However, other studies highlighted no evidence in gene flows in *Ornithodoros coriaceus* and a far more complex situation with *Ixodes uriae*. The ongoing sequencing of *Ixodes scapularis* (vector of the Lyme Disease spirochaete *Borrelia burgdorferi*, the zoonotic *Babesia microti* and the HGE agent now part of the *Anaplasma phagocytophilum* complex). Furthermore, complementing results in genetic improvement in mosquitoes (genetic markers, sexing, genetic sterilization and fail-safe systems) will also increase performance as it has already been shown in field applications in developing countries. Recent results have greatly improved the fitness of genetically-modified insects compared to wild type populations with new approaches such as the post-integration elimination of transposon sequences, stabilising any insertion in genetically-modified insects. Encouraging results using the Sterile Insect Technique (SIT) highlighted some metabolism manipulation to avoid the viability of offspring from released parent insect in the wild, if necessary. Recent studies on vector symbionts would also bring a new angle in vector control capabilities. These new potential approaches will improve the levels of control or even in some cases would eradicate vector species and consequently the vector-borne diseases they can transmit. This paper will review the work on different genetic approaches to understand host/pathogen interface in vectors and new genetically modified techniques used to control them.

(8) A comparative study of Genetic lineages of DENGUE VECTORS, *Aedes aegypti* and *Aedes albopictuS*, from Thailand and France

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Keywords: genetics, *Aedes aegypti*, *Aedes albopictus*, Thailand, France.

In order to compare the genetic diversity among populations of two main vectors of Dengue in Thailand, *Aedes aegypti* and *A. albopictus*, were collected from several sites including urban, rural and forested areas of Bangkok, Nakhonpathom, KhonKaen, ChiangMai and Kanchanaburi Province. Various methods were used such as ovitrap, landing catch and/or aspirator. In addition, *A. albopictus* from France was also collected and manipulated compared with the Thai populations. All adult mosquitoes were species identified and kept at -20°C until processed. DNA extraction was carried out using a classical extraction buffer as previously described (Collins F.H., 1987). Molecular characterization and genetic lineages identification were done, among all collected sample populations, by using three genetic markers including the mitochondrial NADH dehydrogenase subunit 5 (ND5) fragment, the nuclear ribosomal DNA second internal transcribed spacer region (ITS2) and, the mitochondrial cytochrome oxidase I (COI). Aligned sequences of *A. aegypti* and *A. albopictus* 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

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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].

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