

models completed in the mid-1990s (CIMSIM and DENSiM) have been incorporated into a Windows™-based graphical interface for enhanced ease of use. Major updates include resolution of coding bugs and implementation of model structural changes, such as age-dependent adult vector mortality, oviposition site selection, and human density calculations. The new program can be used to compare the impact of single or integrated vector control interventions based on locally-derived entomological, serological and climatic data. For example, space spraying (80% efficacy) every 6 months over a 5 year period was predicted to reduce the adult *Ae. aegypti* population in a 1 hectare simulation area from a baseline of 199.2 down to 186.0 females/day. Resultant reductions in human infection rates were minimal. Conversely, space spraying plus larviciding of 90% of large containers (90% efficacy) every 6 months effectively reduced mosquito populations by a further 66.0%, to 63.3 females/day. The resultant total number of human dengue infections within the simulation area dropped to 7.1-8.0 from a baseline of 18.5-19.0. Sensitivity analyses are being undertaken using a Latin hypercube sampling scheme to identify the most epidemiologically significant parameters. Validations are based on comparison of model outputs to longitudinal pre- and post-intervention entomological and serological field data from the Amazonian city of Iquitos, Peru. The program will be made available in multiple languages, free of charge. We anticipate that it will be utilized by vector control personnel, public health practitioners, and government officials to support the formulation of locally-adapted dengue control strategies.

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RAINFALL AND THE *CULEX PIPPIENS* COMPLEX: HOW MUCH IS TOO MUCH?

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Mosquitoes in the *Culex pipiens* complex are important worldwide as pests and vectors of human pathogens, including several flaviviruses and filarial worms. *Cx. pipiens* s.l. utilizes storm drains and other organically charged larval habitats associated with human development. Although precipitation or anthropogenic water inputs are essential for creation of urban larval habitats, field and lab studies have suggested that intense rainfall flushes larvae out of these habitats, often leading to a reduction in adult abundance. We tested the hypotheses that (1) a moderate level of rainfall, enough to create breeding sources but not so much as to cause flushing, results in larger numbers of adult *Cx. pipiens* s.l. and (2) the precipitation-abundance relationship depends on the condition of the underground drainage system. Predictor variables considered were the amount and frequency of rainfall, combined with urban development dates and household income as surrogates for the condition of drainage systems. These were tested in spatially and temporally explicit Bayesian regression models fitted to a 10-year statewide dataset including 856 sites. In urban areas, high levels of late-winter precipitation were associated with reduction of adult female trap counts by > 50% during spring.

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CHARACTERIZATION OF IMMUNOGENIC PROTEINS IN *ANOPHELES GAMBIAE* SALIVARY GLANDS AND THEIR POTENTIAL USE AS A MARKER OF EXPOSURE TO MALARIA

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During blood feeding, the mosquito injects saliva into the vertebrate host. This saliva contains bioactive components which may play a role in pathogen transmission and in host-vector relationships by inducing an immune response in the vertebrate host. The evaluation of human immune responses to arthropod bites might also represent a research

direction for assessing individual exposure to the bite of a malaria vector. We have previously described that IgG response specific to whole salivary extracts from *Anopheles gambiae* may be a marker of the risk of malaria transmission in young children exposed to malaria in Senegal. The aim of the present study is then to characterize immunogenic salivary proteins of *An. gambiae* by an immuno-proteomic approach. 2DE -blotting were performed with sera from children living in different malaria endemic area. Ten immunogenic proteins were revealed in uninfected saliva after 2DE-blotting with sera from exposed children. Among these proteins, seven were identified by mass spectrometry, several are involved in sugar meal (amylase) and other ones are involved in blood meal (5' nucleotidase, D7 long form and D7-r4). Several of these proteins are now produced under their recombinant form. The next step will be to test which protein has the better potential as a marker of exposure to *Anopheles* bite by ELISA technique on large cohort of malaria exposed individuals. The second step will be to characterize immunogenic proteins present in *Plasmodium falciparum* infected salivary glands. This work opens the way to design new epidemiological tools, to evaluate malaria exposure in the field, similarly to the study of the risk of transmission for other vector-borne diseases.

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MALARIA VECTOR BREEDING SITES AND ASSESSING THEIR IMPACT ON LOCAL MALARIA RISK: PRELIMINARY DATA ON THE RISK FACTORS FOR MALARIA INFECTION

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The study aims to investigate the importance of different vector breeding site types on malaria infection risk. The study was carried out in 3 villages in the Lower Shire Valley in southern Malawi. In an on-going process, longitudinal surveys of malaria parasitemia and mosquito abundance were carried out in the three study villages every 4 months beginning August 2006. Parasitemia was determined using microscopy of field collected thick films in children less than 10 years of age. Adult mosquitoes were collected by pyrethrum knockdown (PKD) to determine mosquito abundance/ density. Here we present preliminary results from the first two surveys carried out in September 2006 (dry season) and April 2007 (end of wet season). The odds ratio of having malaria was 27.79 higher in April 2007 (end of wet season) than in September 2006 ($p < 0.001$). The finding was as expected since malaria transmission peaks towards the end of wet season. The odds ratio of having malaria was 0.08 higher for children living at Nkata village than those living at Nkhwazi ($p < 0.002$). Similarly children living at Kela showed a higher odds ratio (0.14) of having malaria than those living at Nkwazi ($p < 0.013$). No significant differences were found in children living either at Nkata or Kela ($p < 0.411$). The difference in malaria prevalence between the study sites despite the short distance between them could be explained by heterogeneities in malaria transmission but also socio-economic factors. The odds ratio of having malaria was 6.69 higher for children not sleeping under an insecticide treated bed net ($p < 0.020$) compared to children that were sleeping under a treated net. These results were also expected since treated nets have been shown to reduce all cause mortality and morbidity in children and communities using them. Parent education, child age or sex and mosquito abundance were not significant risk factors to malaria infection ($p > 0.5$). It is too early to say that these are not risk factors to malaria infection as the results here are indeed only preliminary. In conclusion, this study has shown that time of survey (season), site or location (village) and use of ITNs were important factors to malaria infection.

Cornélie Sylvie, Senglat M., Doucoure S., Demettre E.,
Remoué Franck (2008)

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