pictures differ in animals infected with mycobacteria cultivated using a continuous cell culture and in those infected with mycobacteria grown on Levenstein-Yensen medium. We have developed a new method of cultivation that allows to remain the most important biological properties unchanged at long-term cultivation on a continuous cell culture.

Identification of genetic diversity within *Brugia* species in feline based on internal transcribed spacer regions

Supatra Areekit, Arda Pakpitchareon, Sunsanee Phasook, Sintawee Khoochareontaworn, Phaisarn Khawsak, and Kosum Chansiri *

* Department of Biochemistry, Faculty of Medicine, Srinakharinwirot University, Bangkok 10230, Thailand

It has been reported that *Brugia malayi* have infected not only human but also animals such as cats, monkeys, and dogs, whereas *B. pahangi* causes morbidity only in cat reserviors. Due to their similarity in morphologies and others, the identification of both brugian species in such carriers based on traditional detection tools can be difficult and mostly lead to misdiagnosis. Hence, the data based on genes is the alternative useful information for not only parasite identification but also their genetic diversities. The internal transcribed spacer (ITS) regions were used to determine the genetic diversity of *Brugia* spp. within domestic cat reservoirs from different geographical areas in Thailand. Microfilaria was separated and their DNA was extracted prior to PCR amplification. The specific primers of ITS1 and ITS2 regions were used to yield the PCR products of 580 bp and 660 bp in size, respectively. The fragments were cloned, sequenced, and aligned in comparison to the reported data of *B. malayi* and *W. bancrofti*. It was found that ITS1 and ITS2 phylogenetic trees demonstrated the genetic variation among *Brugia* spp. Phylogenetic trees based on Neighbor Joining (NJ) and DNA Parsimony (DNA PARS) revealed both single infection of either *B. malayi* (cat 1, 3 and 4) or *B. pahangi* (cat 6 and 7) and mix infection of both *Brugia* spp. (cat 2 and 5). It can be proposed that ITS regions could be used for studying genetic diversity of *Brugia* spp., especially, in cat reservoirs which will be beneficial for epidemiological survey.

Spatial approach of the production of *Aedes aegypti* pupae using GIS and Remote sensing

Philippe Barbazan[1], Wasana Bonyuan[1], Florent Demoraes[1], Marc Souris[1], Walairut Tuntaprasart[2] and Jean-Paul Gonzalez[1].

1. IRD-Mahidol University, CVVD- UR 178, Project, Emerging Viral Diseases and Information System Research, Faculty of Sciences, Mahidol University, Thailand
2. Faculty of Public Health, Mahidol University, Thailand

DHF is a permanent challenge for Public Health authorities in Thailand, as epidemics in 1997-1998 and 2001, spread over most of the country. Wide variations of level of incidence over areas mean that to be efficient the control strategy needs the delineation of risk areas. Classical entomological indices are used by public health authorities to launch local vector control activities but their reliability to

identify areas with higher incidence and to reduce it, is limited. In the frame of a WHO-TDR program to develop new entomological indices based on pupae counts, an exhaustive survey of potential breeding sites has been done in areas with different types of urbanization in Thailand. A GIS has been developed, using the precise localization (GPS) of houses as a basic layer. The characterization of the most productive breeding sites in terms of pupae, the density of human population and socio economical indicators, such as the field description of the type of dwellings (unmanaged urban environment, town houses, residential and administrative areas, villages) were additional layers of information. Most productive BS were similar in the different areas. The containers for water storage produced up to 90% of the pupae which density could reach 0.1 to 2.6 pupae per person. The correlation between the number of potential BS and the number of pupae is higher (0.9) if we consider groups of neighboring houses (density of attributes). A minimal threshold was defined under which stochastic process in BS colonization may lead to an interruption in pupae production. Spatial patterns in the distribution of pupae allows to identify areas were targeted vector control should be easier and more efficient. This method, combining field survey for the characterization of productive breeding sites and GIS technology to delineate areas with a specific type of urbanization, will help to identify similar environments likely to evolve simultaneously in response to the emergence of epidemic phenomena. Control strategies can therefore target the most productive containers but also key areas in the transmission network, for a better efficiency.

The RNA Virus Database

Robert Belshaw[1], Tulio de Oliveira[1] and Andrew Rambaut[2]

1. Department of Zoology, University of Oxford, United Kingdom

2. Institute of Evolutionary Biology, University of Edinburgh, United Kingdom

As concern mounts over the threat posed by RNA viruses, and the amount of genomic information we have for them increases, a single web application providing key genomic resources for all species is timely. We have created the RNA Virus Database to perform six main services for all 700 RNA viral species: Identify submitted viral nucleotide or amino acid sequences, provide curated whole genome nucleotide alignments – with corresponding phylogenetic trees – for each virus, Align submitted nucleotide sequences to the above, provide amino acid sequences for all viral genes, and allow the user to extract the corresponding region from the above whole genome alignments, provide whole translated genomes for each viral species, show links to the more specialised web sites for the viruses of greatest medical importance (including genotyping tools). We also link to other sites providing further taxonomic or biological information for each virus. We are currently using the database to analyse the deep phylogeny of RNA viruses and the relationship between genome size and genome architecture. We expect the website version of the database to facilitate and encourage research into many other aspects of RNA viral evolution. It is freely accessible at http://virus.zoo.ox.ac.uk/

Barbazan Philippe, Bonyuan W., Demoraes Florent, Souris Marc, Tuntaprasart W., Gonzalez Jean-Paul. (2006).

Spatial approach of the production of Aedes aegypti pupae using GIS and remote sensing.

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

Atlanta (USA) ; Bangkok : CDC ; IRD, p. 77-78.

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