

FIRST ISOLATION OF THE RIFT VALLEY FEVER VIRUS FROM *CULEX POICILIPES* (DIPTERA: CULICIDAE) IN NATURE

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Abstract. Following the reemergence of Rift Valley fever (RVF) virus in southeastern Mauritania in 1998, an entomological survey was undertaken in the boundary area in Senegal to assess the extent of the virus circulation. During this study, RVF virus (36 strains) was isolated for the first time from *Culex poicilipes* in nature. The possible role of *Cx. poicilipes* as an RVF vector is discussed regarding its biology and ecology.

Rift Valley fever (RVF) is an African viral zoonosis transmitted by mosquitoes. In September and October 1998, hemorrhagic fever cases were reported in the Ayoun El Atrouss zone, Mauritania (Nabeth P, unpublished data). Rift Valley fever virus was diagnosed using IgM capture, reverse transcriptase-polymerase chain reaction (RT-PCR), and virus isolation at the Pasteur Institute, Dakar, Senegal. Following the confirmation of these RVF cases in Mauritania, entomological survey was carried out in Senegal along the river basin in Thille Boubacar, Kanel, Dembankane, and Diawara (Figure 1) in order to evaluate the extent of virus circulation. These localities are approximately 400 kilometers from the Mauritanian epidemic/epizootic zone.

Mosquitoes were collected using the Centers for Disease Control and Prevention (CDC) light traps with CO₂ set nearby temporary ground pools and CDC light traps without CO₂ set in sheepfolds or cowsheds. They were then sorted and classified into monospecific pools and stored in liquid nitrogen before virological isolation attempts were made. Isolations were performed on Vero and AP 61 (*Aedes pseudoscutellaris*) cell lines. Rift Valley fever virus identification

was made by indirect immunofluorescence,¹ then confirmed by complement fixation and seroneutralization tests.

In total, 31,944 mosquitoes belonging to 6 genera and 20 species were captured. *Culex poicilipes* and *Mansonia uniformis* were the most common species (Table 1). Thirty-six RVF virus strains were isolated from *Cx. poicilipes* captured in Diawara, the locality in which the highest density of *Cx. poicilipes* was obtained (Figure 2). The true infection rate was estimated to be $0.37 \pm 0.06\%$ in Diawara.

To our knowledge, this is the first isolation of RVF virus from *Cx. poicilipes* in nature. Among mosquitoes collected, *Culex antennatus*, *Anopheles pharoensis*, *Mansonia africana* and *Ma. uniformis* were already found naturally infected by the RVF virus.² Previously, RVF virus isolations were obtained in Senegal from mosquitoes *Aedes dalzieli*, *Aedes vexans*, and *Aedes ochraceus*.³ Like most RVF virus vectors, *Cx. poicilipes* is a temporary-ground-pools mosquito well adapted to the Sahelian area. In Barkedji area where an entomological survey has been conducted since 1990, *Cx. poicilipes* is the most represented species after *Ae. vexans*.³ In this area, a high tropism of *Cx. poicilipes* was observed for

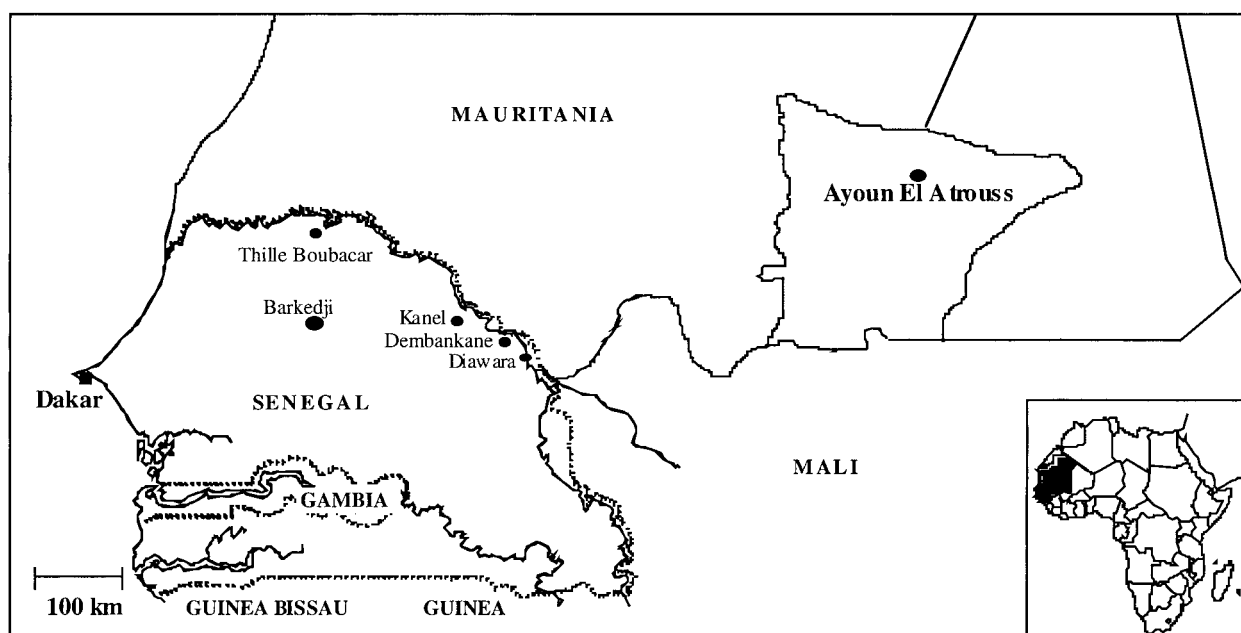


FIGURE 1. Location of the study areas.

TABLE 1
Mosquitoes captured in November 1998 in the Senegal River Basin

Species	No.	No. of Pools	Density*	Abundance (%)†
<i>Culex poicilipes</i> ‡	14,937	299	678.9	46.76
<i>Mansonia uniformis</i>	14,370	290	653.2	44.98
Other species	2,637	95	119.8	8.25
Total	31,944	684	1,452	100

* Number of mosquitoes captured per trap per night.

† Percentage of the number captured for a species/total of the collection.

‡ 36 Rift Valley Fever virus strains isolated.

Other species: *Anopheles ziemanni*, *Anopheles gambiae s.l.*, *Anopheles pharoensis*, *Anopheles rufipes*, *Anopheles wellcomei*, *Aedes sudanensis*, *Aedes vexans*, *Culex antennatus*, *Culex bitaeniorhynchus*, *Culex ethiopicus*, *Culex neavei*, *Culex quinquefasciatus*, *Culex tritaeniorhynchus*, *Mansonia africana*, *Mimomyia mimomyiaformis*, *Mimomyia splendens*, *Uranotaenia balfouri*, and *Uranotaenia mayeri*.

humans, sheep, oxen, and chickens.⁴ In addition, feeding preference studies conducted in the Senegal river basin have shown that *Cx. poicilipes* fed preferentially on humans but also on bovines, ovines, and nonidentified animals, while in Kenya its ornithophilic tendency was unequivocal.^{5,6} These considerations on *Cx. poicilipes* biology and ecology, as well as its experimentally demonstrated vectorial competence to RVF virus⁷ constitute clues pointing to the vector role of the species in RVF virus transmission cycles.

Rift Valley fever virus isolations in Mauritania and Senegal in 1998 were evidence that the virus had emerged at the same period in several locations. Comparable situations were also observed with the 1993 RVF virus circulation in Senegal, Mauritania and Egypt^{3,8,9} and with the recent outbreak in Kenya and Somalia in 1997–1998.¹⁰ At least two hypotheses could explain this widespread RVF virus circulation. The first is the possible virus diffusion from an infected area to a receptive one. Human and livestock movements represent a likely origin of this virus diffusion. Regarding the ornithophilic tendency of *Cx. poicilipes*, the role of birds in RVF virus dissemination merit more thorough investigation, even if some studies invalidated their reservoir role.¹¹ In contrast, the vectors' role in RVF virus propagation could not be taken into account because of their reduced dispersal activity (e.g., 250 m around the breeding site for *Aedes mcintoshi*).¹² Like *Ae. mcintoshi*, *Cx. poicilipes* seems to have a limited activity around temporary ground pools, since in Diawara, no *Cx. poicilipes* specimen was captured in domestic cowsheds. The second hypothesis is the simultaneous emergence of the virus from enzootic maintenance cycles in different geographical areas. In favor of this hypothesis, studies in Eastern Africa have shown that RVF virus is subject to inter-epizootic transovarial maintenance by *Aedes* mosquitoes and that the virus emergence would be dependent on climatic changes.^{13,14} In West Africa factors involved in the virus emergence are still unclear.

Ongoing studies on the genetic variability of strains isolated in Mauritania and Senegal might be expected to provide further insights into the epidemiology of the virus in West Africa.

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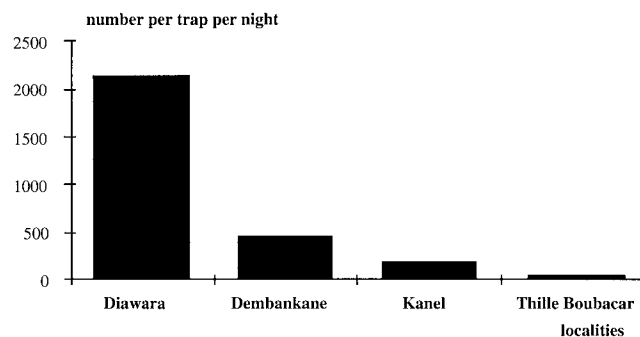


FIGURE 2. *Culex poicilipes* population density in the Senegal River Basin.

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