

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 of 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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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 distinct 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 vulvovaginitis, abortion and neonatal calf mortality leading to temporary or permanent infertility.

Methods: During present study, a mycoplasma 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 ureaplasma isolates against ten selected antibiotics was performed at first stage of their cultivation in U-9B colour test liquid medium.

Results: The mycoplasma 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 found higher in genitally diseased cows (92.907%) 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 shown by 6 isolates to tetracycline, 4 isolates to enrofloxacin, spiramycin and chloramphenicol, 3 isolates to tylosin and erythromycin and one isolate to tiamutin and sparflaxacin.

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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