

## 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.l. 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 *kdr*-based mechanism caused by a single point mutation (leucine TTA to phenylalanine TTT) in the para-sodium channel gene is the main mechanism of pyrethroid 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 di-

agnostic 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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