

among all populations. We have started obtaining sequences of the more conserved mtDNA *Cyt b* gene from the same localities to corroborate our *COI* findings and investigate earlier demographic history of this important malaria vector.

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CHROMOSOMAL PLASTICITY AND EVOLUTIONARY POTENTIAL IN THE MALARIA VECTOR *ANOPHELES GAMBIAE* SENSU STRICTO: INSIGHTS FROM THREE DECADES OF RARE PARACENTRIC INVERSIONS

Marco Pombi¹, Beniamino Caputo¹, Carlo Costantini², Maria Angela Di Deco¹, Mario Coluzzi¹, Alessandra della Torre¹, Frederic Simard³, Nora J. Besansky⁴, Vincenzo Petrarca⁵

¹Dip. Scienze di Sanità Pubblica, Università Sapienza, Rome, Italy,

²Institut de Recherche pour le Développement, UR⁰¹⁶, and Organisation de Coopération pour la Lutte contre les Endémies en Afrique Centrale, Yaoundé, Cameroon, ³Institut de Recherche pour le Développement, UR⁰¹⁶, and Institut de Recherche en Sciences de la Santé, Bobo-Dioulasso, Burkina Faso, ⁴Centre for Tropical Disease Research and Training, Dep. of Biological Sciences, University of Notre Dame, Notre Dame, IN, United States, ⁵Dip. Genetica e Biologia Molecolare, Università Sapienza, Rome, Italy

In the *Anopheles gambiae* complex, paracentric chromosomal inversions are non-randomly distributed along the complement: 18/31 common polymorphic inversions are on chromosome arm 2R, which represents about 30% of the complement. Moreover, in *An. gambiae* sensu stricto, 6/7 common polymorphic inversions occur on 2R and 1 on 2L. Most of these inversions are considered markers of ecological adaptation that increase the fitness of the carriers of alternative karyotypes in contrasting habitats. However, little is known about the evolutionary forces triggering the origin and allowing subsequent establishment of chromosomal inversions in field populations. Here, we present data on 82 previously undescribed rare chromosomal inversions (RCIs) recorded during extensive field sampling in 16 African countries over a 30 year period, which may shed light on the dynamics of chromosomal plasticity in *An. gambiae* s.s. and its adaptive potential. We analyzed breakpoint distribution, length, and geographic distribution of RCIs, and compared these measures to those of the common inversions. We found that RCIs, like common inversions, are disproportionately clustered on 2R, which may indicate that this arm is especially prone to breakages. However, contrasting patterns were observed between the geographic distribution of common inversions and RCIs. RCIs were equally frequent across biomes and on both sides of the Great Rift Valley (GRV), whereas common inversions predominated in arid ecological settings and west of the GRV. Because 17/82 (21%) RCIs were found repeatedly at very low frequencies-- at the same sampling location across different years and/or in different sampling locations-- we suggest that RCIs are early in the process of establishment and subject mainly to drift under unperturbed ecological conditions. Nevertheless, RCIs may represent an important reservoir of genetic variation for *An. gambiae* s.s. in response to environmental change, further testifying to the considerable evolutionary potential hidden within this pan-African malaria vector.

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WHAT IS THE IMPACT OF ARBOVIRAL INFECTION ON VECTOR LONGEVITY?

Louis Lambrechts, Thomas W. Scott

University of California, Davis, CA, United States

The idea that arboviruses should evolve towards a benign relationship with their vectors was prevalent in the early history of medical entomology. The idea was based on the belief that virulence (i.e., negative effects on vector fitness) was necessarily detrimental to the virus because a virus that is harmful to its vector is harmful to itself. Reduction in vector longevity was an example of this view, because arboviruses are generally

transmitted only after an extrinsic incubation period that is close to or exceeds the average lifetime of their vectors. In the 1980's, conflicting observations and theoretical developments on the evolution of host-pathogen interactions challenged this view by supporting the idea that increased levels of virulence could potentially be advantageous provided they concomitantly increased transmission. However, while a number of studies have reported experimental evidence for increased vector mortality due to arboviral infection, others have failed to detect any significant impact; a single study even provided evidence for enhanced vector longevity. Whether this variation in the outcome of studies relies on biological differences between particular vector-virus systems or simply reflects differences in experimental settings remains unclear. Focusing on mosquito-virus interactions, we performed a meta-analysis of published studies to (1) evaluate the overall magnitude and statistical significance (across systems and studies) of the effect of arboviral infection on vector longevity, and (2) identify characteristics of individual studies (e.g., infection method, viral dose, environmental quality, etc.) influencing the magnitude of the observed effect. Our results unravel the biological and experimental factors underlying the impact of arboviral infection on vector longevity and help identify the evolutionary forces driving the virulence of arboviruses to their free-ranging vectors.

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THE EVOLUTION OF ANTI-MALARIAL IMMUNE GENES IN THE *ANOPHELES GAMBIAE* COMPLEX

Michel A. Slotman¹, Aristeidis Parmakelis², Nikolas Poulakakis³, Kirstin B. Dion¹, Jonathon C. Marshall⁴, Christophe Antonio-Nkondjio⁵, Parfait H. Awono-Ambene⁵, Frederic Simard⁶, Adalgisa Caccone¹, Jeffrey R. Powell¹

¹Yale University, New Haven, CT, United States, ²University of Athens, Athens, Greece, ³University of Crete, Heraklion, Greece, ⁴Southern Utah University, Cedar city, UT, United States, ⁵Organisation de Coopération pour la Lutte Contre les Endémies en Afrique Centrale, Yaounde, Cameroon, ⁶Institute de Recherche pour le Development, Ouagadougou, Burkina Faso

The goal of developing malaria resistant transgenic mosquitoes for malaria control has focused much attention on the immune system of *Anopheles gambiae*. Numerous genes are now known that affect the mosquito's ability to transmit *Plasmodium*. In order to narrow down these genes to those that specifically target *Plasmodium*, we have taken an approach that is based on the observation that malaria vectors and their *Plasmodium* parasite co-evolve. That is, we expect immune genes that specifically target *Plasmodium* to show signs of positive selection in those mosquitoes that transmit malaria, but not in closely related non-vector species. We have now investigated the evolution of 20 anti-malarial immune genes in six species of the *An. gambiae* complex, including both vector and non-vector species. Although we previously reported an instance of positive selection of *LRIM1* in the malaria vector *An. arabiensis*, the majority of the investigated anti-malarial immune genes show patterns of purifying selection. However, for TEP1 the two vector species *An. gambiae* and *An. arabiensis* carry two markedly divergent allele classes, indicating that this gene may be subject to balancing selection.

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ASSOCIATIONS BETWEEN URBAN STRUCTURE AND *Aedes Aegypti* LARVAL HABITATS IN PUNTARENAS, COSTA RICA

Adriana Troyo¹, Kristopher L. Arheart², Douglas O. Fuller², Olger Calderon-Arguedas¹, John C. Beier²

¹Universidad de Costa Rica, San Jose, Costa Rica, ²University of Miami, Miami, FL, United States

Geospatial technologies have been increasingly applied to study vector-borne diseases, although their use in urban setting has been limited. In this study, high-resolution satellite imagery from QuickBird was analyzed to determine the relationships that urban structure, determined by tree

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The evolution of anti-malarial immune genes in the
Anopheles gambiae complex

In : 57th American Society of Tropical Medicine and Hygiene
annual meeting. 79 (6), 201-art. 683

ASTMH Annual Meeting, 57., La Nouvelle-Orléans (USA),
2008/12/07-11