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INSENSITIVE ACETYLCHOLINESTERASE (*ACE-1^R*) OF *ANOPHELES GAMBIAE* S.S.: EVENTS OF INTROGRESSION AND DUPLICATION BETWEEN THE M AND S MOLECULAR FORMS

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Studies on insecticide resistance genes provide data on the evolutionary processes involved in the adaptation of insects to environmental changes. Understanding the dynamics and the evolution of genes associated with insecticide resistance between closely related taxa represents a great interest, in terms of understanding resistance evolution in the field. This is a key component in establishing effective long-term resistance management strategies to eventually adapt vector control. In an upstream study, the mutation G119S (generating *ace-1^R* allele) was found in both molecular forms of *An. gambiae* s.s from Benin, Burkina Faso and Côte d'Ivoire. To establish whether the G119S mutation has arisen independently in each form or by genetic introgression, we analysed coding and non-coding sequences of *ace-1* alleles in M and S mosquitoes from representative field populations from West Africa. Our data revealed many polymorphic sites shared by S and M forms, but no diversity was associated with the G119S mutation. This indicates that the G119S mutation was a unique event and that genetic introgression explains its distribution within the two forms. Unexpectedly, sequence analysis of some resistant individuals revealed a duplication of the *ace-1* gene in both *An. gambiae* s.s. M and S forms. Again, the distribution of this duplication in the two forms most likely occurred through introgression. These results impacts on the question of actual levels of gene flow between the two molecular forms in tropical savannah areas. We can conclude that the G119S mutation could spread rapidly in the field and then compromises the use of organophosphate and carbamate compounds in public health as an alternative for indoor residual spraying in areas where malaria vectors are resistant to DDT and pyrethroids. This study underlines the necessity to monitor the G119S mutation in natural populations before planning and implementing malaria control programs based on the use of organophosphate and carbamate.

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ENTOMOLOGICAL EVALUATION OF PERMETHRIN IMPREGNATED BEDNETS AGAINST *ANOPHELES DARLINGI* IN THE PERUVIAN AMAZON

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Millions of Long Lasting Insecticide Treated Nets (LLINs) are to be distributed throughout the Amazon basin between 2007 and 2010. There is however, little understanding of how such interventions might impact upon the number of bites (and hence infections) that the people of that region receive. Bednets are particularly suitable for insects that bite and rest indoors and at night but *Anopheles darlingi*, the principal and anthropophilic vector of malaria in the Amazon, typically bites early in the evening, and is relatively exophilic and exophagic. In this study we present a simple prefabricated design for an experimental hut and a basic window trap. We show that these collect sufficient An. darlingi for the evaluation of interdomiciliary vector-control interventions. Using these tools, we report on the effect of LLINs on entrance and exit rates, and mortality of *An. darlingi*. Huts containing bednets collected ca. 50% fewer mosquitoes in window traps than untreated huts. Treated huts also contained fewer mosquitoes that had entered by other routes. Of those, >90% were collected dead or dying; presumably as a result of contact with bednets. This was in dramatic contrast to untreated huts in which there was less than 5% mortality among mosquitoes that had entered by means other than the window traps. We also note some unusual patterns in parous / nulliparous rates inside and outside the huts that suggest that *An. darlingi* becomes more endophilic and endophagic with experience and age.

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SPATIO-TEMPORAL ORDERING OF A CHAGAS DISEASE VECTOR ELIMINATION CAMPAIGN

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The rational design of interventions is critical to the control of communicable diseases. The Chagas disease vector *Triatoma infestans* has been eliminated from large areas of South America through application of insecticide, but vector control campaigns often fail when the insect returns to treated areas after insecticide wanes. Here we utilize a genetic algorithm, originally developed for the "traveling salesman" problem, in order to identify spatio-temporal designs of insecticide application that maximize the probability of vector elimination. Calibrated to empirical data on *T. infestans* migration, we find that the success of a control strategy is sensitive to the duration of insecticide efficacy, and shows chaotic fluctuations in response to unforeseen delays in the control campaign. Successful strategies feature both coarse and fine-grained geographic correlations. Nevertheless, successful designs generally deviate from a simple, sequential treatment of geographically proximate communities, instead "jumping ahead" to treat distal communities prior to completing treatment of a single area. We study the conditions under which this "jumping-ahead" strategy improves outcomes in a simplified system. Our analysis provides a detailed method to optimize elimination campaigns for an important disease vector as well as elucidates general guidelines to improve other control measures in time and space.

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EFFECTS OF FOREST FRAGMENTATION ON RELATIVE ABUNDANCE, BLOOD MEAL SPECIES COMPOSITION, AND TRYPANOSOME INFECTION OF THE CHAGAS DISEASE VECTOR *RHODNIUS PALLESCENS* IN A PANAMANIAN LANDSCAPE

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Deforestation and forest fragmentation are associated with infectious disease emergence in humans and animals. The objective of this study is to investigate relationships between forest fragmentation, vector populations, and transmission of the zoonotic vector-borne parasite *Trypanosoma cruzi* in a rural landscape of Panama. *Rhodnius pallescens,* the principal reduviid bug vector of Chagas disease in Panama, was collected from its primary habitat, the palm *Attalea butyracea*, from habitat types reflecting a range of anthropogenic disturbance (continuous undisturbed forest, forest fragments, cattle pasture, and peridomicile). *R. pallescens* abundance was estimated for each habitat type, bugs (N=641) were tested for infection with *T. cruzi* and *T. rangeli* by a duplex PCR assay, and

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