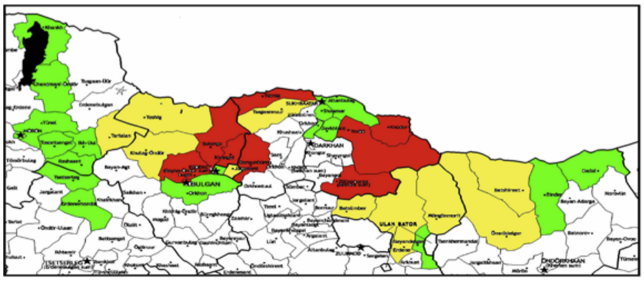
gan aimags (Fig. 2) and intensive measures of prophylaxis are necessary both for residents and for tourists in those provinces. This project has been supported by Russian Fund for Basic Research, grant=08-04-90206-Mong_a.



RED – High risk of infection: high abundance of *I. persulcatus* ticks; the TBE virus had been detected either by ELISA or by RT-PCR; from 1.2 to 5.9% of ticks are infected by TBEV.
YELLOW - Moderate risk of infection: low abundance of *I. persulcatus*, TBEV has not been detected in ticks.
GREEN - Low risk of infection: the natural conditions in some local areas are suitable for *I. persulcatus* but no ticks was found in those territories so far.

Figure 2. Prevalence of TBEV in Northern Mongolia and risk of infection for humans

doi:10.1016/j.ijid.2010.02.449

76.006

Bartonella spp infections diagnosed between 2005 and 2009 by the National Rickettsial Reference Laboratory in Rio de Janeiro, Brazil

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Background: *Bartonellae* are gram negative bacteria that parasitize erythrocytes and endothelium of several mammals, being widespread in nature. Its main source of infection to humans is the domestic cat. *Bartonella* infection is not notifiable, and no national data is available regarding its manifestations in Brazil. The aim of this study is to describe the cases referred with a possible diagnosis of bartonellosis to the National Rickettsial Reference Lab (LNHR) in Rio de Janeiro.

Methods: A Microsoft Excel® datasheet was designed for the study, so as to correlate the Brazilian Ministry of Health Notification requests received by LNHR (SINAN, for Brazilian Spotted Fever, notifiable since 2001) and the Lab's database. The diagnosis of bartonella infection was considered definite when paired samples showed a 4-fold difference in titers detected in the Indirect Immunofluorescence Assay for *B.henselae* IgG antibodies from Bion, USA, and/or the polymerase chain reaction (using primers CAT1/CAT2) was positive in biological samples.

Results: 54 patients had samples sent with the SINAN requests with the clinical suspicion of bartonellosis. Of these, 20 (37%) had definite infection by reactive IFA assay and/or positive PCR results (6 of 20). 19/20 patients were from Rio, 1 from Bahia. Mean age ± standard deviation was 28,9 ± 17,5 years, with median of 26. 12/20 patients (11/15), adenopathy (11/12), hepatoesplenomegaly (7/13), abdominal pain (5/19), prostration (5/9), headache (5/10) and conjunctival injection (4/11). Six patients had neuroretinitis, one of which with associated meningoencephalitis. One of the 20 patients had aortic valve endocarditis which required surgery.

Conclusion: More human samples are gradually being sent for Bartonella testing in LNHR, possibly because of greater medical awareness of this infection. Although classically the agent of cat-scratch disease, severe syndromes such as neuroretinitis, disseminated disease (with fever and hepatosplenomegaly) and endocarditis were seen in this first documented series of cases from Brazil. This deserves public health attention and better information to health care providers.

doi:10.1016/j.ijid.2010.02.450

76.007

Multiplexed diagnostic assays for detection of high consequence foreign and emerging animal disease

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Background: Due to the overwhelming number of foreign and emerging animal diseases a critical challenge to detection and response to outbreaks of animal disease is the availability of rapid, rigorously tested diagnostic assays able to detect multiple disease organisms. Methods currently used for veterinary diagnostics are generally single agent and can be timeconsuming, labor-intensive, and difficult to scale up in the event of an outbreak. Multiplexed PCR detection capabilities provide many advantages over conventional single agent, timeconsuming and labor intensive detection methodologies. Because of these advantages, coupled with their inherent adaptability and multiagent utility, multiplexed PCR assays are ideal for use in detection of foreign and emerging animal disease.

Methods: Our most promising work thus far has been the development of multiplexed RTPCR nucleic acid assays that can detect multiple genome regions of pathogens in a single tube with a high degree of sensitivity and specificity.

Results: We have demonstrated the ability to simultaneously extract and amplify DNA and RNA targets from environmental and clinical samples with a high degree of efficiency. The FMD assay can detect 17 distinct genomic regions from a panel of foreign and domestic viruses that are clinically indistinguishable from Foot and Mouth Disease virus in cattle, sheep and pigs. While our deeply multiplexed avian influenza assay can simultaneously detect and subtype influenza A in a sample from poultry or wild birds and determine if the most common human (H1,2,3) and well as several avian subtypes (H3,5,7,9) are present. The avian influenza assay detect 37 distinct genomic regions located on segment 4 (hemagglutinin), segment 7 (matrix) and segment 8 (non

structural) of influenza A. Of the 37, 34 are targeted exclusively to segment 4 to provide hemagglutining subtyping for influenza A. The other three signatures provide universal detection of influenza A by targeting segment 7 and 8 in the assay.

Conclusion: These multiplex panels have been extensively tested and demonstrated to work with environmental and clinical samples at multiple public health and agricultural laboratories. It is hoped that these assays may be further developed to be acceptable for routine use for the detection of economically important animal diseases.

doi:10.1016/j.ijid.2010.02.451

76.008

Transmission of chikungunya in Singapore, 2008

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Background: Chikungunya is a vector-borne viral febrile disease that is not endemic to Singapore. We describe herein the epidemiology of 718 cases identified during the outbreak in 2008, including probable sources of infection, modes of transmission, and vector species responsible for this outbreak.

Methods: We investigated into all laboratory-confirmed chikungunya cases notified from the healthcare institutions between 30 Dec 2007 and 4 Jan 2009. Cases epidemiologically linked in space and time were defined into clusters and analysed. Vector operations at each cluster were carried out to identify the mosquito species responsible for transmission.

Results: A total of 718 cases of chikungunya were reported in 2008. The outbreak began with a cluster of cases at Little India in Jan—Feb. Sustained local transmission only occurred after a wave of imported cases in Jul. During the period from Jul-Dec, there were 693 cases, of which 173 (25%) were imported infections and 520 (75%) local infections. Among the 173 imported cases, 162 (94%) originated from Malaysia, mainly in people who developed the illness after visiting rural Johor where *Aedes albopictus* activity was reported. 152 (80%) of them were Singaporeans. Among the 520 local cases, majority were males (414, 80%) of working age (mean, 38 years) non-resident (327, 62.9%) labourers (277, 53.3%)). Higher risks of infection were associated with landed property and temporary housing. Cases were distributed in the urban, sub-urban, industrial and agricultural areas of Singapore. Entomological surveys involving species identification of mosquito larva found in these areas implicated *Aedes albopictus* (31 out of 34 clusters with breeding) as the vector responsible for transmission.

Conclusion: Our findings showed that proximity to infective *Aedes albopictus* mosquito vectors, either through travel to rural Johor, or work/stay within local forested areas increased risks of acquiring the chikungunya virus infection.

doi:10.1016/j.ijid.2010.02.452

76.009

Escalation of Japanese encephalitis in India: Evidence from 2005 viral encephalitis outbreak and appraisal of niceties

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Background: Viral encephalitis is a global emerging problem. North India faced a large epidemic of Japanese encephalitis (JE) in 2005. Therefore, the present study was planned to reconfirm the circulation of JE in the area and to get a better view of trend of the disease to slowdown the burden of JE.

Methods: Surveillance was carried out to identify patients with acute encephalitis. Blood and cerebrospinal fluid specimens from suspected cases underwent pathological, serological, demographic investigation and viral testing for evidence of Japanese encephalitis virus (JEV) infection; either by IgM capture ELISA/RT-PCR or both. To identify circulating JEV strain RTPCR, sequencing and phylogenetic analysis was performed. Based on clinical cases reported between 1992-2008, trend of JE infection in the state was analyzed to examine the dynamics of infection.

Results: Our investigations ($n = 38$) revealed that only 55.3% cases were positive for JE. Pathological examination revealed marked pleocytosis in CSF (90 ± 76.9 cells/mm^3), and peripheral leucocytosis (64.7 ± 8.86% neutrophils) with mild anemia. Males were more susceptible than females with ratio of 1.63:1 and significant gender diaerence ($P < 0.05$) was observed in patients below six years. In the patient group with age below six years, rate of infection per million was six fold higher ($P < 0.005$) in males as compared to females. Our phylogenetic study (suggests that circulating novel strain (JEV GP05; submitted in NCBI with FJ979830 accession number) during 2005 JE epidemic was close to GP78 and in future larger epidemic may occur.

Conclusion: The 2005 JE epidemic was possibly because of JEV GP05 (a close member of JEV GP78) and it is spreading in newer areas. The trend of JE (1992 — 2008) suggested that the problem in North India is escalating and larger epidemics may be envisaged in future. Considering possibility of larger epidemic in future, serious steps are necessary for combating JE, including development of more efficient surveillance methods and differential diagnosis.

doi:10.1016/j.ijid.2010.02.453

76.010

What is the current situation with plague in North Africa?

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Background: From Morocco to Egypt, North Africa was widely affected by plague throughout the first half of the twentieth century. Most of the countries had natural foci described. For unknown reasons, human plague disappeared in the 1950 s (outside of very sporadic clusters in Libya, last