

Short communication

West Nile virus in Tunisia, 2014: First isolation from mosquitoes



F. Wasfi^a, K. Dachraoui^a, S. Cherni^a, A. Bosworth^b, W. Barhoumi^a, S. Dowall^b, I. Chelbi^a, M. Derbali^a, Z. Zoghلامي^a, J.C. Beier^c, E. Zhioua^{a,*}

^a Institut Pasteur de Tunis, Laboratory of Vector Ecology, 13 Place Pasteur, 1002 Tunis, Tunisia

^b Public Health England, Porton Down, Salisbury, Wiltshire SP4 0JG, UK

^c Department of Public Health Sciences, University of Miami Miller School of Medicine, Miami, FL 33136, USA

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ABSTRACT

Several outbreaks of human West Nile virus (WNV) infections were reported in Tunisia during the last two decades. Serological studies on humans as well as on equine showed intensive circulation of WNV in Tunisia. However, no virus screening of mosquitoes for WNV has been performed in Tunisia. In the present study, we collected mosquito samples from Central Tunisia to be examined for the presence of flaviviruses. A total of 102 *Culex pipiens* mosquitoes were collected in September 2014 from Central Tunisia. Mosquitoes were pooled according to the collection site, date and sex with a maximum of 5 specimens per pool and tested for the presence of flaviviruses by conventional reverse transcription heminested PCR and by a specific West Nile virus real time reverse transcription PCR. Of a total of 21 pools tested, 7 were positive for WNV and no other flavivirus could be evidenced in mosquito pools. In addition, WNV was isolated on Vero cells. Phylogenetic analysis showed that recent Tunisian WNV strains belong to lineage 1 WNV and are closely related to the Tunisian strain 1997 (PAH 001). This is the first detection and isolation of WNV from mosquitoes in Tunisia. Some areas of Tunisia are at high risk for human WNV infections. WNV is likely to cause future sporadic and foreseeable outbreaks. Therefore, it is of major epidemiological importance to set up an entomological surveillance as an early alert system. Timely detection of WNV should prompt vector control to prevent future outbreaks. In addition, education of people to protect themselves from mosquito bites is of major epidemiological importance as preventive measure against WNV infection.

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1. Introduction

In the Western Mediterranean basin, West Nile virus (WNV) is transmitted mainly by *Culex* mosquitoes (Turell, 2012; Vázquez et al., 2011). In natural foci, the circulation of WNV involves birds as amplifying host and bird-feeding mosquitoes (Jourdain et al., 2007) with humans and equines as incidental hosts. WNV is widely distributed in Africa, Middle East, Asia, Southern Europe and the Americas (Hubálek and Halouzka, 1999). A specific WNV lineage 1 variant was also reported in Australia (Scherret et al., 2001). Most of human WNV infections are asymptomatic with less than 1% of infected individuals developing severe neuroinvasive diseases such as meningitis, encephalitis and flaccid paralysis (Kramer et al., 2007).

* Corresponding author at: Institut Pasteur de Tunis, Laboratory of Vector Ecology, 13 Place Pasteur BP 74, 1002 Tunis, Tunisia.

E-mail addresses: elyes.zhioua@gmail.com, elyes.zhioua@pasteur.rns.tn (E. Zhioua).

In Tunisia, several major outbreaks of human WNV infections occurred during 1997 (Triki et al., 2001), 2003 (Hachfi et al., 2010; Riabi et al., 2014), and 2012 (Bouatef et al., 2012). Sporadic cases were reported in 2007, 2010, and 2011 (Bouatef et al., 2012). Several studies showed an intensive circulation of WNV among humans (Riabi et al., 2010; Bahri et al., 2011), equines (Ben Hassine et al., 2014) and birds in Tunisia (Hammouda et al., 2015). A risk map for WNV infection in equines in Tunisia showed that the governorates of Jendouba, Nabeul, Sousse, Monastir, Sfax, Mednine and Djerba are considered as high-risk areas (Bargaoui et al., 2015). To date, no virological data concerning WNV in mosquitoes for Tunisia are available. In the present study, we performed a preliminary virological screening of mosquitoes for WNV in Tunisia.

2. Materials and methods

2.1. Study sites and mosquito samplings

The study was performed in two villages [(Saddaguia: 35° 05' N, 9° 25' E and El Felta: 35° 16' N, 9° 26' E)] belonging to the governorate

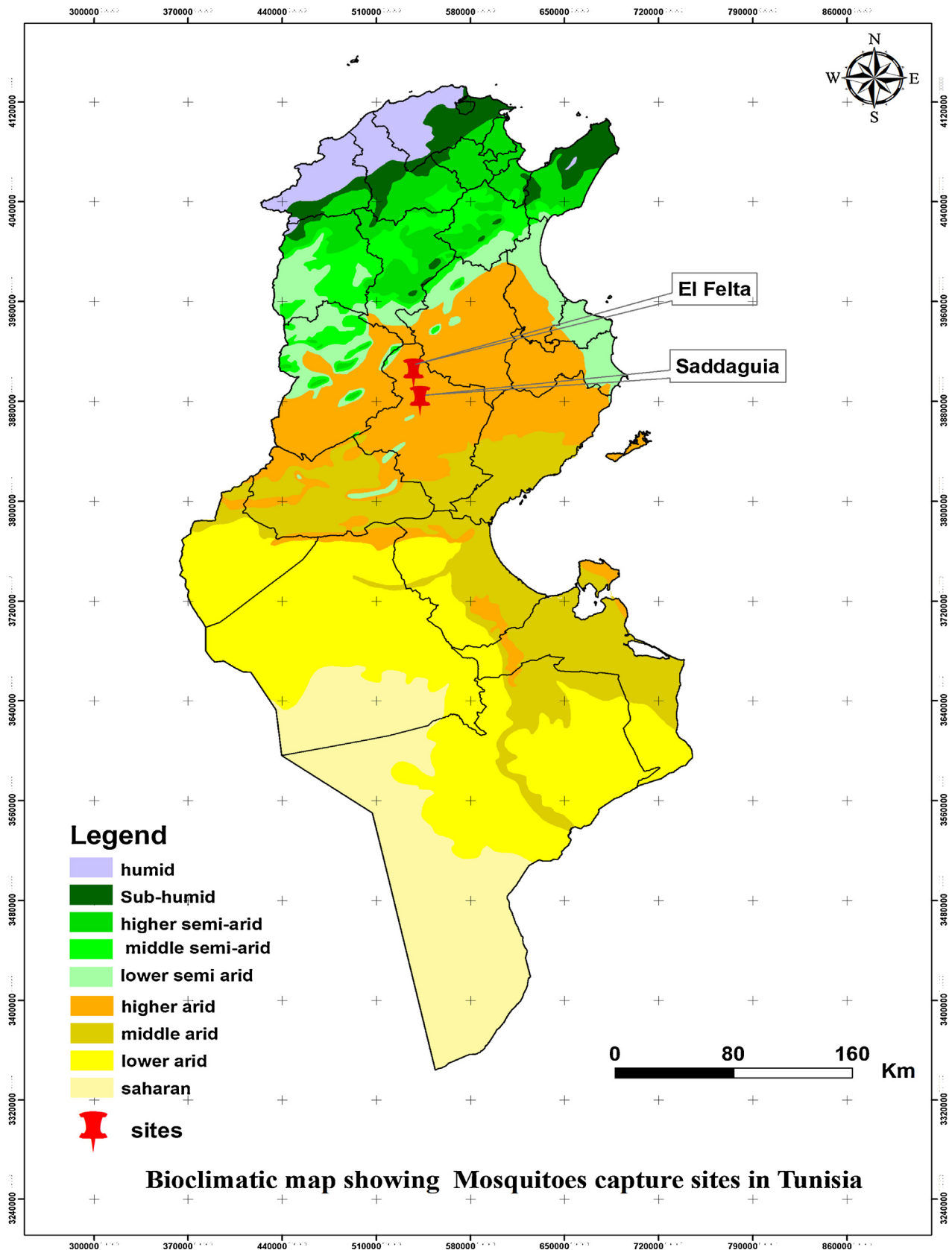


Fig. 1. Bioclimatic map showing mosquitoes capture sites in Tunisia.

of Sidi Bouzid located in Central Tunisia with an arid bio-climate (Fig. 1). During the last 20 years, environmental changes due to irrigation have occurred in these arid areas located in Cen-

tral Tunisia and lead to the establishment of sand fly vectors of zoonotic visceral leishmaniasis previously limited to the humid areas located in Northern Tunisia (Barhoumi et al., 2015), and to

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