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Original Investigation

Estimating habitat suitability for potential hantavirus reservoirs in north-western Patagonia using satellite imagery: Searching for the best predictive tools

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ABSTRACT

We modelled potential distribution maps for four species of rodents known to be reservoirs of the hantavirus disease. These models provide general distribution hypotheses based on a 14-year period and 274 field capture sites. Satellite remote sensing were used to extrapolate climatic and environmental features of potentially suitable habitats for these rodents in Nahuel Huapi National Park and surrounding areas. We tested the accuracy of different satellite sensors for the geographic distribution of *Oligoryzomys longicaudatus*, *Abrothrix longipilis*, *Abrothrix olivaceus* and *Loxodontomys micropus*. When looking for the best method to predict the presence of potential hantavirus reservoir species assemblages, the best prediction levels were obtained using supervised parallelepiped classifications of the SAC-C Normalized Difference Vegetation Index (NDVI) combined with the Digital Elevation Model (DEM) (91.71% for *A. longipilis*, 95.35% for *A. olivaceus*, 91.92% for *L. micropus* and 90.82% for *O. longicaudatus*). These results show that upper components of the landscape structure (e.g. climate and topography) determine the spatial distribution of hantavirus reservoirs independently of the floristic composition of the vegetation patches.

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Introduction

An accurate geographic distribution of small mammal reservoir species is a key factor in the study of transmissible diseases (Ricklefs and Schluter 1993). However, the distribution of many rodent taxa are poorly known in most of the Neotropics (Musser and Carleton 2005). In Argentina, on the one hand, the collecting localities are influenced by the knowledge of the group under consideration and by the presence of specialists in a given region, and the results depict a very conservative version of a distributional hypothesis (Porcasi et al. 2005). On the other hand, the available shaded maps (e.g. Olrog and Lucero 1981; Parera 2002; Bonino 2005) are too general to be useful for epidemiological purposes when decisions need to be made at a local scale. An efficient way to predict accurate distribution maps is under the assumption that a species' spatial distribution is linked to specific habitat requirements. If the distribution of animal species correspond to plant species composition, the prediction level is limited to a local scale and highly dependent

on the knowledge of plant taxonomy and distribution. By contrast, if the distribution of animal species is influenced primarily by environmental and climatic factors, the prediction level can rise to regional scale with high levels of accuracy because satellite tools can be used. Given these facts, the understanding of the correspondence between small mammals and environmental and climatic parameters is a key factor in modelling distribution.

Classical studies found a strong correspondence between small mammal assemblages and vegetation composition. This correspondence has been well documented in research on various types of environments, including deserts (MacMahon 1976), grasslands (Grant and Birney 1979), shrub-steppe (Parmenter and MacMahon 1983), forest-steppe (Pearson and Pearson 1982) and elsewhere (Morton et al. 1994). Small mammals typically occur within and move among habitat patches distinguished on the basis of floristic composition, and thus, a vegetation map should predict small mammal assemblages to some extent.

However, Monjeau et al. (1997) suggested that small mammal assemblages are "more landscape ecologists than systematic botanists" because of their better correspondence to a complex landscape classification based on the hierarchical integration of climate, geology and soil moisture, than to a classification based

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solely on floristic composition. In a comparative study on plants and rodents, Monjeau et al. (1998) suggested that small mammal community composition in Patagonia can be predicted without the aid of a vegetation map and/or floristic information. If climate, geology and geomorphology are the major components structuring landscapes (Klijn and Udo de Haes 1994), then it should be possible to predict small mammal distribution maps using indicators provided by remote sensors that integrate data about environmental factors such as temperature, precipitation and soil properties (e.g. Greenness indices in Rouse et al. 1974), as well as digital elevation models (Sadro et al. 2007). Recent advances in remote sensing of climatic and ecological features via satellite have begun to be used to identify particular environments that are suitable for different species, which represents a great advance in the production of range maps (Skov 2000; Peterson 2001).

Recently, Porcasi et al. (2005) modelled potential distribution maps for one species of small mammal known to be reservoirs of hantavirus (*Oligoryzomys longicaudatus*) and provided a broad hypothetical distribution map for Southern America. This study is aimed at developing a more detailed resolution of the habitat suitability of the reservoir species at regional scale, based on a 14-year period and 274 field capture sites. Our aim is to investigate the habitat suitability of the four species acknowledged as potential reservoirs of hantavirus (*O. longicaudatus*, *Abrothrix longipilis*, *Abrothrix olivaceus* and *Loxodontomys micropus*) using different satellite tools. In addition, we provide a comparison of the predictive capacity of different sensors.

The study case

Hantavirus

Among the most recently emerging diseases are the hemorrhagic fevers transmitted by rodents. Hantaviruses (genus *Hantavirus*, family Bunyaviridae) are rodent-borne zoonotic agents that cause the renal syndrome in Asia and Europe and the hantavirus pulmonary syndrome (HPS) in the Americas (Mills et al. 1999).

The virus Andes, related mainly with *Oligoryzomys longicaudatus*, causes HPS in Argentine Patagonia and adjacent Chile (Levis et al. 1998), where species *Abrothrix olivaceus*, *Loxodontomys micropus* and *Abrothrix longipilis* were also described as hosts (Calderón et al. 1999; Cantoni et al. 2001; Pavletic 2001). Moreover, studies of Cantoni et al. (2001) in Argentinean Patagonia detected hantavirus antibodies with an interannual and seasonal variation in prevalences in these species, which were confirmed also by Ortiz et al. (2004) for the same three species for Chilean Patagonia.

The epidemiology of this disease relies on a thorough understanding of the ecology of small mammals and its relationship to environmental features (Engelthaler et al. 1999), such as the above mentioned climatic factors (i.e. temperature, rainfall), geology and geomorphology (Klijn and Udo de Haes 1994; Monjeau et al. 1998). Prevention measures are essential in mitigating the transfer of the hantavirus from its hosts to humans because no treatment is yet available. In this context, rodent distribution maps could be used to minimize the overlap between human activities and rodents (Mills et al. 1999) through land use zoning, habitat modification, rodent control, and awareness-raising campaigns.

Small mammals in Patagonia

Research by Pearson and Pearson (1982) provided information regarding the correspondence between small mammal species distribution and precipitation. Monjeau (1989) studied the correspondence between small mammal assemblages and 11 envi-

ronmental indicators. Studies by Heinemann et al. (1995), Hillyard et al. (1995), Lozada et al. (1996), Guthmann et al. (1997), Sikes et al. (1997) and Kim et al. (1998) gave information on the ecology and distribution of several species of small mammals in or near the study area. Monjeau et al. (1997) emphasized the correspondence between the composition of small mammal species assemblages and the landscape divisions proposed by Soriano (1983) and del Valle et al. (1995). Monjeau et al. (1998) demonstrated that assemblages of both plants and small mammals corresponded to the upper divisions of these landscape classifications, which are based on climatic and geomorphological features.

Material and methods

Study site

The study area is located between 40°20' and 41°45' latitude South, and 69°30' and 72°00' longitude West (Fig. 1). The study area is characterized by a pronounced gradient in annual rainfall ranging from above 4000 mm in the Andean Valdivian Forest to less than 200 mm in the eastern edge (Prohaska 1976). The western half of the area is also associated with a pronounced altitudinal component. Most of the variation in this West-East gradient takes place in the first 150 km, producing some of the sharpest biotic transitions known (Quintanilla Perez 1983; Veblen and Lorenz 1987). Pearson and Pearson (1982) concluded that the composition of small mammal assemblages changes substantially over very short geographic distances in relation to the rainfall.

Trapline survey

In addition to the near 500 specimens collected by Monjeau and colleagues in previous studies (Monjeau 1989; Heinemann et al. 1995; Hillyard et al. 1995; Lozada et al. 1996; Guthmann et al. 1997; Sikes et al. 1997; Monjeau et al. 1997, 1998; Kim et al. 1998), trapline data were made available by O. P. Pearson, M. I. Christie, D. Sage, J. Kirsch, A. Dickerman, and M. Scott. Two or more lines were run in different land units too close to each other to be discriminated as different points at the scale of the map. During the whole survey, 274 trap lines of Sherman live-traps or Museum Special snap-traps were run to collect small mammals. Trap lines ranged from 200 to 400 traps per night at each locality, with a distance between traps of 10 m. A total of 4663 specimens from these captures are stored in the Museum of Vertebrate Zoology (University of California, Berkeley), the Bell Museum of Natural History (University of Minnesota, Saint Paul), the Zoological Museum of Wisconsin (University of Wisconsin, Madison), the Museum of Comparative Zoology (Harvard University), and the Museo Municipal de Ciencias Naturales, Lorenzo Scaglia (Mar del Plata, Argentina). The 274 trapping sites were geo-referenced in the field. Fig. 1 shows the study area with the 274 trapping sites and the steep gradient that characterizes the landscape.

As we consider data based on different trapping efforts to be inadequate for a reliable quantitative estimate of species abundance, we used only qualitative data in the treatment of small mammal communities. Considering that the presence-data approach is corroborated with larger and more quantitative investigations in the same region, we consider it to provide an accurate representation of the species assemblages.

Remote sensing and meteorological data

Data were generated using three satellites. Static data were obtained from SAC-C MMRS and Landsat TM sensors, and dynamic data in the form of 10-year time series from the NOAA AVHRR sensor that also includes 20 years of rainfall and temperature variation.

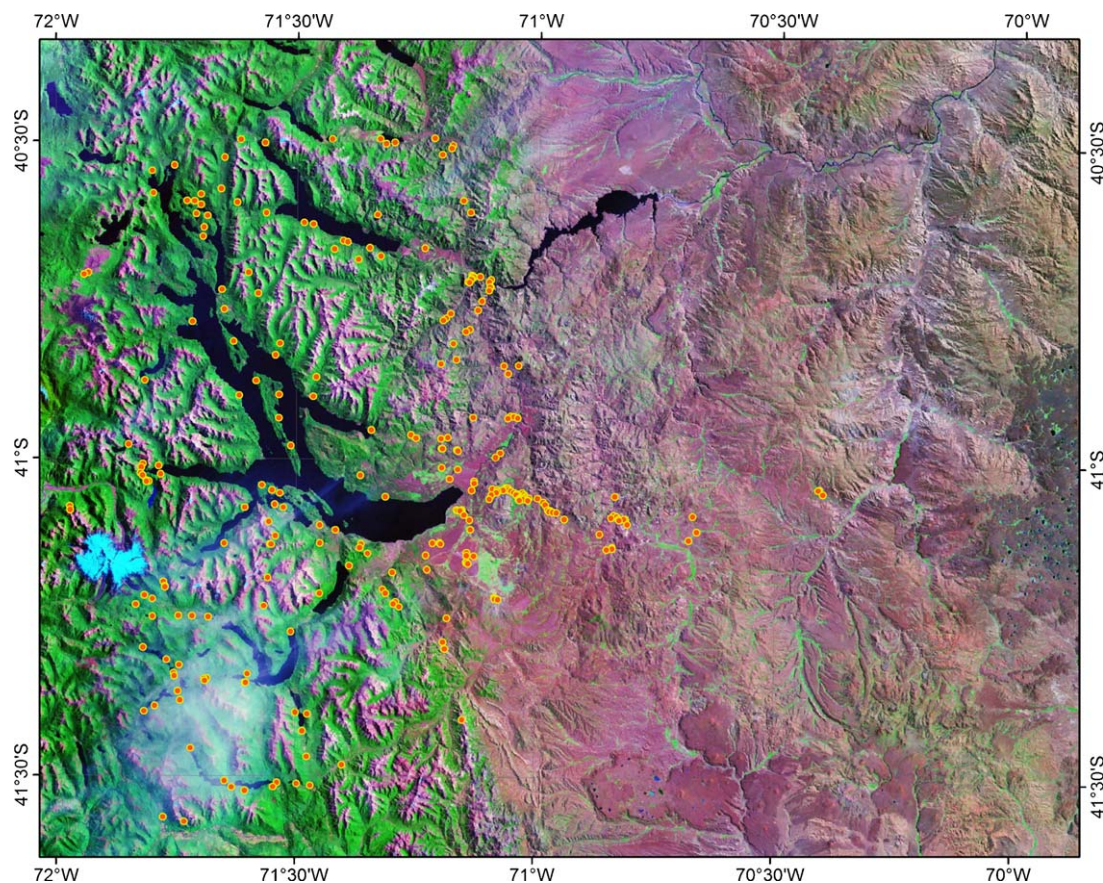


Fig. 1. SAC-C MMRS image (April 12th, 2001 – Path 232 Row 66/97 – R:B5, G:B4, B:B2) of the sampling area, with the location of the 274 trapping sites and the steep landscape gradient.

Data sets incorporate topographic features derived from the Shuttle Radar Topography Mission (SRTM). Composite multi-band images include raw bands of each sensor, the Normalized Difference Vegetation Index (NDVI, Jensen 1986) and digital elevation models. All data analysis and processing operations were performed using ENVI 4.1 software. Values range from -1 to $+1$ for NOAA AVHRR, Landsat and SAC-C MMRS sensor data.

Environmental composite image at the NOAA sensor scale

The database was processed by CONAE (Comisión Nacional de Actividades Espaciales; Argentina) and represents a compilation of three different sources of information resampled at a 1 km pixel size (Porcasi et al. 2005). This database, available at <http://www.daac.ornl.gov>, contains the following environmental variables: (Band 1) rainfall variation is depicted by the first Principal Component of a Principal Component Analysis (PCA) applied to a monthly time series of mean rainfall rasterized grid of an approximately 50 km spatial resolution over a period of 30 years (Leemans and Cramer 1991; Cramer and Leemans 2001); (Band 2) and (Band 3) Normalized Difference Vegetation Index (NDVI) and Land Surface Temperatures (LST) images (Price 1984) were derived from the NOAA-AVHRR meteorological satellite with a post-processing pixel size of 8 km. NDVI and LST datasets are the first Principal Component of the PCA applied to 10 years (1982–1992) monthly averaged NOAA products. This kind of information source has also been widely used in biogeographical modelling with epidemiologic relevance (Rogers et al. 2002). As suggested by Eastman and Fulk (1993) we used a standardized PCA to determine the predominant patterns of variance in such datasets. Finally, (Band 4), Digital Elevation Model (DEM) data, is sampled at 1 km spatial resolution provided

by the US Geological Survey (USGS 2004), available at the following web page: <http://edcdaac.usgs.gov/gtopo30/gtopo30.asp>.

Landsat satellite imagery

Two Landsat 7 ETM images of 30 m pixel resolution (February 1997 – Path 232 Row 88 and Path 232 Row 89 – WRS2) were used to generate a mosaic image of the endemic region of the Patagonian Hantavirus. These images were geo-referenced using the image to image technique (Richards and Jia 2006). A synthetic multi-band image was generated using eight raster layers corresponding to Landsat 7 ETM bands 1–2–3–4–5 and 7, NDVI and a 90 m spatial resolution Digital Elevation Model mosaic (Path 232 Row 88 and Path 232 Row 89 – WRS2) from USGS (2004) also obtained from the GLCF website.

SAC-C imagery

MMRS Real Mode image from the Argentine satellite SAC-C (www.conae.gov.ar) was acquired on April 12th, 2001 (Path 232 Row 66/97) and geo-referenced with a Landsat image mosaic. Even though rodents were captured between 1984 and 1997, we consider possible the assessment of rodent distribution over that period by means of a SAC-C image taken in 2001 because of the relative stability provided by the area's protection status (The Nahuel Huapi National Park). To test this assumption, a radiometric correlation analysis between Landsat TM images acquired in March 1985 and images acquired in December 2001 was performed following Danaher (2002). We carried out a pixel by pixel correlation of "regions of interest" based on the location of the 274 sampling points. Although the two Landsat images used in this analysis were

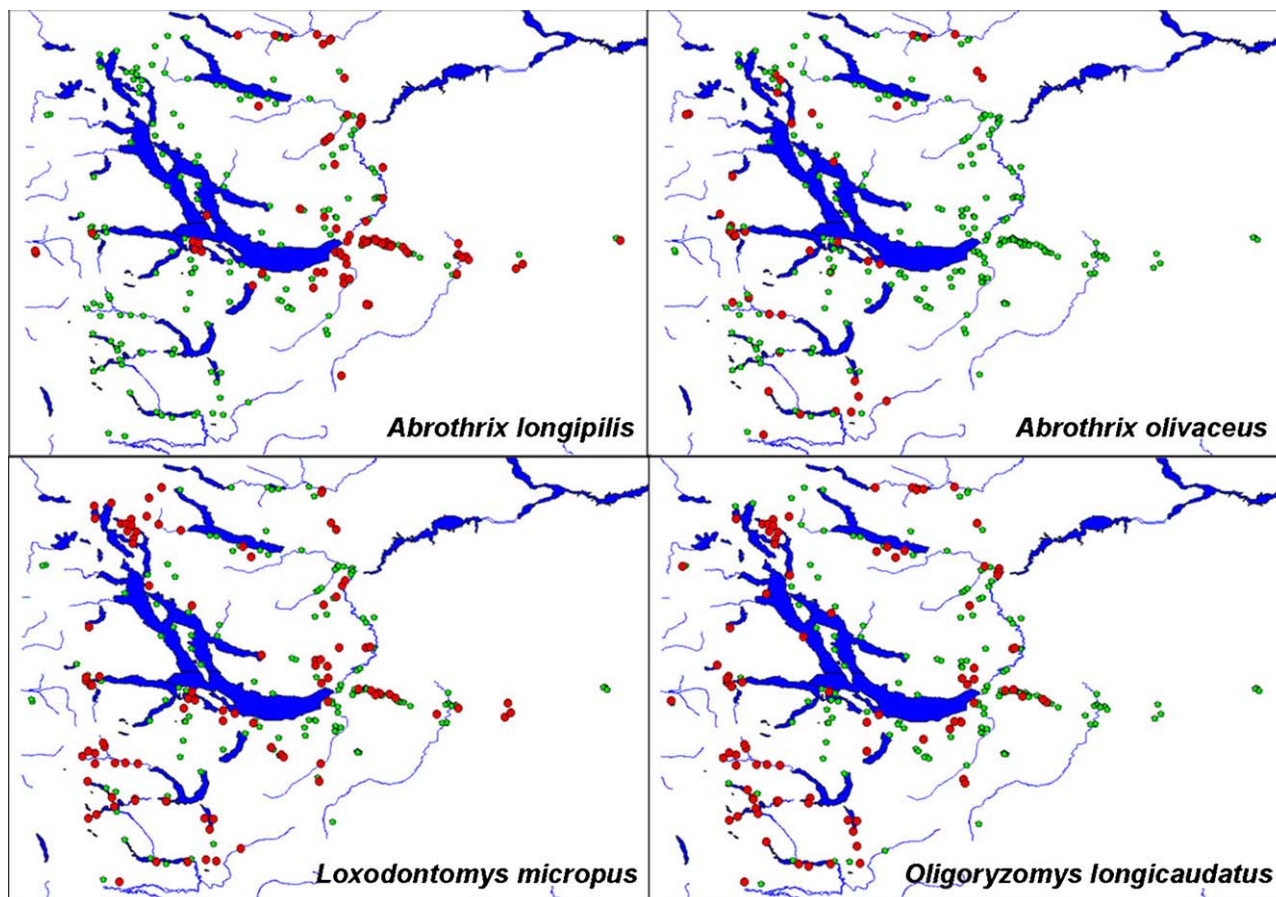


Fig. 2. Capture sites of presence (red big circles) and absence (light green small circles) of the four potential hantavirus reservoirs rodents species for the North Patagonian Region. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of the article.)

taken in two different seasons, we obtained a mean correlation of 84%, with higher values for bands 7 and 2 (90% and 87%), which confirmed the environmental stability of the study area over the time period of interest.

In order to minimize the mountain shadow effect, each SAC-C MMRS band (except band 4) was divided by the value of band 4, obtaining a composite image featuring the following layers: (1) Normalized Different Vegetation Index (same algorithm as for Landsat NDVI), (2) Digital Elevation Model mosaic (058–263 and 058–275) of 90 m spatial resolution (USGS 2004) obtained from the GLCF website, and 3–6) original MMRS bands 1–2–3–5 divided by band 4. The pixel size of different bands was resampled to 175 m.

Classification

Masking

With the aim of avoiding misclassification, we generated masks for each image created by supervised classifications as in Schowengerdt (2007), using training sites of interest with snow, clouds and water bodies (lakes, ponds, rivers and ocean). As classified images often suffer from a lack of spatial consistency (speckle or holes in classified areas), Sieve and Clump post classifications of masks were applied using morphological operators (Schowengerdt 2007). By utilizing these two methods, we avoided the contamination of class information by adjacent classes, which usually takes place when Low pass filtering is applied.

Construction of rodent habitat suitability maps

We generated ROIs (Regions of Interests) of absence and presence of potential hantavirus reservoirs for the three image groups. The images derived from satellite data and environmental variables show the Nahuel Huapi National Park and the adjacent eastward area. As an example, for *Oligoryzomys longicaudatus* we created two regions of interest, for *Oligo* = 0 (176 absence points) and *Oligo* = 1 (98 presence points). A point represents a single pixel of each image. Fig. 2 shows the total of 274 presence–absence sites detailed for each species under study.

Two algorithms of Supervised Classifications were performed for each of the three composite images using ROIs as groundtruthing sites (Schowengerdt, 2007). From the total of ROIs obtained, only 80% were used as training sites. In order to find the most suitable predictive classification method for rodent presence, we tested different combinations of input bands for each composite image.

Supervised parallelepiped classifications were performed using a simple decision rule to classify multi-spectral data. The decision boundaries form an n -dimensional parallelepiped in the image data space. The dimensions of the parallelepiped were decided based on a standard deviation threshold from the mean of the selected class, which was rodent presence. When a pixel value was above the low class threshold and below the high class threshold for all n bands being classified, it was assigned to that class. Areas of the image whose pixel values did not coincide with any of the parallelepipeds were designated as unclassified (Richards and Jia 2006). In parallel,

Table 1

Rodent species presence prediction levels expressed as a percentage of all predicted pixels using as training sites a random subsample of 80% of all ground control points (274 sites). St D indicates the value of the standard deviation used from the mean.

Reservoir species	SAC-C overall accuracy level			
	St D 2	St D 1.7	St D 1.5	Mean accuracy
<i>Abrothrix longipilis</i>	91.71	80.12	77.90	83.24
<i>Abrothrix olivaceus</i>	95.35	76.74	60.47	77.52
<i>Loxodontomys micropus</i>	91.92	85.86	80.81	86.20
<i>Oligoryzomys longicaudatus</i>	90.82	82.47	77.55	83.61
Mean accuracy level	92.45	81.30	74.18	82.64

the Maximum Likelihood classification method was applied considering absence–presence ground data as ROIs (ENVI 4.1. 2004). This method calculates the probability that a given pixel belongs to a specific class by assuming that the statistics for each class in each band are normally distributed. Threshold values closer to 1 indicated strict inclusion of pixels whose values were closer to the means of training sites; when threshold values tended towards 0, the inclusion of pixels took a major dispersion of the values into account. Probability thresholds were selected, and finally each pixel was assigned to the class that had the highest probability (Richards and Jia 2006).

Testing model accuracy

For both classification methods, the prediction accuracy of expected distribution areas was computed using confusion matrixes (Jensen 1986). Then, it was evaluated using a randomly selected subsample (20%) of all presence ROIs as ground control points. We calculated omission and commission errors and the overall accuracy that consisted of the percentage of correctly classified pixels over the complete map (Congalton 1991; Chuvieco 1996) only for presence Parallelepiped classifications. We obtained a Kappa coefficient for the Maximum Likelihood classifications. In this sense, commission errors include both true (over-prediction) and apparent (correctly predicted areas not verifiable as such) commission errors because of the existence of an uncertain absence class (Anderson 2003; Anderson et al. 2003; Porcasi et al. 2005).

Construction of rodent species overlap habitat maps

Using Band Math tool (ENVI 4.1 2004), we summed up all predictive distribution maps obtained from SAC-C and DEM data, by counting presence values of each species as one and absence values as zero. As a result, the overlap habitat map of potential hantavirus reservoirs shows the number of species within each 175 m pixel expressed by a colour gradient ranging from blue (0 species) to red (4 species).

Results

When looking for the best method to predict the presence of potential hantavirus reservoir species assemblages, the most

Table 3

Classification results of the overlap of species with respect to surface units. Prediction areas are expressed as a percentage of the entire SAC-C image area (2nd column) and as square kilometres (3rd column).

Overlap map class	Image area [%]	Habitat area [Km ²]
1 reservoir species	3.1	6658.3
2 reservoir species	1.2	2139.1
3 reservoir species	2.0	3724.8
4 reservoir species	8.0	14652.8
No reservoir species	85.7	156464.1
SAC-C subset scene	100.00	183639.0
Mask	33.5	61210.1

accurate classifications were obtained using the Supervised Parallelepiped classification. These results were obtained using overlays of the NDVI Index derived from a SAC-C data a 90-m DEM derived from the Shuttle Radar Topography Mission (USGS 2004). Using a threshold of 1.7 standard deviations from the mean, we obtained the following accuracy prediction levels per pixel: 80% for *Abrothrix longipilis*, 77% for *Abrothrix olivaceus*, 86% for *Loxodontomys micropus* and 82% for *Oligoryzomys longicaudatus* (Table 1). Fig. 3 shows the predictive distribution map for *O. longicaudatus* in forest and steppe landscapes.

The Maximum Likelihood classifications based on absence–presence data found the highest prediction values when using NOAA input data. Table 2 shows the prediction accuracy levels of the three imagery sets when predicting the distribution of the rodent species.

At a spatial resolution of 1 km × 1 km, the best predictors were time series of composite images of rainfall, NDVI and Land Surface Temperature bands. At this scale, the Digital Elevation Model showed inferior predictive capacity.

Overlap of the predicted distributional range of species

When overlapping the maps of the four species under study (Fig. 4), we noticed that these four species assemblage coexist in most of the humid western part of the study area. In contrast, more than 85% of the predicted areas correspond to potential reservoir absence in the Patagonian steppe (Table 3), where only sprinkled meadows and shrubby riverbands were found suitable for hosting potential hantavirus reservoirs.

Discussion

Predictions, landscape hierarchy and geographical scale—the presence of potential hantavirus reservoir assemblages, *Oligoryzomys longicaudatus*, *Abrothrix longipilis*, *Abrothrix olivaceus* and *Loxodontomys micropus*, can be predicted with high accuracy levels using remote sensors, which record landscape features rather than floristic composition. For instance, a subset of the forest small mammal assemblages is present in isolated patches in the steppe area, although these habitats do not have one single species of flora in common. Thus, climatic, topographic, hydrological, and edaphic

Table 2

Rodent presence–absence prediction levels (expressed as a percentage of predicted pixel by pixel) between observed and predicted values by different sensors (274 sites). The Kappa index expresses the proportion of observed predictions beyond pure chance. RS stands for remote sensing.

RS data	Landsat			SAC-C			NOAA			Mean accur.
	Accur.	Kappa	Bands	Accur.	Kappa	Bands	Accur.	Kappa	Bands	
<i>A. longipilis</i>	72.99	0.44	d15	71.90	0.44	DEM.NDVI	77.01	0.54	All	73.97
<i>A. olivaceus</i>	66.42	0.29	d125	66.06	0.25	DEM.NDVI	77.74	0.46	All	70.07
<i>L. micropus</i>	60.58	0.25	d125	63.87	0.29	DEM.NDVI	73.72	0.45	All	66.06
<i>O. longicaudatus</i>	67.15	0.33	d15	65.69	0.31	DEM.NDVI	78.83	0.54	All	70.56
Mean accur.	66.79	0.33		66.88	0.32		76.82	0.50		70.16

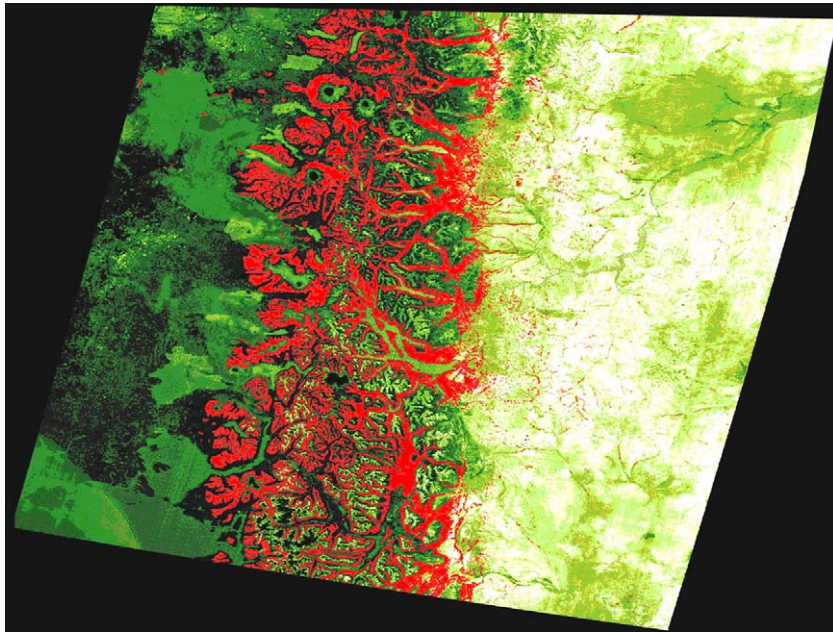


Fig. 3. Predictive distribution map for *Oligoryzomys longicaudatus* in northern Patagonia. Red depicts pixels with rodent presence predicted by the Parallelepiped classification method. Green represents the variation of the NDVI value.

features are the factors that provide habitat suitability for hantavirus reservoirs, and not floristic composition.

Therefore, the results of this research corroborate previous studies by Monjeau et al. (1997, 1998), which showed that the composition of small mammal communities can be predicted without the use of vegetation maps. In these studies, assemblages of

small mammals in northern Patagonia showed a stronger association with the landscape-level classification system proposed by del Valle et al. (1995) than with the vegetation maps established by Soriano (1956) based on floristic composition. This holistic approach is related to the concept of life zones (Holdridge 1947) or land units (Zonneveld 1989). In this frame, the hierarchical struc-

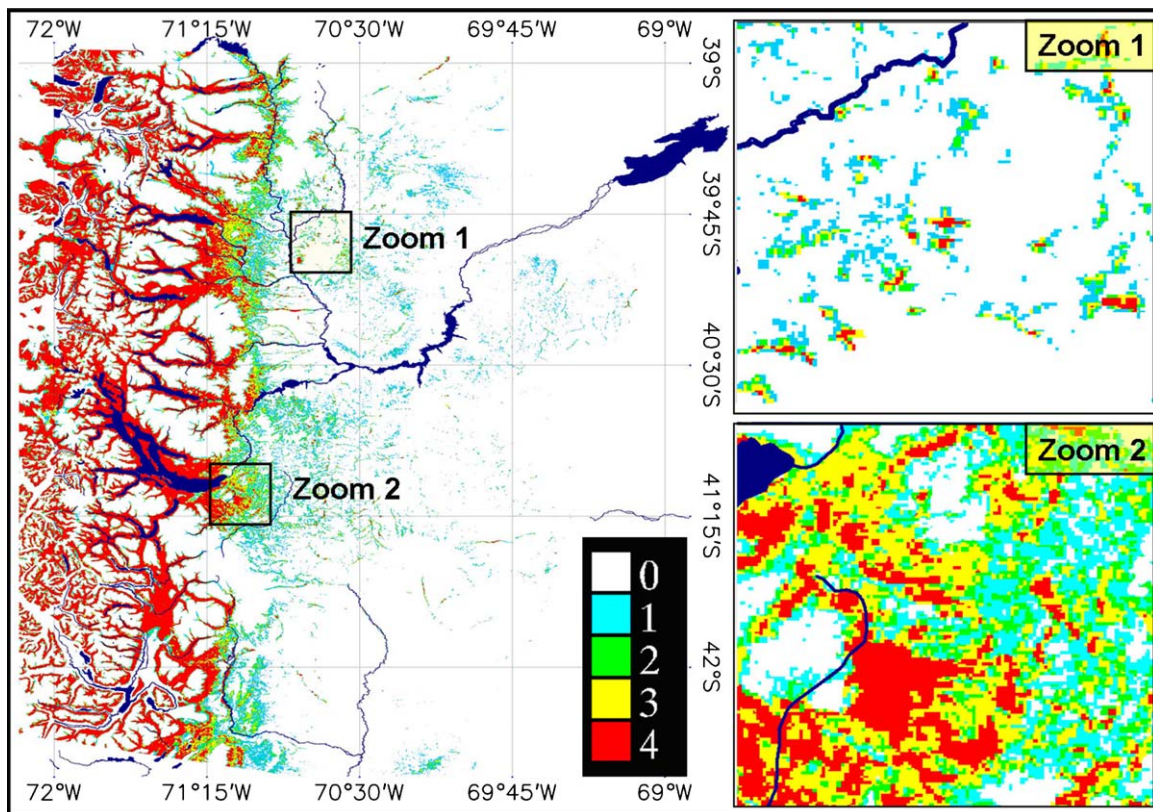


Fig. 4. Different distributions of rodent assemblage for northern Patagonia. Each colour represents the number of potential hantavirus reservoir species that coexist in a 175 m × 175 m predicted area. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of the article.)

ture of nature is a key factor that allows us to predict the presence of hantavirus reservoirs solely with upper level information derived from remote sensing data.

Although information on vegetation is not relevant to predict community assemblages at regional scale (e.g. 1:2,500,000), it is important at local a scale (e.g. 1:50,000). At microhabitat scale, vegetation can function as an indicator of variables that directly influence basic demographic processes such as mortality, natality, and dispersion. As demonstrated by Rogers and Randolph (1993), Randolph and Rogers (1997), Gorla (2002), and Rogers et al. (2002) the spatial distribution of animal species is associated with variability in primary productivity. In addition, other researchers investigated the efficiency of meteorological satellite images by using a vegetation index time series to develop a surveillance system of plagues that depend on microhabitat vegetation cover (Gleiser et al. 1997; Grilli and Gorla 1997). Birney et al. (1976) suggested that, during *Microtus* outbreaks, only those areas that offer sufficient vegetation cover are suited as “source” habitat, where individuals can remain and reproduce. Nevertheless, vegetation coverage acts as a physical component of the landscape providing refuge and food independently of its floristic composition.

Presence/absence data: Considering that this kind of field data is based on disparate trapping efforts, we consider it inadequate for a reliable quantitative estimation of species abundance, essentially because the overlap of the species influences trappability. During hantavirus epidemics in the United States, Childs et al. (1995) and Glass et al. (2002), found that the abundance of HPS reservoirs was related to risk factors around HPS sites. Larrieu et al. (2003) found a correlation between antibody prevalence and human infection. In contrast, there was no correlation found by Larrieu et al. between rodent density and human infection. Cantoni et al. (2001) found no correlation between antibody prevalence and rodent density or human infection. Pearson (2002) confirmed this evidence when describing an outbreak of *Oligoryzomys* in 1997, curiously not locally related with hantavirus, since the number of human infections had reached a peak a year before the rodent outbreak. For all these reasons, we considered the presence–absence data the most suitable source of information to construct our habitat suitability maps as well as future hantavirus risk maps, which would be based on the upper components of landscape structure detected by remote sensors.

Overlap of species: Even though the epidemiological risk associated with the presence and/or abundance of rodent reservoirs is beyond the scope of this study, it is important to clarify that risk does not necessarily increase as you go from one to four species of potential reservoirs (Fig. 4). To the contrary, one could make the case that risk goes down as community complexity increases. For instances, Yahnke et al. (2001) found a decrease in seroprevalence in the primary hantavirus reservoir as the number of species in the small mammal assemblage increased.

Species distribution predicting success: This paper provides the most detailed predictions ever made for hantavirus reservoirs in Patagonia using a combination of satellite tools. It is important to mention that neither the classification based only on NDVI nor the one based only on the DEM attained the prediction levels obtained when combining the data of the two tools using the Supervised Parallelepiped classification.

The lower accuracy levels obtained using the Maximum Likelihood classification in comparison to the Parallelepiped method may be due to our experimental design, which included compiling data from a variety of studies. *Abrothrix longipilis* is extremely “trap-happy” and tends to enter Sherman traps prior to other species, diminishing the effectiveness of the trapping effort for the other species that may be present. For this reason, we were unable to confirm species presence at sites where *Abrothrix longipilis* abundance was high (Monjeau 1989). Finally, in agreement

with Muñoz-Pedrerros et al. (2007), the overlap habitat map shows that less than 15% of the predicted areas correspond to potential reservoir presence, suggesting a low probability of rodent–human encounters in the region. Part of this region is also a national park which would further decrease the probability of rodent–human encounters.

In the Patagonian steppe, 3.1% of the area represents suitable habitat for only one reservoir species: *Abrothrix longipilis* or *Loxodontomys micropus* in meadow patches, or *Oligoryzomys longicaudatus* in shrubby patches, which are non suitable habitat for the other species. The maps created in this study are particularly useful for the Patagonian steppe because they predict patchy habitat suitability with high degree of detail. More specifically, the habitats in the steppe are clearly delineated compared to the forest where the presence of these four species is widely known and their distribution is compact.

Future directions: Our future efforts will seek to produce HPS risk maps based on the probability of seropositive reservoirs overlapped with human HPS positive cases areas, proximity to human population density, distance to main roads, and touristic attractions. We anticipate that these relations will allow us to assess the risk of humans entering in contact with hantavirus reservoirs in northern Patagonia at a regional scale.

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