rheic piglet in Eastern India. The VP4, VP6, NSP4 and NSP5 genes of porcine G12 strain RU172 exhibited genetic relatedness to human Wa-like G12 strains. Although the origin of human G12 genotype remains obscure, some recent studies on human G12 rotaviruses suggested that the G12 genotype might be of porcine origin. To determine the true origin of G12 rotaviruses and decipher the exact genetic relatedness between human and porcine G12 strains, we characterized genetically the remaining six genes (VP1-3 and NSP1-3) of porcine G12 strain RU172.

Methods: The VP1-3 and NSP1-3 gene sequences of porcine G12 strain RU172 were obtained by RT-PCR and direct sequencing using end primers and several internal primers, designed from conserved stretches of several published sequences.

Results: The VP1-3 and NSP1-3 genes of porcine G12 strain RU172 exhibited high sequence identities to Wa-like porcine and human strains, including human G12 strains, and by phylogenetic analyses, clustered within the Wa genogroup along with human Wa-like G12 strains.

Conclusion: Wa-like human and porcine group A rotaviruses are believed to be genetically related and have a common origin. Therefore, based on full genome analyses of porcine G12 strain RU172 and human Wa-like G12 strains, we propose that the Wa-like human G12 strains might have resulted from reassortment events involving Wa-like human non-G12 and porcine G12 strains, or more favorably, both the porcine and human Wa-like G12 strains might have evolved from a common progenitor, maybe of porcine origin. The AU-1-like and DS-1-like G12 strains might be the result of reassortment events involving non-G12 strains of these genogroups and human Wa-like G12 strains. Therefore, the present study deciphers the probable origin of human G12 genotype, and provides evidence for porcine-human transmission of rotaviruses.

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34.007

Veterinary practitioners and the spread of infectious diseases

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Background: There is an increasing overlapping among livestock,pets and human beings, highlighting the need for a well defined biosecurity plan to reduce the opportunity for infectious agents to gain access to and spread within a veterinary premises or any other animal housing unit.And the recent outbreaks of infectious diseases around the world have clearly shown the threats to human and animal health arising from emerging and re-emerging infectious disease, a fact which has huge economic and public health implications.

Methods: In order to provide the best veterinary care possible, veterinarians have to redefine their underlying responsibility to minimize the risk of additional; harm that might unintentionally befall a patient because of their interventions.

spread of infectious diseases.

Conclusion: This paper focused on an investigation to determine the possible roles of veterinary practitioners in the spread of infectious diseases, discusses the need for biosecurity programs in veterinary practices,and relates a practical approach for developing biosecurity practices that are tailored to individual facilities,to help ensure that veterinary practitioners retain their role in the control rather than the spread of infections.

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34.008

Trypanosome infections in dogs from Chagas disease endemic regions in Panama, Central America

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Background: Chagas Disease remains a major parasitic zoonosis in Latin America affecting 9.8 to 11 million people. The infection is caused by *Trypanosoma cruzi*, a protozoan naturally transmitted to mammals, including humans, by triatomines. In endemic areas, humans and animals become mainly infected through contact with parasite-infected excreta from triatomines. The sylvatic triatomine, *Rhodnius pallescens* is considered the main vector of *T. cruzi* and *T. rangeli* in Panama. In many countries, such as Panama, non-domiciliated vectors remain responsible for a significant transmission risk and their control poses a challenge for disease control. Dogs are important reservoirs of the disease in the domestic transmission, and due to the close proximity with humans they may represent a high risk to humans. However, the role of dogs as reservoirs and as risk factor for human transmission in the peridomestic and/or sylvatic habitats has only been partially explored. Consequently we evaluate the prevalence of canine trypanosomiasis rural endemic communities where the non-domicilated *R. pallescens* is responsible for *T. cruzi* transmission to humans.

Methods: During 2007, a cross-sectional study was designed to evaluate the presence of anti-*T. cruzi* antibodies and blood trypanosomes in dogs from the rural communities of Las Pavas and Lagartera Grande in Central Panama. A questionnaire was applied to the dog owners to assess epidemiological data and risk factors associated with the disease.

Results: Of the 94 dogs analyzed, 51 were male and 43 females. The mean age for both males and females was 3.6 years (range 4 months — 15 years).Serological and parasitological tests revealed that 12 dogs (12.8%) were trypanosome infected (Table 1). Nine dogs (9.6%) had antibodies against *T. cruzi*. Trypanosomes were isolated in three (5.3%) hemoculture samples. Molecular analysis showed that isolated trypanosomes were *T. rangeli*. None of these *T. rangeli* positive dogs had detectable antibodies against *T. cruzi*. Four infected dogs belong to people with Chagas disease diagnosis.

Conclusion: In conclusion our data demonstrate that dogs are frequently infected with Trypanosomes in this area o Panama with a prevalence similar to the one observed in the human population. This study improves our understanding of the epidemiology and control of Chagas disease in rural areas of central Panama.

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34.009

Molecular evidence of genetic diversity of *Borrelia burgdorferi* sensu lato detected in *Ixodes granulatus* ticks removed from rodents in Taiwan

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Background: Genetic diversity of *Borrelia* spirochetes in *Ixodes granulatus* ticks of Taiwan remains unknown and needs further identified.

Methods: A general survey was conducted to collect *I. granulatus* ticks removed from trapped rodents in Taiwan. Total genomic DNA was extracted from individual tick specimen by using DNeasy Blood & Tissue Kit (Qiagen). Genetic identities of *Borrelia* spirochetes detected in *I. granulatus* ticks were determined by analyzing the gene sequences amplified by a nested polymerase chain reaction (PCR) assay based on the 5S-23S intergenic spacer amplicon gene of *B. burgdorferi* sensu lato. Phylogenetic relationships of these detected spirochetes were further analyzed by neighbour-joining (NJ) compared with maximum parsimony (MP) methods.

Results: A total of 261 *I. granulatus* ticks (156 adults and 105 nymphs) were tested by nested-PCR assay and *Borrelia* spirochetes were detected in 80 adults and 52 nymphs with an infection rate of 51.3% and 49.5%, respectively. Phylogenetic analysis reveals that all these detected spirochetes constitute two major separate clades distincted from other *Borrelia* genospecies in both NJ and MP methods. Within the clades, 10 strains of *Borrelia* spirochetes detected in *I. granulatus* ticks were closely related to the genospecies of *B. burgdorferi* sensu stricto and 15 strains of detected spirochetes were closely related to *B. valaisiana*.

Conclusion: Our results demonstrate the genetic diversity of *B. burgdorferi* sensu lato spirochetes detected in *I. granulatus* ticks collected in Taiwan. The genetic identities of these detected spirochetes were clarified by analyzing sequence homology of 5S-23S intergenic spacer amplicon gene. Further investigations on *Borrelia* spirochetes detected in variant tick species and reservoir hosts would beneficial to the better understanding of genetic heterogeneity of *Borrelia* spirochetes in Taiwan.

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Occurrence of *Ureaplasma diversum* in cows with various reproductive disorders

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Background: Ureaplasma diversum, a bovine species was first isolated by Taylor Robinson and co-workers in 1967 from cattle. The genital ureaplasmosis in cows occurs in various clinical forms viz. urethritis, endometritis, salpingitis, granular vulvoveginitis, abortion and neonatal calf mortality leading to temporary or permanent infertility.

Methods: During present study, a mycoplasmological examination of cervico-vaginal swabs/vaginal discharges from 136 cows including 86 with various reproductive disorders (22 anoestrus, 25 repeat breeder, 6 cervicitis, 17 metritis, 16 abortion/still-birth) and 50 apparently healthy cows was conducted.The U-9B liquid medium was used for isolation of Ureaplasmas. *In-vitro* antibiotic sensitivity of ureaplasmal isolates against ten selected antibiotics was performed at first stage of their cultivation in U-9B colour test liquid medium.

Results: The mycoplasmological examination of cervico-vaginal swabs/vaginal discharges from 136 cows including 86 with various reproductive disorders and 50 apparently healthy cows resulted in isolation of 14*Ureaplasma* species along with 11 *Mycoplasma* and 8 *Acholeplasma*.The incidence of mollicutes was was found higher in genitally diseased cows 929.07%) as compared to apparently healthy cows (16%). The prevalence of *Ureaplasma diversum* was more in repeat breed cow (20%) than anoestrus (9.8%), cervicitis and metritis (4.9%). However, no*Ureaplasma* strain was isolated from abortion cases. The concentration of nine strains of *Ureaplasma* isolated from cows with various reproductive disorders and 5 from apparently healthy ranged between 5x102 to 5x104ccu/ml. All the test strains of Ureaplasma, were found sensitive for lincospectin and resistant to ampicillin. However, variable resistance was shawn by 6 isolates to tetracycline, 4 isolates to enrofloxacin, spiramycin and chloramphenicol, 3 isolates to tylosin and erythromycin and one isolate to tiamutin and sparfloxacin.

Conclusion: All the fourteen strains of Ureaplasma isolated from cows with various reproductive disorders show multiple drug resistance against tested antibiotics.

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