

1 **A glutathione S-transferase metabolic resistance to insecticides is associated**
2 **with higher *Plasmodium* infection in the African malaria vector *Anopheles***
3 ***funestus***

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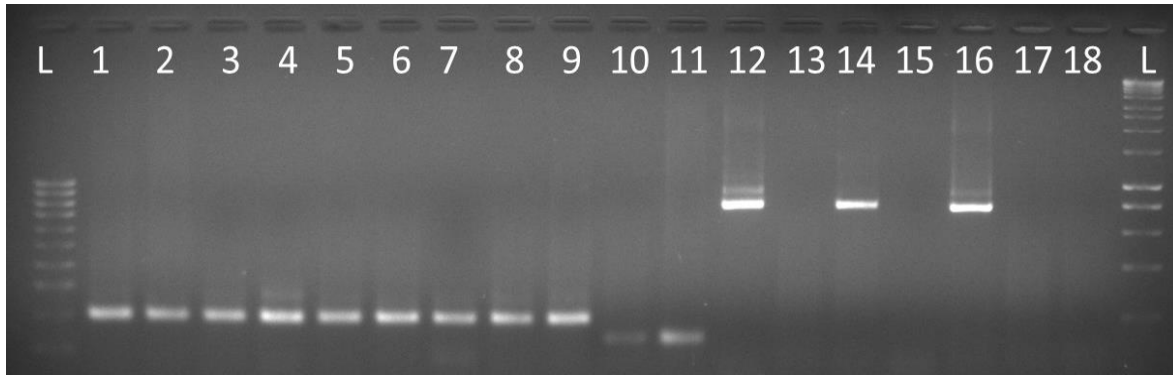


Figure S1 : Nested PCR on mosquitoes positive by Taqman; L= ladder 100bp-1kb, 1-9 = *P. falciparum* (205bp); 10-11 = *P. malariae* (144bp); 12, 14, 16 = *P. ovale* (800bp), 13, 15, 17 =No amplification; 18= negative control; L= ladder 0.1-10kb. This gel image was cropped from the original gel.

HAP	Freq	0011111112333334444445 77112345938899900333353 06594918084501456046746	Infection status
H1 (R)	1	TTGAACAAGGTTACGAGTCCATA	nI
H2 (R)	1	...T.....G.....	nI
H3 (R)	7G.....	nI, I
H4 (R)	6	G..T.....G.....	nI, I
H5 (S)	6G.....C.	nI, I
H6 (S)	1	..C.....G.....CC	nI
H7 (S)	3CC	nI
H8 (S)	1G.....C.	nI
H9 (S)	1G.....C.	nI
H10 (S)	2	..C.....AG.....C.	nI, I
H11 (S)	1	..C....G....G..G.C...CC	nI
H12 (S)	2G.T.....CC	nI
H13 (S)	1G.....TTTCC	nI
H14 (S)	1C.	nI
H15 (S)	2T.....A.....C.	nI, I
H16 (R)	1G.T.....TTT..	nI
H17 (R)	1	...T.....G.....	nI
H18 (S)	1G..TTTC.	I
H19 (S)	2GA.....G.....C.	I
H20 (S)	1C.....C.	I
H21 (R)	1	.A..C.....	I
H22 (R)	1T.....TTT.C	I
H23 (R)	1	G..T.....	I
H24 (S)	1GA.....CC	I
H25 (S)	2	G.C...G...AC.....C.	I
H26 (S)	1T.....TTTCC	I
H27 (S)	1	..C....G.....C.	I
H28 (S)	2T.....A.....CC	I

Figure S2: Polymorphic sites of the GSTe2 gene sequences between infected and non-infected *An. funestus* mosquitoes in Mibellon. nI is for non-infected; I is for infected. The number in red indicate the nucleotide position of the substitution site. Each line represents an haplotype (H) whereas R or S stand for resistant or susceptible haplotype.

Table S1: Assessment of association between different genotypes for RDL mutation on infection by *Plasmodium spp.* in *Anopheles funestus* s.s in Mibellon as RDL is nearly fixed in Obout for whole mosquitoes.

Génotypes	Rdl	
	Odds ratio	P-value
RR vs RS	0,10 (0,10 – 1,19)	0,08
RR vs SS	0,38 (0,04 – 3,77)	0,37
RS vs SS	4 (1,24 – 12,86)	0,03*

Abbreviations: RR, homozygous resistant; RS, heterozygous; SS, homozygous susceptible; for odds ratio, confidence interval at 95% are given in brackets; *,significant.

Table S2: Assessment of association between different genotypes for RDL combined with GSTe2 mutations on infection by *Plasmodium spp.* in *Anopheles funestus* s.s.

Genotypes	<i>Oocyst infection</i>		<i>Sporozoite infection</i>	
	Odds ratio	P-value	Odds ratio	P-value
RR/RR vs RS/RR	1.69 (0.7 – 2.19)	0.318	2.42 (0.76 – 2.8)	0.29
RR/RR vs SS/RR	2.7 (0.8-3.9)	0.16	Inf (inf)	<0.0001
RS/RR vs SS/RR	1.59 (0.58 – 3.1)	0.36	Inf (inf)	0.003

Table S3: genetic diversity parameters of *GSTe2* sequences according to the infection status and the L119F genotypes

Samples	N	S	h (Hd)	Syn	NSyn	π (k)	D	F*
<i>P. falciparum</i>								
Infected	22	20	16 (0,97)	4	7	0,006 (4,90)	- 0,39 ^{ns}	0,26 ^{ns}
uninfected	30	17	17 (0,94)	4	5	0,005 (3,64)	- 0,52 ^{ns}	- 0,35 ^{ns}
GSTe2								
Resistant (RR)	14	11	8 (0,87)	3	3	0,004 (3,03)	- 0,49 ^{ns}	- 0,56 ^{ns}
Heterozygote (RS)	12	13	7 (0,89)	3	5	0,004 (3,30)	- 0,99 ^{ns}	- 1,17 ^{ns}
Susceptible (SS)	26	19	19 (0,97)	5	3	0,005 (3,98)	- 0,71 ^{ns}	- 0,71 ^{ns}
GSTe2 × <i>P. falciparum</i>								
RR × <i>P. fal</i> +	2	7	2 (1)	2	2	0,009 (7)	//	//
RR × <i>P. fal</i> -	12	9	6 (0,82)	2	2	0,003 (2,44)	- 0,74 ^{ns}	- 1,22 ^{ns}
RS × <i>P. fal</i> +	8	13	7 (0,96)	3	5	0,005 (4,21)	- 0,81 ^{ns}	- 0,96 ^{ns}
RS × <i>P. fal</i> -	4	3	3 (0,83)	1	2	0,002 (1,67)	0,17 ^{ns}	0,15 ^{ns}
SS × <i>P. fal</i> +	12	15	9 (0,96)	4	3	0,006 (4,73)	- 0,21 ^{ns}	0,27 ^{ns}
SS × <i>P. fal</i> -	14	14	11 (0,96)	3	3	0,004 (3,37)	- 0,95 ^{ns}	- 1,41 ^{ns}
Total	52	23	28 (0,96)	5	7	0,005 (4,19)	- 0,57 ^{ns}	0,07 ^{ns}

N : number of sequences analysed ; (2n) ; S : number of polymorphic sites; h : number of haplotypes (dh : haplotypic diversity) ; Syn : number of synonymous mutations ; NSyn : number of non-synonymous mutations; π : nucléotidique diversity (k : mean number of nucléotidic differences between sequences) ; D: Tajima index ; F* : Fu & Li index. ; ns : no significant

Table S4: Details of primer sequences used to analyse for *L119F GSTe2* mutation.

Primers	Sequence (5' to 3')
NdeI_Gste2F	GGAATTCCATATGACCAAGCTAGTTCTGTACACGCT
XbaI_Gste2 R	TCTACATCAAGCTTTAGCATTTCCTCCTT
L119F-Res	CGGGAATGTCCGATTTTCCGTAGAA tAA
L119-F-Sus	CATTCTTATTCTCATTACAGGAGCGTA aTC