Report of a novel pathogenic orthohantavirus in Tucuman, Argentina
Journal Club sessions

Brignone, Julia *et al*., 2025. Revista Argentina de Microbiología (IF 1.8, Q4)
Presented on March 31, 2025

FACULTAD DE
MEDICINA
UASLP

LABORATORIO DE GENOMICA VIRAL Y HUMANA
FACULTAD DE MEDICINA
UASLP

MSc. JM Mendoza-Mendez
SE Guerra-Palomares
CA García-Sepúlveda

Laboratorio de Genómica Viral y Humana
Facultad de Medicina
Universidad Autónoma de San Luis Potosí

Hantaviruses in Argentina

Hantavirus pulmonary syndrome (HPS): acute viral disease caused by members of the genus Orthohantavirus, family Hantaviridae.

Main transmission route to humans through aerosolization of rodent excreta.

Andes virus a major concern due to person-to-person transmission & high mortality (25-35%).

The International Committee on Taxonomy of Viruses (ICTV) recognizes the circulation of two HPS-causing hantavirus species in Argentina:

- Orthohantavirus andesense (Andes, Lechiguanas & Orán viruses)
- Orthohantavirus negraense (Laguna Negra virus)

Other orthohantavirus circulating in Argentina that do not meet ICTV criteria for classification into the recognized orthohantavirus species::

- HPS-associated (Juquitiba, Bermejo, HU39694 & Alto Paraguay)
- Not-associated to human disease (Maciel, Pergamino, Leyes & Seoul)

Hantaviruses in Argentina

Before 2016, Tucuman was not considered endemic for hantavirus, although suitable rodent reservoirs had been identified.

Since 2016, three confirmed cases with no history of travel outside the province were identified.

Two 2016 HPS cases identified with probable exposure in Burruyacú department both deceased.

One 2017 HPS case with probable exposure in Leales department, survived.

Orthohantavirus HU39694 genotype4 identified.

The aim of this report is to describe the first clinical case of HPS caused by an **unknown orthohantavirus genotype** in the province of Tucuman, Argentina.

2021 HPS in Tucuman province (1st case)

Previously healthy young woman resident of Tucuman.

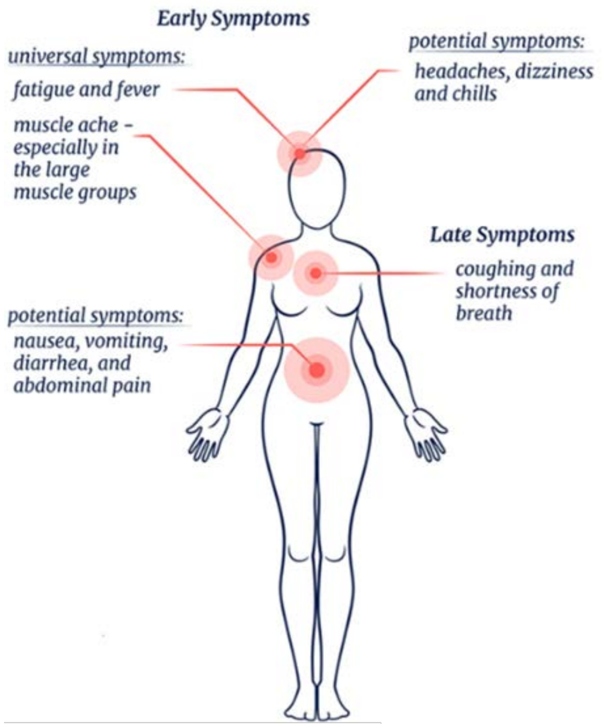
Previous visits to rural areas known as potential exposure sites.

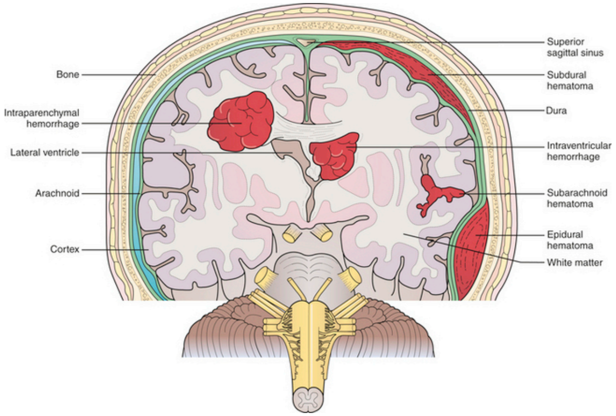
Oct 18, 2021. Debut
- Fever & asthenia.

Oct 21, 2021. Labs
- Nasopharyngeal swab (NPS) SARS-CoV-2 negative.
- Serum sampled (for confirmatory ELISA).

Oct 22, 2021. Labs
- Nasopharyngeal swab (NPS) SARS-CoV-2 negative.

Oct 23, 2021. Admitted to hospital
- Acute respiratory illness progresses to respiratory failure.
- ICU and mechanical ventilation.
- Thrombocytopenia, haemo-concentration & lactic acidosis.
- Cerebral/pulmonary parenchymal haemorrhage.
- Death within few 2 hours.





2021 HPS in Tucuman province (2nd case)

Young healthy male resident of Tucuman.

Previous three-day cammping trip to area known as potential exposure sites 25 days prior to debut.

Oct 20, 2021. Debut

- Fever, nausea, headache & abdominal pain.

Oct 24, 2021. Labs

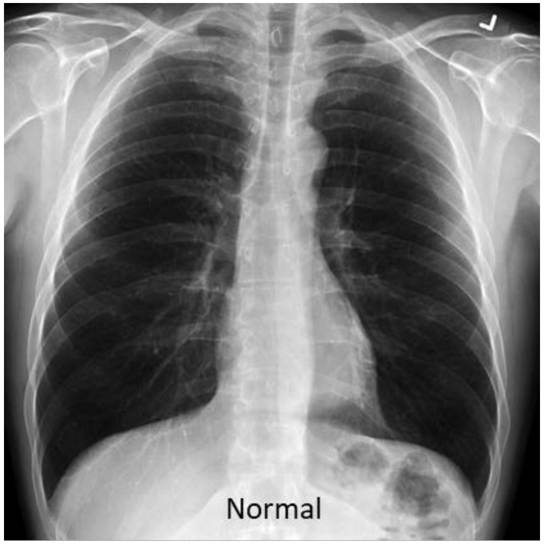
- Diagnosed with right basal pneumonia.
- Empiric antibiotics.
- High-flow cannula ventilation til Oct 26.
- DENV, SARS-CoV-2, Leptospira & other bacterial assays proved negative.

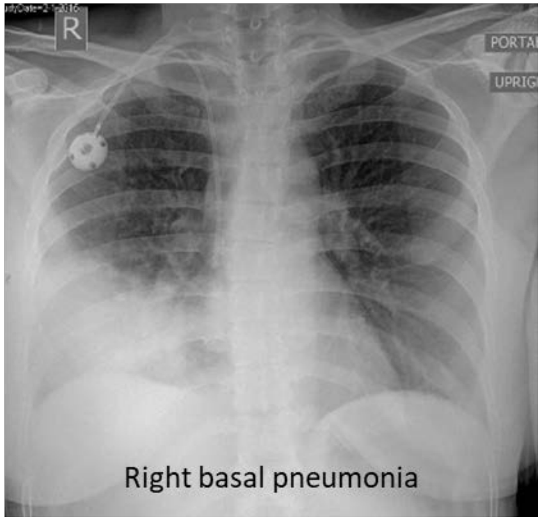
Oct 29, 2021.

- Serum sampled (for confirmatory ELISA)

Nov 2, 2021 (nine days after admission).

- Dicharged due to favourable evolution.





Methodology

Anti-Maciel orthohantavirus IgG/IgM ELISA.

Nested RT-PCR genomic identification and molecular analysis.

Total RNA Qiamp kit from serum.

Nested RT-PCR amplification of orthonatavirus:

- S Segment (NP) targeting 447 bp amplicon.
- M Segment (G2) targeting 513 bp amplicon.

QIAquick Gel Extraction purification of amplicons.

Sanger sequencing of amplicons in 3500 Avant genetic analyzer.

Homology analysis through BLAST.

Sequence alignment with Muscle and AliView.

Evoilutionary model determination with ModelFinder.

Maximum likelihood phylogenetic analysis with W-IQ Tree.

Ultrafast bootstrap analysis of 2000 replicates for clades statistics visualized with FigTree.

Nucleotide similarity percentages calculated with MEGA11

Epidemiological investigation (both cases)

Serum samples from both cases (on different days, D9 and D18) submitted to Instituto Nacional de Enfermedades Virales Humanas (INEVH-ANLIS) in Pergamino, Argentina.

Diagnostic confirmation of HPS by serum ELISA IgM with titre ≥ 6400.

IgG not detected in Case 1 but 1600 in Case 2 by day +9.

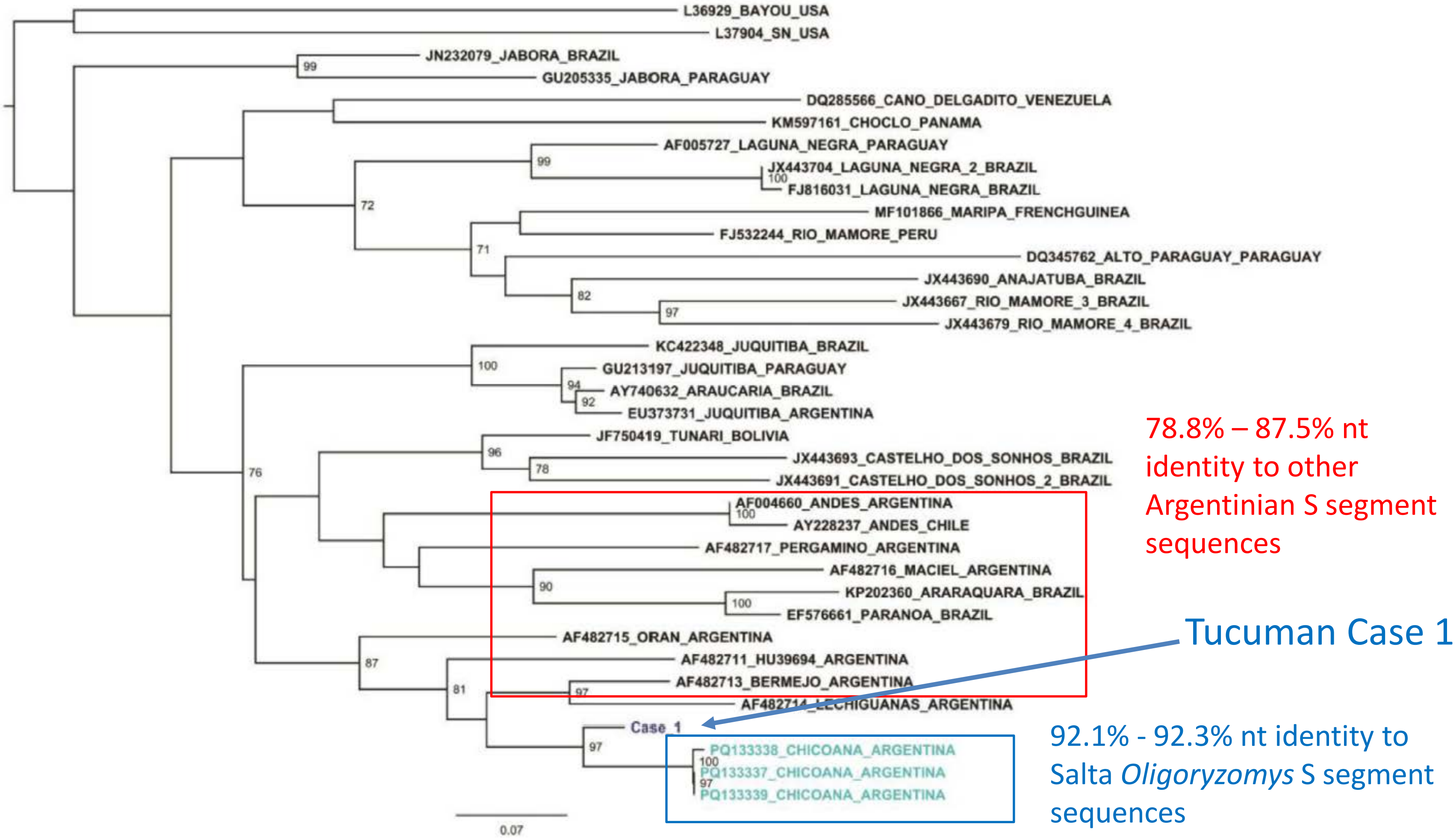
Genomic amplification Case 1

S Segment (NP) PQ248942
M Segment (G2) PQ248943

Global identity to other hantaviruses 82-87% (suggests new genotype).

92-96% identity to sequences obtained from *Oligoryzomys* of Salta province (2014).

Results



78.8% – 87.5% nt identity to other Argentinian S segment sequences

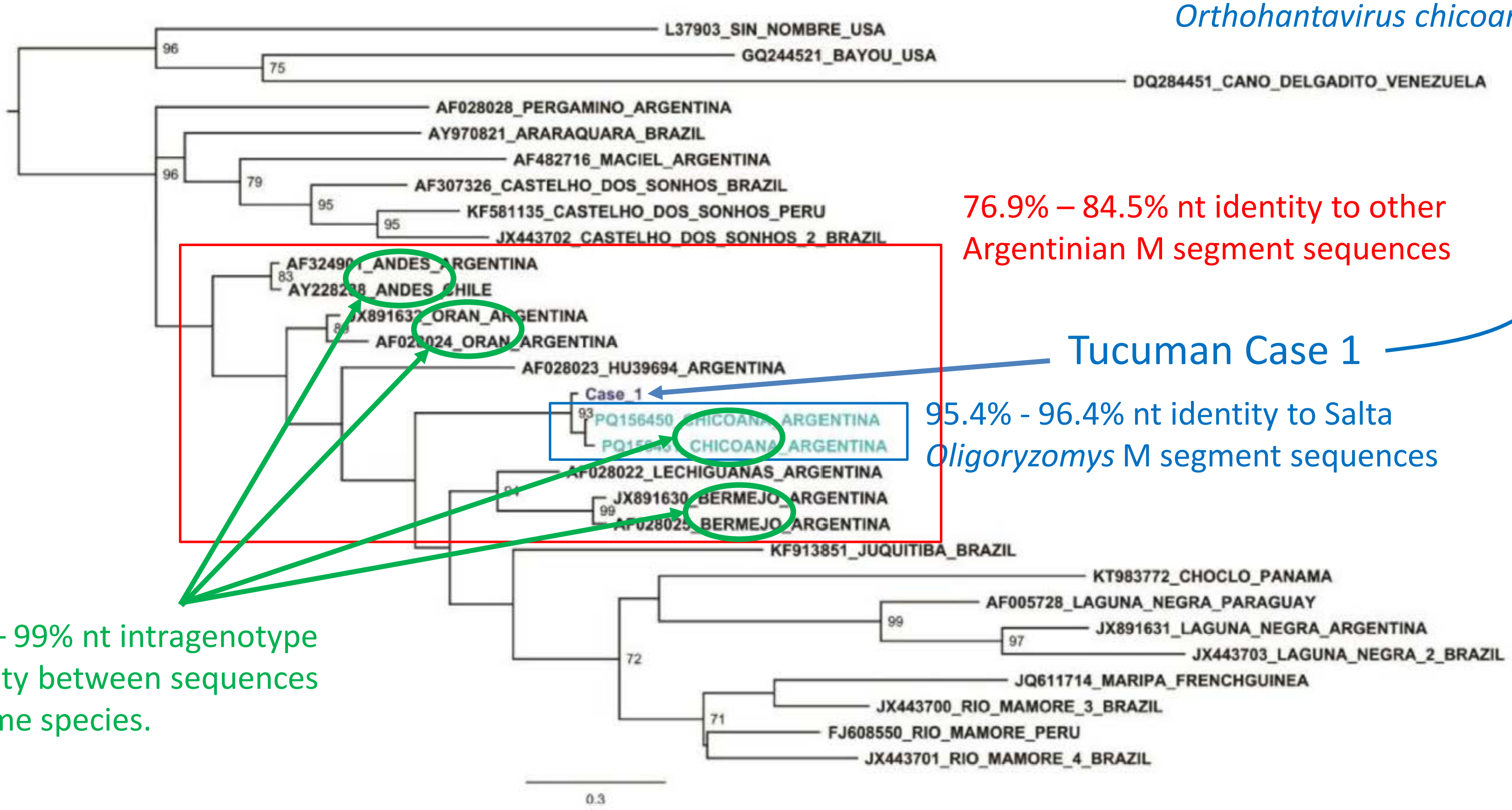
Tucuman Case 1

92.1% - 92.3% nt identity to Salta *Oligoryzomys* S segment sequences

Maximum likelihood tree for a 428 nt fragment of the NP (S segment), using TIM2+F+I+G4 as nucleotide substitution model for the S dataset. Only bootstrap support ≥ 70% shown.

Results

Case 1 HPS very likely due to *Orthohantavirus chicoanense*



76.9% – 84.5% nt identity to other Argentinian M segment sequences

Tucuman Case 1

95.4% - 96.4% nt identity to Salta *Oligoryzomys* M segment sequences

92% – 99% nt intragenotype identity between sequences of same species.

Maximum likelihood tree for a 329 nt fragment of the G2 (M segment), using TIM2+F+I+G4 as nucleotide substitutionmodel for the M dataset.

RVPVE

Red de
Vigilancia de
Patógenos
Virales
Emergentes

FACULTAD DE MEDICINA UASLP
FACULTAD DE INGENIERÍA
CEFPPE - SLP
CIAAS - CIACYT
CENTRO COLABORADOR OMS/OPS UASLP-MÉXICO

Christian A. García-Sepúlveda — Laboratorio de Genómica Viral & Humana, Medicina UASLP
Sandra E. Guerra-Palomares — Laboratorio de Genómica Viral & Humana, Medicina UASLP
Dulce Ma. Hernández Piña — Laboratorio de Genómica Viral & Humana, Medicina UASLP
J. Manuel Mendoza Méndez — Laboratorio de Genómica Viral & Humana, Medicina UASLP
Andreu Comas García — Departamento de Microbiología, Medicina UASLP
Mauricio Comas García — Unidad de Microscopía de Alta Resolución, CICSAB Ciencias UASLP
Guillermo Espinosa Reyes — Centro de Investigación Aplicada en Ambiente y Salud (CIAAS), Medicina UASLP
Fernando Díaz-Barriga Martínez — Centro de Investigación Aplicada en Ambiente y Salud (CIAAS), Medicina UASLP
Juan Carlos Cuevas Tello — Algoritmos de Inteligencia Artificial Aplicados, Ingeniería UASLP
Ignacio Amezcua Osorio — Comité Estatal para el Fomento y Protección Pecuaria de San Luis Potosí.

www.genomica.uaslp.mx
GenomicaUASLP
GenomicaUASLP

Laboratorio Nacional CONAHCYT
Alta Contención Biológica
LANCOBI
IPN
UNAM
UASLP

Laboratorio de Genómica Viral & Humana BSL-3, Facultad de Medicina UASLP

- Dr. Christian A. García-Sepúlveda (Operaciones BSL-3, Virología Molecular)
- Dra. Sandra E. Guerra-Palomares (Virología molecular)
- Dr. Andreu Comas García (Epidemiología molecular)
- Dra. Sofia Bernal Silva (Virología molecular)
- Dr. Fernando Díaz-Barriga Martínez (Una salud integral)
- Dr. Mauricio Comas García (Microscopía electrónica y virología estructural)
- Dr. Roberto González Amaro (Inmunología)
- Dr. Juan Carlos Cuevas Tello (Aplicaciones de algoritmos de inteligencia artificial)

Laboratorio Nacional de Vacunología y Virus Tropicales, Escuela Nacional de Ciencias Biológicas IPN

- Dra. Ma. Isabel Salazar Sánchez (Virología molecular e inmunología)
- Dr. Jesús Miguel Torres Flores (Operaciones BSL-3)
- Dr. Joel Armando Vázquez Pérez (Virólogo especializado en Influenzavirus)
- Dr. Rosa Elena Sarmiento Silva (Viróloga especializada en virus respiratorios)

Departamento de Inmunología del Instituto de Investigaciones Biomédicas UNAM

- Dra. Clara Inés Espitia Pinzón (Operaciones BSL-3)
- Dr. Antonio García Knight (Inmunólogo viral con énfasis en virus emergentes)
- Dr. Renato León Rodríguez (Virología molecular)
- Dr. Wenceslao Coronado Aceves (Evaluación de fármacos in vitro e in vivo)
- Dra. Georgina Diaz Herrera (Médica Veterinaria pequeñas especies)
- Maestra Erika Segura Salinas (Evaluación de fármacos potenciales)