Knock down resistance (kdr) of *Anopheles gambiae* complex (Diptera: Culicidae), an eye opener on resistance surveillance in Zimbabwe.

1Aramu Makuwaza, 1Nobert Mudare, 1Wietske Mushonga, 4Joel Mouatcho, 4David Nyasvisvo, 4Shadreck sande, 3Joseph Mberikunashe, 2Susan Mutambu 4Hieronymo T. Masendu, & 1Sungano Mharakurwa

*1Africa University, Mutare, Zimbabwe.*

*2National Institute of Health Research (NIHR), Harare, Zimbabwe.*

3*National Malaria Control Programme-Zimbabwe.*

4*Abt Associates, Harare, Zimbabwe.*

**Background**

Establishing the extent, geographical distribution and mechanisms of insecticide resistance in malaria vectors is a prerequisite for effective resistance management. The current monitoring of insecticide resistance in Zimbabwe is often performed reactively or dependent upon local projects being conducted. Use of adult *Anopheles* mosquitoes raised from larvae for insecticide resistance monitoring raises the risk of inclusion in the test of high numbers of non-vectors. Basing on a combination of different sampling methods, we report findings on the distribution of kdr in the major malaria vector, *An. gambiae* sl across Zimbabwe.

**Methods**

Adult mosquito samples were collected by pyrethrum spray catches, CDC light night-landing proxy catches, CDC light catches (indoor and outdoor) and raising of adults from larval collections. These samples were collected from end of year 2016 to end of year 2017 from 16 sentinel sites nationwide. Vector identification and the detection of kdr resistance alleles were determined by PCR.

**Results**

There was evidence of emerging kdr resistance alleles, ranging from 1.2 to 19.2 %, among 2282 samples of *Anopheles gambiae* complex sibling species submitted by sentinel sites for species identification after collection of adults in and around living structures and adults raised from wild collected larval stages. Also demonstrated was the existence of high numbers of, *An. quadriannulatus* within the *An. gambiae* complex sibling species collected as adults and when raised to adults from larvae which can significantly bias results of resistance tests conducted without confirmatory identification by PCR.

**Conclusions**

There are emerging kdr mutants among vectors collected from sentinel sites. Continued monitoring is recommended at least biennially to enable timely interventions before escalation to levels that can trigger programme failure. Confirmatory PCR identification is recommended for vector resistance tests as high abundance of non-vector sibling species can substantially bias the findings.

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