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genes
MDPI

Influence of a major mountainous landscape barrier (Mount Cameroon) on the spread of metabolic (*GSTe2*) and target-site (*Rdl*) resistance alleles in the African malaria vector *Anopheles funestus*

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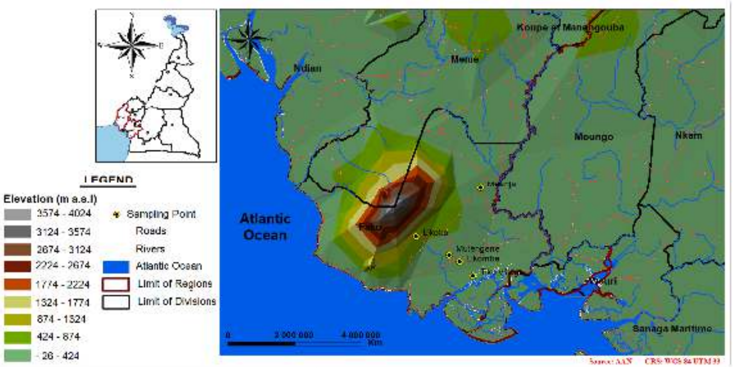
Rationale of the study

Major landscape modifications such as the Rift Valley (East Africa) have been suggested as main barrier to the spread of insecticide resistance alleles in *An. funestus* populations. It remains to know whether the Mount Cameroon, the highest peak in West Africa (4,100 meters above the sea level) could also influence the resistance gene flow between vector populations in order to improve the management of insecticide resistance.



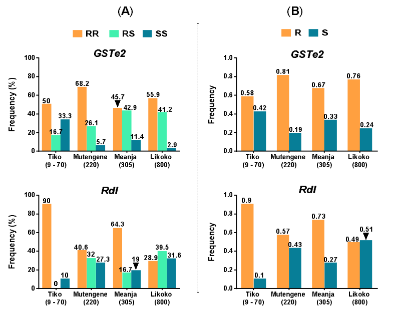
Map of the study area

Materials and Methods

- ❖ Entomological surveys were carried out between the year 2010 and 2014.
- ❖ The landing catch on human volunteers was the main technique used for adult females' mosquitoes.
- ❖ Morphological identification followed molecular ID species and insecticide resistance genotyping using classical PCR and TaqMan.
- ❖ Direct sequencing of *GSTe2* and *Rdl* full length DNA fragments (both strands) using ABI technologies.

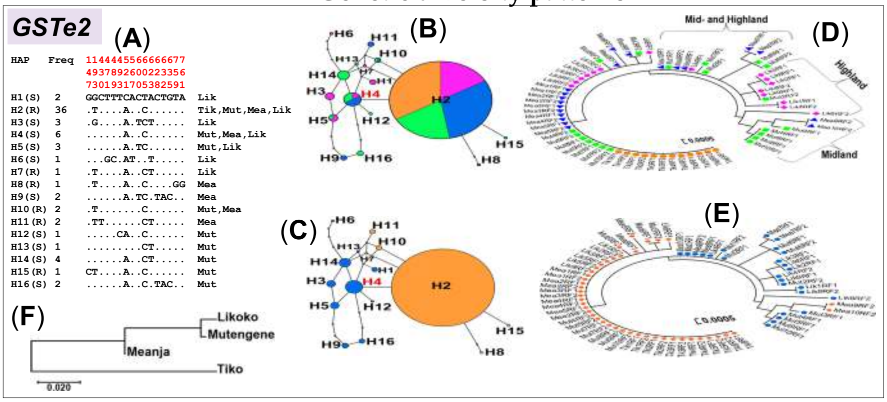
Results

Genotype (A) and allele (B) frequency distributions



Notes: increased resistance allele frequencies of *GSTe2* whereas *Rdl* decreased following altitudinal increments. Altitude in brackets under localities.

Genetic diversity patterns



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HAP    Freq  1144445566666677
             4937892600223356
             7301931705382591
H1(S)   2    GGCTTTCACTACTGTA  Lik
H2(R)   36   .T....A..C......  Tik,Mut,Mea,Lik
H3(S)   3    .G....A.TCT.....  Lik
H4(S)   6    ......A..C......  Mut,Mea,Lik
H5(S)   3    ......A.TC......  Mut,Lik
H6(S)   1    ...GC.AT..T.....  Lik
H7(R)   1    .T....A..CT.....  Lik
H8(R)   1    .T....A..C....GG  Mea
H9(S)   2    ......A.TC.TAC..  Mea
H10(R)  2    .T.......C......  Mut,Mea
H11(R)  2    .TT......CT.....  Mea
H12(S)  1    .....CA..C......  Mut
H13(S)  1    .........CT.....  Mut
H14(S)  4    ......A..CT.....  Mut
H15(R)  1    CT....A..C......  Mut
H16(S)  2    ......A..C.TAC..  Mut
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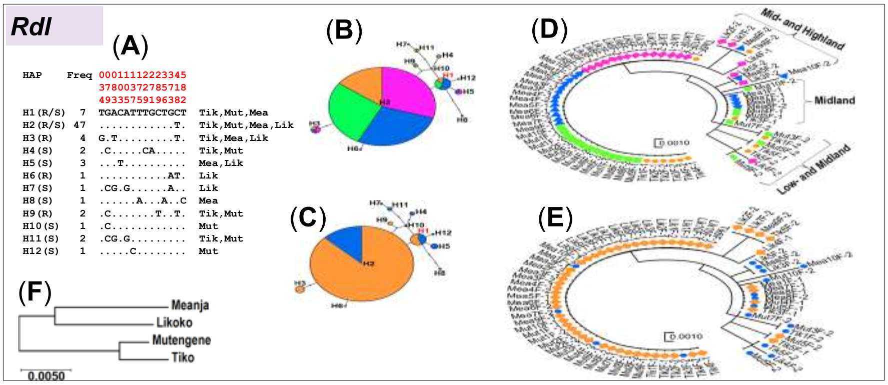

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HAP       Freq 0001111222334 5
               3780037278571 8
               4933575919638 2
H1(R/S)   7    TGACATTTGCTGCT  Tik,Mut,Mea
H2(R/S)  47    ............T.  Tik,Mut,Mea,Lik
H3(R)     4    G.T.........T.  Tik,Mea,Lik
H4(S)     2    .C.....CA.....  Tik,Mut
H5(S)     3    ...T..........  Mea,Lik
H6(R)     1    ...........AT.  Lik
H7(S)     1    .CG.G......A..  Lik
H8(S)     1    .......A...A..C Mea
H9(R)     2    .C.......T..T.  Tik,Mut
H10(S)    1    .C............  Mut
H11(S)    2    .CG.G.........  Tik,Mut
H12(S)    1    .....C........  Mut
```

Notes: Genetic diversity patterns

(A) Haplotype diversity patterns in surveyed sites; R = resistant; S = susceptible; polymorphic sites are in *red*. TCS haplotype networks showing haplotype's generation within resistance gene in *An. funestus* s.s with respect to localities **(B)** and allelic profiles **(C).** Maximum likelihood phylogenetic trees of DNA sequences among localities **(D)** and allelic profiles **(E). (F):** Neighbour-joining tree of the genetic distances showing a genetic relatedness to the landscape along the Mountain altitudinal transect

Legend (B) and (C) 🟧 Tiko 🟦 Meanja 🟩 Mutengene 🟪 Likoko

(D) and (E) 🟧 Resistant 🟦 Susceptible

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