SCIENTIFIC NOTE

FIRST REPORT OF A *kdr* MUTATION IN *ANOPHELES ARABIENSIS* FROM BURKINA FASO, WEST AFRICA

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ABSTRACT. The leu-phe kdr mutation was detected in a specimen of Anopheles arabiensis during an extensive survey of pyrethroid resistance in An. gambiae s.I. in Burkina Faso. The detection of this mutation in An. arabiensis, which had so far been observed only in An. gambiae s.s., is important at both epidemiologic and fundamental levels. It can be useful to understand the history of this gene throughout the range of An. gambiae complex.

KEY WORDS Anopheles arabiensis, kdr, pyrethroid resistance, Burkina Faso

Identified since 1954 in Musca domestica, knockdown resistance to dichlorodiphenyltrichloroethane (DDT) is characterized by a marked reduction in the intrinsic sensitivity of the insect nervous system to this compound (Milani 1954). It confers resistance to both DDT and pyrethroids, which share a similar mode of action. Pyrethroid resistance in Anopheles gambiae was 1st reported from Côte d'Ivoire by Elissa et al. (1993), and kdr involvement was subsequently found by Martinez-Torres et al. (1998). It has probably been selected by the intensive use of DDT and, later, pyrethroids used for cotton crop protection. Recently, a survey in Burkina Faso demonstrated that An. gambiae pyrethroid resistance patterns were in accordance with the agricultural use of these insecticides (Diabaté et al. 2002a). As in several other insect species, a kdrbased mechanism caused by a single point mutation (leucine TTA to phenylalanine TTT) in the parasodium channel gene is the main mechanism of pvrethroid resistance in An. gambiae s.l. (Knipple et al. 1994, Matinez et al. 1998). This mutation is specifically observed in West Africa. A different kdr mutation (leucine TTA to serine TCA) was found to confer pyrethroid resistance in An. gambiae s.s. from East Africa (Ranson et al. 2000). Recently, pyrethroid resistance with a monooxygenase-based mechanism was observed in both An. funestus and An. gambiae (Hargreaves et al. 2000, Etang et al. 2003). Following the availability of a molecular diagnostic test for detection of kdr, several studies were conducted on the prevalence and distribution of the leu-phe mutation in An. gambiae s.l. populations from Africa (Chandre et al. 1999). The kdr mutation was 1st detected in the recently described S molecular form of An. gambiae (Chandre et al. 1999, Favia et al. 2001) only, whereas it was not observed either in the sympatric M molecular form or in An. arabiensis. These results, observed in the savannah area of West Africa, provided strong evidence for restricted gene flow within the An. gambiae species and forms (Coluzzi et al. 1985, della Torre et al. 2001). Then, in a subsequent study carried out in the south forested area of Benin and a rice field of Burkina Faso, the leu-phe kdr mutation was identified in the M molecular form, and sequencing of a large upstream intron suggested that this highly adaptive mutation arose in the M form through genetic introgression from the S form (Weill et al. 2000, Diabaté et al. 2002b, Diabaté et al. 2003). This was so far the situation of the kdr mutation in the An. gambiae complex from West Africa.

For the 1st time, we report here the leu-phe kdr mutation in the species An. arabiensis. This event was detected in the framework of a large ongoing survey of pyrethroid resistance in An. gambiae s.l. populations in Burkina Faso. Overall, 165 An. arabiensis specimens sampled from different areas have been analyzed by the Martinez-Torres et al. (1998) polymerase chain reaction (PCR) protocol, and a heterozygous mutation was observed in 1 An. arabiensis specimen from an agricultural area subject to intensive use of insecticides. Anopheles arabiensis was often observed at low frequency (14%) sympatrically with both molecular M and S forms of An. gambiae, but its frequency consistently increased in the north of the country (33%) and, depending on locality, could reach 60%. Previous studies have already shown wide kdr mutation distribution in the S form throughout the coun-

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try (Diabaté et al. 2002a). Mosquito samples were collected at the larval stage and brought back to the laboratory for rearing to the adult stage. Genomic DNA was extracted from single mosquitoes and PCR-amplified for species identification within the *An. gambiae* complex (Scott et al. 1993) and *kdr* detection (Martinez-Torres et al. 1998). Sequencing in the laboratory is ongoing to determine whether this *kdr* mutation in *An. arabiensis* is inherited through genetic introgression from the S molecular form of *An. gambiae*, as has already been observed with the M form.

This 1st report of *kdr* occurrence in *An. arabiensis*, a 2nd major vector in Africa, is of great significance at both fundamental and applied levels. Its potential effect on the efficacy of malaria vector control interventions will have to be evaluated and results taken into consideration by malaria control programs. Further characterizations of this new allele is needed to investigate the history of the onset and spread of this gene within species and forms of the *An. gambiae* complex.

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