

of such an effort. Because of their geographic isolation, islands are simplified settings for natural experimental studies of vector control strategies. Two potential sites for these studies are the islands of São Tomé and Príncipe located off the west coast of Africa. In this study we carried a phylogeographic analysis aimed at understanding the evolutionary origins of *A. gambiae* populations from both islands using mitochondrial and nuclear loci. Mosquito samples were collected from São Tomé (~100 individuals from 2 populations), Príncipe (~50 individuals from one population) and various countries from continental and insular Africa (~400 individuals from 9 countries). We sequenced portions of the ITS region of the rDNA, and the ND5 mitochondrial gene. Analysis of the mtDNA gene revealed extensive genetic divergence between São Tomé and Príncipe island populations. Results also suggest a recent origin of mtDNA haplotypes possibly from Nigeria, Cameroon, and the Central Republic of Africa. On the contrary, analysis of the nuclear genes indicates a possible origin of the island populations from Angola. Possible explanations of these results are discussed, particularly in relation to historical human migration routes.

(ACMCIP Abstract)

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THE EFFECT OF MOSQUITO SALIVA ON *PLASMODIUM YOELII* INFECTION

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Immunity to the saliva of hemataphagous insects has considerable effects on the pathogens they transmit. Work has shown that the pathology associated with disease models, including Lyme's disease and Leishmaniasis, is modulated by immune responses against vector saliva. Mosquito saliva also has the ability to elicit strong hypersensitivity reactions, evidenced by the swollen, itchy, red bumps associated with mosquito bites. Mosquito bites in areas of high malaria endemicity can number as high as 100 per day, and their saliva has a glut of pharmacologically active compounds. These molecules have anti-hemostatic, anti-inflammatory, and immunosuppressive activities. In this study we demonstrate that exposure to *Anopheles stephensi* saliva prior to malaria infection skews the local and systemic immune response toward a Th1 bias, subsequently limiting *Plasmodium yoelii* development with in Balb/c mice. This has been evidenced by a lowered hepatic parasite burden that strongly correlates to an increase in both local and systemic interferon γ (IFN γ) production, as well as increased production of hepatic inducible nitric oxide synthase (iNOS). This protective effect was fully abrogated in IFN γ -deficient animals, demonstrating the importance of the host's response to vector saliva. The protective effect associated with mosquito presensitization makes salivary components strong candidates for use as adjuvants in malaria vaccine development. This study demonstrates the necessary attention that must be paid to the host-vector interaction, further highlighting the complexity of vector-transmitted diseases.

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A NEW PUUMALA HANTAVIRUS AS CAUSE OF AN NEPHROPATHIA EPIDEMICA OUTBREAK IN SOUTH-EAST GERMANY IN 2004

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A micro-epidemic of hantavirus infections occurred in Lower Bavaria, South-East Germany, starting in April 2004. While only three cases were registered from 2001 to 2003, a dramatically increased number of clinically apparent hantavirus infections (n=38) was observed in 2004, plus 7 additional cases until June 2005. To determine the reservoir responsible for the infections, a total of 61 rodents were trapped in Lower Bavaria. Serological and genetic investigations revealed that Puumala virus (PUUV) is dominant in the local population of bank voles. Partial PUUV S segment nucleotide sequences originating from bank voles at four different trapping sites showed a low divergence (up to 3.1%). This is contrasted by a nucleotide sequence divergence of 14-16% to PUUV strains recognized in Belgium, France, Slovakia or North-Western Germany. PUUV sequences from Lower Bavaria represent a new PUUV subtype which seems to be responsible for the observed increase of human hantavirus infections in 2004/2005.

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IMPACT OF LAND COVER CHANGE ON HANTAVIRUS ECOLOGY IN THE INTER-ATLANTIC FOREST OF PARAGUAY

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Recently, we reported the discovery of several additional rodent species as potential reservoirs of hantavirus in western (*Holochilus chacarius*) and eastern Paraguay (*Akodon montensis*, *Oligoryzomys chacoensis*, and *O. nigripes*). The discovery of hantavirus in three areas of eastern Paraguay was surprising, since cases of hantavirus pulmonary syndrome have only been reported in western Paraguay. To further explore the phylogenetic relationships of hantavirus strains in Paraguay to others in South America, we have amplified and sequenced portions of the hantavirus S- and M-segments from these four animal species. Phylogenetic analysis showed that these sequences along with the other South American sequences formed a clade distinct and unique from North American hantaviruses. Interestingly, two of the hantavirus strains, AIPa from the Alto Pargauay Department in the Chaco and Itapúa16 from the Itapúa Department in eastern Paraguay showed strong homology to known hantaviruses in comparisons of their M-segment sequences, but not in their S-segment sequence. These results suggest that reassortment may play a role in the complex evolution of South American hantaviruses. Since the occurrence of hantavirus in rodent hosts has been correlated to a number of climatic and environmental factors, including



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