genes from six localities were compared pairwise. The preliminary result showed marqued differences in nucleotide composition among *Aedes* mosquito populations of Nakhonpathom Province as compared to the others. This study reveals information on divergence of dengue vector from endemic areas and will help to understand vector competence and efficiency in transmitting the virus. Furthermore, it will serve as an informative knowledge on the species dispersal modalities and mean for implementing control strategies.

"Student Symposium"

(9) Molecular characterization of Thai *Ehrlichia* canis and *Anaplasma platys* strains isolated from dogs

Danai Pinyoowong[1], Sathaporn Jittapalapong[2] Fanan Suksawat[3], Roger W. Stich[4] and Arinthip Thamchaipenet[1]

1. Department of Genetics, Faculty of Science, Kasetsart University, Thailand; 2. Department of Parasitology, Faculty of Veterinary Medicine, Kasetsart University, Thailand; 3. Department of Medicine, Faculty of Veterinary Medicine, Khon Kaen University, Thailand; 4. Department of Veterinary Pathobiology, University of Missouri, Columbia, MO, USA.

Keywords: *Ehrlichia canis*, *Anaplasma platys*, PCR, Thailand, Dogs

Canine monocytic ehrlichiosis caused by *Ehrlichia canis* is veterinary importance worldwide. In Thailand, there has been little information available on *E. canis* and its phylogeny. The objective of this study was to characterize and establish molecular structure and phylogeny of Thai *Ehrlichia* and *Anaplasma* strains. *Ehrlichia*-positive blood samples of dogs were extracted for genomic DNAs. 1.5 Kb PCR products of 16S rRNA gene were obtained using designed genus-specific primers for *Ehrlichia* and *Anaplasma*. Nearly complete sequences of the 16S rRNA gene were compared with other sequences available in the Genbank database. Percentage of similarity as well as secondary structure analysis of 16S rRNA sequences indicated that they are new *E.* canis and *A. platys* strains. Phylogenetic analysis revealed that two strains of Thai *E. canis* were closely related and formed a single cluster within the cluster amongst previously published *E. canis* from different countries. *A. platys* found in this study showed close relationship with earlier report of *A. platys* in Thailand. This report represents the first molecular characterization of *E. canis* in dogs from Thailand.

(10) *Leishmania braziliensis*: population structure and reproductive modes.

Rougeron V[1]., De Meeûs T.[1], Hide M.[1], Waleckx, E.[1], Arevalo, J.[2], Bermudez, H[3], Llanos-Cuentas, A[2], Dujardin, J-C[5], Bañuls A-L[1].

1. Laboratoire GEMI UMR CNRS-IRD 2724, centre IRD, Montpellier, France; 2. Alexander Von Humboldt Institute of Tropical Medicine, Universidad Peruana Cayetano Heredia, Lima, Peru; 3. Faculty of Medicine, Universidad Mayor San Simon, P.O. Box 4866, Cochabamba, Bolivia; 4. Department Parasitology, Institute of Tropical Medicine, Antwerp, Belgium.

Leishmaniases are severe diseases affecting humans and animals caused by protozoan parasites belonging to the *Leishmania* genus and transmitted by female sandflies' bites. These parasitoses are widespread over all continents, except Antarctica. Nowadays, leishmaniases still pose considerable public health problems. At present, it is suggested and even admitted that *Leishmania* species present a basically clonal population structure associated to rare sexual recombination events. However, such a statement mostly relies on population genetics studies that may be criticised. The markers used were little adapted (lack of resolution or dominant markers) and clonality was inferred from the analysis of linkage disequilibria across loci that are far from ideal in that respect. *Leishmania braziliensis* is an important leismaniasis agent in South America. The principal objective of our work was to study the population structure and reproductive mode of this species in Peru and Bolivia and, for the first time, using microsatellite markers. On the whole, 124 human isolates (68 from Peru and 56 from Bolivia) were genotyped on 12 microsatellite loci. Various population genetics tests were applied. The results obtained appear in contradiction with a simple clonal propagation. Indeed, strong homozygosities found at each locus, associated to strong linkage disequilibria across loci, advocated for an inbred reproductive strategy. Further analyses suggest that a significant part of the high heterozygote deficits observed in our samples is likely the consequence of a Wahlund effect, i.e. the coexistence of strongly differentiated genetic entities within each sample. This work brings key information concerning the biology of these organisms and opens new prospects on the study of this species and other members of the genus.

(11) Clonal strains of *Pseudomonas aeruginosa* isolated from patients with cystic fibrosis

Pholawat Tingpej[1], Mark Elkins[2], Veronica Yozghatlian[1], Barbara Rose[1], Jim Manos[1], Peter Bye[2,3], Colin Harbour[1*]

1. Department of Infectious Diseases and Immunology
2. Department of Respiratory Medicine, Royal Prince Alfred Hospital, Sydney, Australia
3. Medicine, University of Sydney, Sydney, Australia

* Corresponding author: Associate Professor Colin Harbour, Department of Infectious Diseases and Immunology, Blackburn Building DO6, University of Sydney, 2006, NSW Australia, Tel: 61 2 93514334, Fax: 61 2 93514731, Email: charbour@infdis.usyd.edu.au

Cystic Fibrosis (CF) is the most common genetic condition among Caucasians. Eighty percent of people with CF are infected with *Pseudomonas aeruginosa* by adulthood and most die from complications arising from chronic lung infections. *P. aeruginosa* is widespread in various environments including hospitals. It was once generally accepted that individual CF patients acquired *P. aeruginosa* from their environments and thus each patient carried their own unrelated (or unique) strain. Recently however, clonal (or epidemic) strains have been reported in Europe and Australia. In this study, DNA restriction fragment length polymorphisms (RFLP) of *P. aeruginosa* isolates from 112 patients attending an adult CF clinic at Royal Prince Alfred Hospital in Sydney, Australia were analysed using pulsed-field gel electrophoresis (PFGE). Cluster analyses were performed using

Rougeron V., De Meeûs Thierry, Hide Mallorie, Waleckx E., Arevalo J., Bermudez H., Llanos-Cuentas A., Dujardin J.C., Banuls Anne-Laure. (2006).

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