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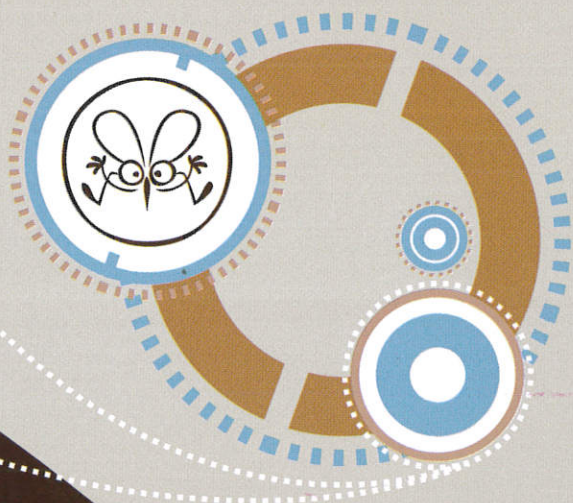
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When epidemic
becomes endemic:
a global challenge
towards vector
control

Abstract Book



Vector-pathogen association: lack of congruence of phylogeographical pattern of the vector tick *Amblyomma variegatum* (Acari: Ixodidae) and of the Rickettsiales *Ehrlichia ruminantium*?

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The hard ticks *Amblyomma variegatum* is the main vector of *Ehrlichia ruminantium* the pathogen responsible for heart water or cow driosis, a tropical disease of ruminants. This tick originates from sub-Saharan Africa and is now widely widespread. *A. variegatum* has been described for the first time in Madagascar in 1899, but its introduction is probably older and very likely concomitant with livestock introduction from Africa. *A. variegatum* has also been described in the Comoros, Mayotte, La Reunion and Mauritius islands. *A. variegatum* was probably introduced in the Caribbean area in the middle of the 18th century through cattle trade. Together with the tick, *E. ruminantium* was also introduced in these areas.

Numerous and complex factors have an influence on the epidemiology of vector-borne diseases. Environmental factors, which may be deeply altered by human activities, have a direct impact on the system bacterium/vector. The creation of communication and trade routes have allowed human movements but also movement of animals, pathogens and vectors. These complex interactions may determine whether or not the vector and the pathogen would share similar phylogeographical patterns.

The aim of this study was to investigate the genetic and demographic phenomena that have shaped the present distribution and structure of *A. variegatum* together with the bacteria *E. ruminantium*. A phylogeographic approach has been carried out on *A. variegatum*, by analysing of two mitochondrial-DNA genes and on *E. ruminantium* using 2 multi-locus approaches, MLST (multilocus sequence typing) on 5 housekeeping genes and MLVA on 7 VNTRs (Multiple Loci VNTR Analysis).

On *A. variegatum*, this study has led to the identification of two main lineages one covering all the species distribution area on another one restricted to East Africa and Indian Ocean area while the MLST analysis of *E. ruminantium* shows two main clusters, one worldwide cluster including Caribbean, Indian Ocean and West and South Africa and one restricted to West Africa. This apparent lack of congruence will be discussed according to MLVA data expected to present a higher polymorphism than MLST.