

High insecticide resistance mediated by different mechanisms in *Culex quinquefasciatus* populations from the city of Yaoundé, Cameroon

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Supplementary Table S1 Details of the qPCR assays that were applied for the gene expression analysis of major detoxification genes

Gene	Primers	Sequence	Reacti on efficie ncy	R ²	%CV	Dyn amic Rang e (Ct valu es)	Melt ing curv e	Agarose gel electrophoresis
RPS3	F	AGCGTGCCAAGTCG ATGAAG	97.32 %	0.9 918	<10%	17.5- 31.5	Singl e peak	Single band in the expected size
	R	ACGTACTCGTTGCA CGGATCTC						
	R	GCATCAAGCGCCAC CATATAGG						
RPL8	F	GCTGGCCGAAGGT GCGTGGT	91.3%	0.9 985	<10%	14.8- 30.0	Singl e peak	Single band in the expected size
	R	TTGCGACCTGGCGG CGTTCC						
CYP9 M10	F	GCAAAGAGAAGAG CACAACATTG	105%	0.9 987	<10%	23.0- 32.3	Singl e peak	Single band in the expected size
	R	CTCCGTTGAGGACT GAAGATG						
CYP6Z 10	F	AGCGGTTCTTCGAG GAAAGC	97.2%	0.9 997	<10%	22.1 8- 30.0	Singl e peak	Single band in the expected size
	R	GTTGGACAGCAGCA TTATGAGG						
CYP6A A7	F	ATGACGCTGATTCC CGAGACTGTT	97.2%	0.9 999	<10%	21.9- 31.1	Singl e peak	Single band in the expected size
	R	TTCATGGTCAAGGT CTCACCCGAA						
Esterase A	F	GGCGCACTTGGTAT GATATGTG	99.5%	0.9 88	<10%	27.3- 32.7	Singl e peak	Single band in the expected size
	R	TCTGGTCCTTTAGTC CGGCA						
Esterase B	F	ACGGTCCGGATTTC TTGGTT	105%	0.9 996	<10%	23.2- 31.3	Singl e peak	Single band in the expected size
	R	TCCTGCACCGATTG ACAACA						
CYP4H 34	F1	CCGTTCAGCGTGGG ATCG		N/A (Gene expression was not detectable)				
	R1	GCAGCACCAGGTCC ATCTTG						

	F2	CATCCAGCTGGCAA AGCACC		
	R2	GACTTCTGCGCCGA GTACG		
	F3	TTTACGATGCTGTT GTTTGCGATTG		
	R3	CTGCACCCTAATCG GAATCC		
	F4	GCCGAACCCACCAA TCAGTA		
	R4	GGGTGGAAAATGC GCTTCAG		
	F5	CTCGGGCATTTCCTT CACCA		
	R5	TTGGTTAAGGGGTG CGGTTT		

Suppl Table S2 Overexpression fold changes of detoxification genes in four *Culex quinquefasciatus* mosquito populations compared to the S-lab susceptible mosquito strain.
Bold letters indicate statistically significant upregulation.

Populations	Detoxification genes fold changes (95% CI), P value				
	<i>CYP9M10</i>	<i>CYP6AA7</i>	<i>CYP6Z10</i>	<i>Esterase A</i>	<i>Esterase B</i>
Mendong	0.519 (0.265 - 0.889) P = 0.009	7.54 (3.72 - 21.1) P = 0.002	23.1 (15.1 - 36.6) P = 0.017	2.83 (0.611 - 14.6) P = 0.144	18.7 (7.61 - 71.9) P = 0.011
Nkolbisson	0.400 (0.162 - 0.926) P = 0.004	7.46 (3.77 - 17.0) P = 0.003	4.32 (3.16 - 5.79) P = 0.005	21.3 (1.63 - 199) P = 0.009	15.4 (8.91 - 39.5) P = 0.012
Tongolo	0.486 (0.304 - 0.824) P = 0.015	10.24 (4.34 - 40.5) P = 0.014	5.01 (3.46 - 6.79) P = 0.029	50.4 (3.94 - 304) P = 0.018	14.8 (8.82 - 37.7) P = 0.011
Etam-Bafia	1.23 (1.075 - 1.492) P = 0.002	14.5 (7.20 - 32.1) P = 0.002	5.36 (1.79 - 9.28) P = 0.002	6.54 (1.77 - 26.4) P < 0.001	19.0 (7.7 - 60.9) P < 0.001

Note: CYP4H34 gene was also tested but no expression profile was detected.