target of selection is probably directed against the EGF-like domain, and may involve recognition of pathogen associated molecular patterns (PAMPs). Biological studies that seek to identify the interacting target(s) of the EMR1 receptor can shed further insight into the nature of the evolution of the gene, and its involvement (if any) in susceptibility to infections.

Symposium "Medical entomology 1"

(5) *Aedes aegypti*: experimental data supports a genetic background for shape variation.

Jirakanjanakit N.[1], Leemingsawat S.[2] and Dujardin J. P.[3]

1. Center for Vaccine Development, Institute of Science and Technology for Research and Development, Mahidol University, Salaya, Puttamonthon, Nakhonpathom, Thailand

2. Department of Medical Entomology, Faculty of Tropical Medicine, Mahidol Unversity, Bangkok, Thailand

3. IRD Montpellier, GEMI, UMR CNRS-IRD 2724, Montpellier, France

Keywords: *Aedes aegypti*, isofemale line, shape variation, metric disparity

Shape variation of the wing of *Aedes aegypti* was examined in three isofemale lines A, B and C under controlled laboratory conditions during ten generations. The landmark coordinate data were collected from cross veins and junctions for morphometric analysis. To quantify shape variation, we used the "metric disparity" index, known to be independent of sample sizes. Statistical comparisons were performed by non-parametric tests (bootstraps). It was assumed that isofemale lines had been founded by parents having different genotypes, and that no new genotypes appeared during the 10 generations of follow-up. Metric disparity was scored across lines within a given generation and across different generations within a given line. It was shown that the metric disparity index behaved as expected for an indicator of genetic diversity: increasing when mixing different lines, not increasing when adding individuals of the same line. In addition, a simple classification tree of the total sample showed that even after ten generations, the wings were clustered into three groups according to the initial founders. This study suggests a genetic basis for wing geometry of *Aedes aegypti*. The epidemiological interest of wing shape behaving as a genetic character would be to help in detecting natural patterns of population structuring at a low cost. In the same way three experimentally isolated lines were recognized by individual wing traits, it is expected that any isolated field population could also be detected. Similar conclusions were obtained previously on various old laboratory lines of *Aedes aegypti*.

(6) Population structure of main malaria vectors in Asia, members of *Anopheles* species complexes: Implications on vector control

Manguin Sylvie*[1], Garros Claire[1,a], Dusfour Isabelle[1,b] & Coosemans Marc[2]

1. Institute of Research for Development (IRD), Centre of Biology and Management of Populations, Montpellier, France

2. Institute of Tropical Medicine (ITM), Antwerp, Belgium.
a. University of California, Irvine, College of Health Sciences, Program in Public Health, 3501 Hewitt Hall, Irvine, CA 92697-4050, USA; b. Uniformed Services University of the Health Sciences (USUHS), dept PMB, 4301 Jones Bridge Road, Bethesda, MD 20814, USA.
* Corresponding author: Manguin Sylvie' CBGP, Campus international Agropolis de Baillarguet, CS 30016, 34988 Montferrier-sur-Lez cedex , France ; e-mail: manguin@mpl.ird.fr

In Asia, the anopheline biodiversity is very rich and the main malaria vectors belong to complexes in which species are morphologically indistinguishable. Recent advances in systematics and molecular identifications have allowed a clarification of phylogenetic relationships and a simplification of species identification among and within the sibling species or *Anopheles* groups. This is of primordial importance for applying appropriate vector control programs. The presentation of the latest data on the main malaria vectors in southern Asia will highlight the importance of precisely identifying the species, assessing relationships among members of complex, and testing phylogenetic hypotheses involving closely related *Anopheles* species to conduct adequate and efficient vector control strategies. The Minimus Complex is widely distributed on the Asian Continent and is composed of two species considered as malaria vectors in SE Asia. This complex belongs to the Funestus Group which comprises 27 closely related species distributed in Africa and in Asia. Based on molecular and morphological characters and a complete phylogenetic work, a new systematic scheme was recently presented which reflects the evolutionary relationships within species of this group. The Sundaicus Complex is distributed along the coast of Asia and is known as one of the main malaria vector in southern Asia. Recent molecular works on this complex have allowed the recognition of at least three species for which phylogeographic evolutionary scenario will be presented along with the malaria risk linked to specific human activities. Other *Anopheles* complexes with major malaria vectors will be mentioned such as the Dirus, Fluviatilis, and Culicifacies in relation to systematics and malaria transmission.

(7) From population structure to genetically-engineered vectors: new ways to control vector-borne diseases?

Olivier Sparagano*
* School of Agriculture, Food and Rural Development, Newcastle University, Agriculture Building, Newcastle-upon-Tyne, NE1 7RU, UK, e-mail: Olivier.Sparagano@ncl.ac.uk
Keywords: ticks, mosquitoes, biodiversity, genetic flow, genetic manipulations.

Epidemiological studies on ticks and the pathogens they can carry (such as Lyme Disease) are showing some correlations between infection rates and biodiversity highlighting the “dilution” effects on potential vectors while other studies comparing sympatric small rodent species demonstrated that rodent species transmitting more pathogens are parasitized by more ectoparasite species. Further studies on host dispersion also showed some impacts on genetic diversity in the ticks with some other comparisons between tick sex, location and genetic flows within these ectoparasite populations.

Manguin Sylvie, Garros Claire, Dufour Isabelle, Coosemans M. (2006).

Population structure of main malari vectors in Asia, members of Anopheles species complexes : implications on vector control.

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

Atlanta (USA) ; Bangkok : CDC ; IRD, p. 28-29.

International Meeting on Molecular Epidemiology and Evolutionary Genetics in Infectious Diseases, 8.