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SHORT COMMUNICATION

Immunoinformatics Analysis of Mojiang Virus G Protein Epitopes

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ABSTRACT

Mojiang virus (MojV), a rodent-borne parahenipavirus, is closely related to Nipah and Hendra viruses. Located in the tropical–subtropical Asia emerging-disease hotspot, MojV highlights One Health risks at the wildlife–human interface amid land-use change and climate-driven reservoir shifts. With no vaccines or treatments available, we used immunoinformatics to identify conserved B- and T-cell epitopes in the attachment glycoprotein (G). Four high-scoring, non-toxic, non-allergenic epitopes were prioritised: B-cell epitope LGTGGGGYQVL (385–395), CTL epitope DTTIKPIEY (174–182), CTL/HTL epitope LRFGITPDISVRSTT (465–479), and HTL epitope KDEIWCIAITEGKKQ (572–586). These epitopes offer promising candidates for multiepitope vaccines, improved diagnostics, and cross-henipavirus research. This study provides a framework to support vaccine preparedness against understudied zoonotic threats in tropical and subtropical regions.

Keywords: paramyxovirus, immunoinformatics, emerging zoonotic virus

Introduction

Mojiang virus (MojV) is a zoonotic paramyxovirus first identified in 2012 from *Rattus flavipectus* rats after a cluster of three fatal pneumonia cases among miners in Mojiang, Yunnan Province, China (Wu et al., 2014). Phylogenetically related to the Henipavirus genus within the Paramyxoviridae family, MojV possesses a ~18 kb negative-sense single-stranded RNA genome encoding structural and nonstructural proteins, including nucleocapsid (N), phosphoproteins (P/V/W/C), matrix (M), fusion (F), attachment (G), and large (L) proteins (Wu et al., 2014). Like other parahenipaviruses, MojV entry is mediated by G and F glycoproteins, where G binds host receptors to trigger F-mediated membrane fusion (Da Silva et al., 2021). Located at the tropical–subtropical Asia interface, an established hotspot for emerging zoonoses driven by intensive human–wildlife contact, land-use change, mining activities, and climate-mediated reservoir expansion, MojV exemplifies critical One Health challenges at the animal–human–environment interface. Despite its unclear human pathogenic potential, the virus underscores the growing threat of rodent-associated paramyxoviruses in rapidly changing ecosystems of Southeast and South Asia. Currently, no vaccines, therapeutics, or specific diagnostic tools exist for MojV or related rodent-borne parahenipaviruses. In this context, understanding conserved immunogenic epitopes on the G glycoprotein, the primary target of neutralising antibodies and T-cell responses in parahenipaviruses is essential for advancing serological surveillance, risk assessment, and regional preparedness. Here, we employed immunoinformatics to predict and prioritise safe, antigenic, and conserved B- and T-cell epitopes in the MojV G protein, providing a foundational framework for monitoring and mitigating spillover risks from understudied wildlife-associated viruses in tropical and subtropical emerging-disease hotspots.

Materials and methods

The complete amino acid sequences of Mojiang virus attachment glycoprotein (G) (GenBank accessions: YP_009094095.1, AHM23777.1, and PDB: 5NOP chains A and B) were retrieved from NCBI and PDB databases. Multiple sequence alignment was performed using Clustal Omega. Prediction, screening, and ranking of linear B-cell epitopes, cytotoxic T-lymphocyte (CTL) epitopes, and helper T-lymphocyte (HTL) epitopes were carried out using an immunoinformatics pipeline integrating tools for antigenicity (VaxiJen v2.0), allergenicity (AllerTOP v2.0), toxicity (ToxinPred), immunogenicity (IEDB MHC I Immunogenicity Tool), population coverage

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(IEDB Population Coverage Tool), surface accessibility and topology (TMHMM v2.0), and cross-conservation within Paramyxoviridae (IEDB Conservancy Tool). All analyses followed the workflow described by Ting et al. (2025), with default threshold parameters unless otherwise specified. The final selection of potential epitopes was based on combined high scores, non-allergenicity, non-toxicity, surface exposure, absence of human homology, and conservation across the analysed sequences.

Results and discussion

Multiple sequence alignment of the four available Mojiang virus (MojV) attachment glycoprotein (G) sequences (YP_009094095.1, AHM23777.1, and PDB 5NOP chains A and B) using Clustal Omega revealed 72.4% overall identity, with the highest conservation in the globular head domain and greatest variability in the N-terminal signal peptide and stalk region around residues 164–165 (Figure 1). This pattern is typical of henipaviruses, where the receptor-binding head domain is under strong evolutionary constraint to preserve viral entry function, making it an ideal source of stable, broadly reactive epitopes (Larsen et al., 2025). After selection for toxicity, antigenicity (VaxiJen ≥0.4), allergenicity, immunogenicity, surface accessibility, and conservation within Paramyxoviridae, only 19 epitopes remained safe and immunogenic. From these, four potential candidates were prioritised (Table 1): the dominant helper T-cell epitope KDEIWCIAITEGKKQ (572–586; VaxiJen 1.8937), overlapping CTL/HTL epitope LRFGITPDISVRSTT (465–479; VaxiJen 1.4636), CTL epitope DTTIKPIEY (174–182; VaxiJen 1.3147), and linear B-cell epitope LGTGGGGYQVL (385–395; VaxiJen 0.5193), located in a solvent-exposed loop of the receptor-binding domain and thus promising for neutralising antibodies. All four candidate epitopes were non-toxic, non-allergenic, surface-exposed, and highly conserved, with overlapping CTL/HTL regions likely to drive robust, long-lasting immunity. These epitopes represent critical targets for intervention in the tropical–subtropical Asia hotspot, where mining, deforestation, and climate-driven expansion of Rattus species are increasing the frequency of human–rodent contact (Blasdell et al., 2022; Bai et al., 2023). The 2012 MojV spillover in an abandoned mine highlights a distinct rodent-to-human transmission pathway that complements the bat-driven route of Nipah and Hendra viruses. The identified epitopes, therefore, provide useful markers for (i) broad serological surveillance in at-risk occupational and rural populations, (ii) improved diagnostic differentiation of paramyxovirus-like illness, and (iii) potential cross-protective antigen design, which are critical steps for integrated human–animal–environmental health strategies in dynamic ecosystems. The current study demonstrates that immunoinformatics can deliver rapid, cost-effective solutions for understudied zoonotic threats, supporting proactive regional preparedness against future parahenipavirus spillovers. The findings from this study provide the basis for experimental validation of peptide-MHC binding and immunogenicity assays in the future.

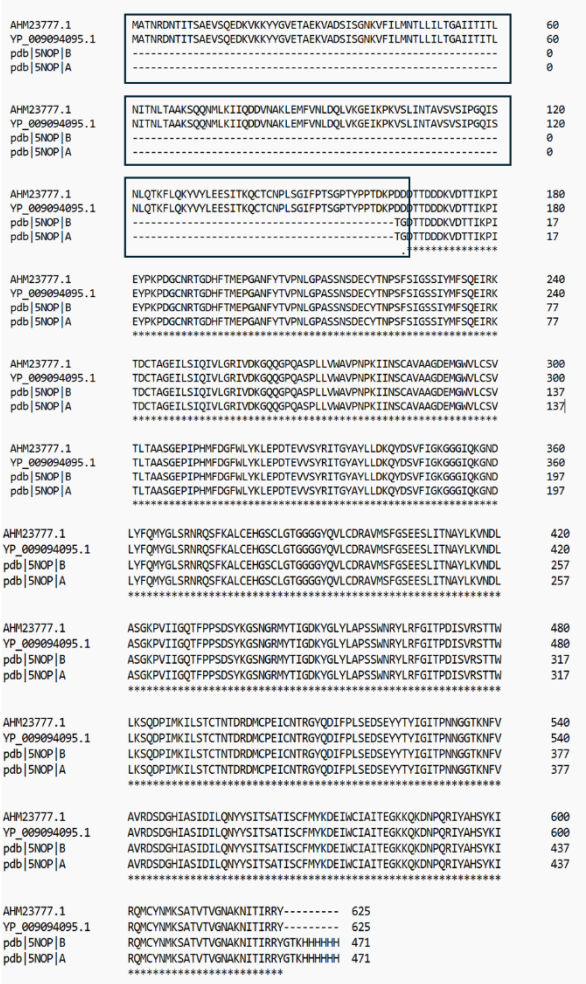

Figure 1. Multiple sequence alignment of the four available Mojiang virus (MojV) attachment glycoprotein (G) sequences (YP_009094095.1, AHM23777.1, and PDB 5NOP chains A and B). The region with the greatest variability in the N-terminal is indicated by a thick black frame, while the other regions are highly conserved.

Table 1. Predicted linear epitopes of MojV G protein and their antigenicity, allergenicity, toxicity, immunogenicity, conservancy and surface accessibility.

	Sequence	Position	Antigenicity	Allergenicity	Toxicity	Immunogenic	Conservancy (≥90%)	Surface accessibility
HTL	KDEIWCIAITEGKKQ	572–586	1.8937	Non-allergen	Non-toxin	Yes	Yes	Outside
CTL/HTL	LRFGITPDISVRSTT	465–479	1.4636	Non-allergen	Non-toxin	Yes	Yes	Outside
CTL	DTTIKPIEY	174–182	1.3147	Non-allergen	Non-toxin	Yes	Yes	Outside
BCL	LGTGGGGYQVL	385–395	0.5193	Non-allergen	Non-toxin	Yes	Yes	Outside

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Conflict of interest statement

The authors declare no conflicts of interest.

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