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Computational Evaluation of the B-Cell Epitope of 37-kDa Outer Membrane Protein H *Pasteurella multocida* Type B from Nusa Tenggara Timur, IndonesiaTenggara Timur, Indonesia

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ABSTRACT

HS is still a frequently reported endemic disease, with outbreaks in Indonesia. HS vaccines distributed in Indonesia exhibit various limitations. This study computationally evaluated the B-cell epitope of the 37-kDa OmpH derived from the amino acid sequence of Pasteurella multocida from the NTT and Katha strains and compared the epitopes of the two strains. Amino acid sequences were obtained from NCBI and analyzed for multiple sequence alignment, and homology was analyzed using the BLASTp program at NCBI. Epitope prediction was performed using the IEDB B-cell epitope and ABCPred prediction tools. The VaxiJen v.2 online platform was used for antigenicity analysis, and IEDB was used for epitope conservancy analysis. The results of the homology analysis revealed that local NTT isolates had a high (>95%) identity with the Katha strain and isolates from China, India, Iran, Japan, and the USA. The epitope predictions from both methods were cross-checked, overlapping epitopes were shortlisted, and only five epitopes were predicted. Among the five, one epitope, ALEVGLN, appeared to be antigenic to both NTT and Katha strains. The antigenic sequence of 37 kDa OmpH can be used for peptide-based vaccine development and immunotherapeutic design.

Keywords

Haemorrhagic Septicemia, P. multocida, Outer membrane protein H (OmpH), Epitope, Antigenicity

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Abbreviations

HS: Haemorrhagic Septicemia
OmpH: Outer membrane protein H
kDa: Kilo Dalton
NCBI: National Center for Biotechnology Information
NTT: Nusa Tenggara Timur
IEDB: Immune Epitope Database
WOAH: World Organization for Animal Health

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Introduction

HS, also known as snoring disease in Indonesia, is caused by Pasteurella multocida, a gram-negative bacterium that commonly infects cattle and buffalo [1].

HS has a wide distribution, especially in tropical regions, such as Middle-East, Central Africa, North-East Africa, South Africa, South Asia, and South-East Asia [2]. In Indonesia, 12,058 cases of HS were reported between July 2007 and December 2019, with cases in buffaloes (4,047), cattle (5,809), pigs (2,108), goats/sheep (64), and Equidae (30) [3].

The disease causes huge losses due to livestock mortality, as well as losses in the meat- and dairy-related industries [4]. The economic loss of the livestock industry is estimated at 792 million USD per year [5], and the mortality rate of HS is up to 100% [6]. Considering its socioeconomic impact, HS is classified as one of 22 strategic infectious diseases in Indonesia, where control measures are coordinated at the central level [7].

The disease remains endemic in Indonesia, and several regions continue to report outbreaks [8, 9, 10] despite vaccination efforts. Currently, the disease is present in multiple areas of Indonesia, including Bali, Bengkulu, DKI Jakarta, Java, Aceh, West Nusa Tenggara, East Nusa Tenggara, North Sumatra, South Kalimantan, South Sumatra, Jambi, Riau, Central Sulawesi, West Sumatra, East Kalimantan, and Central Kalimantan [3].

The HS vaccines in Indonesia are administered once annually in the form of either an oil adjuvants vaccine or an aluminum precipitate vaccine, both of which are developed using the Katha strain from Burma [7]. The most effective option in the market is the oil adjuvant vaccine, which can provide immunity for up to one year. However, this vaccine has limitations, including the high viscosity of the solution, which makes injection challenging and can lead to swelling and abscesses at the injection site [2, 11]. Furthermore, this type of vaccine has a short storage time because it is susceptible to damage caused by temperature fluctuations [12].

The OmpH is a prominent protein in the purified envelope of P. multocida envelope and was identified as an immunodominant porin. Ongoing research has explored the feasibility of utilizing OmpH as a subunit vaccine in both native and recombinant forms to combat avian cholera, bovine respiratory illness, and HS [4, 13-16]. Vaccination with the recombinant form of OmpH, which has a molecular weight of 37 kDa, can induce both antibody- and cell-mediated immune responses in dairy calves and swamp buffaloes, protecting HS [4, 17]. Research conducted by Maulana et al. (2018) demonstrated that 37-kDa OmpH from a local strain of P. multocida isolated from NTT and Katha strains exhibit similar B-cell epitopes [18].

Immunoinformatics is a valuable technique for identifying new antigenic epitopes that can be used to design new vaccines against a variety of infectious diseases, including peptide-based vaccines. Given the advancement of immunoinformatics technologies, more accurate prediction of B-cell epitopes can now be made. Compared to strict laboratory studies, employing immunoinformatics methods to anticipate epitopes and develop peptide-based vaccines minimizes costs and saves time, whilst also elevating precision [19, 20].

This study was conducted to computationally evaluate the B-cell epitope of the 37-kDa OmpH derived from the amino acid sequence of P. multocida from NTT and Katha strains, and compare the epitopes of the two strains. The results can be used for further evaluation in the development of a peptide-based vaccine candidate.

Results

Multiple Sequence Alignment and Homology Analysis

Conserved and varied regions of the 37 kDa OmpH from NTT and other sources were evaluated through homology analysis and multiple sequence alignment as depicted in Figure 1. Specifically, Clustal W was employed to assess seven different sequences of the OmpH gene from NTT-Indonesia, China, Japan, India, Iran, the USA, and Katha strains. Most of the alterations were point mutations, whereas there were identified insertions at positions 66-71, and deletions at positions 60-61, 189, and 196-197. The Entropy (Hx) Plot in Figure 2 indicates high entropy, revealing a significant variation between each sequence. The highest entropy values of 0.95570 were was recorded at positions 6. The homology analysis results showed that the 37 kDa OmpH asam amino sequence in local NTT isolates was significantly similar (>95%) to the Katha strain and isolates from China, India, Iran, Japan, and the USA (Table 1).

Prediction of the B-Cell Epitope of the OmpH P. multocida isolates of NTT and Vaccines

Kolaskar and Tangoankar method was employed to predict both the NTT isolates and Katha strain, possessing 11 potential B-cell epitopes within the 37 kDa OmpH gene that met the specified threshold value. In addition, the ABCpred prediction server was utilized in this study for predicting linear B-cell epitope regions in an antigen sequence through an artificial neural network. The results of both methods

Figure 1.
Multiple alignment of amino acid sequences of 37 KDa gene OmpH P. multocida NTT isolates compared with and isolates from GenBank

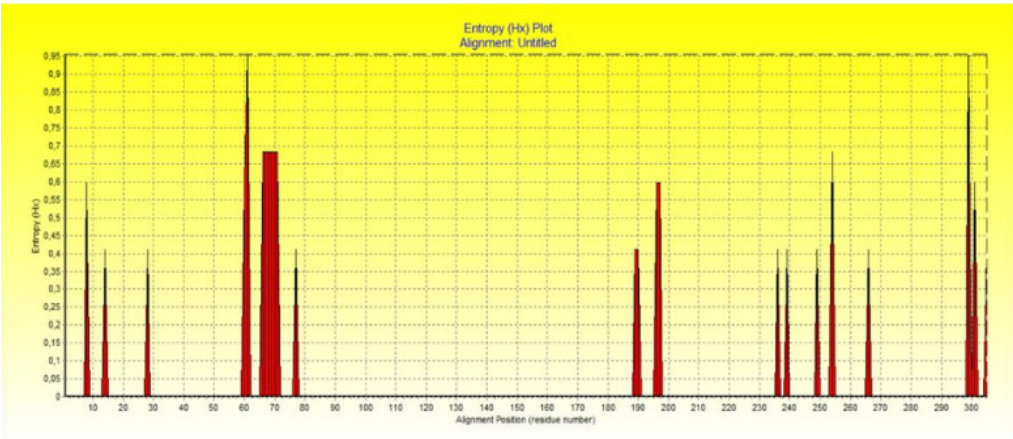

Figure 2.
Entropy (Hx) Plot graphic of multiple sequence alignment of all amino acid sequence of 37 KDa gene OmpH P. multocida NTT isolates with vaccines and isolates frim GenBank

Table 1.
Homological value of the nucleotide sequences of OmpH *P. multocida* NTT isolate and vaccine

Comparison isolate (Data GenBank)	NTT Isolate QDC35621 (%)	Katha Strain QDF60493.1
Outer membrane protein [Pasteurella multocida]. Accession Number ABR24803.1 - China	99.30%	98.95%
Adhesive protein, partial [Pasteurella multocida]. Accession Number ABX58059.1 - India	98.95%	100.00%
Outer membrane protein, partial [Pasteurella multocida]. Accession Number AAC02257.1 -USA	96.92%	95.24%
OmpH, partial [Pasteurella multocida]. Accession Number AQM74565.1 - Iran	96.54%	95.53%
Outer membrane protein [Pasteurella multocida]. Accession Number ABD94067.1 - Japan	95.85%	94.85%
Katha Strain Accession Number QDC35621	98.95%	100%

$\chi 2(3)=1532$, $p =< 0.001$

were cross-checked, and overlapped epitopes were shortlisted. Next, only five epitopes were ultimately selected and listed in Tables 2 and 3.

Antigenicity Analysis

Antigenicity analysis was conducted using the VaxiJen test with a threshold value of 0.5 (tables 4 and 5). Out of the five epitopes, one appeared to be antigenic in both NTT and Katha strains with the same peptide sequence ALEVGLN and a score of 1.3471.

Conservancy Analysis

Conservation analysis was performed on 100 sequences retrieved from the NCBI database via the BLASTp tool against the NTT isolate. Only ALEVGLN was deemed as a possible antigen when it came to antigenicity, while both GFVVAGL and ALEVGLN showed relatively high conservation levels (93%) (Table 6).

Table 2.
Potential shortlisted BCL epitopes of OmpH *P. multocida* NTT isolate using Kolaskar and Tongaonkar antigenicity method and ABCpred method

Kolaskar and Tongaonkar Antigenicity Method	Amino Acid Position	ABCpred Method	Start Position
DVGVSDYTYFLG	100-111	DVGVSDYTYFLGGINN	98
GAYVFSA	136-142	GFTFGGAYVFSADADK	131
GFVVAGL	154-160	RGFVVAGLYNRKMGDV	153
SQKYVTVA	177-184	AGYSQKYVTVAKQEKE	174
ALEVGLN	223-229	ALEVGLNYDINDKAKV	223

Table 3.
Potential shortlisted BCL epitopes of OmpH *P. multocida* Katha strain using Kolaskar and Tongaonkar antigenicity method and ABCpred method

Kolaskar and Tongaonkar Antigenicity Method	Amino Acid Position	ABCpred Method	Start Position
DVGVSDYTYFLG	100-111	DVGVSDYTYFLGGINN	100
GAYVFSA	138-144	GFTFGGAYVFSADADK	133
GFVVAGL	156-162	RGFVVAGLYNRKMGDV	155
SQKYVTVA	179-185	AGYSQKYVTVAKQEKA	179
ALEVGLN	223-229	ALEVGLNYDINDKAKV	223

Table 4.
Prediction of B-cell epitope antigenicity from outer membrane protein H (OmpH) amino acid sequences of *P. multocida* local isolates NTT

Antigenicity test by Vaxijen v 2.0		
Sequences	Score*	Probability
DVGVSDYTYFLG	0.2146	Probable Non-Antigen
GAYVFSA	-0.1360	Probable Non-Antigen
GFVVAGL	-0.1978	Probable Non-Antigen
SQKYVTVA	0.2844	Probable Non-Antigen
ALEVGLN	1.3471	Probable ANTIGEN

*threshold score 0.5

Table 5.
Prediction of B-cell epitope antigenicity from outer membrane protein H (OmpH) amino acid sequences of Katha vaccine strain

Antigenicity test by Vaxijen v 2.0		
Sequences	Score*	Probability
DVGVSDYTYFLG	0.2146	Probable Non -Antigen
GAYVFSA	-0.1360	Probable Non -Antigen
GFVVAGL	-0.1978	Probable Non -Antigen
SQKYVTVA	0.2844	Probable Non -Antigen
ALEVGLN	1.3471	Probable ANTIGEN

*threshold score 0.5

Table 6.
Conservation analysis of selected peptides from *P. multocida* NTT isolate and Katha strain through the IEDB epitope conservancy analysis website

Peptide Sequence	%Protein Sequence Identification
DVGVSDYTYFLG	84.00% (84/100)
GAYVFSA	74.00% (74/100)
GFVVAGL	93.00% (93/100)
SQKYVTVA	28.00% (28/100)
ALEVGLN	93.00% (93/100)

Discussion

The OmpH is an antigenic surface protein in the envelope of P. multocida. It has been identified in all bovine isolates and is being considered a vaccine candidate by some researchers [2]. Conserved and varied regions of the 37 kDa OmpH protein from NTT and other sources were assessed through multiple sequence alignment. The entropy (Hx) plot graphs were utilized to illustrate the variations between sequences. The entropy values had a range of 0-1. The more varied a sequence, the higher the entropy value. The positions with the highest entropy were 61 and 299. Sequences resulting in high entropy alignment are unlikely to make good vaccine candidates. An entropy value of 0 was observed in regions 1-7, 14-27, 29-59, 78-188 191-195, 198-235, 240-248, 254-265, and 267-298. In the low-entropy alignment, it is crucial to consider regions that correspond to very low entropy when designing peptide vaccines. This highly conserved region across antigens results in the formation of antibodies by the peptide, which protects against pathogens of different serotypes. Furthermore, this region demonstrates several critical functions due to its high level of conservation, making it resistant to mutation under positive selection pressure. In addition, the binding of antibodies to this region deactivates essential functions [21]. The 37 kDa amino acid sequence of OmpH local isolates in NTT showed high identity (>95%) with the Katha strain and isolates from China, India, Iran, Japan, and the USA, suggesting that the nucleotide sequences of NTT, vaccines, and other reference isolates may share a common ancestor [22].

A B-cell epitope refers to a defined region on the surface of an antigen that binds to an antibody. There are two categories of epitopes, comprising continuous (linear or sequential) and discontinuous (non-linear or conformational) epitopes [23]. Linear B-cell epitopes are made up of peptides that can be readily used in immunization and antibody production as substitutes for antigens [24]. The Kolaskar and Tangoankar methods revealed that both the NTT isolates and Katha strain possess 11 potential B-cell epitopes in the 37 kDa OmpH gene that surpass the specified threshold value in this study. The Kolaskar and Tongaonkar antigenicity techniques evaluate the antigenicity dependent on the physiochemical properties of amino acids as well as the number of experimentally confirmed epitopes [25].

Another prediction method for B-cell epitopes utilized in this study was the ABCpred prediction server. This server implements an artificial neural network to predict the linear regions of B-cell epitopes in an antigen sequence. The methodology for this server is developed on a recurrent neural network (machine-based technique), which relies on fixed-length patterns. The accuracy of this prediction method is 65.93%.

ABCpred was utilized to identify potential B-cell epitopes from 37 kDa OmpH P. multocida NTT isolate and Katha strain. The results from both methods were cross-checked, narrowed down, shortlisted to overlapping epitopes, and only five were selected. The combination of both methods can enhance the results of the prediction accuracy of B-cell epitope [26].

The peptides in the epitope prediction were chosen using the Kolaskar and Tongaonkar antigenicity methods and subsequently verified with the ABCpred method. They were then tested for antigenicity using the VaxiJen test, with a minimum threshold value of 0.5. VaxiJen is a pioneering server for the alignment-independent prediction of protective antigens [27]. Out of the five epitopes, one appeared to be antigenic in both NTT and Katha strains with the same peptide sequence ALEVGLN, scoring 1.3471. The high antigenicity value of this peptide sequence indicates its potential as an ideal vaccine candidate. A higher antigenicity value translates to a greater ability to induce the production of specific antibodies by B-cells [28].

The 37 kDa OmpH peptides with fairly high conservation (93%) comprise GFVVAGL and ALEVGLN, although only ALEVGLN is considered a probable antigen. In a study conducted by Bui et al. [29], conservation refers to the part of a protein sequence that contains an epitope that is considered to be at or above a certain level of identity. Regions with lower variability in the parts of the protein sequence that contain epitopes indicate greater epitope uniqueness. This indicates the degree of variability or uniqueness of the epitope. Therefore, these regions often serve as good targets for the development of epitope-based vaccines since the targeted epitopes are present in various strains of specific pathogens.

Conclusion

According to the findings of our bioinformatics studies, there was only one epitope of 37 kDa OmpH P. multocida both from NTT isolate and Katha strain that met the selected criteria of antigenicity and conservancy analysis. The epitope "ALEVGLN" is hypothesized to be the most potential candidate for a seed epitope/peptide vaccine within the 37 kDa OmpH. Further studies are needed to investigate the conserved regions of OmpH and assess their efficacy as vaccines against P. multocida infection.

Materials & Methods

Data Retrieval

The amino acid sequences of the 37 kDa OmpH P. multocida isolate retrieved from NCBI with accession numbers QDC35621 and QDF60493, as well as other reference isolates with accession numbers ABR24803.1, ABX58059.1, AAC02257.1, AQM74565.1, and ABD94067.1 were analyzed [31].

Multiple Sequence Alignment

Amino acid sequences obtained from NCBI were analyzed for multiple sequence alignment by employing the CrustalW method in the BioEdit program. Amino acid sequences of seven different strains were included in this analysis to identify the conserved regions of 37 kDa OmpH [32].

Homology Analysis

Homology analysis was performed using the BLASTp program at NCBI [22]. Specifically, the amino acid sequence of the 37 kDa OmpH of the NTT local isolate was compared to the Katha strain and five other isolates from different countries retrieved from GenBank, NCBI.

Epitope Prediction

Epitope prediction was performed using the IEDB B-Cell epitope prediction tool (http://tools.iedb.org/bcell/) with default thresholds. The Kolaskar and Tongaonkar antigenicity method was employed, which can predict antigenic determinants with approximately 75% accuracy. Moreover, ABCpred (http://crdd.osdd.net/raghava/abcpred/) was utilized, which can achieve an accuracy of up to 65.93% using recurrent neural networks with a 0.5 threshold [24]. Predicted peptides were acquired and analyzed further for their antigenicity using the VaxiJen v 2.0 tools [27].

Antigenicity Analysis

The antigenicity analysis was completed using VaxiJen v.2 online platform (http://www.ddg-pharmfac.net/vaxijen/VaxiJen/VaxiJen.html). The targeted proteins in VaxiJen2.0 were predicted using the auto-cross covariance method with a threshold of 0.5 [30].

Conservancy Analysis

The epitope conservancy analysis tool used in this study was epitope conservancy analysis (http://tools.iedb.org/conservancy/) at the IEDB (Immune Epitope Database) webserver with sequence identity threshold set at 100%. Selected peptide sequences from the previous step were assessed for their conservation among 100 homologous sequences of P. multocida retrieved from the NCBI database where BLASTp was performed against the NTT isolate [29].

Authors' Contributions

F.K.M and D.H conceived and planned the experiments. F.K.M carried out the experiments. F.K.M and D.H. contributed to the interpretation of the results. F.K.M took the lead in writing the manuscript. All authors provided critical feedback and helped shape the research, analysis and manuscript.

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Conflict of interest

The authors declare that there is no conflict of the interest

References

1. Prihandini SS, Noor SM, Kusumawati A. Deteksi serotipe, karakterisasi molekuler dan studi kekerabatan genetik isolat lokal Pasteurella multocide. JITV. 2017; 22(2): 91-9. DOI: 10.14334/jitv.v22i2.1630.

2. Almoheer R, Abd Wahid ME, Zakaria HA, Jonet MAB, Al-shaibani MM, Al-Gheethi A, Addis SNK. Spatial, Temporal, and Demographic Patterns in the Prevalence of Hemorrhagic Septicemia in 41 Countries in 2005–2019: A Systematic Analysis with Special Focus on the Potential Development of a New-Generation Vaccine. Vaccines. 2022; 10(2): 315. DOI: 10.3390/vaccines10020315.

3. [WOAH] World Organization of Animal Health. World Animal Health Information System (Surveillance and control measures: Hemorrhagic Septicemia). 2022. Available online: https://wahis.woah.org/#/dashboards/control-measure-dashboard [accessed 11 June 2022]

4. Muenthaisong A, Nambooppha B, Rittipornlertrak A, Tankaew P, Varinrak T, Muangthai K, Atthikanyaphak K, Sawada T, Sthitmatee N. An Intranasal Vaccination with a Recombinant Outer Membrane Protein H against Haemorrhagic Septicemia in Swamp Buffaloes. Vet Med Int. 2020 May 26;2020:3548973. DOIi: 10.1155/2020/3548973.

5. Shome R, Deka RP, Sahay S, Grace D, Lindahl JF. Seroprevalence of hemorrhagic septicemia in dairy cows in Assam, India. Infect Ecol Epidemiol. 2019;9(1):1604064. DOI: 10.1080/20008686.2019.1604064.

6. Clemmons EA, Alfson KJ, Dutton JW 3rd. Transboundary Animal Diseases, an Overview of 17 Diseases with Potential for Global Spread and Serious Consequences. Animals (Basel). 2021; 11(7):2039. DOI: 10.3390/ani11072039.

7. Noor SM, Prihandani SS, Desem MI, Purba HHS and Andriani. Antibody response in cattle after local isolate SE vaccine administration. IOP Conf. Series: Earth and Environmental Science. 2021;860:012071. DOI:10.1088/1755-1315/860/1/012071.

8. Nasution SS, Azfirman LP, Hutagaol NM, Azizi RA. Investigasi Kasus Septicaemia Epizootica (SE) pada Ternak Kerbau dan Sapi di Kabupaten Aceh Singkil. Buletin Veteriner Tahun. 2021; Edisi 2. URI: http://repository.pertanian.go.id/

handle/123456789/15518.

9. Narcana IK, Suardana IW, Besung INK.Molecular characteristic of Pasteurella multocida isolates from Sumba Island at East Nusa Tenggara Province, Indonesia. Veterinary World. 2020;13(1):104-9. DOI: www.doi.org/10.14202/vetworld.2020.104-109.

10. Berek HSD, Nugroho WS, Wahyuni AETH. Protektivitas Sapi di Kabupaten KupangTerhadap Penyakit Ngorok (Septicaemia Epizootica). J. Vet. 2015.;16 (2): 167-73.

11. Tanwar H, Yadav AP, Singh SB, Ganju L. Immunity against Pasteurella multocida in animals vaccinated with inactivated Pasteurella multocida and herbal adjuvant 'DIP-HIP'. Journal of Vaccines and Immunology. 2016;2(1):010-4. DOI: 10.17352/jvi.000014.

12. Herliani H, Abrani Sulaiman M, Ilmi Hidayat. Potency of Cell Wall Protein of Pasteurella multocida as Hemorrhagic Septicemia Vaccine on Swamp Buffaloes Journal of Wetlands Environmental Management. 2020; 8(1): 33–44. DOI: 10.20527/10.20527/jwem.v8i1.200.

13. Varinrak T, Poolperm P, Sawada T, Sthitmatee N. Cross-protection conferred by immunization with an rOmpH-based intranasal fowl cholera vaccine. Avian Pathol. 2017;46(5):515-525. DOI: 10.1080/03079457.2017.1321105.

14. Ahmad TA, Rammah SS, Sheweita SA, Haroun M, El-Sayed LH. Development of immunization trials against Pasteurella multocida. Vaccine. 2014;32(8): 909-17. DOI: 10.1016/j.vaccine.2013.11.068.

15. Joshi S, Tewari K, Singh R. Comparative immunogenicity and protective efficacy of different preparations of outer membrane proteins of Pasteurella multocida (B:2) in a mouse model. Veterinarski arhiv. 2013; 83(6): 665-76.

16. Okay S, Özcengiz E, Gürsel I, Özcengiz G. Immunogenicity and protective efficacy of the recombinant Pasteurella lipoprotein E and outer membrane protein H from Pasteurella multocida A:3 in mice. Res Vet Sci. 2012; 93(3):1261-5. DOI: 10.1016/j.rvsc.2012.05.011.

17. Muangthai K, Tankaew P, Varinrak T, Uthi R, Rojanasthien S, Sawada T, Sthitmatee N. Intranasal immunization with a recombinant outer membrane protein H based Haemorrhagic septicemia vaccine in dairy calves. J Vet Med Sci. 2017;80(1):68-76. DOI: 10.1292/jvms.17-0176.

18. Maulana FK, Handijatno D, Plumeriastuti H, Ernawati R, Tyasningsih W, Mufasirin M. Sequence Homology and Epitope Prediction of 37 kDa Outer Membrane Protein H(ompH) Gene of Pasteurella multocida Type B Isolate from Nusa Tenggara Timur (NTT). Indian Journal of Public Health Research & Development. 2019;10(12): 1708-13. DOI:10.37506/v10/i12/2019/ijphrd/192109.

19. Potocnakova L, Bhide M, Pulzova LB. An Introduction to B-Cell Epitope Mapping and In Silico Epitope Prediction. J Immunol Res. 2016;2016:6760830. doi: 10.1155/2016/6760830.

20- Muenthaisong A, Rittipornlertrak A, Nambooppha B, Tankaew P, Varinrak T, Pumpuang M, Muangthai K, Atthikanyaphak K, Singhla T, Pringproa K, Punyapornwithaya V, Sawada T, Sthitmatee N. Immune response in dairy cattle against combined foot and mouth disease and haemorrhagic septicemia vaccine under field conditions. BMC Vet Res. 2021;17(1):186. DOI: 10.1186/s12917-021-02889-8.

20. TopuzoĞullari M, Acar T, Pelİt Arayici P, UÇar B, UĞurel E, Abamor EŞ, ArasoĞlu T, Turgut-Balik D, Derman S. An insight into the epitope-based peptide vaccine design strategy and studies against COVID-19. Turk J Biol. 2020;44(3):215-227. DOI: 10.3906/biy-2006-1.

21. Ganguly B. Computational Prediction of Immunodominant Epitopes on Outer Membrane Protein (Omp) H of Pasteurella multocida Toward Designing of a Peptide Vaccine. Methods Mol Biol. 2016;1404:51-57. doi: 10.1007/978-1-4939-3389-1_3.

22. Pearson WR. An introduction to sequence similarity ("homology") searching. Curr Protoc Bioinformatics. 2013;Chapter 3:3.1.1-3.1.8. DOI: 10.1002/0471250953.bi0301s42.

23. Ghaffar A, Tariq A. In-silico analysis of Pasteurella multocida to identify common epitopes between fowl, goat and buffalo. Gene. 2016;580(1):58-66. DOI: 10.1016/j.gene.2016.01.020.

24. Sanchez-Trincado JL, Gomez-Perosanz M, Reche PA. Fundamentals and Methods for T- and B-Cell Epitope Prediction. J Immunol Res. 2017;2017:2680160. DOI: 10.1155/2017/2680160.

25. Oany AR, Emran AA, Jyoti TP. Design of an epitope-based peptide vaccine against spike protein of human coronavirus: an in silico approach. Drug Des Devel Ther. 2014;8:1139-49. DOI: 10.2147/DDDT.S67861.

26. Khan MT, Islam R, Jerin TJ, Mahmud A, Khatun S, Kobir A, et al. Immunoinformatics and molecular dynamics approaches: Next generation vaccine design against West Nile virus. PLoS ONE. 2021; 16(6): e0253393. DOI: 10.1371/journal.pone.0253393.

27. Doytchinova IA, Flower DR. VaxiJen: a server for prediction of protective antigens, tumour antigens and subunit vaccines. BMC Bioinformatics. 2007;5;8:4. DOI: 10.1186/1471-2105-8-4.

28. Wattimena MN, Wijanarka W. In Silico Analysis Prediction of B-Cell Epitope as a Vaccine Candidate for SARS-CoV-2 B.1.617.2 (Delta) Variant. Journal of Biomedicine and Translational Research [Online]. 2022;1:7-15. DOI:10.14710/jbtr.v1i1.13113

29. Bui H-H, Sidney J, Li W, Fusseder N, Sette A.. Development of an Epitope ConservancyAnalysis Tool to Facilitate the Design of EpitopeBased Diagnostics and Vaccines. BMC Bioin-

formatics. 2007; 8:361. DOI: 10.1186/1471-2105-8-361

30. Azam F, Saad M, Rahim R, Chumnanpoen P, E-kobon T, Othman S. Antigenic outer membrane proteins prediction of Pasteurella multocida serotype B:2. AsPac J. Mol. Biol. Biotechnol. 2020;28 (4) : 102-16. DOI: 10.35118/apjmbb.2020.028.4.

31. Maulana FK, Handijatno D, Plumeriastuti H, Ernawati R, Tyasningsih W, Mufasirin. Sequence Homology and Epitope Prediction of 37 kDa Outer Membrane Protein H(Omph) Gene of Pasteurella multocida Type B Isolate from Nusa Tenggara Timur (NTT). Indian Journal of Public Health Research and Development. 2019;10(12):1708-13. DOI: 10.37506/v10/i12/2019/ijphrd/192109.

32. Nouri MAA, Almofti YA, Abd-elrahman KA, Eltilib EEM. Identification of Novel Multi Epitopes Vaccine against the Capsid Protein (ORF2) of Hepatitis E Virus. American Journal of Infectious Diseases and Microbiology. 2019;7(1): 26-42. DOI: 10.12691/ajidm-7-1-5.

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