ASSOCIATION BETWEEN HOST ABUNDANCE, ANDES VIRUS ANTIBODIES AND ENVIRONMENTAL VARIABLES IN SOUTHERN ARGENTINA

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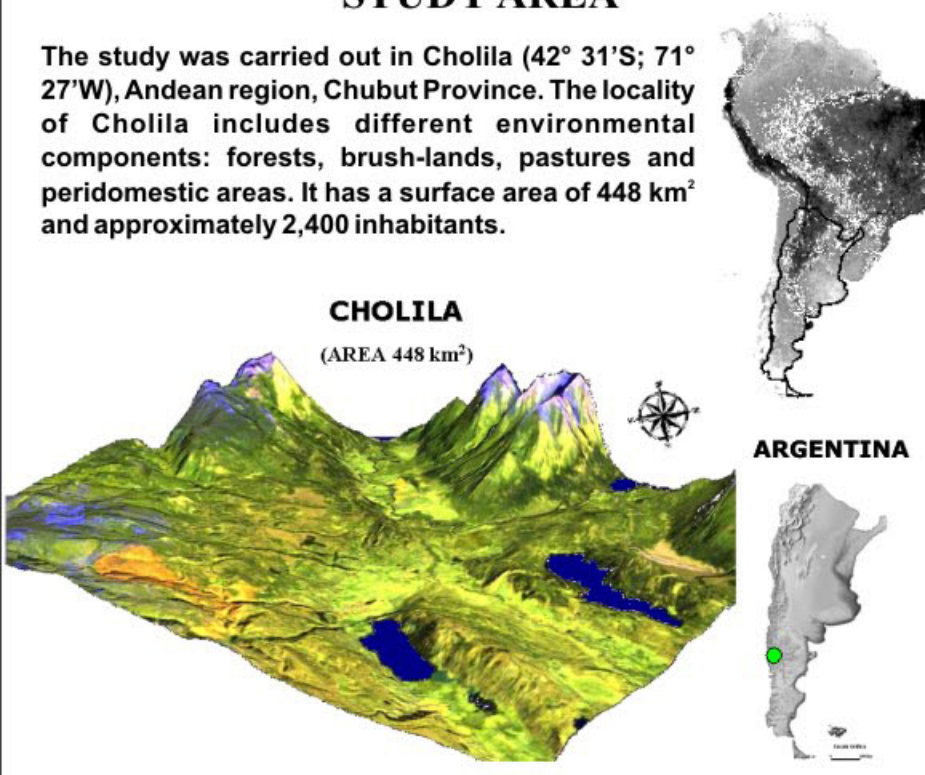
INTRODUCTION

Oligoryzomys longicaudatus **(Bennett, 1832), commonly known as long-tail rice rat is the main hantavirus reservoir in southern Argentina. Its distribution occurs in the east Andean zone of the Patagonic forests and extends to the Atlantic Ocean in Río Negro and Chubut provinces. However, the causes of landscape and local distribution of this species are poorly known. Since 2003 to 2008, intensive ecological studies have been carried out in Cholila, Chubut (Argentina), to improve our understanding of hantavirus-host system. The objective of this work was to identify environmental factors associated with high *Oligoryzomys longicaudatus* bundance and infection by Andes virus to develop predictive models of HPS risk for humans in this region.**

STUDY AREA

The study was carried out in Cholila (42° 31'S; 71° 27'W), Andean region, Chubut Province. The locality of Cholila includes different environmental components: forests, brush-lands, pastures and peridomestic areas. It has a surface area of 448 km² and approximately 2,400 inhabitants.



Oligoryzomys longicaudatus

MATERIALS AND METHODS

The rodent host records in each habitat were obtained by a system of trap lines with a total of 258 sites of capture in brush-lands, 344 in forests and 290 in pastures. Each trap line was identified with two conditions: rodent population abundance (high or low) and infection status. Thirty meteorological and environmental variables were extracted from different databases (Landsat, Alos, Modis and Bioclim) to characterize each trap site. All raster maps and vectors were rectified to a common UTM coordinate system.

The environmental variables were used to perform logistics regression analyses (stepwise) with the statistical software R. Akaike´s information criterion was used to select the model that best fit the particular dataset. Predictive models were developed using GRASS 6.3.

RESULTS

A logistic regression model showed that high abundances (table 1) were significantly associated with 7 variables: precipitation (annual, seasonal and wettest quarter), maximum temperature of warmest month, slope and summer and spring NDVI.

The presence of antibody positive animals (table 2) was significantly explained by variables related to temperature, precipitation, slope and summer NDVI.

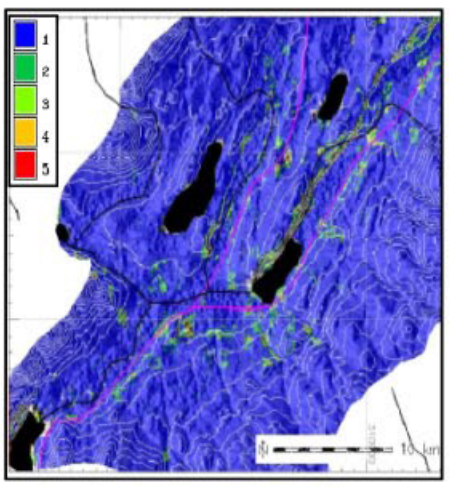
Table 1: Logistic regression abundance model

	Estimate	Std. Error	z value	Pr(>|z|)	
(Intercept)	56,920	24,060	2,370	0,020	*
Maximum temperature of warmest month	-0,340	0,130	-2,750	0,010	**
Annual precipitation	0,520	0,130	-4,140	0,000	***
Seasonal precipitation	2,090	0,460	4,570	0,000	***
Precipitation of wettest quarter	1,000	0,250	3,930	0,000	***
Tree	0,080	0,060	1,440	0,150	
Herbaceous	0,090	0,060	1,600	0,110	
Aspect	0,000	0,000	-1,450	0,150	
Slope	0,050	0,020	2,680	0,010	**
Shaded	-0,040	0,020	-1,890	0,060	
NDVI (summer)	-3,020	0,960	-3,150	0,000	**
NDVI (spring)	-2,550	1,030	-2,490	0,010	*
Significance level:	0	0,001***	0,01**	0,05*	0,1 ' '

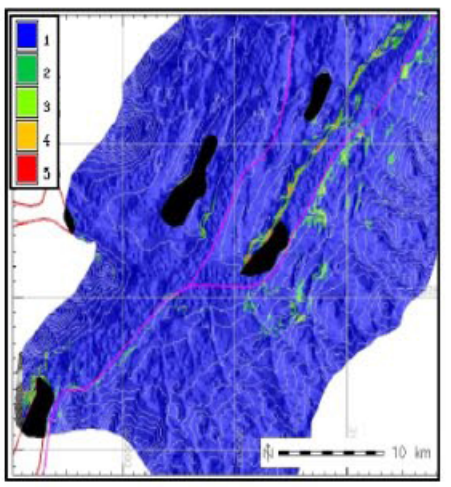
Table 2: Logistic regression infection model

	Estimate	Std. Error	z value	Pr(>|z|)	
(Intercept)	-95,893	46,601	-2,058	0,040	*
Mean diurnal range of temperature	0,827	0,364	2,263	0,024	*
Mean temperature of coldest month	-0,627	0,350	-1,792	0,073	.
Mean temperature of coldest quarter	0,769	0,345	2,231	0,026	*
Mean temperature of wettest quarter	-0,248	0,073	-3,399	0,001	***
Seasonal precipitation	0,911	0,276	3,304	0,001	***
Slope	0,060	0,018	3,293	0,001	***
NDVI (summer)	-1,953	0,992	-1,969	0,048	*
Significance level:	0	0,001***	0,01**	0,05*	0,1 ' '

Predictive model for rodent abundance



Predictive model for rodent infection



Reference: Probability (1) very low; (2) low; (3) moderate; (4) high and (5) very high

CONCLUSION

The predictive models generated allowed us to improve the identification of sites with favorable environmental conditions for *O. longicaudatus* that would increase the HPS risk for humans. Long-term studies will be necessary to understand the spatiotemporal patterns in Hantavirus-host-disease dynamics.