

ment and defines the spectrum of illness and the relation to place of exposure for the most significant health risks that face travelers.

Founded in 1996, the communications and data collection network currently comprises 50 travel/tropical medicine ISTM (International Society of Travel Medicine) clinics on 6 continents operating in cooperation with the US CDC. Returning travelers seen at relatively few sentinel sites provide a sample of disease agents in over 230 different countries. As of December 1, 2009, over 114,000 patient records increasing by 20,000/yr, track trends against a 12-year long baseline for over 500 diagnoses in order to monitor anomalies that might herald disease emergence.

Real time data entry via internet onto a central server allows monitoring of alarming sentinel events to generate immediate network wide queries and enhanced surveillance during focal or widespread outbreak situations. The GeoSentinel response arm disseminates alerts and advisories through CDC, ProMedMail, ISTM, ASTMH, and other partner networks and agencies.

Examples have included: imported traveler-related cases/outbreaks of SARS, 2009 H1N1 influenza, leptospirosis from Borneo, Hantavirus from Chile, Hajj meningitis from Singapore, first-ever dengue from Easter Island, and schistosomiasis from Tanzania.

The presentation will include advances, observations, lessons and limitations from the experience of the global GeoSentinel surveillance network. Data from sentinel travelers upon their return to medically sophisticated environments can also benefit local populations in resource-limited countries.

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Advances from the laboratory (Oral Presentation)

47.001

Epidemiological description of infection with agents of the *Rickettsia* genus in rodents, ectoparasites and humans in the northern coast of Antioquia, Colombia

J.C. Quintero Vélez^{1,*}, A. Londoño¹, V. Quiroz², F. Díaz², P. Agudelo³, M. Arboleda³, J. Rodas²

¹ *Universidad de Antioquia, Medellín, Colombia*

² *Universidad de Antioquia, Medellín, Colombia*

³ *Instituto Colombiano de Medicina Tropical-CES, Sabaneta, Colombia*

Background: *Rickettsia* is a worldwide usually rodent-carried tick, flea or lice-borne bacteria. In Colombia, few reports have been performed, first in the mid-thirties causing an outbreak in the population of Tobia Cundinamarca, and from the years 2006 to 2008 in the Northern region of Colombia known as Urabá. Our main goal was to perform an epidemiological description of the infection in the endemic mentioned area in Colombia.

Methods: Samples were obtained from the municipalities of Apartadó, Turbo y Necoclí, where 335 rodents were captured and parasites were collected from 33 of them. 220 double-blood human samples were also taken

Indirect Immunofluorescence (IFI), was used to detect rickettsial infection in humans and rodents. Additionally, PCR was performed in liver-DNA from rodents searching for specific genetic sequences of *Rickettsia* genus (Citrate Synthase gene, *gltA*) and pathogenic *Rickettsias* (*OmpB* gene).

Results: We obtained 23 rodent DNA samples positive to *gltA* but only 6 of them, positive for the *OmpB* gene, resulting on a 6.8% DNA frequency of infection to *Rickettsias* by PCR. Some PCR products for the *gltA* gene, were sequenced and showed 98% similarity with the *Rickettsia prowazekii* species, but the phylogenetic analysis suggests that these sequences form a separated cluster indicating that these *Rickettsias* could represent a new species or sub-species. 89 of the 220 human sera were tested by IFI and 11 came up positive in dilution 1:64 (10 of the samples were positive in the convalescence period M2, and one in the acute phase, M1). Most of the ectoparasites collected were identified as hard ticks (*Amblyomma* sp, Ixodidae family), soft ticks (*Ornithodoros alectorobius puertoricensis*, Argasidae family) and fleas (*Xenopsylla* sp genus). These samples still remain to be tested for rickettsial infection using both *gltA* and *OmpB*.

Conclusion: This is the first of a series of studies that will allow us to characterize ecologically this endemic site and contribute to recommend the measures to prevent future human cases in this important risk area.

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47.002

Distinct pathological signatures after lethal avian H5N1 and swine H1N1 influenza infections suggest variable pathogenesis

M.-M. Garigliany^{1,*}, A. Habyarimana², B. Lambrecht², E. Van de Paar¹, A. Cornet¹, T. Van den Berg², D. Desmecht¹

¹ *Faculty of Veterinary Medicine - University of Liège, Liège, Belgium*

² *Veterinary and Agricultural Research Center, Brussels, Belgium*

Background: Influenza annual epidemics result in up to 500,000 deaths in human population, and different pandemics occurred over the 20th century, among which the 1918 pandemic was accountable for more than 50 million deaths. Lethal seasonal or pandemic influenza infections are all associated either to secondary bacterial infections or acute respiratory distress syndrome (ARDS). Since antibiotics will help in treating bacterial pneumonias, it is crucial for public health to understand the pathogenesis of influenza-associated ARDS in order to fight it or to prevent its occurrence. Descriptions of the lung alterations in fatal influenza infections in human and mouse all depict similar lung dysfunctions and lesions. Here we describe the ARDS associated with the inoculation of identical doses of two influenza strains highly pathogenic for mice.

Methods: A clade 1 avian H5N1 virus (A/crested_eagle/Belgium/1/2004) and a porcine H1N1 virus (A/swine/lowa/4/1976) were rendered highly pathogenic for mice by serial lung-to-lung passaging in