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Insecticide resistance in *Bemisia tabaci* Gennadius (Homoptera: Aleyrodidae) and *Anopheles gambiae* Giles (Diptera: Culicidae) could compromise the sustainability of malaria vector control strategies in West Africa

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ABSTRACT

Insecticides from the organophosphate (OP) and pyrethroid (PY) chemical families, have respectively, been in use for 50 and 30 years in West Africa, mainly against agricultural pests, but also against vectors of human disease. The selection pressure, with practically the same molecules year after year (mainly on cotton), has caused insecticide resistance in pest populations such as *Bemisia tabaci*, vector of harmful phytoviruses on vegetables. The evolution toward insecticide resistance in malaria vectors such as *Anopheles gambiae sensus lato* (*s.l.*) is probably related to the current use of these insecticides in agriculture. Thus, successful pest and vector control in West Africa requires an investigation of insect susceptibility, in relation to the identification of species and sub species, such as molecular forms or biotypes. Identification of knock down resistance (*kdr*) and acetylcholinesterase gene (*Ace1*) mutations modifying insecticide targets in individual insects and measure of enzymes activity typically involved in insecticide metabolism (oxidase, esterase and glutathion-*S*-transferase) are indispensable in understanding the mechanisms of resistance. Insecticide resistance is a good example in which genotype–phenotype links have been made successfully. Insecticides used in agriculture continue to select new resistant populations of *B. tabaci* that could be from different biotype vectors of plant viruses. As well, the evolution of insecticide resistance in *An. gambiae* threatens the management of malaria vectors in West Africa. It raises the question of priority in the use of insecticides in health and/or agriculture, and more generally, the question of sustainability of crop protection and vector control strategies in the region. Here, we review the susceptibility tests, biochemical and molecular assays data for *B. tabaci*, a major pest in cotton and vegetable crops, and *An. gambiae*, main vector of malaria. The data reviewed was collected in Benin and Burkina Faso between 2008 and 2010 under the Corus 6015 research program. This review aims to show: (i) the insecticide resistance in *B. tabaci* as well as in *An. gambiae*; and (ii) due to this, the impact of selection of resistant populations on malaria vector control strategies. Some measures that could be beneficial for crop protection and vector control strategies in West Africa are proposed.

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1. Introduction

Most pesticides used in West Africa are for crop protection on cotton, especially in Sudano-Sahelian countries. Six liters of insecticide per hectare are distributed on credit each year to cotton farmers by ginning companies (Martin et al., 2005). But these insecticides are also sold on the informal market, and used on other crops such as vegetables (Ahouangninou et al., 2011). They belong mainly to the pyrethroids (PY) and organophosphate (OP) chemical families. The whitefly *Bemisia tabaci* Gennadius (Hemiptera: Aleyrodidae) is one of the major pests of cotton and vegetable crops worldwide. This pest causes damage both directly by feeding and indirectly through the excretion of honeydew (Jones, 2003). *B. tabaci* is also a vector of *Tomato yellow leaf curl virus* (TYLCV), a complex of geminiviruses infecting tomato cultures worldwide (Berlinger, 1986). At present, invasions of virus-bearing *B. tabaci* continues to be a critical barrier to establishment of tomato crops in open fields (Berlinger, 1986). There is a considerable genetic and biological variability of *B. tabaci* leading to the opinion that *B. tabaci* is in fact a complex of morphologically indistinguishable species/biotypes (Perring, 2001; Simon et al., 2003; Pascual and Callejas, 2004; Boykin et al., 2007; McKenzie et al., 2009; De Barro and Ahmed, 2011; De Barro et al., 2011). We have retained the commonly used term biotype here to link this study with previous studies. To date, approximately 30 *B. tabaci* biotypes have been identified that differ with regard to various characteristics as host range, fecundity, ability to transmit plant viruses, endosymbionts diversity and insecticide resistance (Dittrich et al., 1990; Byrne and Toscano, 2002; Otoidobiga et al., 2002; Horowitz et al., 2003, 2005; Musa and Ren, 2005; Gnankiné et al., 2002, 2007; Xu et al., 2010). PYs and OPs were introduced in agriculture for the control of cotton pests about 30 years ago. They exerted a huge selection pressure on *B. tabaci* populations, which resulted to the selection of insecticide resistance in populations from West Africa (Houndété et al., 2010). In Burkina Faso indeed, *B. tabaci* populations in cotton fields were shown to be resistant to cypermethrin, methamidophos and omethoate (Houndété et al., 2010). Sub-Saharan Africa Silverleafing (ASL) and Q1 biotypes were identified on cotton plants, tomatoes, and okra by *Cytochrome Oxidase1* (*CO1*) (Gnankiné et al., 2013a). Generally, Q1 biotypes are found predominantly and preferentially on cotton plants. ASL biotype is found in sympatry with Q1 on vegetable crops. A recent report done by Gnankiné et al. (2013b) showed the presence of the mutations that are responsible for the *kdr* and *ace-1*^{R} resistance. These results clearly indicate that different biotypes/genetic groups co-exist in West Africa and exhibit variations in insecticide resistance. Regarding resistance, F331W mutation in the acetylcholinesterase gene (*ace1*) was closed to fixation in Q1 and ASL individuals, but all Q3 individuals were susceptible. For *kdr*, the L925I mutation was observed only in Q1 populations. Thus, insecticide treatments rapidly selected for resistant individuals of Q biotypes; for instance, B biotype is known to be more susceptible to several chemical compounds than the Q biotype explaining why it sometimes displaces the B biotype (Horowitz et al., 2005; Chu et al., 2010).

The evolution toward insecticide resistance in malaria vectors such as *Anopheles gambiae* Giles (Diptera: Culicidae) is partly related to the current use of these insecticides in agriculture (Corbel et al., 2007; Djogbénou et al., 2010; Yadouleton et al., 2011). The residues in plots are known to contaminate mosquito-breeding sites, resulting in delayed growth rates and development of resistance in larvae (Akogbeto et al., 2006). To date, malaria vector control has predominantly focused on targeting the adult mosquito through house spraying and long lasting insecticide net (LLIN) use (Kelly-Hope et al., 2008; Raghavendra et al., 2011). Unfortunately, OPs and PYs currently used in control of agricultural pests as *B. tabaci* are also the same ones used for vector control increasing the potential for resistance selection in mosquitoes as *An. gambiae*.

An. gambiae is also a complex, with seven sibling species that are closely related and morphologically indistinguishable from each other by routine taxonomic methods (Gillies and Coetzee, 1987). It includes some of the most important malaria vector species of sub-Saharan Africa i.e. *An. gambiae s.s.* and *An. arabiensis*, Patton. Genetic differentiation also occurs within the highly polymorphic *An. gambiae s.s.* species subdivided into five cytoforms: Forest, Savanna, Bamako, Mopti, and Bissau. They differ in their arrangement of chromosomal inversion and appear more or less genetically isolated in the field (Coluzzi et al., 1985, 2002). In addition, studies using molecular markers such as X-linked ribosomal DNA revealed the presence of two distinct molecular forms within *An. gambiae s.s*: the M and S forms that co-exist in West Africa (Della Torre et al., 2005). In the dry savannahs of West Africa, the S form preferentially breeds in temporary aquatic habitats and is found during the rainy seasons, whereas the M form is present all year round, breeding in man-made permanent aquatic habitats (Simard et al., 2009). In Burkina Faso, genes conferring resistance to insecticides display large frequency differences in M and S forms and also within *An. arabiensis* (Dabiré et al., 2012). Resistance of *An. gambiae s.l.* to DDT and pyrethroids is especially conferred in West Africa by mutation of the sodium channel target site, the L1014F *kdr* (Martinez-Torres et al., 1998; Diabaté et al., 2002a,b;

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