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Analysis of the B glycoprotein of Bovine Alphaherpesvirus 1 and 5 as a vaccine candidate against Infectious Bovine Rhinotracheitis



Analysis of the B glycoprotein of Bovine Alphaherpesvirus 1 and 5 as a vaccine candidate against Infectious Bovine Rhinotracheitis

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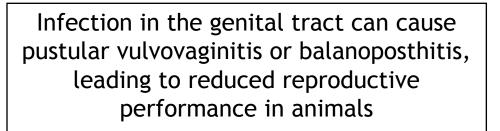




Disease produced

Infectious Bovine Rhinotracheitis (IBR) and Bovine Meningoencephalitis

The disease is characterized by symptoms in the upper respiratory tract, including purulent rhinorrhea, conjunctivitis, fever, prostration, and loss of appetite.



Responsible for serious economic losses due to restrictions on international cattle trade, abortions (25-60%), weight loss and reduced milk production.



Neural problems





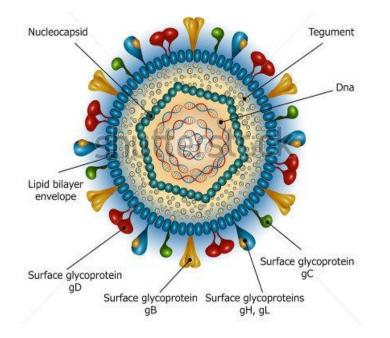
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Alphaherpesvirus Bovino (BoHV) 1 y 5

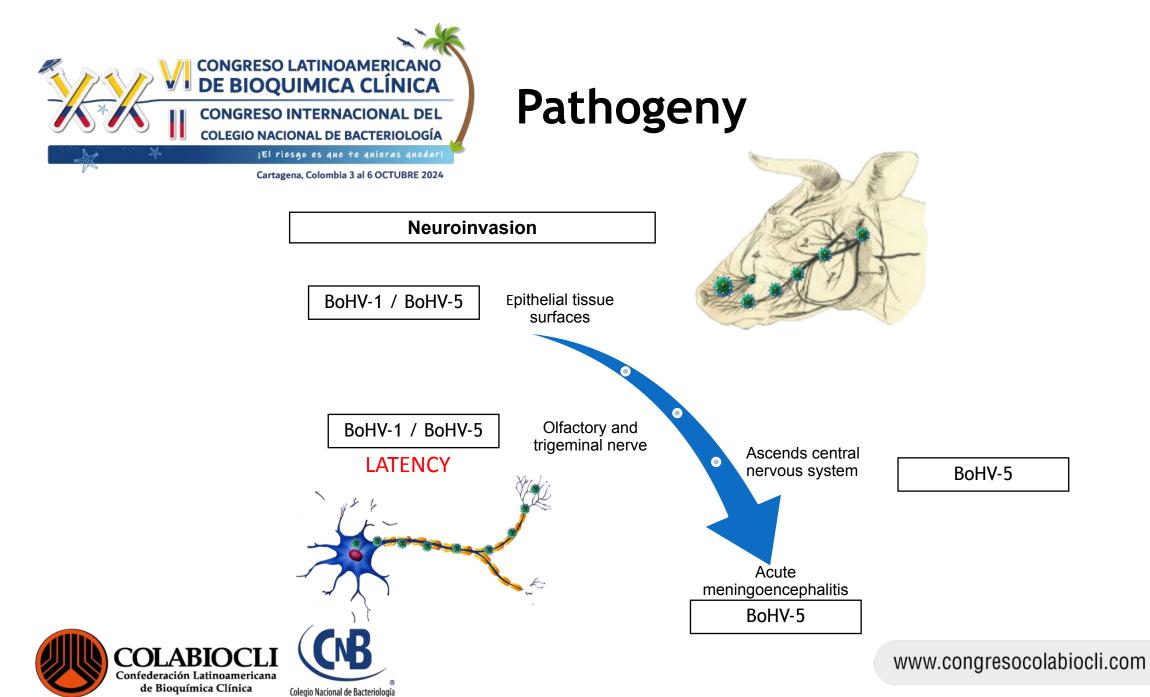
Características				
Family	Herpesviridae			
Subfamily	Alphaherpesvirinae.			
Gender	Varicellovirus			
Genoma	DNA double chain			
Structure	lcosahedral capsid. Envelope			



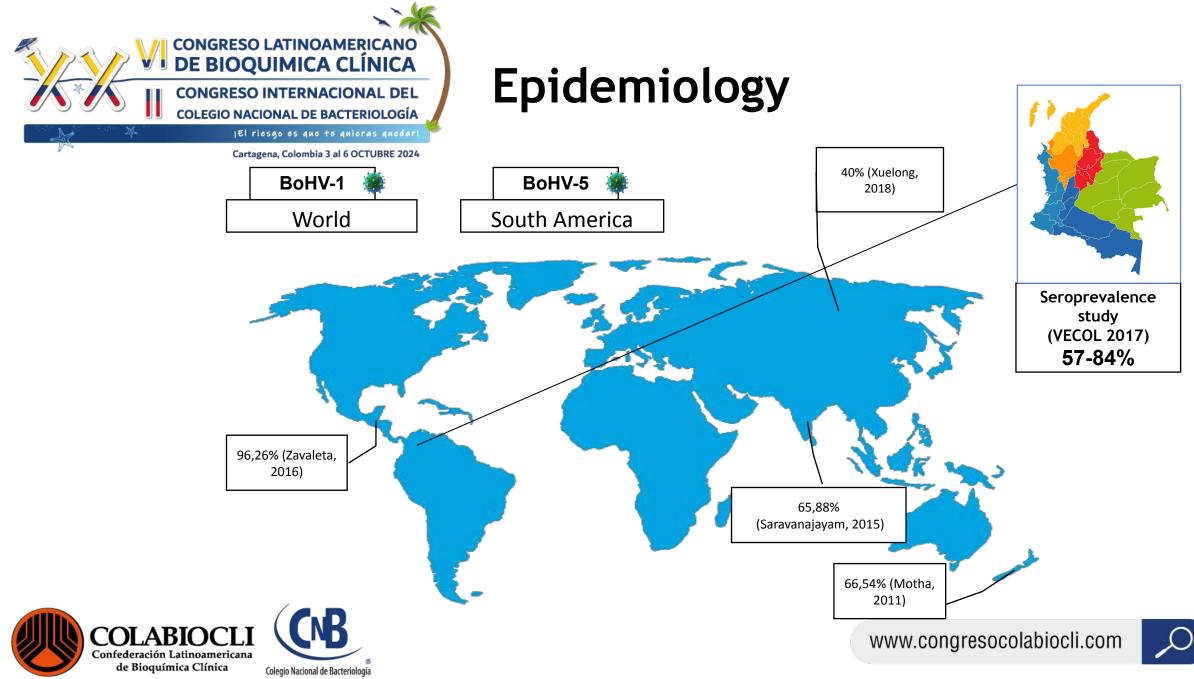


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Gerdts et al., 2000; D´Offay et al., 1993; Roels et al., 2000; Muylkens et al., 2007



Straub, 2001; Metzler et al. 1986; Ackermann et al., 2006; VECOL, 2018.



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Current vaccines

The World Organisation for Animal Health (OIE) reports that vaccination against BoHV-1/5 can be effective in reducing clinical manifestations and, consequently, economic losses. However, it does not provide complete protection against infection.

Inactivated	Modified live virus
Vecol S.A	Zoetis
Novartis	Fort Dodge
Virbac	Pfizer
Tecnovax	

For this reason, a wide variety of vaccine agents have been developed in recent years, ranging from classical inactivated vaccines to those utilizing new technologies.

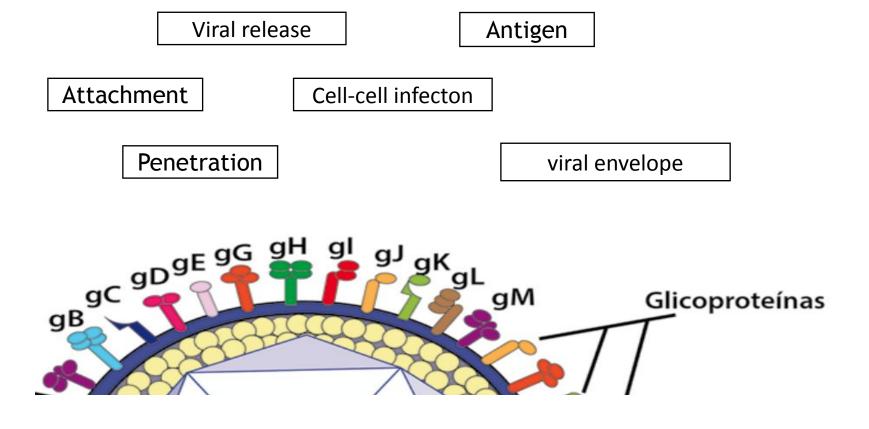








BoHV glycoproteins





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Glycoprotein evidence

Fisher et al., 2007

BoHV-5i + Propoleo

Dummer et al., 2014

gD BoHV-5 P. pastoris

gD BoHV-1/5 P. pastoris

Araujo et al., 2018

Santos et al., 2021

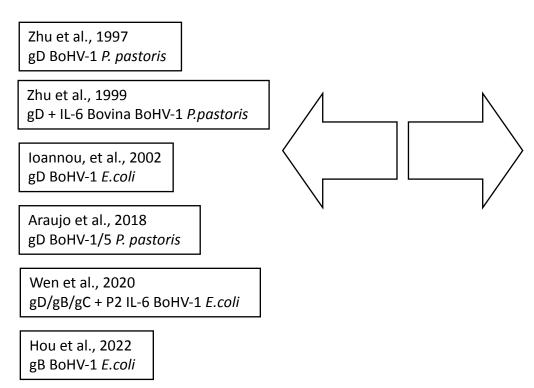
Araujo et al., 2022 gD BoHV-5 *P. pastoris*

Toyonensis BoHV-5 P.

gD + Esporas B.

pastoris

Babiuk et al., 1987 gB/gC/gD BoHV-1 Native



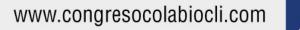






Could be the B glycoprotein of BoHV-1/5 a vaccine candidate against IBR??



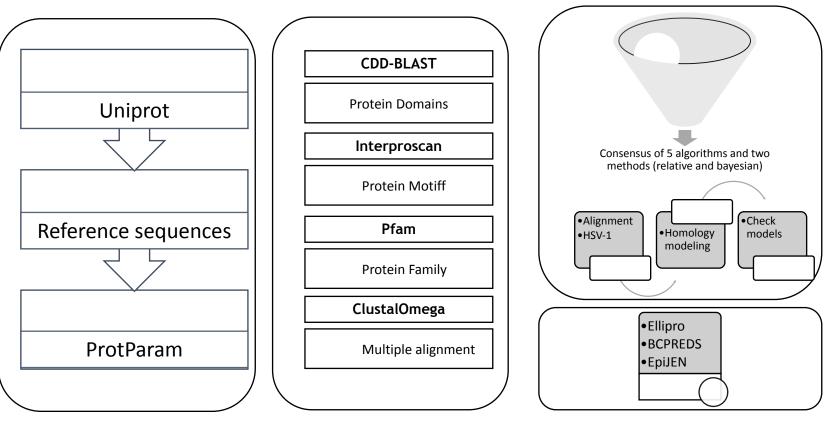




Bioinformatic approach

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gD gN gH **GLYCOPROTEIN** gB gC gΜ gE gl 5 5 5 5 5 1 5 1 5 1 1 5 1 1 1 1 VIRUS STRAIN 932 947 521 417 417 96 95 438 419 575 599 842 380 387 486 848 Amount of aa Molecular 101.19 102.45 55.38 51.44 44.92 44.62 10.26 10.31 45.51 43.17 61.16 63.54 88.37 88.99 39.91 39.67 weight(Kda) 9.77 10.47 9.81 4.71 8.88 8.60 pl theoretical 8.46 8.73 8.61 8.97 5.18 5.10 9.77 4.81 8.66 10.97 Total number of negatively charged 104 103 51 45 49 47 6 6 18 24 77 82 71 77 24 33 residues Total number of positively charged 109 111 56 53 38 36 11 11 36 35 47 58 77 85 49 38 residues 45.86 49.91 50.27 53.15 38.98 30.77 53.84 37.97 65.92 47.79 47.18 57.63 59.80 44.12 53.22 38.49 Instability index 78.56 77.84 68.43 70.99 63.12 68.47 98.65 104.84 114.09 116.06 79.74 72.62 93.61 92.29 81.42 80.75 Aliphatic index Average (-0.352)(-0.377) (-0.286) 0.604 (-0.161) (-0.311) 0.239 0.212 (-0.029) 0.052 (-0.273)(-0.272)(-0.261)0.477 0.558 0.543 hydropathicity (GRAVY) Alignment idendity **91.878** 75.287 79.905 78.125 78.475 69.772 85.984 70.951 (%) Cell-cell Attachment Attachment Penetration Morphogenesis Morphogenesis Cell-cell infection Cell-cell infection infection Funtion emPAI 0.778 3.786 0.551 1.683 0.413 0.688 0.389

Physicochemical properties of glycoproteins

Bioinformatic results

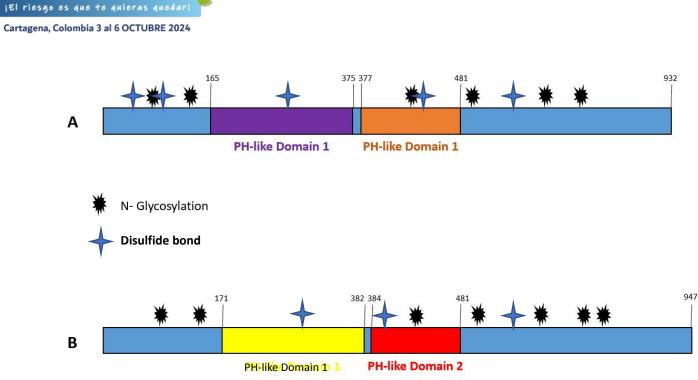




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Schematic representation of the B glycoproteins of BoHV-1 and BoHV-5

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1A. BoHV-1 B glycoprotein. PH-like domain 1 found between 165 to 375 and PH-like domain 2 found between 377 to 481; N-glycosylation sites (105, 153, 441, 483, 640 and 706). 1 B. BoHV-5 B glycoprotein. PH-like domain 1 found between 171 to 382 and PH-like domain 2 found between 384 to 481; N-glycosylation sites (111, 159, 448, 490, 594, 654 and 720).





Bioinformatic results



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	LAQAAGENSRFFVCPPPSGATVVRLAPARPCPEYGLGRNYTEGIGVIYKENIAPYTFKAY LAQAAGENSRFYVCPPPSGATVVRLAPARPCPEYELGRNYTEGIGAIYKE <u>NIAPYTFKAY</u>	174 180
Glycoprotein B of BoHV-1 Glycoprotein B of BoHV-5	IY-KNVIVTTTWAGSTYAAITNQYTDRVPVGMGEITDLVDKKWRCLSKAEYLRSGRKVVA IYYKNVIVTTTWAGSTYAAITNQYTDRVPVGLGEITDLVDKKWRCLSKAEYLRSGRKVVA	233 240
	EDRDDDDWEAPLKPARLSAPGVRGWHTTDDVYTALGSAGLYRTGTSVNCIVEEVEARSVY FDRDEDPWEAPLKPARLSAPGVRGWHTTDEVYTALGSAGLYRTGTSVNCIVEEVEARSVY ****:	293 300
	PYDSFALSTGDIIYMSPFYGLREGAHREHTSYSPERFQQIEGYYKRDMATGRRLKEPVSR PYDSFALSTGDIIYMSPFYGLRDGAHREHTSYSPERFQQIEGYYKRDMATGRRLKEPVSR	353 360
	NFLRTQHVTVAWDWVPKRKNVCSLAKWREADEMLRDESRGNFRFTARSLSATFVSDSHTF NFLRTQHVTVAWDWVPKRKNVCSLTKWREADEMLRDESRGNFRFTARSLSATFVSDGHTF	413 420
	ALQNVPLSDCVIEEAEAAVERVYRERYNGTHVLSGSLETYLARGGFVVAFRPMLSNELAK ALQNVPLSDCVTEEAGAAVERVYRERFNATHVLSGGLETYLARGGFVVAFRPMLSNALAK	473 480
	LYLQELARSNGTLEGLFAAAAPKPGPRRARRAAPSAPGGPGAANGPAGDGDA LYLQELARSNGTLEGLFAAGGSGAAAAAAPKPVPRRARRSASPTPPAP-AASGDGGDGDA *******************************	525 539

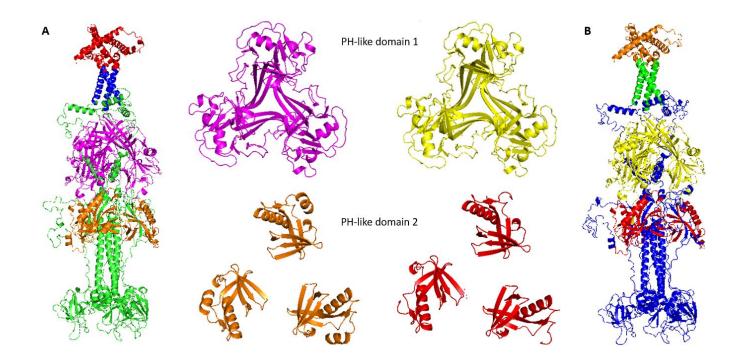
Sequence alignment of the B-glycoprotein domains of BoHV-1 and BoHV-5. "*" Represents identical aa, red and blue lines represent PH-like domain 1 and PH-like domain 2 respectively.





Bioinformatic results

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Modeling of the B glycoproteins of BoHV-1 and BoHV-5

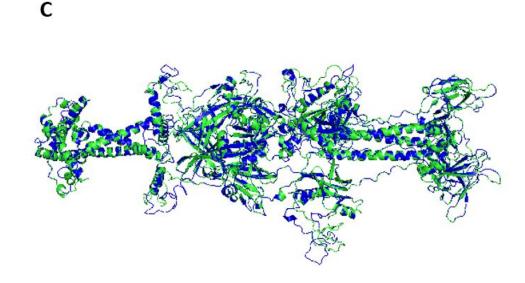
4A. BoHV-1 glycoprotein B. Green: general structure. Magenta: domain similar to PH 1. Orange: domain similar to PH 2.4B. BoHV-5 glycoprotein B. Blue: general structure. Yellow: domain similar to PH 1. Red: domain similar to PH 2.





Bioinformatic results

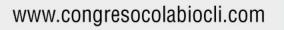




Modeling of the B glycoproteins of BoHV-1 and BoHV-5

4C. Overlapping patterns of BoHV-1 B-glycoprotein (green) overlaid with the BoHV-5 B-glycoprotein pattern (blue). RMSD value (0.081)



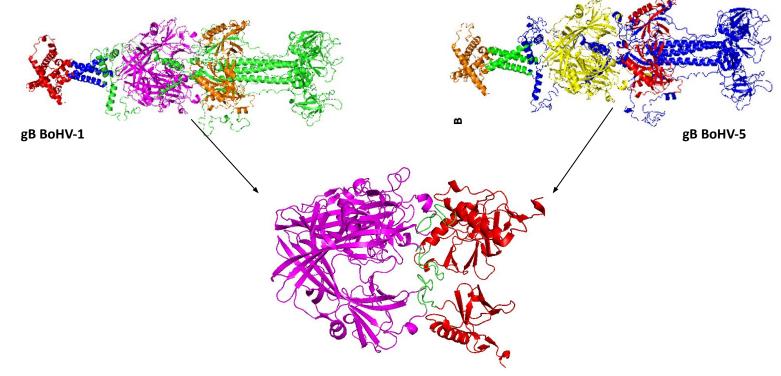




Vaccine design

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Domain 1 (BoHV-1) + Linker (GS) x8 + Domain 2 (BoHV-5)

3D modeling of the vaccine candidate.





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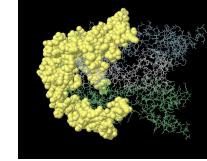
A. Ellipro

0,782

Vaccine design

0,781





0,779

B. BCpreds

Position	Epitope	Score	
273	SDCVIEEAEAAVERVYRERY	1	
210	KNVCGSGSGSGSGSGSGSGSGS	1	
119	NCIVEEVEARSVYPYDSFAL	1	
169	QQIEGYYKRDMATGRRLKEP	1	
231	KWREADEMLRDESRGNFRFT	1	
86	ARLSAPGVRGWHTTDDVYTA	1	
148	PFYGLREGAHREHTSYSPER	0.999	
252	RSLSATFVSDSHTFALQNVP	0.99	
314	AFRPMLSNELAKLYLQELAR	0.986	
27	TYAAITNQYTDRVPVGMGEI	0.952	
6	YTFKAYIYYKNVIVTTTWAG	0.829	

C. EpiJen

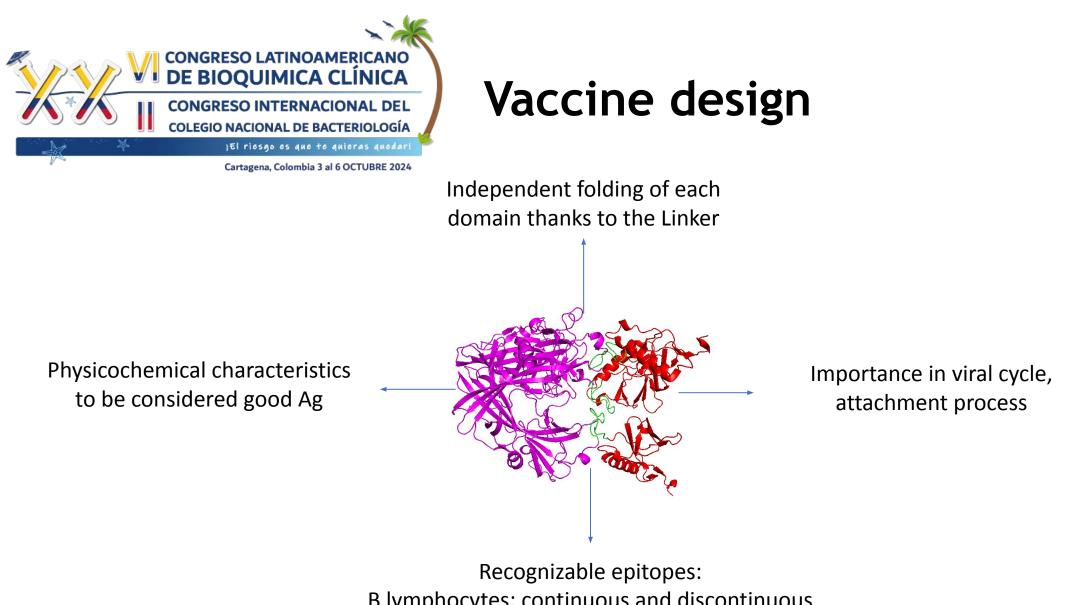
Starting position	Peptide	Predicted -logIC50 (M)	Predicted IC50 Value (nN
137	ALSTGDIIY	9.175	0.67
6	YTFKAYIYY	8.772	1.69
20	TTTWAGSTY	8.622	2.39
142	DIIYMSPFY	8.367	4.30
155	GAHREHTSY	8.25	5.62
297	VLSGSLETY	7.523	29.99
11	YIYYKNVIV	7.436	36.64
113	RTGTSVNCI	7.341	45.60
3	IAPYTFKAY	7.115	76.74
104	TALGSAGLY	6.953	111.43
319	LSNELAKLY	6.906	124.17
103	YTALGSAGL	6.89	128.82
305	YLARGGFVV	6.88	131.83
98	TTDDVYTAL	6.789	162.55
294	GTHVLSGSL	6.73	186.21
27	TYAAITNQY	6.353	443.61
120	CIVEEVEAR	6.264	544.50

Epitope prediction. A. Prediction of B-lymphocyte discontinuous epitopes. B. Prediction of continuous epitopes B lymphocytes. C. Prediction of continuous epitopes T lymphocytes









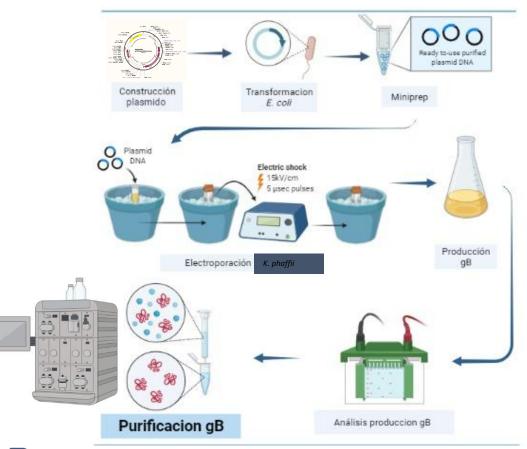


B lymphocytes: continuous and discontinuous T lymphocytes: Continuous

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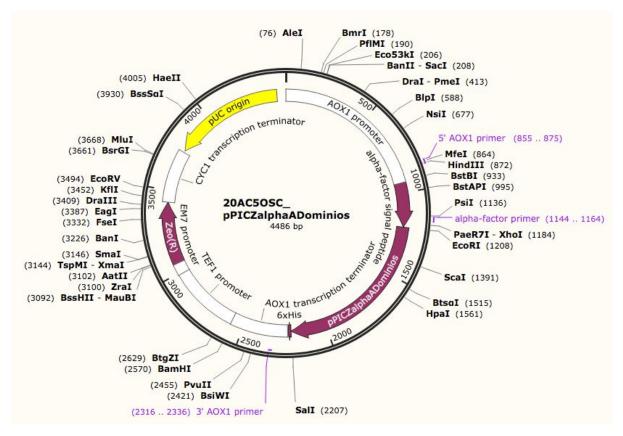




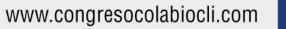


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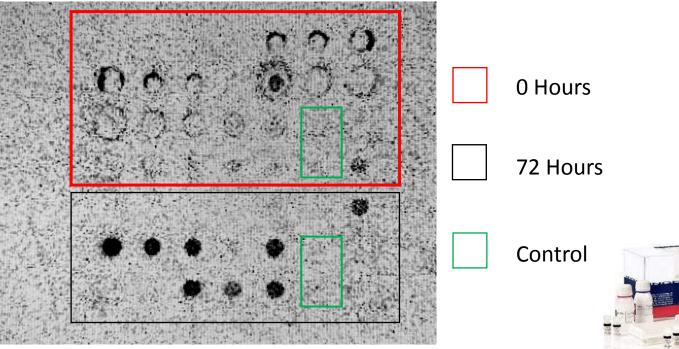






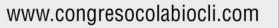






Dot blot of the crude extract of the K. phaffii GS115 clones





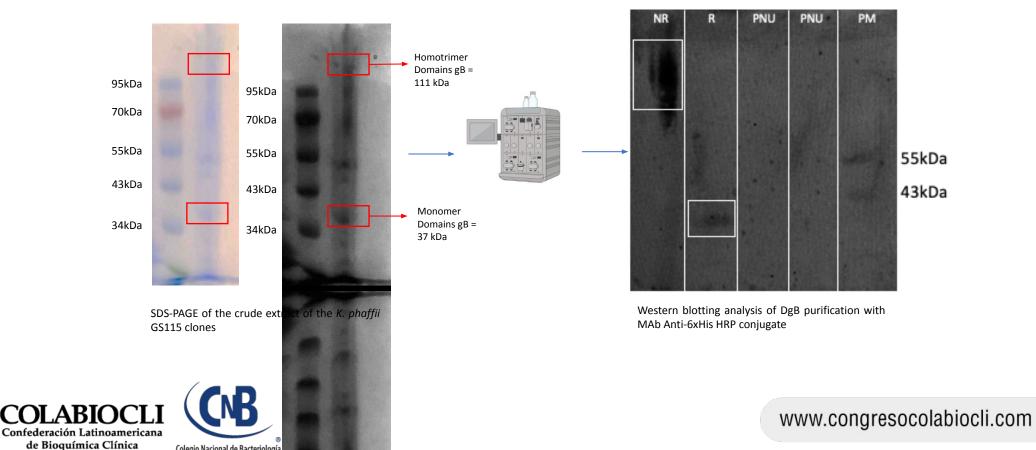


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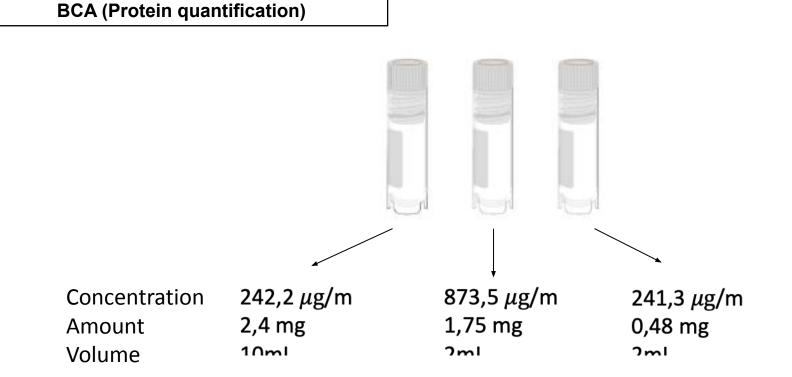
Colegio Nacional de Bacteriología

NR = Non-reducing R= Reducing PNU= Unbound protein MP=Weight marker



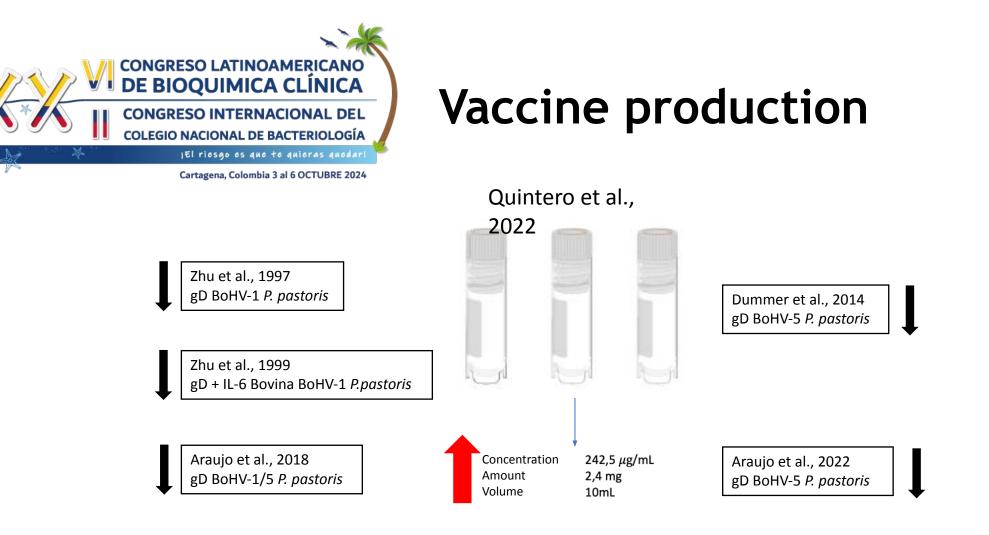










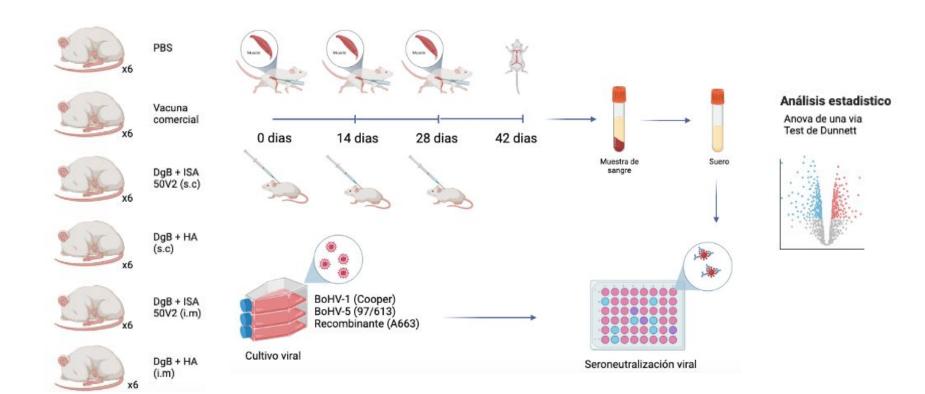


The improved performance of our candidate is attributed to its optimal size, reduced complexity, and absence of post-translational rearrangements, which eliminates the need for bioreactor production, unlike glycoprotein D











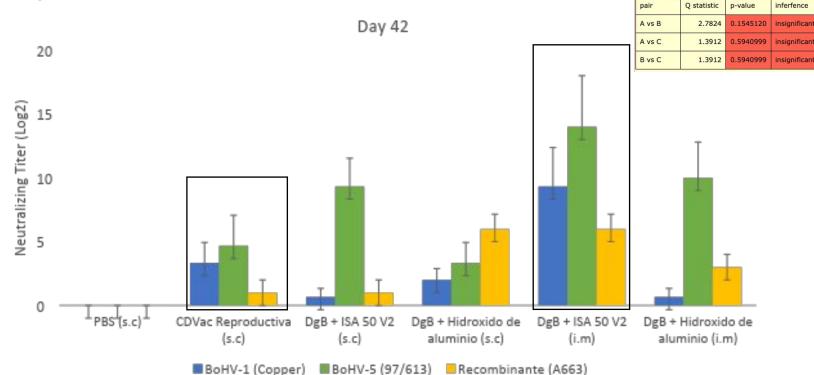


treatments

Tukey HSD

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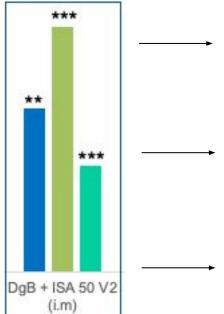


Data represent the mean \pm S.E.M of log2 transformed data and are expressed as the reciprocal of the highest dilution that completely inhibited virus-induced CPE. Statistical analysis was performed by one-way ANOVA followed by Dunnett's multiple comparisons test. *P < 0.05, **P < 0.01, and ***P < 0.001. s.c.: subcutaneously; i.m: intramuscularly.



Tukey HSD Tukey HSD





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> > The exposure time to the antigen in intramuscular tissues is longer than that via the subcutaneous route

Oil adjuvants prolong antigen retention in tissues, leading to greater recruitment of antigen-presenting cells

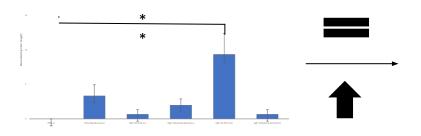
No significant differences were found between the antibody titers against the different viruses, indicating that our candidate is effective against all three viruses





Henriksen-Lacey et al., 2010; Tacken et al., 2011; Coffman et al., 2010; Smith et al. al., 2007; Batista-Duharte et al., 2014; cook et al., 2007; Schynder et al., 2021





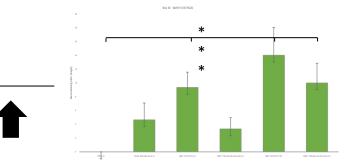
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> > Our obtained neutralizing antibody titers against BoHV-1 are comparable or higher (Zhu et al., 1997; Zhu et al., 1999; Ioannou, et al., 2002; Araujo et al., 2018; Wen et al., 2020; Hou et al., 2022)

Our neutralizing antibody titers were higher against BoHV-5 (Fisher et al., 2007; Dummer et al., 2014; Araujo et al., 2018; Santos et al., 2021; Araujo et al., 2022)



To the best of our knowledge, this is the first vaccine candidate tested for its ability to neutralize a naturally occurring recombinant strain.





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The subunit vaccine against Neisseria meningitidis is the first vaccine designed using reverse vaccinology

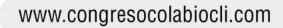
Bioinformatics tools enable the rapid and safe study of infectious agents in a controlled environment

Advantages reverse vaccinology

Vaccines can be designed in laboratories with a lower biosafety level than that required for handling the pathogen itself







The binding of different antigens could enhance protection against various pathogens, a concept known

as chimeric vaccines



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Quintero Barbosa et al. BMC Veterinary Research (2023) 19:28 https://doi.org/10.1186/s12917-023-03590-8 **BMC Veterinary Research**

Open Access

RESEARCH

Characterization and expression of domains of Alphaherpesvirus bovine 1/5 envelope glycoproteins B in *Komagataella phaffi*

Juan Sebastián Quintero Barbosa^{1*}, Heidy Yohana Triana Rojas², Janneth Gonzalez³, Angela Johana Espejo-Mojica², Carlos Javier Alméciga Díaz² and María Fernanda Gutierrez¹

Abstract

Background Bovine herpes virus (BoHV 1 and BoHV-5) are the causative agents of infectious bovine rhinotracheitis (BR). IBR is responsible for important economic losses in the cattle industry. The envelope glycoprotein B (gB) is essential for BoHV infection of cattle's upper respiratory and genital tract. gB is one of the main candidate antigens for a potential recombinant vaccine since it induces a strong and persistent immune response.

Results In this study, gB of BoHV-1 and BoHV-5 was characterized in terms of function, structure, and antigenicity through bioinformatics tools. gB showed conserved sequence and structure, so, both domains named PH Like 1 and 2 domains of each virus were selected for the design of a bivalent vaccine candidate. The immunoinformatic study showed that these two domains have epitopes recognizable by B and T lymphocytes, followed by this, the cDNA domains from BoHV-1/5 gB (Domains-gB) were transformed into the yeast *Komagataella phaffii* GS115 (previously known as *Pichia pastoris*). A recombinant protein with molecular weight of about 110 kba was obtained from the culture media. The vaccine candidate protein (Domains-gB) was recognized by a monoclonal antibody from a commercial ELISA kit used for IBR diagnostic, which may suggest that the epitopes are conserved of the entire infectious virus.

Conclusion Overall, it was shown that the recombinant domains of BoHV-1/5 gB have antigenic and immunogenic properties similar to the native gB. This vaccine candidate is promising to be used in future studies to assess its immunogenicity in an animal model.

Keywords Alphaherpesvirus bovine, Vaccine, Recombinant protein, IBR

vaccines

Articles produced

Articl

Humoral Immune Response of Mice against a Vaccine Candidate Composed of a Chimera of gB of Bovine Alphaherpesviruses 1 and 5

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Abstract: Infectious bovine rhinotrachetiis (IBR) and bovine meningcencephallis are caused by tonine alphakergewines (BoHV) types 1 and 5, which seriously threaten the global cattle industry. Vaccination to improve immunity is the most direct and effective means to prevent these conditions. Glycoprotein B (gB) is essential for the attachment of both viruses to permissive cells, and is a major target of the host immune system, inducing a strong humoral response. The aim of this study was to evaluate, in a murine model, the immune response of a candidate vaccine formulation composed of a chimeric BoHV-1 and BoHV-5 gB (DgB), expressed in Konsgottefle phaffii. The chimeric DgB vaccine adjuvanted with Montanide 50 ISA V2 or aluminum bydroxide was administered intramuscularly or subcutaneously. A control group and a group that received a commercial vaccine formulation administered intramuscularly. The results demonstrated that the chimeric DgB conserved important epitopes that were able to stimulate a humoral immune response capable of neutralizing BoHV-1, BoHV-5, and the recombinant strain, suggesting that the vaccine antigen is a promising candidate to be further evaluateflin.



Citation: Quintero Barbosa, J.S.;

Almsicips-Diaz, C.I.: Pérez, S.E.:

Gatierrez, M.F. Humoral Immune

Response of Mice against a Vaccine

Candidate Composed of a Chimera

at gB of Bovine Alphaherpesviruses





MDPI

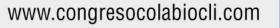




Gracias

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