

infected and not immunosuppressed group (CI). By the way an increase of encephalic lesions in animals immunosuppressed during the CP in relation to CI was observed. Although parasitemia reactivation was not observed in animals infected with *T. cruzi* II clones, an increase of inflammatory process in the heart and skeletal muscle, but not in the brain, was observed among animals infected with Bug2148cl1. These results showed that the genetic diversity of *T. cruzi* has an important role on the reactivation of the infection after immunosuppression and corroborates the working hypothesis subjacent to the model clonal theory in *T. cruzi*.

Identification of *Theileria* in Endangered Serow and Endangered Eld's Deer in Thailand

P. Sanyathitiseree¹, P. Lertwatcharasarakul¹, N. Thoughtip¹, S. Phatthanakunanan¹, S. Jala¹, W. Tanwattana², J. Thaewner² and W. Waijwalku^{1*}

1. Faculty of Veterinary Medicine, Kasetsart University, Kamphaensaen, Nakhon Pathom, Thailand 73140

2. K Kheow Open Zoo, Chonburi, Thailand

* Corresponding author. Tel.: + (66 81) 9811545, -mail address: fvetwww@yahoo.com

Keywords: Theileria, 18s rRNA, Reverse line blot hybridization.

The blood samples of eld's deer and in the zoo and poaching serow were collected for DNA extraction. Polymerase Chain Reaction (PCR) was performed with the 18s rRNA specific primer for babesia and theileria. The PCR products were determined species specific by species-specific probe of TBD-RLB KIT (Isogen®). Two PCR products of Eld's deer and also of the serow hybridized to *Theileria/Babesia* common probe but not found hybridization to species specific probe position. Moreover, nucleotide sequences of PCR products were determined by using BigDye Terminal Cycle Sequence Kit and analyzed with blast program which closely related with *Theileria sp.* The sequence of the parasite from the serow, *Theileria sp.* (Khao Yai), showed most similarities with *Theileria sp.* (OT1) of the ovine reported in Spain and from elder's deer, *Theileria sp.* (Khao Khaew) was highest similarity with *Theileria sp.* of deer in Japan. The completely sequence of 18srRNA will be done soon. This is the first report of theileriosis in the wildlife serow and elder's deer in the zoo in Thailand.

Using a climate dependent matrix model to predict mosquito abundance: application to *Aedes (Stegomyia) africanus* and *Aedes (Diceromyia) furcifer* (Diptera: Culicidae), two main vectors of the yellow fever virus in West Africa.

Brigitte Schaeffer,¹ Bernard Mondet,² and Suzanne Touzeau¹

1. INRA, Jouy-en-Josas, France

2. IFP/IRD-UR 178, Pondicherry, India

Keywords: Vector population, mathematical model, climate dependency.

Mosquitoes, acting as vectors of diseases, are particularly involved in the transmission of viruses. Thus the abundance of some tree-hole breeding species strongly depends on weather, specially rainfall. The aim of this paper is to provide a tool to predict vector abundance. In order to describe the

dynamics of these mosquito populations, we developed a matrix model integrating climate fluctuations. The population is structured in five stages: two egg stages (immature and mature), one larval stage and two flying stages (nulliparous and parous adult females). We considered the water availability in breeding-sites as the main environmental factor affecting the mosquito life cycle. The model represents the evolution of the mosquito abundance in each stage over time, in connexion with water availability. This model was used to simulate the abundance trends over three years of two mosquito species, *Aedes africanus* (Theobald) and *Aedes furcifer* (Edwards), vectors of the yellow fever in Côte d'Ivoire, West Africa. Water dynamics in the tree-hole was reproduced from daily rainfall data. The results we obtained show a good match between the simulated population and the field data over the time period considered.

Human Immunodeficiency Viruses Type 1 Circulating in the Comunitat Valenciana (Spain).

Sentandreu¹ V., Bracho¹ M.A., Alastrue² I., Belda³ J. González-Candelas¹ F.

1. Cavanilles Institute for Biodiversity and Evolutionary Biology (University of Valencia, Spain)

2. Center for AIDS Information and Prevention. Public Health Department of Valencia (Spain)

3. Center for AIDS Information and Prevention. Public Health Department of Alacant (Spain)

Human immunodeficiency virus type 1 (HIV-1) mutates rapidly and nucleotide substitutions, deletions, insertions, and rearrangements resulting from recombination events are the main factors contributing to its high degree of genetic heterogeneity. Nucleotide sequence analyses allow the recognition of phylogenetic relationships and the classification of HIV-1 into different subtypes and recombinant forms. The prevalence of multiple HIV-1 subtypes in a single geographic region might result in an increased frequency of mixed infections. Eventually, recombinants between more than one variant can be found. HIV-1 subtype B is the most prevalent variant in Spain, although non-B subtypes have been reported, mainly among African immigrants. Classification of HIV-1 into subtypes is based primarily on the analysis of sequences coding for the *env* gene. However, the *pol*-coding region has also been validated for this purpose and is currently used much more since drug resistance testing is undertaken routinely at a large scale. Here we describe the main features of HIV-1 subtypes circulating in the Comunitat Valenciana (Valencia and Alacant provinces). We have amplified and sequenced the HIV-1 protease and partial reverse transcriptase (PR-RT) genes from isolates of 75 patients. Samples were obtained from two Centers of AIDS Information and Prevention and 40% of them correspond to immigrants. Subtype identification was performed by phylogenetic analyses, taking as reference a panel of 120 HIV-1 sequences representing all subtypes and recombinant forms described. We have found 60 (80%) subtype B sequences. Non-B subtypes were mainly represented by recombinant forms (14/15, 18.7%) from patients coming from Africa and South America and only one for subtype A. At least one drug resistance mutation in the *pol* gene was detected in 86.7% of sequences. This study demonstrates that most viruses circulating in Spain (Valencia-Alacant) are in fact inter-subtype recombinants, with CRF02_AG being the most prevalent recombinant form.

Schaeffer B., Mondet Bernard, Touzeau S. (2006).

Using a climate dependent matrix model to predict mosquito abundance : application to *Aedes (Stegomyia) africanus* and *Aedes (Diceromyia) furcifer* (Diptera : Culicidae), two main vectors of the yellow fever virus in West Africa.

In : Tibayrenc Michel (ed.). MEEGID 8 : 8th international meeting on molecular epidemiology and evolution genetics in infectious diseases.

Atlanta (USA) ; Bangkok : CDC ; IRD, p. 100-101.

International Meeting on Molecular Epidemiology and Evolutionary Genetics in Infectious Diseases, 8., Bangkok (THA), 2006/11/30 .