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MACEIÓ . ALAGOAS

Abstracts selected for

HGP Award

HGP.1 to HGP.6

SBV 40 ANOS

HGP.1

Effects of albumin nanoparticles loaded with *Pseudomonas aeruginosa* infective phages in an acute pulmonary infection model.

Cunha GA[1], Marangoni GS[1], Durante MFR[1], Sanchietta L[1], Gozzi WP[1], Gabriel MLC[1], Malaquias LCC[1], Oliveira CE[1], Dutra LAL[2], Almeida GMF[2], Coelho LFL[1] - [1]Universidade Federal de Alfenas, [2]Universidade Ártica da Noruega

Pseudomonas aeruginosa is a critical opportunistic pathogen in immunocompromised patients, whose multidrug resistance limits conventional antibiotic therapy options. In response to the need for new antimicrobial alternatives, this study developed and characterized bovine serum albumin nanoparticles loaded with bacteriophages (NPPha) specific to *P. aeruginosa*. Scanning electron microscopy revealed that NPPha exhibited a uniform morphology with an average diameter of 220 nm. To assess the *in vivo* antimicrobial effect, an acute lung infection model in C57BL/6 mice was used, comparing NPPha administration with non-encapsulated phages (VAC1). The animals were anesthetized with intraperitoneal injections of xylazine (10 mg/kg) and infected with 20 uL of *P. aeruginosa* (4×10^7 CFU/ nostril) and then treated intranasally with 10 uL of NPPha or VAC1 (3×10^{11} PFU/mL) per nostril. The results demonstrated that treatment with NPPha preserved alveolar architecture, significantly reduced inflammatory infiltrate, and promoted viral adhesion to the mucosal epithelium. Furthermore, the nanostructured formulation reduced the pulmonary bacterial load by 2-3 $\log_{10}$, whereas the group treated with non-encapsulated VAC1 exhibited severe tissue destruction and no reduction in bacterial density. In conclusion, the albumin-based delivery system enhances the stability and biological activity of bacteriophages, constituting a promising strategy for controlling acute pulmonary infections. Future studies will focus on improving the long-term stability and effects of NPPha against *P. aeruginosa* biofilms.

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HGP.2

REEMERGENCE OF DENV-3 IN BRAZIL: PHYLOGEOGRAPHIC RECONSTRUCTION OF VIRAL SPREAD AND ITS ASSOCIATION WITH DISEASE SEVERITY

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After nearly 15 years, DENV-3 reemerged in Brazil in 2023 through the newly detected lineage 3III_B.3.2. We investigated the spatiotemporal dispersion of this lineage and its epidemiological impact in Brazil. We generated 87 near-complete DENV-3 genomes sampled across nine Brazilian states and analysed them alongside publicly available sequences, enabling the most comprehensive assessment of lineage 3III_B.3.2 spread in Brazil to date. Phylogeographic analyses reconstructed viral introductions and spatial spread of lineage 3III_B.3.2. In parallel, dengue case notifications (2023–2025) were used to fit multivariable logistic regression models evaluating associations between DENV serotypes and severe dengue while adjusting for demographic and spatiotemporal covariates. Lineage 3III_B.3.2 entered Brazil at least 14 times between 2023 and 2024, followed by diversification into six region-specific transmission clades and heterogeneous regional expansion, with multiple introductions likely originating from the Caribbean. Compared with DENV-1, infections caused by DENV-2 and DENV-3 were associated with higher odds of severe dengue (adjusted ORs 1.24–1.71 and 1.47–1.94, respectively). Sensitivity analyses restricted to children ≤2 years suggested that the DENV-2 association persisted, whereas DENV-3 estimates were not statistically significant. Our results reveal a dynamic pattern of multiple introductions and regionally structured spread of 3III_B.3.2 rather than a single expansion event. Although the observed associations of DENV-2 and DENV-3 with severe dengue may be influenced by secondary infections, our findings suggest co-circulation of multiple DENV serotypes may contribute to more severe outcomes, reinforcing the importance of sustained surveillance.

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HGP.3

Uncovering the viral diversity of amazonian rivers

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The Amazon region contains the vastest river network of the globe and has an invaluable importance to worldwide climate and water safety. This study investigated viral diversity, gene content, life strategies, phage-host relationships, and environmental interactions across four amazonian rivers. A total of 5 samples per city in triplicate (60 samples) were collected from four rivers belonging to four different cities in the state of Pará, The samples were filtered for DNA extraction and shotgun sequencing, and had their physicochemical parameters measured alongside georeferencing data. Samples were assembled with Metaspades and viral sequences were predicted with VirSorter2, DeepVirFinder, CheckV and Genomad. IPHOP was used for host prediction. Viral relative abundances were retrieved using Bowtie2 and the relative abundances of the viral scafolds were used to calculate viral alpha and beta diversity, to calculate correlations with the collected environmental parameters. The study identified a total of 6648 viral operational taxonomic units (vOTUs), including diverse bacteriophages, *Nucleocytoviricota*, and *Maveriviricetes*. While relative abundance patterns varied by river, cyanophages from the *Kyanoviridae* family consistently dominated. The Marabá and Altamira rivers displayed the highest alpha diversity. Viral community structure was primarily driven by pH (beta diversity), while alpha diversity correlated positively with dissolved oxygen, temperature, and pH, but negatively with deforestation. The analysis revealed viral-host linkages to 28 microbial phyla, predominantly showcasing a lytic lifestyle. Additionally, 514 auxiliary metabolic genes (AMGs) were identified, linking 27 microbial families to key biogeochemical cycles (carbon, phosphorus, nitrogen, methane, and sulfur), underscoring viruses' critical role in freshwater ecosystems.

HGP.4

ECOLOGICAL AND EVOLUTIONARY ANALYSIS OF *ORTHOHANVIRUS* REVEALS SPECIES-SPECIFIC CODON USAGE AND HOST ADAPTATIONS TO *OTHOHANTAVIRUS ANDESENSE*

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Hantaviruses, members of the genus *Orthohantavirus*, circulate as emerging zoonotic viruses, but very little is known about their transmission dynamics. The Andes Virus (*Orthohantavirus andesense*, ANDV) is a zoonotic rodent-borne pathogen, which was at the center of the cruise ship-outbreak, between April and May of 2026. Considering the unprecedented nature of this episode, we aimed to characterise the ecological and evolutionary drivers of ANDV' reemergence in a human-to-human transmission chain. In this context, we retrieved from GenBank near-complete genomic data, and from the curated dataset, we applied evolutionary and codon usage analyses to investigate ecological and evolutionary patterns related to human transmission. We found a major evolutionary and geographical distinctions considering Old and New world *Orthohantavirus*. To ANDV, we attested the existence of two major lineages within the species, with most of the genomes obtained from Argentina, Chile and Brazil, showing high congruence through the phylogenetic reconstruction for each genomic segment (L, M and S). The codon usage analyses showed a great bias within host and biogeographical patterns of distribution. Also, the inter-host codon usage analyses showed a higher adaptiveness to human and rodent hosts. At the intra-host analyses for distinct human tissues, we observed a congruence of the results to all the segments, with higher adaptation to testis, liver and kidney. In conclusion, the results indicate patterns of codon usage for *Orthohantavirus* in their different natural hosts, corroborating a long period of coexistence between the organisms and also evidence of *Orthohantavirus* adaptation to humans as its dead end host.

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HGP.5

CHARACTERIZATION OF THE VIROME ASSOCIATED WITH GLOBALLY DISTRIBUTED PHLEBOTOMINE SANDFLIES

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Arthropod-associated viral diversity is vast and largely uncharacterized. Human activities such as deforestation and agricultural expansion alter natural habitats, modifying vector-host dynamics and increasing the risk of viral spillover. Phlebotomine sandflies (Diptera: *Psychodidae*) are blood-feeding vectors of major medical and veterinary importance, transmitting *Leishmania* and economically relevant viruses, yet their resident virome remains poorly explored. Characterizing these viral communities is crucial to understand vector ecology and its potential impact on animal and agricultural health. We conducted a metatranscriptomic survey of viral diversity across New and Old World lineages, mining 125 public RNA-seq libraries from 15 sandfly species with a validated metaviromic pipeline. We recovered 37 non-redundant putative viral sequences representing 32 unique species across 13 families. Plant- and fungus-associated viruses, particularly *Tombusviridae*, were distributed among Old World *Phlebotomus* species. In *Sergentomyia schwetzi*, a species with no confirmed role in human pathogen transmission, we recovered two of the longest genomes of the survey, belonging to *Iflaviridae* and *Dicistroviridae*. In the New World, we identified a putative nodavirus in *Nyssomyia neivai*, expanding the phlebotomine genera associated with nodaviruses beyond *Lutzomyia*. Most viruses were insect-specific and host-restricted, possibly reflecting the predominance of laboratory-derived libraries. Detection of a Lutzomyia nodavirus in an embryonic-stage library, although at low abundance, is compatible with vertical transmission. These findings show that Phlebotominae viromes reflect their ecological niches and dual-feeding behaviors, providing the most comprehensive RNA virome characterization of this subfamily to date and highlighting public transcriptomic data for environmental surveillance. Financial Support: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 00.

HGP.6

Acute IFN-γ responses predict and mediate chronic pain caused by arthritogenic alphavirus infection

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Chikungunya virus (CHIKV), a mosquito-borne alphavirus, causes 17.7 million musculoskeletal cases annually, of which 848,000 progress to debilitating chronic disease. We combined an intra-articular CHIKV infection model in mice, genetic and pharmacological IFN-γ manipulation, and a prospective patient cohort to investigate chronic pain mechanisms. We found that CHIKV infection induced prolonged mechanical hypersensitivity, joint inflammation, cartilage catabolism, and sensory neuron stress despite the absence of detectable viral dissemination to dorsal root ganglia. CHIKV-infected joints exhibited elevated levels of IFN-γ associated with infiltrating T cells. Administration of recombinant IFN-γ into joints recapitulated pain hypersensitivity and neuronal stress, whereas genetic deletion of IFN-γ or pharmacological blockade of its receptor abrogated pain development without affecting viral load. We identified that ~50% (12/24) of CHIKV-infected mice developed persistent pain and exhibited elevated systemic IFN-γ levels during both the acute and chronic phase. Chronic CHIKV pain was associated with peripheral nerve injury and central sensitization features, including reduced nerve conduction velocity, marked ultrastructural myelin disruption, sensory-neuron caspase-3 activation, and increased dorsal horn neuronal pERK and GFAP. Consistently, patients who developed chronic arthralgia had higher acute-phase IFN-γ than those who recovered. Finally, approximately 40% of Mayaro virus-infected mice (04/10) developed persistent pain, extending this phenotype to another arthritogenic alphavirus. Collectively, these findings establish IFN-γ as a neuroimmune mediator between antiviral responses and neural dysfunction, supporting its potential as a biomarker and therapeutic target for chronic diseases caused by arthritogenic alphaviruses.

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