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Phylogenetic and immunoinformatic analysis of VP4, VP7, and NSP4 genes of rotavirus strains circulating in children with acute gastroenteritis in Indonesia

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Abstract

Rotavirus is a major cause of diarrhea in Indonesian children. However, rotavirus vaccines have not been introduced in the national immunization program of Indonesia. Understanding the genetic diversity and conserved antigenic regions of circulating strains are therefore essential to assess the potential efficacy of rotavirus vaccines. We collected fecal samples from hospitalized children less than 5 years of age with acute diarrhea. Rotavirus genotyping was performed by reverse transcriptase polymerase chain reaction, followed by sequencing of the VP4, VP7, and NSP4 genes of representative strains. Phylogenetic analysis was performed to investigate their relationship with globally circulating strains. Conservational analysis, immunoinformatics, and epitope mapping in comparison to vaccine strains were also performed. The sequence analyses showed that differences of multiple amino acid residues existed between the VP4, VP7, and NSP4 antigenic regions of the vaccine strains and the Indonesian isolates. However, many predicted conserved epitopes with higher antigenicity were observed in the vaccine and Indonesian strains, conferring the importance of these epitopes. The identified epitopes showed a higher potential of rotavirus vaccine to be employed in Indonesia. It could also be helpful to inform the design of a peptide vaccine based on the conserved regions and epitopes in the viral proteins.

KEY WORDS

epitopes, genotyping, Indonesia, phylogenetic analysis, rotavirus

1 | INTRODUCTION

Infectious diseases, such as pneumonia, diarrhea, and malaria, are the leading cause of worldwide morbidity and mortality in children less than 5 years of age.^{1,2} Recent estimates demonstrated that rotavirus is the most frequent cause of severe diarrhea episodes resulting in death among children less than 5 years of age, followed by

Enteropathogenic Escherichia coli and calicivirus.³ It was estimated in 2013 that rotavirus infection caused approximately 215 000 deaths in children less than 5 years of age.⁴

The rotavirus genome consists of 11 double-stranded RNA segments which encode six structural proteins (viral proteins [VPs]) and six nonstructural proteins (NSPs). The outer layer is comprised of two neutralizing antigens, VP7 and VP4 proteins. These two genes are the basis for the binary classification of rotavirus into G- and P-genotype, respectively.⁵ Because these two antigens are encoded

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by two separate RNA segments, they are able to undergo reassortment between different human and/or animal rotavirus strains, creating new G-P genotype combinations and ultimately leading to the generation of rotavirus diversity.⁶ In fact, novel G- and P-genotype combinations, as well as reassortants of human and animal strains, have been continuously reported.⁷⁻¹¹

Indonesia is among the South-East Asian countries with a high burden of rotavirus diarrhea-related deaths.¹² As a member of the Asian Rotavirus Surveillance Network, a national surveillance program was established to monitor the circulation of rotavirus strains in the country.¹³⁻¹⁵ The national surveillance conducted in 2006, and between 2009 and 2015 showed that rotavirus was responsible for approximately 47.5%-52.0% of hospital admissions due to acute diarrhea in children under 5 years of age.^{13,16} Genotyping studies showed that G1P[8], G1P[6] and G2P[4] strains were the most common cause of rotavirus diarrhea in Indonesia,^{13,14} in agreement with findings of worldwide studies.¹⁷ Interestingly, changes of dominant strains circulating in Indonesia were observed by year,¹³ including the predominant of G3P[8] since 2013.¹⁶ These findings support the necessity of continuous surveillance in the country.

Currently, there are two commercially available live-attenuated rotavirus vaccines, Rotarix and RotaTeq, that differ in their antigenic specificity. Rotarix (GlaxoSmithKline Biologicals) is comprised of a monovalent G1P[8] strain, derived from the human rotavirus strain RIX 4414.¹⁸ RotaTeq (Merck) is a human-bovine reassortant vaccine, containing five reassortant strains derived from human (G1, G2, G3, and G4) and bovine WC3 (P[8]) strains.¹⁸ Both vaccines provide effective protection against severe rotavirus diarrhea in many countries.^{19,20} However, some reports indicated a reduced efficacy of rotavirus vaccines in developing, low-income countries in Asia and sub-Saharan Africa.^{21,22} The marked variability of antigenic rotavirus proteins has posed a serious obstacle in the effectiveness of rotavirus vaccines.²³

Although rotavirus detection and genotyping were regularly conducted in Indonesia,^{13,14,16} no further sequence analysis of Indonesian rotavirus strains has been performed. Consequently, the genetic evolution of rotavirus strains over time in Indonesia is unknown. Therefore, the objective of this study is to better understand the genetic variations of rotavirus strains circulating in Indonesia in 2006 and 2009. During the period, mass vaccination against rotavirus was not widely implemented. Rotarix and RotaTeq vaccines have been commercially available in Indonesia since 2011. However, they have not been included yet in Indonesia's National Immunization Program (NIP).¹⁶ Therefore, the diversity of rotavirus genes observed in this study was mostly due to the natural evolution of rotavirus in Indonesian pediatric population.

In the present study, we compared the VP4, VP7, and NSP4 genes of human rotavirus strains circulating in Indonesia with global strains and performed phylogenetic analysis. In addition, the immunoinformatic analysis was performed to investigate the potential antigenic differences between Indonesian and vaccine strains (Rotarix and RotaTeq). Conservational analysis and epitope

mapping were employed to investigate the conserved regions and epitopes among these genes to validate the importance of the vaccines in the Indonesian population.

2 | MATERIALS AND METHODS

2.1 | Sample collection and rotavirus detection

This study was a part of the Indonesian Rotavirus Surveillance study conducted in six teaching hospitals in Indonesia (Muhammad Hussein General Hospital, Palembang; Cipto Mangunkusumo General Hospital, Jakarta; Dr. Sardjito General Hospital, Yogyakarta; Hasan Sadikin General Hospital, Bandung; Sanglah General Hospital, Denpasar, Bali; and Mataram General Hospital, Mataram).^{13,14} Fecal samples were collected from children less than 5 years of age hospitalized due to acute diarrhea in the first 48 hours of admission based on the World Health Organization (WHO).²⁴

Fecal samples were transported to the Department of Microbiology, Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada, Yogyakarta. All fecal samples were then aliquoted and stored at -80°C. The presence of group A rotavirus was detected by enzyme immunoassay (EIA), using IDEIA Rotavirus (DakoCytomation) kit according to the instructions provided by the manufacturer.

For the 2006 surveillance year, there were 2293 stool samples collected and 1245 of them (54.3%) were positive for rotavirus. For the 2009 surveillance year, 959 stool samples were collected and 456 of them (47.5%) were positive for rotavirus.^{13,14}

2.2 | Rotavirus genotyping

Rotavirus RNA was extracted from rotavirus-positive stool samples using the QIAamp RNA stool Minikit (Qiagen) according to the manufacturer instructions. Rotavirus RNA was subsequently analyzed to determine both the VP7 (G-type) and the VP4 (P-type) genotypes using reverse transcriptase polymerase chain reaction (RT-PCR), as previously described.²⁵⁻²⁹ The PCR products were first assigned to G- and P-genotype based on size comparison after electrophoresis on 2% agarose gel and ethidium bromide staining. The results of rotavirus detection and genotyping have been previously published.^{13,14}

2.3 | Sequence analysis, multiple alignments, and phylogenetic analysis

Viral RNA was denatured by boiling at 97°C for 4 minutes and then transferred immediately to the ice for 1 minute. The PCR reaction was conducted with a final volume of 30 μL containing 1.5 μL (20 μM) forward primer; 1.5 μL (20 μM) reverse primer; 1 μL dNTP mix (10 μM each); 5 μL 5X buffer; 1 μL one step RT-PCR enzyme mix (Qiagen); 16 μL nuclease-free water; and 4 μL RNA template. Reverse transcription was performed at 42°C for 30 minutes, 97°C for 15 minutes and followed by 35 cycles of 94°C for 30 seconds; 42°C for 30 seconds and 72°C for 60 seconds. The

PCR product was electrophoresed on 1.2% agarose gel and visualized with ultraviolet light.

The PCR products were purified using the Wizard SV Gel for PCR Clean-Up System (Promega) according to the manufacturer's protocol, and then sequenced using an ABI PRISM BigDye Terminator Cycle Sequencing Reaction Kit (Applied Biosystems, Foster City, CA) in an Applied Biosystems 3730xl DNA Analyzer (Applied Biosystems). Sequencing of VP4, VP7, and NSP4 genes were conducted for selected samples with the particular genotyping result, sampling location, and timing of sample collection. Electropherograms were visually analyzed and contiguous DNA sequences were created utilizing the Sequencher Software program version 5.0.1 (Gene Codes Corp Inc, Ann Arbor, MI) for each gene segment.

We selected 20 strains for sequencing; 2, 4, 5, and 9 strains were G1P[6], G1P[8], G2P[4], and G9P[8], respectively. However, not all three genes of each strain were successfully sequenced. Therefore, in total, we generated 37 sequences in this study, consisted of 16, 18, and 3 sequences of VP4, VP7, and NSP4 genes, respectively (Table S1). All sequences obtained in this study were deposited in the GenBank under the accession numbers JQ837877-JQ837884, JQ837886-JQ837888, and MK814541-MK814567 (Table S1).

The VP4, VP7, and NSP4 gene sequences from different regions of Indonesia were compared for homology with strains from other countries obtained from GenBank. For phylogenetic analysis, all complete and partial sequences from different Indonesian regions were included to be compared with strains derived from other countries. The multiple sequence alignments were performed by using Muscle algorithm in MEGA version X.³⁰ The optimal evolutionary model was selected based upon the Akaike information criterion (corrected) ranking implemented in jModelTest.³¹ Maximum likelihood phylogenetic trees were generated using the selected models of nucleotide substitution: Hasegawa, Kishino and Yano (HKY +G₄) (G1 VP7), HKY+I (G2 VP7), General Time Reversible (GTR +G₄) (G9 VP7, P[4] VP4), GTR+I (P[8] VP4) and Tamura-Nei (TrN +G₄) (NSP4). The robustness of branches was assessed by bootstrap analysis using 1000 pseudoreplicate runs and nodes with values >70% were considered to be strongly supported in the phylogenetic analysis. Nucleotide and amino acid distance matrixes were calculated using the p-distance algorithm in MEGA version 10.³⁰

2.4 | Immunoinformatic analysis

For further comparative analysis of the sequenced genes, vaccine sequences of Rotarix and RotaTeq for the VP4 (Rotarix: JN849113; RotaTeq: GU565044, GU565055, GU565066, GU565077, GU565088), VP7 (Rotarix: JN849114; RotaTeq: GU565057, GU565068, GU565079, GU565090, GU565046) and NSP4 (Rotarix: KX954623).³² The amino acid sequence similarity of the vaccine strains was compared with Indonesian strains generated in this study. The antigenic regions of the Indonesian VP4, VP7, and NSP4 rotavirus proteins were also compared with the vaccine strains.³³⁻³⁵

2.4.1 | Analysis of conserved regions

Conserved regions are known to be the best and most effective drug and immune targets. Conservation analysis was performed among the rotavirus vaccine strains and Indonesian rotavirus VP4, VP7, and NSP4 proteins (complete sequences) to determine the conserved regions comprised of ≥9 amino acid residues.³⁶

2.4.2 | Epitope mapping

For the comparative analysis of the putative antigenic regions of vaccine and Indonesian strains, epitope prediction was performed. The Immune Epitope Database and Analysis Resource³⁷ and ABCpred servers³⁸ were used for the prediction of B cell epitopes. ProPred-I³⁹ and ProPred⁴⁰ were utilized for the prediction of CD4+ (MHC II) and CD8+ (MHC I) T cell epitopes. ProPred-I and ProPred predict 47 types of MHC I and 57 types of MHC II allele-specific binding peptides in a provided protein, respectively. Epitopes that bound to the maximum number of alleles were selected for further analysis. All predicted selected epitopes were further cross-checked for homology with human proteomes by BLASTp⁴¹ to prevent any possibility of autoimmune reactions.

2.5 | Ethical approval

This study has received the ethical clearance from the Ethical Committee of the Faculty of Medicine, Public Health and Nursing, Universitas Gajah Mada, Yogyakarta, Indonesia (KF/FK/519/EC).

3 | RESULTS

3.1 | Phylogenetic analysis of the VP4 gene of P[4] and P[8] Indonesian strains

The VP4 gene of the three Indonesian G1P[8] strains were sequenced along with the VP4 gene of nine Indonesian G9P[8] strains. Phylogenetic analysis revealed the majority of strains formed multiple clusters within the same lineage. The G1P[8] strains and a single G9P[8] strain (RVA/Human-wt/IDN/MT-7346/2006/G9P8) clustered within a sublineage interspersed with Indonesian equine-like G3P[8] strains circulating between 2014 and 2015 and contemporary global strains. Six G9P[8] strains formed multiple clusters within a sublineage comprised of global contemporary strains. A single strain, RVA/Human-wt/IDN/BL-5114/2006/G9P[8], clustered within a separate lineage closely related to the strain RVA/Human-wt/Fin-302/1988/G1P[8] (Figure 1A). The Indonesian strains from this study shared 87.2%-100% nucleotide (nt) and 87.8%-100% amino acid (aa) similarity.

The VP4 gene of four Indonesian G2P[4] strains were sequenced. The two strains from 2009 (RVA/Human-wt/IDN/YK-RVY47/2009/G2P[4] and RVA/Human-wt/IDN/MT-RVM113/2009/G2P[4]) clustered together, closely related to contemporary G2P[4] strains circulating in Australia and Taiwan. The two strains from 2006

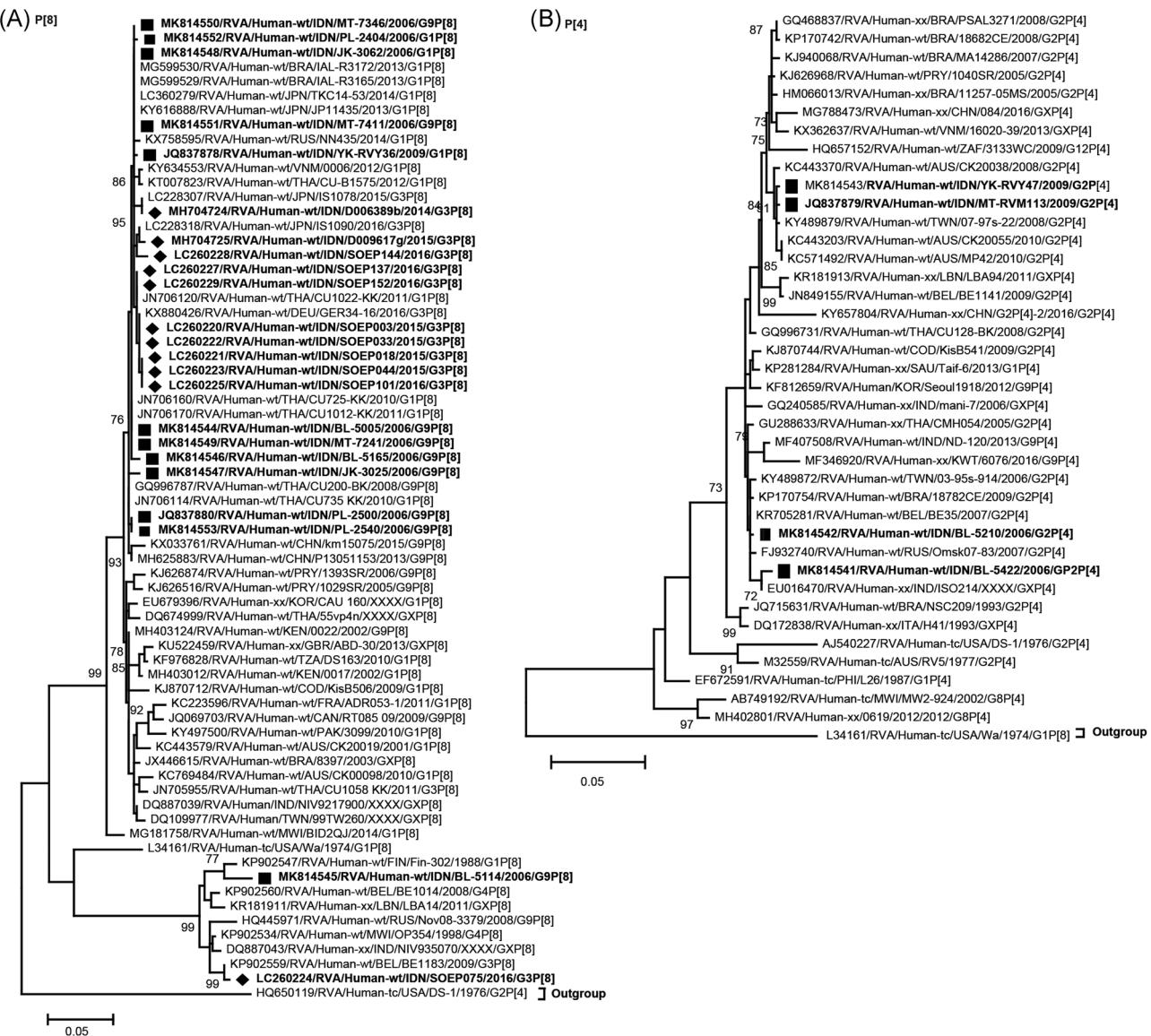


FIGURE 1 Maximum likelihood phylogenetic analysis of the VP4 gene of Indonesian P[8] (A) and P[4] (B) strains. Strains characterized in this study (marked by ■) were analyzed with global isolates obtained from GenBank. Bootstrap values $\geq 70\%$ are shown. Scale bar shows substitutions per nucleotide

(RVA/Human-wt/IDN/BL-5210/2006/G2P[4] and RVA/Human-wt/IDN/BL-5422/2006/GP2P[4]) clustered distinctly to the 2009 strains and were closely related to contemporary strains from Taiwan, Brazil, Belgium, Russia, and India (Figure 1B). The four Indonesian strains shared 97.3%-99.6% nt and 97.9%-100% aa similarity.

3.2 | Phylogenetic analysis of the VP7 gene of G1, G2, and G9 genotypes of Indonesian strains

The VP7 genes of four Indonesian G1P[8] and two Indonesian G1P[6] strains sequenced in this study clustered within the same lineage and were closely related to contemporary strains from Japan, Thailand, and Vietnam (Figure 2A). The six Indonesian strains shared 97.7%-100% nt and 98.4%-100% aa similarity.

The VP7 gene of four Indonesian G2 strains sequenced in this study formed two subclusters. RVA/Human-wt/IDN/BL-5210/2006/G2P[4] and RVA/Human-wt/IDN/YK-RVY47/2009/G2P[4] clustered with contemporary strains from Thailand. RVA/Human-wt/IDN/MT-RVM113/2009/G2P[4] and RVA/Human-wt/IDN/BD-4034/2006/G2P[4] clustered with contemporary strains from Australia, the Philippines, Taiwan, and China (Figure 2B). The four Indonesian strains shared 92.8%-99.9% nt and 95.2%-99.6% aa similarity.

The VP7 gene of eight Indonesian G9P[8] strains sequenced in this study clustered within the same lineage with contemporary strains from Asia and Europe (Figure 2C). The eight Indonesian strains shared 98.0%-100% nt and 98.0%-100% aa similarity.

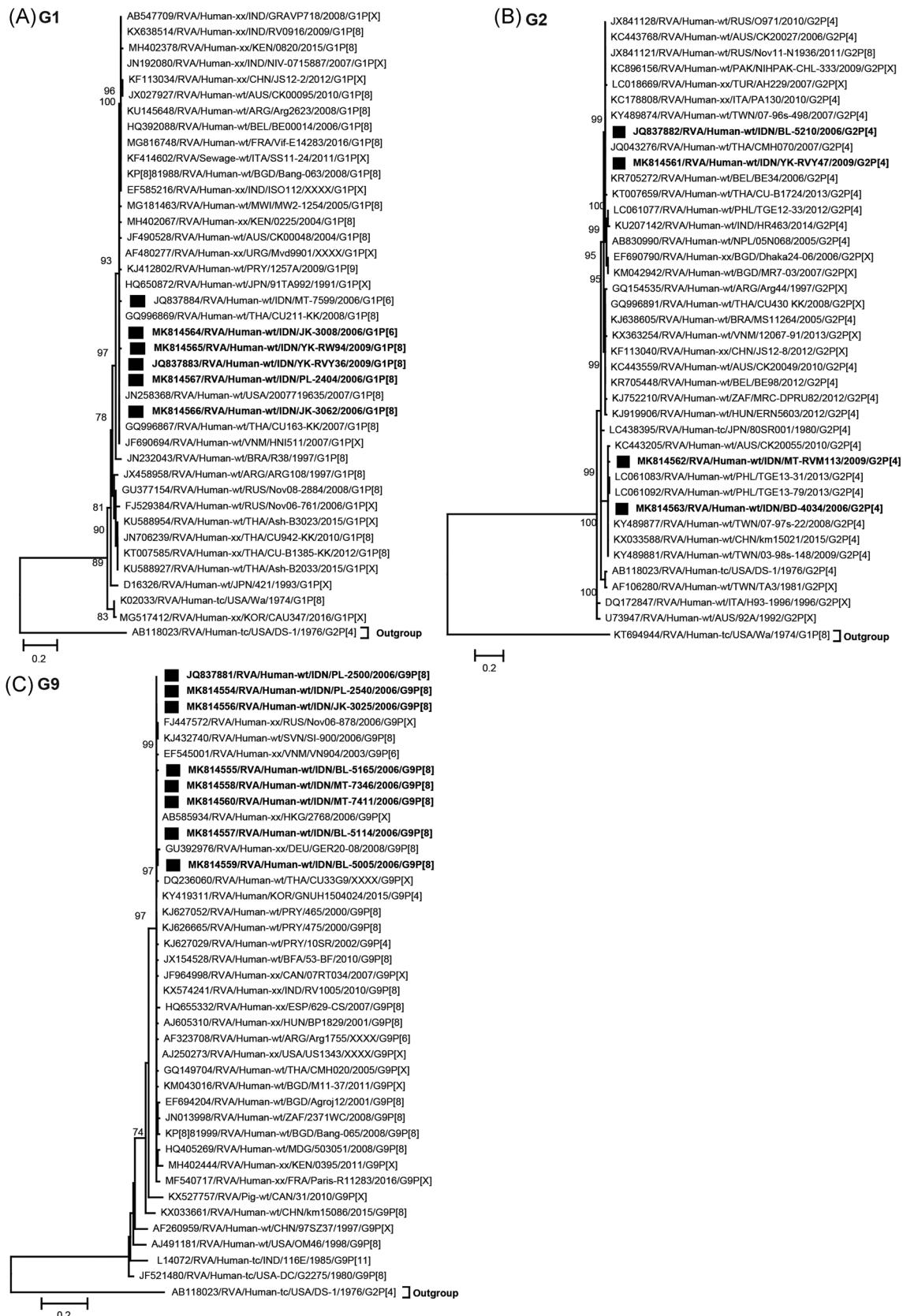


FIGURE 2 Maximum likelihood phylogenetic analysis of the VP7 gene of Indonesian G1 (A); G2 (B); and G9 (C) strains. Strains characterized in this study (marked by ■), and Indonesian strains from the GenBank (marked by ◆) were analyzed with global isolates obtained from GenBank. Bootstrap values ≥70% are shown. Scale bar shows substitutions per nucleotide

3.3 | Phylogenetic analysis of NSP4 genes of Indonesian strains

Three NSP4 genes were sequenced from one G1P[8] strain and two G2P[4] strains (Figure 3). The G1P[8] strain (RVA/Human-wt/IDN/YK-RVY36/2009/G1P[8]) clustered within the E1 lineage closely related to

strains from the USA and India. The two G2P[4] strains (RVA/Human-wt/IDN/MT-RVM113/2009/G2P[4] and JQ837886/RVA/Human-wt/IDN/BL-5210/2006/G2P[4]) clustered within the E2 lineage closely related to strains from India, Korea, and Italy (Figure 3). The two E2 NSP4 genes shared 98.3 nt and 98.7% aa similarity.

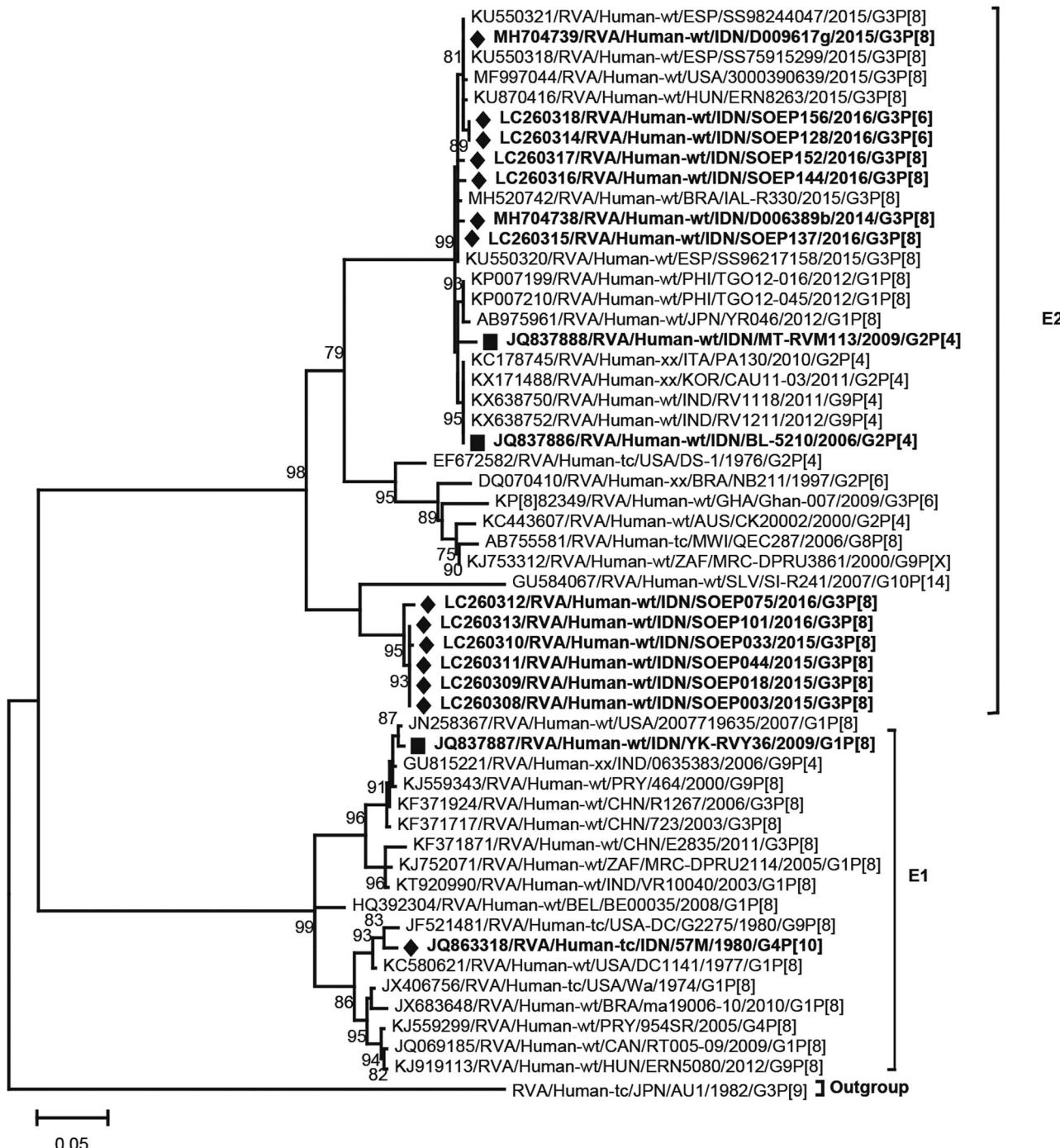


FIGURE 3 Maximum likelihood phylogenetic analysis of the NSP4 gene of Indonesian isolates. Strains characterized in this study (marked by ■), and Indonesian strains from the GenBank (marked by ◆) were analyzed with global isolates obtained from GenBank. Bootstrap values $\geq 70\%$ are shown. Scale bar shows substitutions per nucleotide

3.4 | Comparison of the VP4, VP7, and NSP4 antigenic regions of Indonesian and vaccine strains

The complete sequences of VP4, VP7, and NSP4 genes were obtained to compare the antigenic regions within these VPs with vaccine strains.^{33,34} In VP4, there are four antigenic regions (8-1, 8-2, 8-3, 8-4)³⁴ (Figure 4A). When compared with RotaTeq and Rotarix vaccine strains (P8) four mutations were observed in the 8-1 region and five mutations in the 8-3 region. No mutations were observed in 8-2 and 8-4 regions. Indonesian

P4 strains exhibited two mutations in region 8-1, three mutations in region 8-3 but no mutations were observed in regions in 8-2 and 8-4 when the Indonesian strains were compared with the RotaTeq P8 strain (Figure 4B). Although there was a strain difference between Indonesian and vaccine (RotaTeq) strains, interestingly only a few variations were observed in 8-1 and 8-3 regions; while 8-2 and 8-4 regions were conserved. This region (VP4) also possesses fewer variations in comparison to the variations observed in P8 strains of Indonesia and vaccine strains.

Strains	VP4																		VP7						NSP4																																			
	8_1										8_2				8_3						8_4				7_1a							7_1b					7_2			ASIII										ASII										
Strains	100 146 148 150 188 190 192 193 194 195 196 180 183	113 114 115 116 125 131 132 133 135	87 88 89	7_1a	7_1b	7_2	112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133	136 137 138 139 140 141 142 143 144 145 146 147 148 149 150																																																				
ROTARIX	D S Q E S T N L N N I T A	N P V D S S N D N	N T N	T T N G E W K D Q S V V D K Q N V D N T K D Q N L S M N G			M I D K L T R E I E Q V E L L K R I H D N T R P V D V I D M S K E F I N Q																																																					
ROTAQE	* * * * * * * * * * * * * * * * * * * *	* * * * * * * * * * * * * * * * * * * *	* * * * * * * * * * * * * * * * * * * *				*																																																					
YK-RVY36_G1P[8]	* A * * D * * * * * * * * * * * *	D S * * N R R	D D	* * * * * * * * * * * * * * * * * * * *			* * * * * * * * * * * * * * * * * * * *																																																					
PL-2500_G9P[8]	* A * * * * * * * * * * * * * * *	D N R	D D	* * * * * * * * * * * * * * * * * * * *			* * * * * * * * * * * * * * * * * * * *																																																					
ROTAQE	G S D D Y V N Y A S V T A	T S E T S S N A D T G P																																																										
RVM113_G2P[4]	* A * * * * * * * * * * * * * *	G *	D																																																									
BL-5210_G2P[4]	* A * * * * * * * * * * * * * *	G *	D																																																									
ROTAQE	A N S D E W E N Q D T M N K Q D V S N S R D N T L D I S G																																																											
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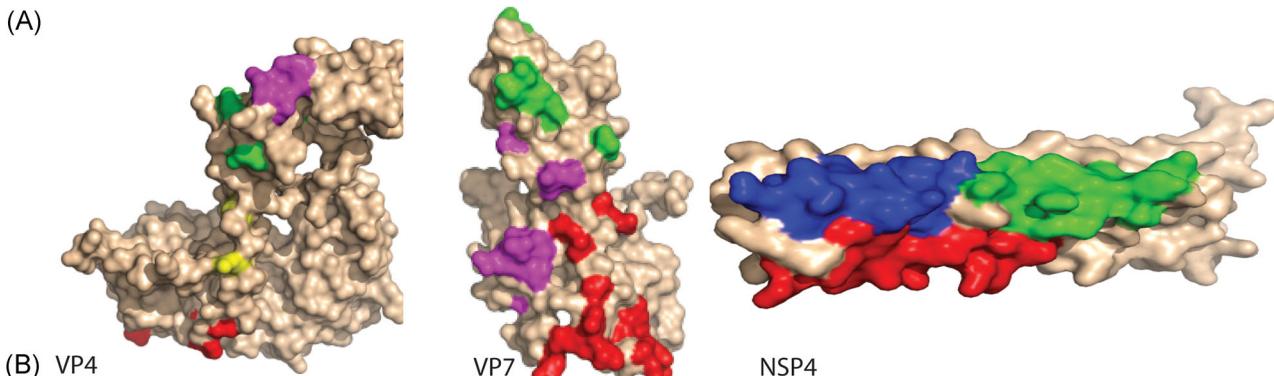


FIGURE 4 A, Alignment of antigenic residues in VP4, VP7, and NSP4 between the strains contained in Rotarix, RotaTeq, and Indonesian circulating strain. Antigenic residues are divided in four antigenic epitopes (8-1, 8-2, 8-3, 8-4) in VP4 protein; three antigenic epitopes (7-1a, 7-1b, and 7-2) in VP7; and three antigenic epitopes (ASI, ASII, and ASIII) in NSP4 protein. Amino acid residues that differ between the vaccine and Indonesian strains are indicated in colored boxes (black triangle). B, Surface representation of VP4, VP7, and NSP4 proteins. Antigenic epitopes are colored in red (8-1), yellow (8-2), green (8-3), and purple (8-4) in VP4; red (7-1a), green (7-1b), and purple (7-2) in VP7; and red (ASI), blue (ASII) and green (ASIII) in NSP4. Only the surface showing the antigenic epitopes are presented by rotating at 180°

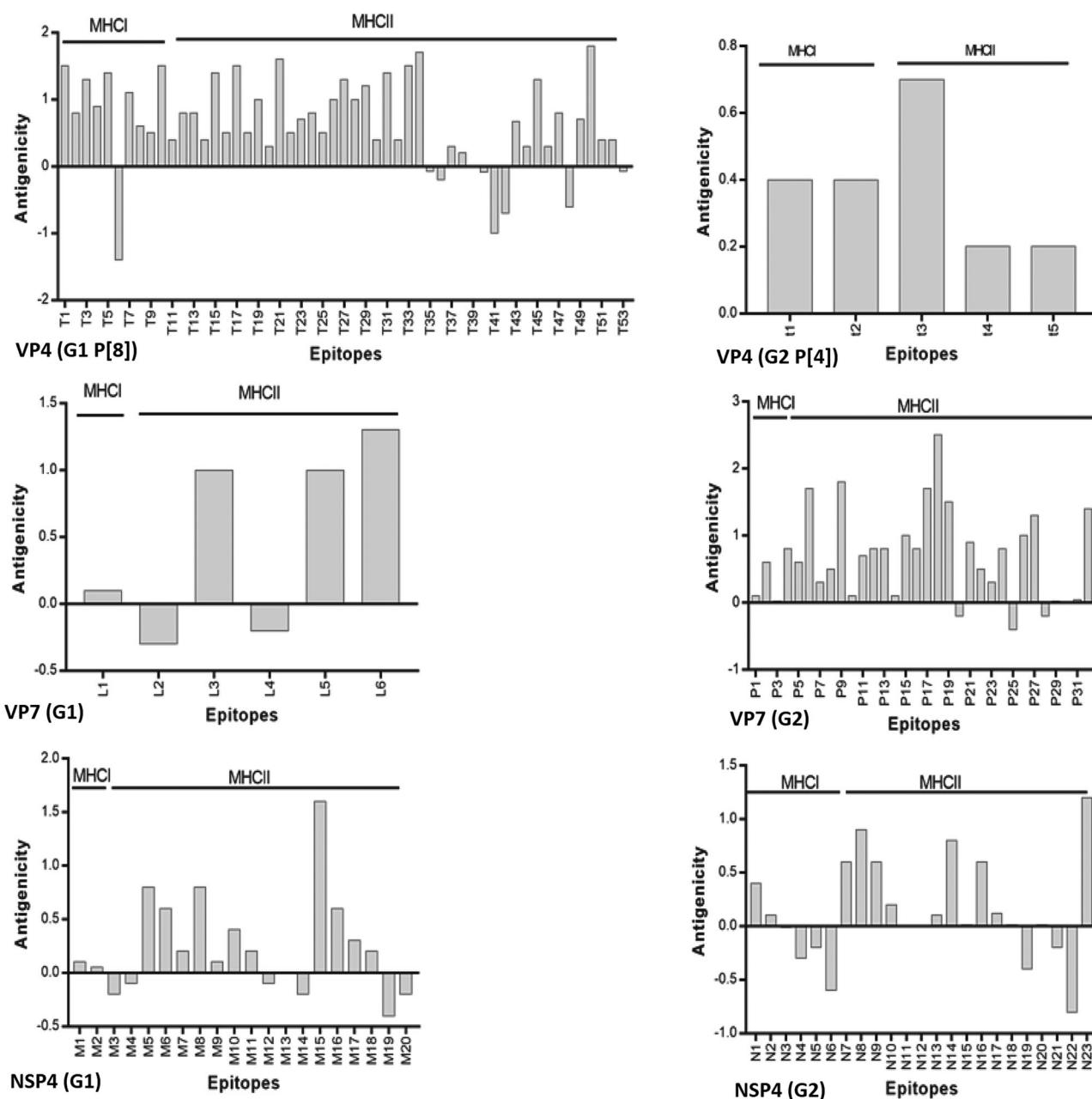


FIGURE 5 Antigenicity of the conserved T cell (MHC I and MHC II) epitopes among the vaccines and Indonesian strains

In VP7 there are three antigenic regions (7-1a, 7-1b, 7-2)³³ (Figure 4A). When compared with vaccine strain (G1) seven mutations were observed in region 7-1a, five in region 7-1b, and six in region 7-2. In Indonesian G2 strains only three variations were observed in 7-1b region when it was compared with the vaccine strain (G2) (Figure 4B).

In NSP4 three antigenic sections are present (ASI, ASII, ASIII) (Figure 4A).³⁵ When Indonesian strains were compared with the vaccine strain, seven variations were observed in ASI, 10 in ASII, and 2 in ASIII (Figure 4B).

3.5 | Conserved regions among VP4, VP7, and NSP4 genes

We have analyzed all complete sequences of Indonesian VP4, VP7, and NSP4 and compared with RotaTeq and Rotarix vaccine strains to highlight all possible conserved regions in these VPs. In VP4, 27 conserved regions were found among the vaccine (Rotarix, RotaTeq) and P[8] Indonesian strains, while 14 conserved regions were observed in the vaccine and Indonesian strains (G2) (Table S2A). In the case of VP7, 9 conserved regions were observed in the vaccine

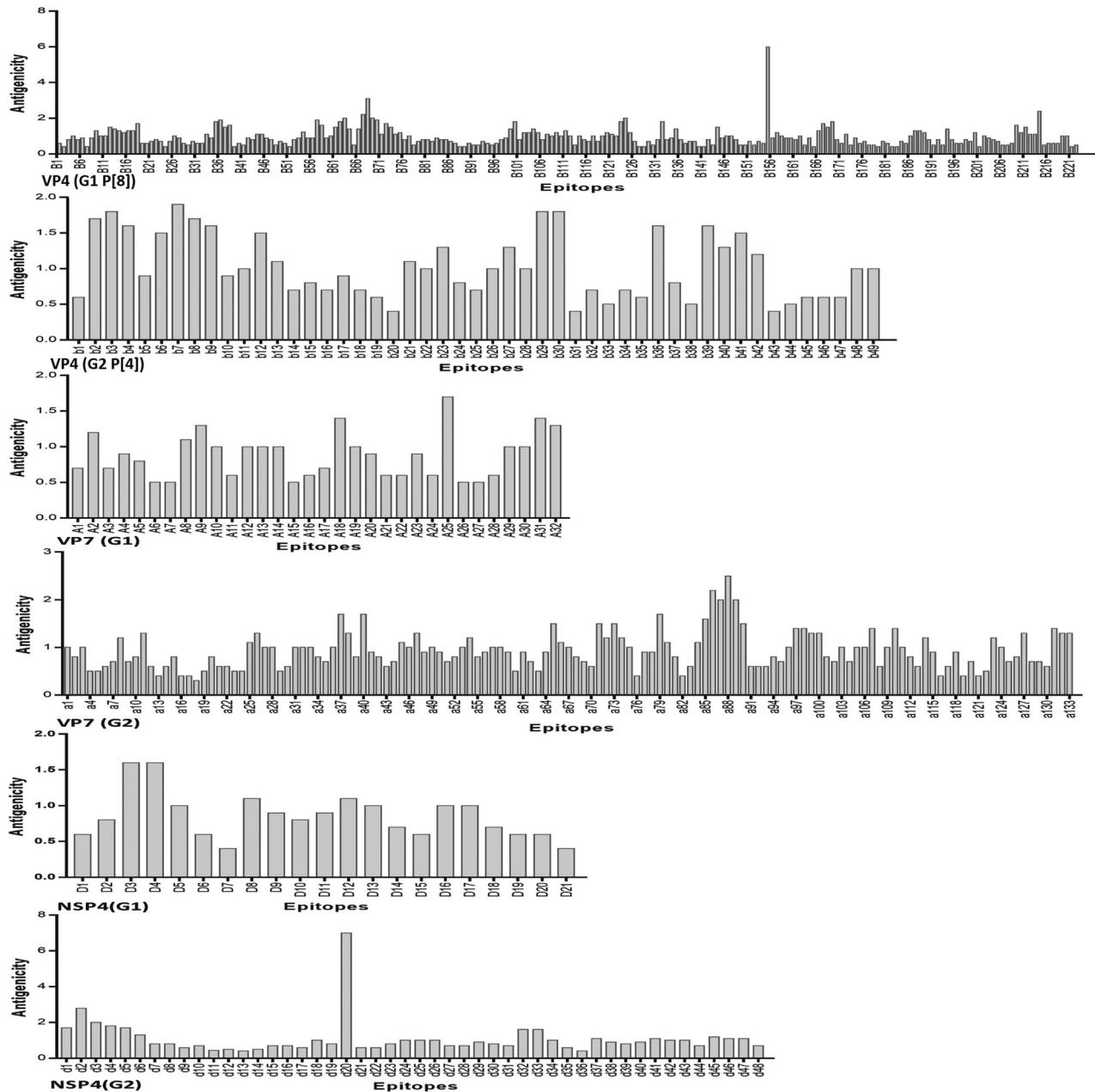


FIGURE 6 Antigenicity of the conserved B cell epitopes among the vaccines and Indonesian strains

and P8 Indonesian strains, while 10 conserved regions were found conserved between the vaccine and Indonesian strain (G2) (Table S2B). Indonesian NSP4 (G1) possessed only three conserved regions in comparison with vaccine strain, but Indonesian NSP4 (G2) were shown to possess six conserved regions (Table S2C). It was observed that despite intergenotypic differences, various conserved regions were common among the vaccine and Indonesian strains.

3.6 | Epitope mapping of VP4, VP7, and NSP4 proteins

Epitope mapping of both vaccine and Indonesian strains was performed to determine B and T cell epitopes that are conserved among them and are present among the conserved regions. The conserved epitopes were

further investigated for their antigenicity by using the online tool Vaxijen.⁴² The epitopes were selected for their higher antigenicity, that is, ≥ 0.4 . It was observed that most of the B cell epitopes lying within the conserved regions have more antigenicity conferring the importance of conserved regions as potential antigenic regions (Figure 6). Some of the conserved T cell epitopes (MHC I and II) also showed high antigenicity (Figure 5), thus showing the potential of these regions. The details of the epitope sequence were provided in Table S3.

4 | DISCUSSION

Rotavirus is known to be a major cause of severe diarrhea globally. The WHO has recommended rotavirus vaccines to be included in

worldwide through NIPs.⁴³ It has been reported that rotavirus infection accounts for a substantial disease burden in children less than 5 years of age in Indonesia.¹⁴ However, rotavirus vaccines have not been introduced in the NIP of Indonesia. The decision to introduce the rotavirus vaccine in Indonesia is delayed due to the lack of awareness of the importance of rotavirus vaccines as well as the financial constraints of the government.⁴⁴ In this report, we performed an investigational study of circulating rotavirus strains and immunoinformatic comparison with the vaccine strains to raise awareness of rotavirus vaccine introduction in Indonesia.

G1P[8], G2P[4], and G9P[8] strains were dominant during this study. We observed that rotavirus genotypes circulating in Indonesia were similar in comparison to global strains.¹⁷ It was recognized that G1P[8], G2P[8], and G9P[8] were the dominant genotypes of circulating strains in Indonesia during 2006-2009, which were also reported in previous global studies.¹⁷ Within each genotype, strains detected in 2006-2009 clustered in a single common lineage and were closely related to contemporary strains detected globally. However, it was suggested that the predominant rotavirus genotypes in Indonesia vary by year and location, underlying the importance of a continuous investigation on circulating genotypes.^{13,45}

One mechanism of generating genetic diversity is the accumulation of point mutations (genetic drift) in each replication cycle of circulating rotavirus strains.³⁴ In the present study, we compared amino acid sequences of the VP4, VP7, and NSP4 antigenic domains of Indonesian and vaccine strains to determine the possible variations that could affect vaccine efficacy. We observed that certain variations were present among Indonesian and vaccine strains. These variations were distributed heterogeneously on the surface of the protein (Figure 4).

Genetic heterogeneity of various rotavirus genotypes could affect the immune responses against the vaccine.⁴⁶ Hence, more specific and conserved epitopes need to be targeted to design a highly protective vaccine against circulating rotavirus genotypes. Furthermore, knowledge of currently circulating strains is required before the initiation of a vaccination program in Indonesia. The most appropriate vaccine design requires information about the distribution of pathogen genotypes as well as HLA alleles.⁴⁷ Through this method, more specific epitopes could be selected which can be valuable to design epitope-based vaccines to efficiently elicit potent B and T cell responses.⁴⁸ On the basis of these observations, we further determined the conserved regions among the vaccine and Indonesian strains. Further B and T cell epitope prediction was performed for both vaccine and Indonesian strains. Only those epitopes that laid in the conserved regions and have high antigenicity were then selected. Our analysis showed that there are a wide variety of conserved epitopes that are common between the vaccine and Indonesian strains, conferring the importance of the available rotavirus vaccine in the Indonesian population.

Thus, our present study describes a comparison between the rotavirus strains circulating in Indonesia with Rotarix and RotaTeq vaccine strains as well as with global strains. The genotyping and immunoinformatic analysis from the present data provides necessary information to identify novel and emerging rotavirus strains but also

an immunoinformatic strategy for vaccine development. However, they should be further validated in functional assays of cross-protection experiments or field-based analysis to prove the biological relevance of our findings.

5 | CONCLUSIONS

The present study provides comprehensive data about the genetic diversity of circulating rotavirus strains in several regions in Indonesia. Continuous surveillance is essential to monitor circulating genotypes and the emergence of novel variants as well as to predict the vaccine efficacy both before and after the introduction of mass vaccination.

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CONFLICT OF INTERESTS

The authors declare that there are no conflict of interests.

AUTHOR CONTRIBUTIONS

HN, CMD, and AI contributed to the study concept and design, acquisition of data, analysis and interpretation of data, and drafting the manuscript; TW and ATA contributed to acquisition and interpretation of data as well as critical revision of the manuscript; CDK, YS, and QP contributed to the scientific discussion, provide facilities, and critical revision of the manuscript; MSH contributed to study concept and design, study supervision, finalization, and critical revision of the manuscript.

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SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section.

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