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Poster Session I

Emerging infectious diseases

Reservoirs of the emerging pathogens *Bartonella* spp. and *Yersinia pestis* in Peru

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Objectives

Despite of the high amount of previous data about human-infecting *Bartonella* species, and the high number of plague cases reported each decade in Peru, there are few works concerning which rodent species are acting as *Bartonella* and plague reservoirs in this country. The objectives of this study were to determine the possible infection of several rodent species from Peru with *Bartonella* spp. and *Yersinia pestis*, evaluate the genetic heterogeneity of the *Bartonella* strains in this country and estimate the importance of our results from the point of view of the public health.

Methods

A total of 28 rodents were captured during 2010-2011 from three villages belonging to La Convención Province, Peru. Spleens of the animals were collected and preserved in 100% ethanol until DNA extraction. Rodents were examined for the presence of *Bartonella* DNA by PCR targeting a 767-bp fragment of the citrate synthase gene (*gltA*). On the other hand, the screening for plague was performed by using a PCR targeting the plasminogen activator protein encoded by the *Y. pestis*-specific pPLA plasmid. With regard to *Bartonella* sequences, the neighbor-joining (NJ) method by Kimura's two-parameter distance method and bootstrap calculation was carried out with 1,000 resamplings.

Results

The captured rodents belonged to the species *Rattus rattus* (n=24), *Hylaeamys perenensis* (n=3) and *Oecomys* spp. (n=1). Five out of them were positive for *Bartonella* spp. and six for *Y. pestis*, and consequently the overall prevalences for both bacteria in rodents were 17.9% and 21.4%, respectively. Furthermore, coinfections with both bacteria were found in three rodents (10.7%). Both pathogens were found in rodents from almost all the studied habitats. Sequence analysis allowed the identification of two *gltA* genotypes, similar to a genotypic variant previously cultured from *Oryzomys palustris* in United States. Considering the NJ tree and the genetic distance found between these two new *Bartonella* genotypes and the rest of the genotypic variants, we propose these as new genotypes.

Conclusions

The results of this study indicate that infections of rodents with *Bartonella* spp. and *Y. pestis* are common and widespread throughout La Convención, Peru. This study constitutes the first report of *Bartonella* spp. and *Y. pestis* in new host rodent species. Because most identified *Bartonella* species have been reported as human infectious agents elsewhere, our results could be considered of public health concern. Our study also enlarges the distribution of plague in Peru, which was thought to be limited to the northern part of the country.