

# *Anopheles gambiae* s.l. *Kdr* Polymorphism and *Plasmodium falciparum* Carriage in Zimbabwe

Brenda Makonyere<sup>5</sup>; Aramu Makuwaza<sup>1</sup>; Nobert Mudare<sup>1</sup>; Wietske Mushonga<sup>1</sup>; Joel Mouatcho<sup>2</sup>; David Nyasvisvo<sup>2</sup>; Shadreck Sande<sup>2</sup>; Hieronymo Masendu<sup>2</sup>; Noe Rakotondrajaona<sup>3</sup>; Joseph Mberikunashe<sup>6</sup>; Sungano Mharakurwa<sup>1</sup>

<sup>1</sup>Africa University, Zimbabwe; <sup>2</sup>VectorLink Zimbabwe, Zimbabwe; <sup>3</sup>Zimbabwe Assistance Programme in Malaria, Zimbabwe; <sup>4</sup>President's Malaria Initiative, Zimbabwe; <sup>5</sup>University of Zimbabwe, Zimbabwe; <sup>6</sup>National Malaria Control Programme, Ministry of Health and Child Care, Zimbabwe

## Background

- Malaria remains a life-threatening disease in most parts of Africa including Zimbabwe.
- The mainstay national malaria control programme interventions include prompt case management and vector control through indoor residual spraying and provision of long-lasting insecticidal nets.
- The effectiveness of vector control interventions can be affected by the development of resistance in mosquitoes under selection pressure from insecticide use.

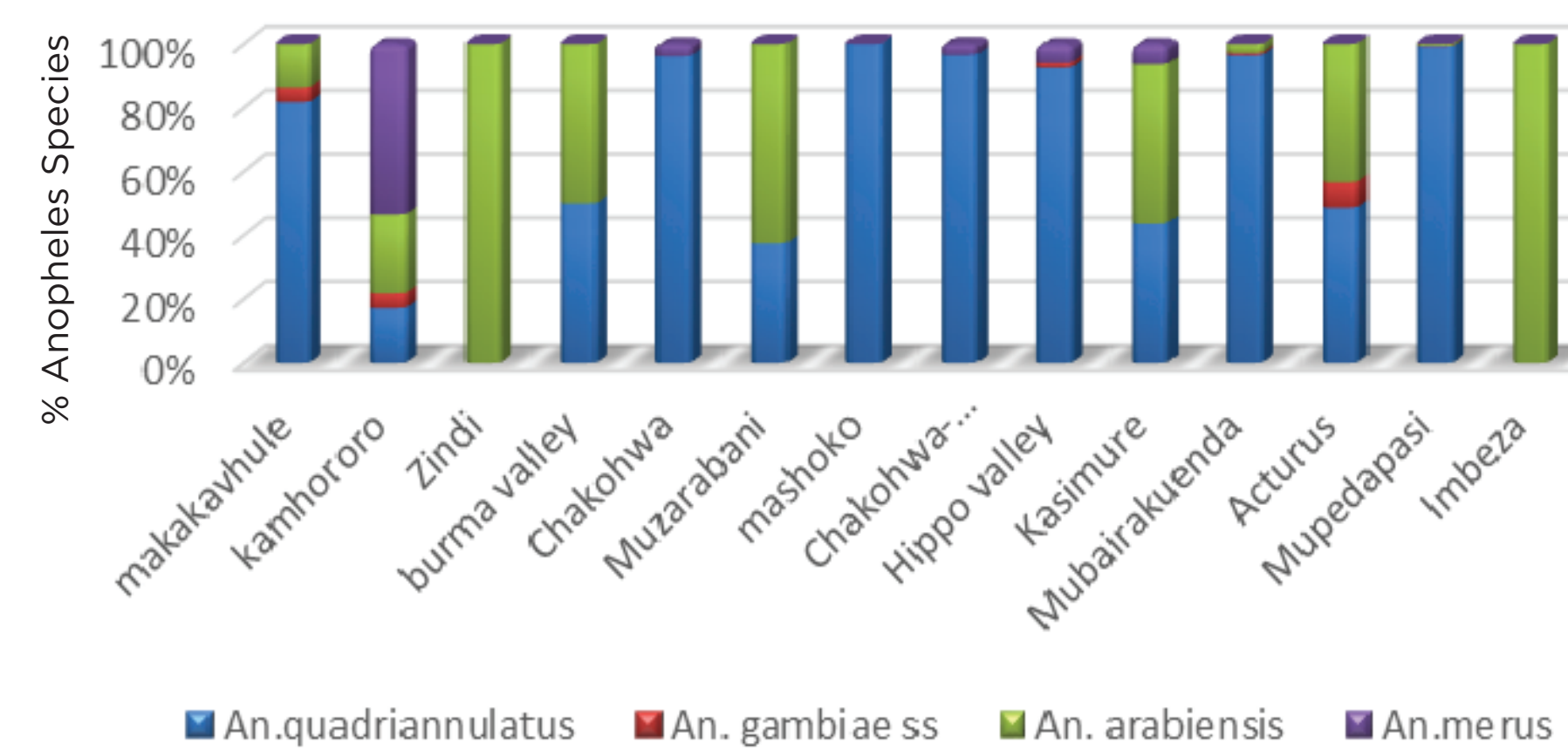
## Main Objective

- To examine the association between the knockdown resistance (*Kdr*) genotype and *Plasmodium falciparum* infection rate among wild *An. gambiae* s.l. vector mosquitoes.

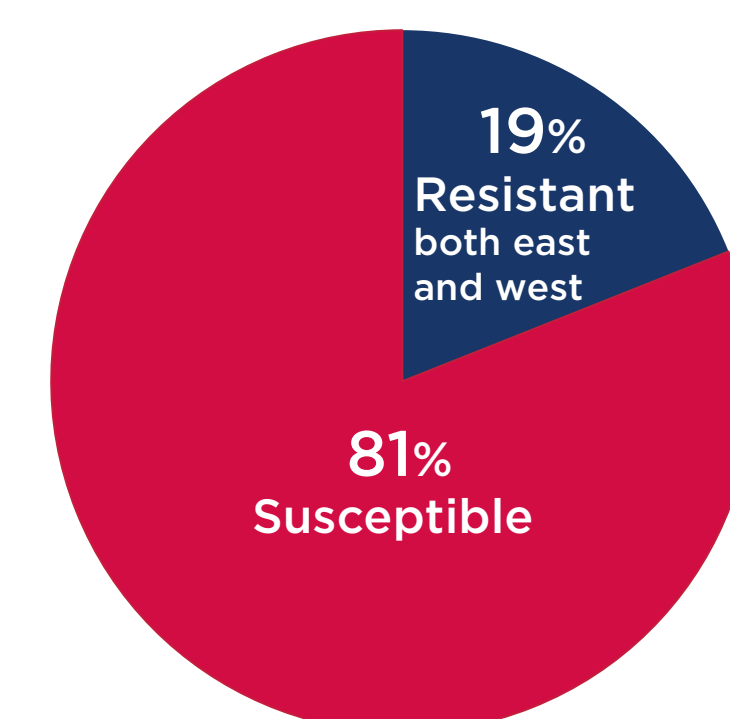
## Methods

- 1518 adult mosquitoes collected from 14 sentinel sites were morphologically identified by entomologists.
- Confirmatory molecular identification conducted using the Wilkins vector sibling species differentiation PCR protocol.
- All vector mosquitoes were subjected to PCR for detection of the *Vgsc*-L1014F and *Vgsc*-L1014S knock down resistance alleles.
- P. falciparum* sporozoite infection among the *An. gambiae* s.l. was detected using circumsporozoite ELISA and confirmed by PCR.

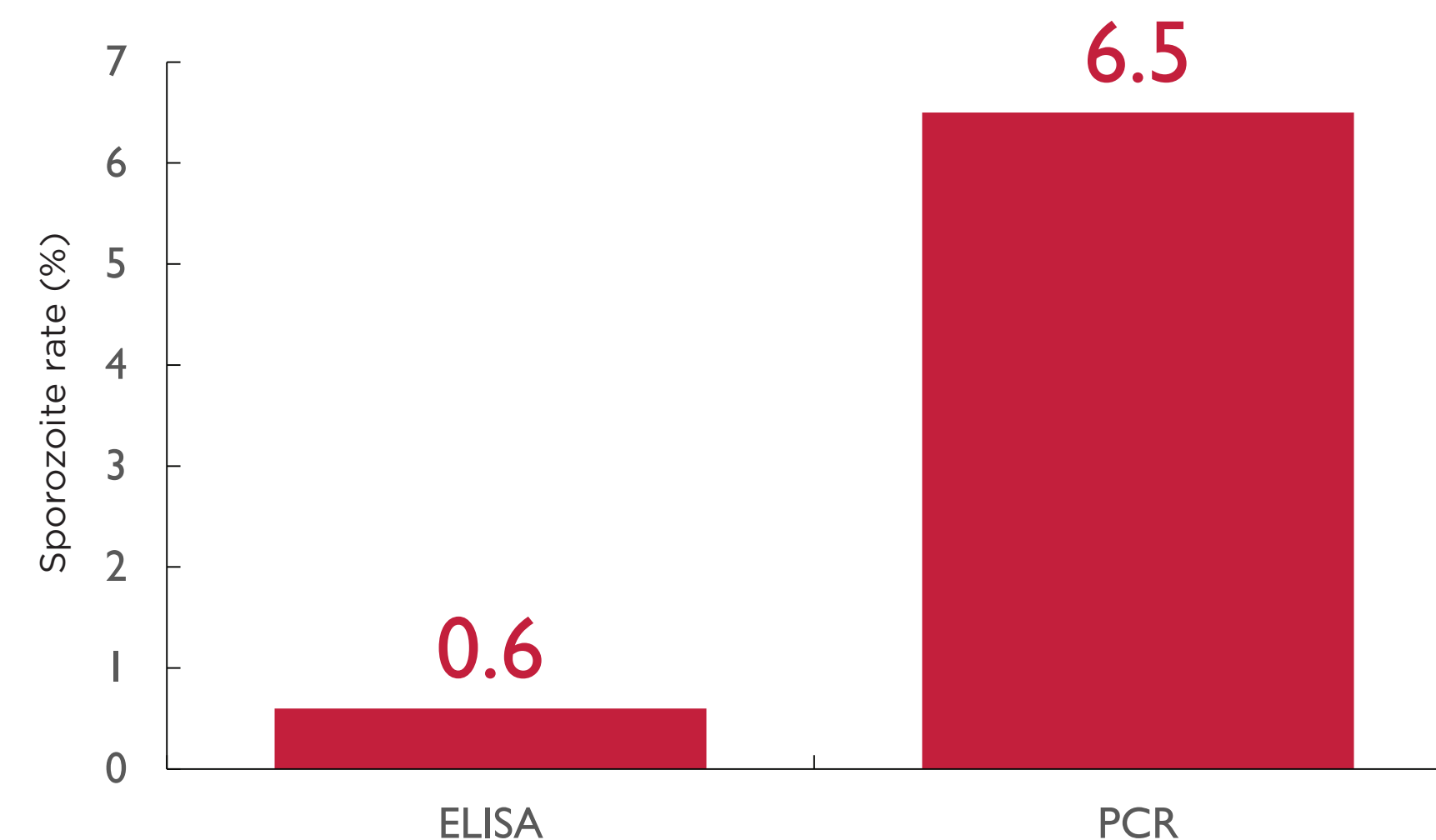
*An.gambiae* s.l. species in different sentinel sites



Resistance distribution



*P. falciparum* infection rate (%)



## Results

*Plasmodium* sporozoite infection status by vector by *Kdr* East genotype

Vector	<i>Kdr</i> East genotype	<i>P. falciparum</i>		Total	P
		Positive	Negative		
<i>An. arabiensis</i>	Mutation present	1 (16.7%)	5 (83.3%)	6 (100%)	1.000
	Wild type	71 (19.3%)	296 (80.7%)	367 (100%)	
	Total	72 (93.3%)	301 (80.7%)	373 (100%)	
<i>An. gambiae</i> ss	Mutation present	0 (0.0%)	2 (100%)	2 (100%)	-
	Wild type	0 (0.0%)	12 (100%)	12 (100%)	
	Total	0 (0.0%)	14 (100%)	14 (100%)	
<i>An. quadriannulatus</i>	Mutation present	2 (15.4%)	11 (84.6%)	13 (100%)	0.435
	Wild type	20 (6.0%)	313 (94.0%)	333 (100%)	
	Total	22 (6.4%)	324 (93.6%)	346 (100%)	
<i>An. merus</i>	Mutation present	0 (0%)	0 (0%)	0 (0%)	-
	Wild type	4 (1.7%)	232 (98.3%)	236 (100%)	
	Total	4 (1.7%)	232 (98.3%)	236 (100%)	
TOTAL	Mutation present	3 (14.3%)	18 (85.7%)	21 (100%)	0.783
	Wild type	95 (10.0%)	853 (90.0%)	948 (100%)	
	Total	98 (10.1%)	871 (89.9%)	969 (100%)	

*An. gambiae* s.l. *Kdr* polymorphism by species

Species	<i>Kdr</i> East wild type	<i>Kdr</i> East mutated	<i>Kdr</i> West wild type	<i>Kdr</i> West mutated
<i>An. gambiae</i> ss (N=18)	88.9%	11.1%	100.0%	0.0%
<i>An. arabiensis</i> (N=397)	98.5%	1.5%	99.7%	0.3%
<i>An. quadriannulatus</i> (N=553)	97.6%	2.4%	98.9%	1.1%
<i>An. merus</i> (N=236)	100.0%	0.0%	49.1%	50.9%

- Individual primary and secondary *An. gambiae* s.l. vectors that bore the *kdr*-resistant alleles were found with lower sporozoite carriage than their counterparts that bore the *Kdr* wild type susceptible allele but the data did not attain statistical significance, possibly due to small numbers of mutants.

*Plasmodium* sporozoite infection status by vector by *Kdr* West genotype

Vector	<i>Kdr</i> West genotype	<i>P. falciparum</i>		Total	P
		Positive	negative		
<i>An. arabiensis</i>	Mutation present	0 (0.0%)	1 (100.0%)	1 (100%)	1.000
	Wild type	72 (19.5%)	298 (80.5%)	370 (100%)	
	Total	72 (19.4%)	299 (80.6%)	371 (100%)	
<i>An. gambiae</i> ss	Mutation present	0 (0.0%)	0 (0%)	0 (0%)	-
	Wild type	0 (0.0%)	12 (100%)	12 (100%)	
	Total	0 (0.0%)	12 (100%)	12 (100%)	
<i>An. quadriannulatus</i>	Mutation present	1 (20.0%)	4 (80.0%)	5 (100%)	0.729
	Wild type	21 (6.1%)	325 (93.9%)	346 (100%)	
	Total	22 (6.3%)	329 (93.7%)	351 (100%)	
<i>An. merus</i>	Mutation present	3 (2.5%)	116 (97.5%)	119 (100%)	0.638
	Wild type	1 (0.9%)	114 (99.1%)	115 (100%)	
	Total	4 (1.7%)	230 (98.3%)	234 (100%)	
TOTAL	Mutation present	4 (3.2%)	121 (96.8%)	125 (100%)	0.006
	Wild type	94 (11.2%)	749 (88.8%)	843 (100%)	
	Total	98 (10.1%)	870 (89.9%)	968 (100%)	

## Conclusions

- Further studies are required to establish the association of resistant *kdr* mosquito variants and sporozoite infection rate in areas where the primary vectors of malaria are dominant and *Kdr* frequencies are high.