136-142Figure 6.1Schematic representation of an in-silico strategy followed for prediction of B- and T-cell epitope using proteome of rotavirus.158Localization of selected linear B-cell epitope in native rotavirus protein. A.VP2; 189-AVENKNSRDAGK-200, B. VP3; 238- TIKLKQERWLGK-249, C. VP4; 208-IPRSEESKCTEYI-220, D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262- WKEMQYNRDI- 271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139- WNLQNRRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J.Figure 6.2VP7; 308-QVMSKRSRSLNSA- 320, K. NSP2; 267- QNWYAFTSSMKQGNT-281, L. NSP3; 108- LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK- 128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group D); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 943- SRRENPVYEYKNPM-156.Figure 6.3Structure modeling of rotavirus proteins using I-TASSER. A. VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.			
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Prediction of B- and 1-cell epitope using proteome of rotavirus.Localization of selected linear B-cell epitope in native rotavirus protein. A.VP2; 189-AVENKNSRDAGK-200, B. VP3; 238- TIKLKQERWLGK-249, C. VP4; 208-IPRSEESKCTEYI-220, D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262- WKEMQYNRDI- 271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139- WNLQNRRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J.Figure 6.2VP7; 308-QVMSKRSRSLNSA- 320, K. NSP2; 267- 168 QNWYAFTSSMKQGNT-281, L. NSP3; 108- LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK- 128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156.Figure 6.3VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.			150
protein. A.VP2; 189-AVENKNSRDAGK-200, B. VP3; 238- TIKLKQERWLGK-249, C. VP4; 208-IPRSEESKCTEYI-220, D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262- WKEMQYNRDI- 271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139- WNLQNRRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J. Figure 6.2 VP7; 308-QVMSKRSRSLNSA- 320, K. NSP2; 267- QNWYAFTSSMKQGNT-281, L. NSP3; 108- LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK- 128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156. Figure 6.3 Structure modeling of rotavirus proteins using I-TASSER. A. VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.	Figure 0.1	prediction of B- and T-cell epitope using proteome of rotavirus.	138
TIKLKQERWLGK-249, C. VP4; 208-IPRSEESKCTEYI-220, D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262- WKEMQYNRDI- 271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139- WNLQNRRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J.Figure 6.2VP7; 308-QVMSKRSRSLNSA- 320, K. NSP2; 267- QNWYAFTSSMKQGNT-281, L. NSP3; 108- LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK- 128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156.Figure 6.3Structure modeling of rotavirus proteins using I-TASSER. A. VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.		Localization of selected linear B-cell epitope in native rotavirus	
D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262- WKEMQYNRDI- 271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139- WNLQNRRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J. VP7; 308-QVMSKRSRSLNSA- 320, K. NSP2; 267- 168 QNWYAFTSSMKQGNT-281, L. NSP3; 108- LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK- 128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156. Figure 6.3 VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.		protein. A.VP2; 189-AVENKNSRDAGK-200, B. VP3; 238-	
WKEMQYNRDI- 271, F. VP4; 657-PDIVTEASEKF-667, G. VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139- WNLQNRRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J.Figure 6.2VP7; 308-QVMSKRSRSLNSA- 320, K. NSP2; 267- QNWYAFTSSMKQGNT-281, L. NSP3; 108- LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK- 128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156.Figure 6.3Structure modeling of rotavirus proteins using I-TASSER. A. VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.		TIKLKQERWLGK-249, C. VP4; 208-IPRSEESKCTEYI-220,	
VP6;   9-KTLKDARDKIVEG-21,   H.   VP6;   139-     WNLQNRRQRTG-149, I. VP6;   373-NYSPSREDNLQR-384, J.   168     VP7;   308-QVMSKRSRSLNSA-   320,   K.   NSP2;   267-     QNWYAFTSSMKQGNT-281,   L.   NSP3;   108-     LSSKGIDQKMRVL-120,   M.   NSP4;   117-TTREIEQVELLK-     128,   N.   NSP5;   170-KCKNCKYKKKYFAL-183,   O.   VP6 (Group     A);   74-ISTDDYDDMRSGI-86,   P.   VP6 (Group B);   197-     GMDSEHRFTVELKTR-211,   Q.   VP6 (Group C);   93-     EAVCDDEIVREA-104,   R.   VP6 (Group C);   143-     SRRENPVYEYKNPM-156.   Structure modeling of rotavirus proteins using I-TASSER.   A.     Figure 6.3   VP2, B.   VP3, C.   VP4, D.   VP7, E.   NSP1, F.   NSP4 and   169     H.   NSP5.   I		D. VP4; 241-RDVIHYRAQANED-253, E. VP4; 262-	
Figure 6.2WNLQNRRQRTG-149, I. VP6; 373-NYSPSREDNLQR-384, J. VP7; 308-QVMSKRSRSLNSA- 320, K. NSP2; 267- QNWYAFTSSMKQGNT-281, L. NSP3; 108- LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK- 128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156.Structure modeling of rotavirus proteins using I-TASSER. A.Figure 6.3VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.169		WKEMQYNRDI- 271, F. VP4; 657-PDIVTEASEKF-667, G.	
Figure 6.2VP7; 308-QVMSKRSRSLNSA- 320, K. NSP2; 267- QNWYAFTSSMKQGNT-281, L. NSP3; 108- LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK- 128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156.168Figure 6.3Structure modeling of rotavirus proteins using I-TASSER. A. VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.169		VP6; 9-KTLKDARDKIVEG-21, H. VP6; 139-	
QNWYAFTSSMKQGNT-281,L.NSP3;108-LSSKGIDQKMRVL-120,M.NSP4;117-TTREIEQVELLK-128,N.NSP5;170-KCKNCKYKKKYFAL-183,O.VP6 (GroupA);74-ISTDDYDDMRSGI-86,P.VP6 (Group B);197-GMDSEHRFTVELKTR-211,Q.VP6 (Group C);93-EAVCDDEIVREA-104,R.VP6 (Group C);143-SRRENPVYEYKNPM-156.Structure modeling of rotavirus proteins using I-TASSER.A.Figure 6.3VP2, B.VP3, C.VP4, D.VP7, E.NSP1, F.NSP4 and H.169			
LSSKGIDQKMRVL-120, M. NSP4; 117-TTREIEQVELLK- 128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156. Figure 6.3 Structure modeling of rotavirus proteins using I-TASSER. A. VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.	Figure 6.2		168
128, N. NSP5; 170-KCKNCKYKKKYFAL-183, O. VP6 (Group A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156.Figure 6.3Structure modeling of rotavirus proteins using I-TASSER. A. VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.			
A); 74-ISTDDYDDMRSGI-86, P. VP6 (Group B); 197- GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156. Figure 6.3 Structure modeling of rotavirus proteins using I-TASSER. A. VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.			
GMDSEHRFTVELKTR-211, Q. VP6 (Group C); 93- EAVCDDEIVREA-104, R. VP6 (Group C); 143- SRRENPVYEYKNPM-156.Figure 6.3Structure modeling of rotavirus proteins using I-TASSER. A. VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.			
EAVCDDEIVREA-104,R.VP6 (Group C);143-SRRENPVYEYKNPM-156.Figure 6.3VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.			
SRRENPVYEYKNPM-156.Figure 6.3Structure modeling of rotavirus proteins using I-TASSER. A. VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.			
Figure 6.3Structure modeling of rotavirus proteins using I-TASSER. A. VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and H. NSP5.169			
Figure 6.3 VP2, B. VP3, C. VP4, D. VP7, E. NSP1, F. NSP3, G. NSP4 and 169 H. NSP5.			
H. NSP5.	Figure 6.3		169
Figure 0.4 [Summary of rotavirus protein-derived B- and I-cell epitopes.] 191	Figure 6.4	Summary of rotavirus protein-derived B- and T-cell epitopes.	191

	Heat mapsho wing the distribution of (A) linear (continuous) B- cell epitopes, (B) HLA-class I and (C) HLA-class II epitopes across the structural and non-structural protein sequences of rotavirus. Strong binding affinity epitopes with <0.5% rank and 2% rank, to HLA class I and class II, respectively, for each HLA molecule are represented here. Red color represents likely antigenic epitopes that were predicted using the methods described in Figure 6.1.	
Figure 6.5	Schematic diagram of multi-epitope chimeric constructs. The multi-epitope constructs sequence consisting adjuvant followed by T- and B-cell epitope. Adjuvant and CTL epitope has been joined by EAAAK linker, whereas the AAY, KK and GGGGS linkers were used to join the CTL, HTL and linear/conformational B-cell epitopes, respectively. A. Construct 1 (VP6A/B/C), B. Construct 2 (VP6/4/7), C. Construct 3 (VP2/3/4/6/7), D. Construct 4 (NSP2/3/4/5) and E. Construct 5 (VP2/3/4/6/7), D. Construct 4 (NSP2/3/4/5) and E. Construct 5 (VP2/3/4/6/7-NSP2/3/4/5), F. Construct 6 (VP6A/B/C–B), G. Construct 7 (VP4/6/7-B), H. Construct 8 (VP4/A), I. Construct 9 (VP6/A) and J. Construct 10 (VP7/A); (BL-Linear B-cell epitope, BC- Conformational B-cell epitope). A/B/C: VP6 sequence of group A, B and C rotaviruses; A: group A rotavirus; B: B-cell epitopes (Both linear and conformational).	201
Figure 6.6	Graphical representation of secondary structure obtained for the multiepitope constructs using PSIPRED server. A. Construct 1, 52.2% helix, 3.0% sheet and 44.8% coil, B. Construct 2, 10.43% helix, 9.71% sheet and 79.86% coil, C. Construct 6, 28.5% helix, 4.0% sheet and 67.5% coil and D. Construct 7, 19.2% helix, 4.8% sheet and 76.0% coil, E. Construct 3, 36.2% helix, 11.0% sheet and 52.8% coil, F. Construct 4, 25.39% helix, 11.92% sheet and 62.69% coil, G. Construct 5, 34.0% Helix, 3.7% Sheet and 62.3% Coil, H. Construct 8, 11.5% helix, 32.7% sheet and 55.8% coil, I. Construct 9, 40.2% helix, 2% sheet and 57.8% coil and J. Construct 10, 59.4% helix, 11.6% sheet and 29% coil.	205-207
Figure 6.7	Tertiary structure modeling of multi-epitope constructs. Cyan color represents CTL epitopes, orange represents HTL epitopes, blue represents linear B- cell epitopes and conformational B-cell epitope is highlighted with green. A. Construct 1; B. Construct 2; C. Construct 3; D. Construct 4; E. Construct 5; F. Construct 6; G. Construct 7; H. Construct 8; I. Construct 9; and J. Construct 10.	208
Figure 6.8	Molecular dynamics simulation study of final multi-epitope constructs representing root mean square deviation. A.	209

	Simulation was carried out for time duration of 20 ns for construct 1, 2, 6 and 7, B. Simulation for construct 5 was performed for the time duration of 40 ns, C. Simulation for 20ns for constructs 3,4,8,9 and 10.	
Figure 6.9	Structure prediction and validation of final multi-epitope constructs. Ramachandran plot analysis of the simulated structures. Summary of residues in favored, allowed and in outlier part is provided in Table 4.	210
Figure 6.10	Surface accessibility of linkers in the final multi-epitope constructs. A. Construct 1; B. Construct 2; C. Construct 3; D. Construct 4; E. Construct 5; F. Construct 6; G. Construct 7; H. Construct 8; I. Construct 9; and J. Construct 10. Blue color represents AAY linker, cyan represents KK linker and GGGGS is represented by red color.	212
Figure 6.11	Conformational B-cell epitopes prediction for the final multi- epitope constructs by Ellipro. A. Construct 1, B. Construct 2, C. Construct 3, D. Construct 4, E. Construct 5, F. Construct 6, G. Construct 7, H. Construct 8, I. Construct 9 and J. Construct 10. The epitopes are represented as colored spheres in the final vaccine model where each color represents one epitope.	213
Figure 6.12	Docked complex of multi-subunit vaccine constructs with integrin receptor. A. Construct1 interaction with $\alpha$ IIb $\beta$ 3 B. Construct 1 with $\alpha$ V $\beta$ 3 C. Construct 2 with $\alpha$ IIb $\beta$ 3 D. Construct 2 with $\alpha$ V $\beta$ 3 E. Construct 6 with $\alpha$ IIb $\beta$ 3 F. Construct 6 with $\alpha$ V $\beta$ 3 G. Construct 7 with $\alpha$ IIb $\beta$ 3 H. Construct 7 with $\alpha$ V $\beta$ 3. Integrin receptor chain A and B has been shown in cyan and silver color, respectively, whereas magenta color represents the multiepitope vaccine constructs in the docked complex.	221
Figure 6.13	Cloning, expression, and affinity purification of four chimeric constructs in E. coli. A) Confirmation of recombinant clones using PCR. Construct 1 (expected gene size 693 bp); Construct 2 (expected gene size 837 bp with 201 bp from vector sequence due to use of T7 forward primer), Construct 6 (expected gene size 603 bp) and Construct 7 (expected gene size 690 bp) were synthesized and cloned into champion pET directional TOPO expression vector (pET100/D-TOPO). C: Negative control without template DNA; M: GeneRuler 1 kb DNA ladder (SM0311, Thermo Scientific). B) pET100/D-TOPO vector map, C) SDS-PAGE analysis showing the expression of recombinant chimeric proteins induced with IPTG (200 µM) at 18°C, 25°C and 37°C induction temperature. Construct 1 (expected size 28.9 kDa including tag); Construct 6 (expected size 28.9 kDa including tag);	226

	Construct 7 (expected size 34 kDa including tag); UI: uninduced	
	E. coli whole cell lysates.	
Figure 6.14	A. Analysis of recombinant protein in soluble and insoluble fractions of bacterial whole cell lysate. SDS-PAGE analysis showing the expressed recombinant chimeric proteins induced with IPTG (200 $\mu$ M) at 25°C in soluble fraction. Construct 1 (expected size 28.9 kDa including tag); Construct 2 (expected size 34 kDa including tag); Construct 6 (expected size 28.9 kDa including tag); Construct 7 (expected size 34 kDa including tag); M: Protein Marker, UI: uninduced E. coli whole cell lysates, SO: Soluble fraction, IN/S: Insoluble Supernatant, IN/P: Insoluble Pellet, B. Purification of soluble protein by Ni-NTA affinity chromatography and confirmation by SDS-PAGE followed by silver staining. Construct 1 (expected size 28.9 kDa including tag); Construct 2 (expected size 34 kDa including tag); Construct 6 (expected size 28.9 kDa including tag); Construct 7 (expected size 34 kDa including tag); M: Protein Marker, FT: Flow Through, W1: First Wash, W2: Second Wash, E1, E2 and E3: First, second and third elute. Inset table: Expected size of construct 1 & 2 and concentration of protein estimated (ng/ $\mu$ l) for 100 $\mu$ l elution, C. Purification of soluble protein by Ni-NTA affinity chromatography and confirmation by SDS-PAGE followed by silver staining. Construct 1 (expected size 28.9 kDa including tag); Construct 2 (expected size 34 kDa including tag); Construct 1 & 2 and concentration of protein estimated (ng/ $\mu$ l) for 100 $\mu$ l elution, C. Purification of soluble protein by Ni-NTA affinity chromatography and confirmation by SDS-PAGE followed by silver staining. Construct 1 (expected size 28.9 kDa including tag); Construct 2 (expected size 34 kDa including tag); Construct 6 (expected size 28.9 kDa including tag); Construct 7 (expected size 34 kDa including tag); M: Protein Marker, FT: Flow Through, W1: First Wash, W2: Second Wash, E1, E2 and E3: First, second and third elute. Inset table: Expected size of construct 6 & 7 and concentration of protein estimated (ng/ $\mu$ l) for 100 $\mu$ l elution.	227-228
Figure 6.15	Silver stained-SDS-PAGE gel electrophoresis showing the purity of multi-epitope antigens. Different concentrations of BSA were loaded to determine the approximate concentration of purified proteins estimated using Bradford assay. M: Prestained protein ladder (Cat. 26616, Thermo Scientific).	229

LIST OF TABLES		
Table No.	Table title	Page No.
Table 2.1	Rotavirus structural and non-structural proteins.	11
Table 2.2a	Vesikari clinical severity scoring system (VSS). VSS was determined to scale the severity of rotavirus induced acute gastroenteritis based on seven clinical parameters recorded at the hospital	25
Table 2.2b	Vesikari Clinical Severity Scoring System Severity Rating Scale	25
Table 3.1	Numbers and proportions of children enrolled, tested for rotavirus and having rotavirus-positive stool specimens, December 2015 – March 2019	61
Table 3.2.	Characteristics of rotavirus-infected and -uninfected children (≤5 years) hospitalized with acute gastroenteritis.	62
Table 3.3	Consensus and G/P typing primers used for the amplification VP7, VP4, VP6, NSP4 and NSP5 genes.	65
Table 3.4	Age wise prevalence of rotavirus in chidren ( $\leq 5$ years) hospitalized with acute gastroenteritis.	69
Table 3.5	Genotype distribution at the surveillance site during the 3 years study period in children $\leq$ 5 years.	72
Table 3.6	Oligonucleotide primers used for PCR amplification of other enteric viruses detected in clinical stool samples; norovirus, adenovirus and astrovirus genes.	82
Table 3.7	Enrolment criteria for collection of stool specimens from RIMS, Imphal, Manipur.	56
Table 4.1	Summary of VP7 and VP4 lineage, date of isolation, and available patient information for rotavirus strains from Imphal analyzed in this study and rotavirus vaccine strains Rotavac, Rotarix and RotaTeq.	98
Table 4.2	The nucleotides and amino acids differences of VP7 and VP4 proteins of Manipur strains with rotavirus vaccine strains. Intragenotype similarities with Rotarix are colored in blue. Intragenotype similarities with RotaTeq are colored in orange. Intragenotype similarities with Rotavac are colored in green.	99
Table 4.3	Alignment of antigenic residues in VP7 between the strains contained in Rotarix, RotaTeq and Rotavac and strains circulating in Imphal. Antigenic residues are divided in three epitopes (7-1a, 7-1b, and 7-2). Amino acids that differ between Rotarix, RotaTeq and Rotavac are indicated in boldface. Red colored residues are residues that are different from Rotarix, and Green colored residues are different from the most similar genotype in RotaTeq. Residues colored in Blue are different	102

from both Rotarix and RotaTeq, Residues colored in Orange are	
different from Rotavac. Amino acid changes that have been	
shown to escape neutralization with monoclonal antibodies	
(Mcdonald SM 2009) are indicated with asteric.	
Alignment of antigenic residues in VP4 (VP8*) between the	
strains contained in Rotarix, RotaTeq and Rotavac and strains	
circulating in Imphal. Antigenic residues are divided in four	
epitopes (8-1, 8-2, 8-3 and 8-4). Amino acids that differ	
between Rotarix and RotaTeq are indicated in boldface. Orange	
Table 4.4   colored residues are residues that are different from Rotarix,	103
and Green colored residues are different from the most similar	
genotype in RotaTeq. Residues colored in Blue are different	
from both Rotarix and RotaTeq. Amino acid changes that have	
been shown to escape neutralization with monoclonal	
antibodies (Mcdonald SM 2009) are indicated with asteric.	
Assembly and genotyping details of the RVA RM251122016	
Table 5.1 Table 5.1 genome.	123
Surveillance of mutations in antigenic region of VP7 between	
Table 5.2 Surveinance of inductions in untigence region of v17 between   RM251122016, strains from VP7 tree and vaccine strain.	126
Surveillance of mutations in antigenic region of VP4 between	
Table 5.3	144
RM251122016, strains from VP4 tree and vaccine strain.	
Table 5.4 Surveillance of mutations in antigenic region of VP6 between   DM251122016 starting from VD7 too or down in a training starting	145
RM251122016, strains from VP7 tree and vaccine strain.	
Surveillance of mutations in antigenic region of VP6 between	146
Table 5.5   RM251122016, RVA sequence in NCBI database and vaccine strain	146
Physico-chemical analysis and prediction of antigenicity of	
Table 6.1 Travirus proteins	164
Summary of linear B-cell epitopes predicted by Bcepred. Four	
physicochemical properties namely, hydrophilicity (Property	
Table 6.21), flexibility (Property 2), polarity (Property 3) and exposed surface (Property 4) were considered for prediction of B-cell	166-167
epitopes. The selected epitopes used for designing multi-	
epitope vaccine constructs are highlighted in bold.	
Summary of predicted conformational B-cell epitopes. Four	
servers were used based on amino acid sequence dependent,	
Table 6.3 CBTOPE (1) and three structure-dependent tools, Ellipro (2),	170-171
Discotope (3) and EPSVR (4). The selected epitopes used for	
designing multi-epitope vaccine constructs are highlighted in	
bold	
Table 6.4aList of HLA class supertype alleles used in this study	173
Table 6.4b   List of HLA class II supertype alleles used in this study	174

-		
	tools were used and servers that predicted the corresponding	
	epitope are numbered as IEDB Proteasomal cleavage/TAP	
	transport/MHC class I combined predictor (1), nHLAPred (2)	
	and RankPep (3). The selected epitopes used for designing	
	multi-epitope vaccine constructs are highlighted in bold	
	Summary of predicted MHC II binding epitopes. Three	
	different tools were used and servers that predicted the	
Table 6.5b	corresponding epitope are numbered as NetMHCpan 3.1 (1),	177-178
10010 0.50	ProPred (2) and RankPep (3). The selected epitopes used for	177 170
	designing multi-epitope vaccine constructs are highlighted in	
	bold	
	Molecular docking of predicted CTL epitopes with MHC I	
Table 6.6a	complexes. The selected epitopes used for designing multi-	180-186
	epitope vaccine constructs are highlighted in bold	
	Molecular docking of predicted HTL epitopes with MHC II	
Table 6.6b	complexes. The selected epitopes used for designing multi-	187-190
	epitope vaccine constructs are highlighted in bold	
-	Rotavirus proteins, total number of epitopes predicted and the	
Table 6.7	immunogenicity/antigenicity/allergenicity as obtained from	192-195
	immune epitope database	
	Predicted B- and T-cell epitopes obtained from the immune	
<b>T</b> 11 C 0	epitope database. The amino acid sequence of selected epitopes	100.000
Table 6.8	used for design of final multi-subunit chimeric antigen	198-200
	constructs	
	Physico-chemical parameter of final multi-epitope constructs.	
<b>T</b> 11 CO	Number of residues, theoretical pI, molecular weight, aliphatic	202
Table 6.9	index, and grand average of hydrophobicity (GRAVY) by	203
	ProtParam	
<u> </u>	Summary of amino acid residues of vaccine constructs in the	
<b>T</b> 11 (10)	energetically favored, allowed and residues in the outlier region	011
Table 6.10	as analyzed by physico-chemical parameter of final multi-	211
	epitope constructs	
<u> </u>	Verification of conformational B-cell epitopes. The epitopes in	
	the final vaccine constructs were superimposed with their	
Table 6.11	native structure by Phymol and Yale alignment server. The	
	corresponding B-cell epitopes or part of the epitope predicted	214-216
	using four servers are numbered as CBTOPE (1), Ellipro (2),	
	Discotope (3) and EPSVR (4).	
	Conformational B-cell epitopes prediction for the final multi-	
Table 6.12	epitope vaccine construct by Ellipro	217-219
Table 6.13	A list of interacting residues of docked multi-subunit vaccine	
	constructs with integrin receptor complex	222
	constructs with integrin receptor complex	

## **ABBREVIATIONS**

RV	Rotavirus
RVA	Group A rotavirus
GE	Gastroenterits
ICTV	International Committee on Taxonomy of Viruses
DLP	Double-layer particle
TLP	Triple-layer particle
dsRNA	Double-stranded RNA
VP	Viral proteins
NSP	Non-structural proteins
WHO	World Health Organization
ROTA	Rotavirus Organization of Technical Allies
NRSN	National Rotavirus Surveillance Network
UIP	Universal Immunization Program
NER	North-eastern states
EM	Electron Microscopy
RdRp	RNA dependent RNA polymerase
LRI	Long Range Interactions
ADRV-N	Novel Adult Diarrhoea Rotavirus
AGMK	African green monkey kidney
HBGA	Histo Blood Group Antigens
EE	Early Endosomes
ME	Maturing Endosomes
ILVs	Intraluminal Vesicles
LEs	Late Endosomes
TCs	Transcription Complexes
LDs	Lipid Droplets
PABP	Poly (A)-Binding Protein

CSF	Cerebrospinal Fluid
AGE	Acute Gastroenteritis
Native-PAGE	Native Polyacrylamide Gel Electrophoresis
E-type	Electropherotypes
NGS	Next Generation Sequencing
BQR	Brequinar
LFM	Leflunomide
DHODH	Dihydroorotate Dehydrogenase
EE	Environmental Enteropathy
OPV	Oral Polio Vaccine
DRC	Democratic Republic of the Congo
EtBr	Ethidium Bromide
MEGA	Molecular Evolutionary Genetics Analysis
NCBI	National Center for Biotechnology Information
RIMS	Regional Institute of Medical Sciences
EIA	Enzyme Immunoassay
ELISA	Enzyme Linked Immuno-sorbent Assay
RT-PCR	Reverse Transcription Polymerase Chain Reaction
PROVEAN	Protein Variation Effect Analyzer
I-TASSER	Iterative Threading ASSEmbly Refinement
RMSD	Root Mean Square Deviation
ViPR	Virus Pathogen Database and Analysis Resource
WGS	Whole genome sequencing
SVR	Support Vector Regression
LINCS	Linear Constant Solver
CTL	Cytotoxic T lymphocytes
HTL	Helper T-cell
RGD	Integrin binding motif
MD	Molecular dynamics
SA11	Simian Agent 11
IEDB	Immune Epitope Database
IS	Intussusception