

Natural hosts of different hantavirus genotypes in south America: who is who?

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Abstract

Accurate species identification of the genus *Oligoryzomys* is particularly important because several species act as natural hosts of hantaviruses affecting humans. We used molecular phylogenetic and a phylogeographic approaches to assign the specific status to individuals from a wide geographical area of Central and South America. We summarize here the rodent-hantavirus relationship emerging from our results and from those available in the literature.

Keywords: Hantavirus, molecular phylogeny, natural hosts, *Oligoryzomys*, phylogeography

Introduction

The genus *Oligoryzomys* (Rodentia, Cricetidae) groups American native rodents distributed from Mexico to the south of South America. Several species of the genus have been recognized as natural hosts of the etiological agents of Hantavirus Pulmonary Syndrome (HPS) (Levis et al., 1998; Padula et al., 2000). In some cases, two different viral lineages have been associated with the same species of *Oligoryzomys*, contradicting the hypothesis that hantavirus genotypes are host-related (Schmaljohn et al., 1985). These results could be explained by the confusing specific taxonomy of *Oligoryzomys*, mainly because of the high similarity in discrete morphological characters and the lack of revisions taking into account regional differences. To contribute to the knowledge of taxonomy, distribution and evolutionary relationships of *Oligoryzomys*, we analyzed sequences of mitochondrial (mt) DNA in individuals from a vast geographical area of Central and South America. We used standard phylogenetic methodologies but, when different well supported clades within a recognized species were detected, a phylogeographic approach was applied to infer their taxonomic status. We also integrated our results with host-parasite relationships reported for the genus *Hantavirus*.

Material and methods

Tissues were collected from live-trapped animals from Argentina, Chile and Uruguay. The mtDNA control region and *cytochrome b* (*cyt b*) were used as genetic markers, following procedures described in Rivera et al. (2007) and González-Ittig et al. (2010). All the sequences of different species of *Oligoryzomys* from Central and South America available in GenBank were incorporated to the phylogenetic inferences, and when appropriate to the phylogeographic analyses. Data were analyzed using maximum parsimony (MP), maximum likelihood (ML) and Bayesian methods. Regarding the phylogeographic analyses, we obtained a median-joining network, performed a hierarchical analysis of molecular variance (AMOVA), a mismatch distribution analysis and calculated standard diversity indices.

Results and Discussion

The phylogenetic trees obtained with both mtDNA segments, using MP, ML and a Bayesian approach presented similar topologies. On the bases of the monophyletic clades recovered, their statistical node support, and in the context of previous available information from cytogenetics and geographical distribution, the following species of *Oligoryzomys* were validated: *O. chacoensis*, *O. destructor*, *O. fornesi*, *O. longicaudatus*, *O. microtis*, *O. nigripes*, *O. stramineus*, *O. moojeni*, *O. fulvescens*, *O. vegetus*, *O. delicatus* and *O. rupestris*. Recently, Hanson et al. (2011) compared *cyt b* sequences of specimens of *Oligoryzomys* captured in Panama and western Venezuela with those from GenBank assigned to *O. fulvescens*; the authors suggest that *O. delicatus* and *O. costaricensis* are separated species from *O. fulvescens*. The specific status of *O. magellanicus*, *O. griseolus*, *O. victus*, *O. andinus*, and *O. arenalis*

are still dubious and should be revised carefully in integrative studies based on molecular, cytogenetic and morphological data from samples covering a wider geographical range.

Regarding the nominal species *O. flavescens*, our phylogeographic analysis revealed the existence of at least four different lineages allopatrically distributed (three of them are present in Argentina). The species *O. flavescens sensu stricto* would have experienced a recent range expansion.

Tab. 1 Species of *Oligoryzomys* acting as reservoirs of different hantavirus genotypes and geographic distribution of rodent natural hosts (*according to Hanson et al., 2011)

Species	Distribution	Hantavirus genotype
<i>O. longicaudatus</i>	Southern Argentina and Chile	Andes
<i>O. flavescens</i> “West”	NW Argentina, SW Bolivia and W Paraguay	Bermejo
<i>O. flavescens sensu stricto</i>	E Argentina and S Uruguay	Lechiguanas
<i>O. nigripes</i>	NE Argentina, E Paraguay and S Brazil	Juquitiba
<i>O. microtis</i>	NE Bolivia, E Perú and W Brazil	Rio Mamore
<i>O. chacoensis</i>	N Argentina, SE Bolivia and Paraguay	Oran
<i>O. costaricensis</i> *	West Panama and Costa Rica	Choclo
<i>O. delicatus</i> *	Venezuela and Surinam	Maporal

The integrative analysis of the information on hantavirus genotypes recovered from humans or rodents, and the available data on species delimitation and geographic distribution in *Oligoryzomys*, supports the following relationships between natural hosts and viral genotypes:

The assignation of accurate relationships among different hantavirus genotypes and their hosts is essential to delimit areas in which the HPS could be endemic.

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