

## Polymorphism of exon-20 in the voltage-gated sodium channel gene of *Anopheles gambiae* s.s. populations from wetlands across the Cameroon volcanic line

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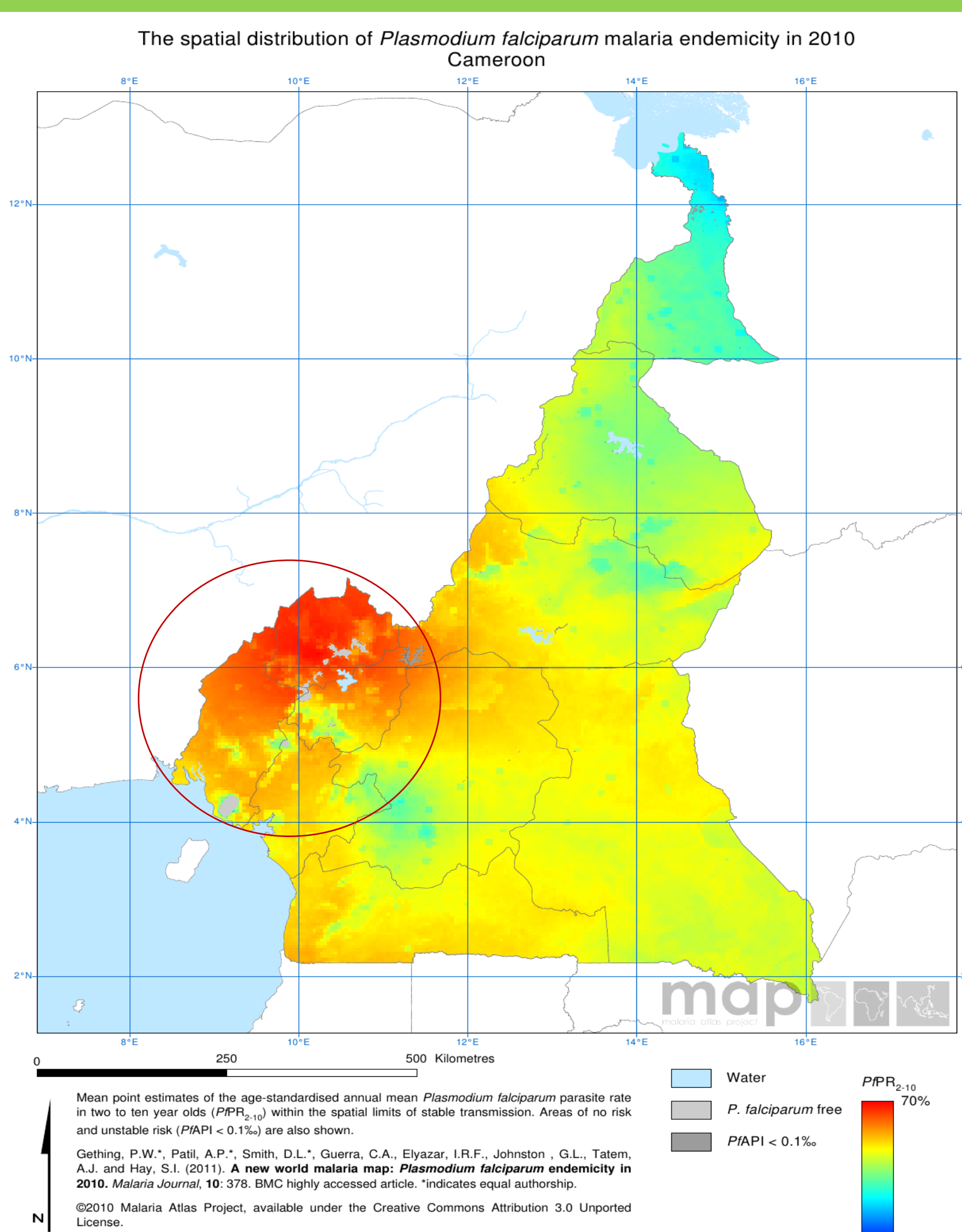
### Background

➤ **Malaria** a major public health burden.

#### In Cameroon

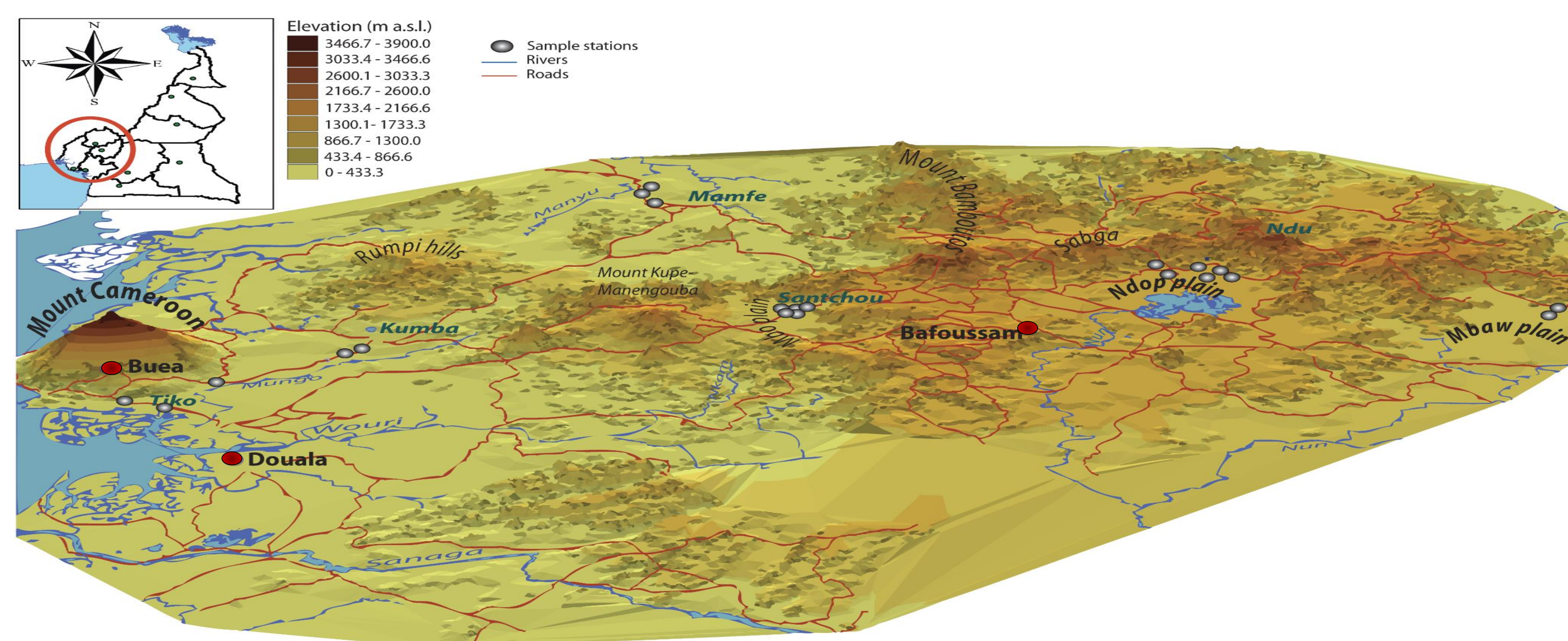
➤ Disparities of knowledges concerning the vector biology and control parameters, especially the **level and spread of insecticide resistant genes in *Anopheles* vectors**:

- Northern/South/Centre parts of the country well studied.
- Limited informations available in the Cameroon hill tract.

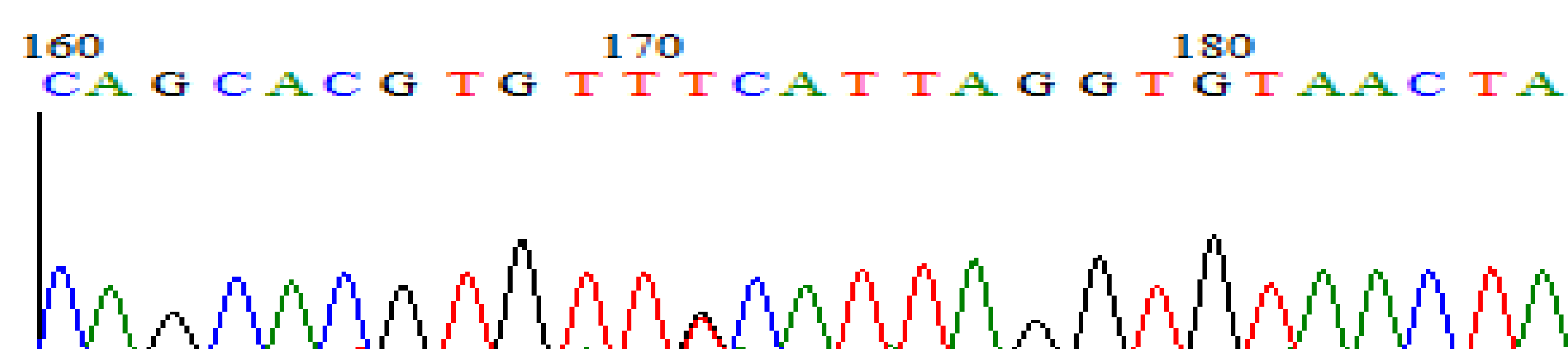


**Aim of the study:** to identify and determine the spread of knockdown resistant (kdr) genes in *Anopheles gambiae* s.s.

### Methods



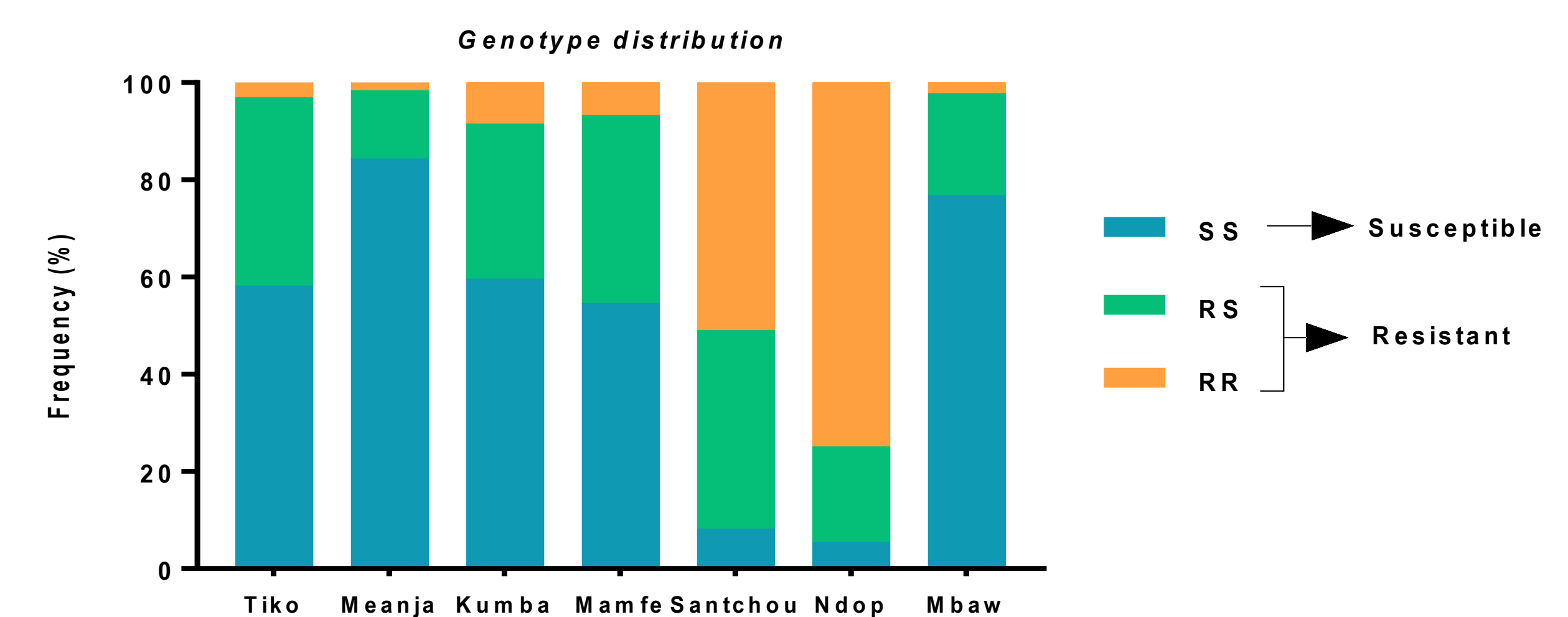
- Cross-sectional surveys during the rainy season months (September and October 2014) using HLC, spray catch and CDC light traps.
- Morphological identification followed molecular ID species and insecticide resistance profile using PCR-based assays (c-PCR & TaqMan).
- Sequencing of a 500bp region in exon-20 of the VGSC gene (kdr):



### Wetlands



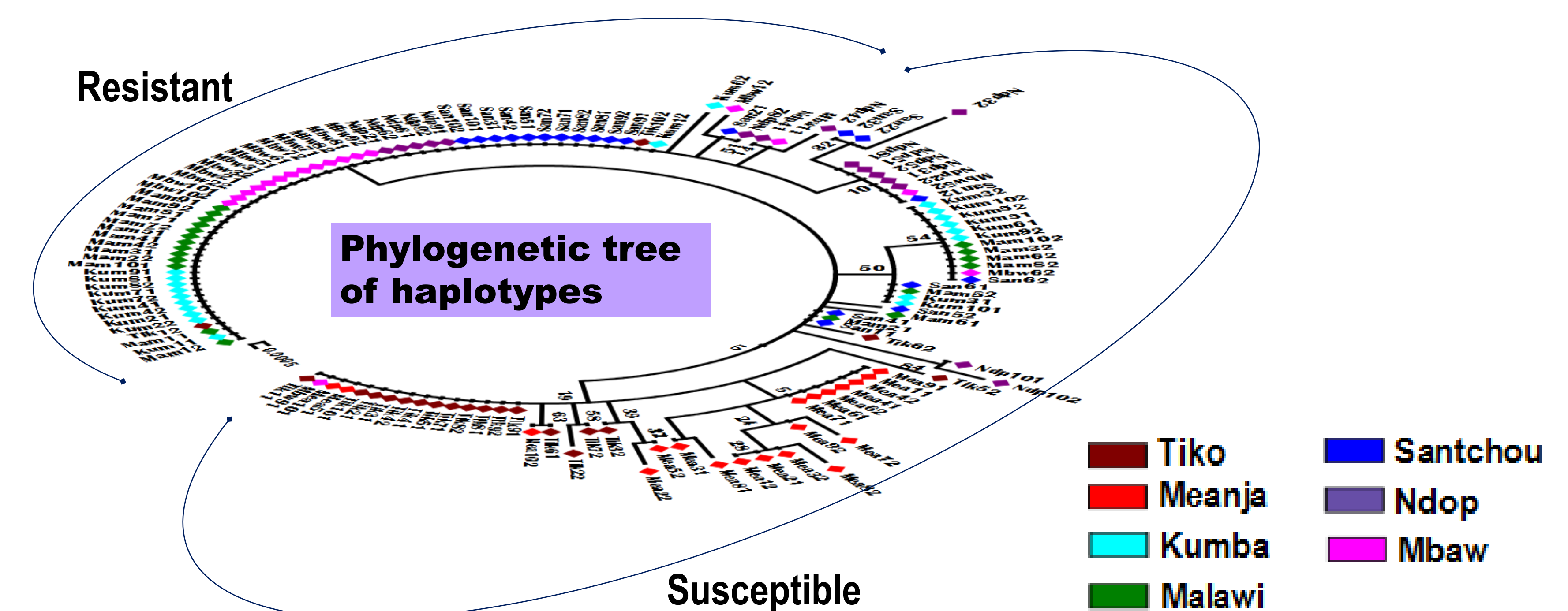
### Results



**Table 1.** genetic variability parameters of the 500bp exon-20 VGSC gene

| Wetland      | N          | S         | h (hd)           | Syn      | NSyn     | $\pi$ (k)           | D                          | F*                         |
|--------------|------------|-----------|------------------|----------|----------|---------------------|----------------------------|----------------------------|
| Tiko         | 20         | 7         | 8 (0.65)         | 0        | 1        | 0.002 (1.22)        | - 1.26 <sup>ns</sup>       | - 0.89 <sup>ns</sup>       |
| Meanja       | 20         | 7         | 11 (0.87)        | 0        | 3        | 0.004 (1.86)        | - 0.18 <sup>ns</sup>       | - 0.02 <sup>ns</sup>       |
| Kumba        | 20         | 4         | 4 (0.63)         | 1        | 1        | 0.003 (1.59)        | 1.19 <sup>ns</sup>         | 0.52 <sup>ns</sup>         |
| Mamfe        | 20         | 4         | 5 (0.56)         | 0        | 2        | 0.003 (1.31)        | 0.47 <sup>ns</sup>         | 0.3 <sup>ns</sup>          |
| Santchou     | 20         | 7         | 8 (0.7)          | 1        | 4        | 0.003 (1.34)        | - 1.05 <sup>ns</sup>       | - 0.82 <sup>ns</sup>       |
| Ndop         | 16         | 9         | 8 (0.83)         | 2        | 5        | 0.004 (2.05)        | - 0.9 <sup>ns</sup>        | - 0.73 <sup>ns</sup>       |
| Mbaw         | 18         | 7         | 6 (0.49)         | 1        | 4        | 0.002 (0.97)        | - 1.77 <sup>ns</sup>       | - 2 <sup>ns</sup>          |
| <b>Total</b> | <b>134</b> | <b>18</b> | <b>32 (0.81)</b> | <b>2</b> | <b>7</b> | <b>0.005 (2.29)</b> | <b>- 0.83<sup>ns</sup></b> | <b>- 0.26<sup>ns</sup></b> |

N = number of sequences (2n); S, number of polymorphic sites; h: number of haplotype (hd: Haplotype diversity); Syn, Synonymous mutations; NSyn, Non-synonymous mutations;  $\pi$ , nucleotide diversity (k= mean number of nucleotide differences); D and F\* Tajima's and Fu and Li's statistics; ns, not significant.



### Implication in community health

We educate populations of the study area on the mosquito fauna present in their community, the vector biology and behaviour, and the measures used to reduce the proliferation and vector-human contact.