Quest for novel viruses in mosquitoes collected in the area of the Taï National Park, Côte d'Ivoire

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Vector-borne pathogens are among the most important emerging and re-emerging viruses that cause epidemics in the human population. As part of a comprehensive study on the distribution of arboviruses and their vectors in different ecological habitats, 7,067 mosquitoes were collected along a straight transect from the inside of the Taï National Park to surrounding fields and villages. From a total of 437 female mosquito pools, 98 (22.4%) caused a cytopathic effect in cell culture. 30 pools were analysed by electron microscopy. Three rhabdoviruses, one flavivirus, one bunyavirus, one orbivirus, one corona-like virus and 10 pools with uncharacterised viral particles were found. From 7 morphologically pre-characterized pools viral sequence information was retrieved by random PCR amplification. Sequence homology to known viruses was low, and relationships were mostly found only on amino acid level. Our system of vector analysis is a powerful tool for routine screening and for the identification of novel viruses. In our screen only new viruses were found, demonstrating that viral diversity in tropical rainforests is still far from being understood.

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* The reference list may be obtained by request or at the poster in the congress.