The genetic architecture of target-site resistance to DDT and pyrethroids in the malaria vectors *Anopheles gambiae* and *Anopheles coluzzii*

DRAFT

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[4]MalariaGEN @@TODO

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Abstract

TODO

Introduction

The malaria vectors *Anopheles gambiae* and *Anopheles coluzzii* are evolving insecticide resistance asdlkj dsalkj daslkjd aslkjdas lkadsj lkadsj adslkj adslkja dslkadsj lkadsj lkasd jlkads jlkadsj lkads jlakds alksdj asdlk jasdlk adslk jadslkj adslkj adslkj adslkj adslk jasd

This is the second paragraph of the introduction, asdlkjio weipo ewrpoi ewrpoi rwepoi werpoiwre poi rewpoi rwepoi erwpoi rewpoi rwepoi rwepoi rwepoi rewpo iwrepoi rwepoi wrepoi wrepoi rwpeo irwpo irwepoi rwepo ipoewi rpow ierwe

Third paragraph zcx,m ncxz,mxczn ,mxczn,mxcz n,mcnxz ,mxczn ,mz ncx,m zcxn

Fourth paragraph asdlkj dsakljdsalkj dsalkj daslkj daslkj dsalkj daslkj sda

TODO

Results

Let's add some results qweoi qewoiewqoip peqwpoi ewqpoi ewqpoieqwipo ewqipo eqwpio eqwipo ewqoip ewqoip ewqiop eqw

Isn't Figure 1 interesting! Table 2 is pretty interesting too.

Mutation			Population allele frequency (%)									LD (D')	
Position[1]	*Ag*[2]	*Md*[3]	AO*Ac*	BF*Ac*	GN*Ag*	BF*Ag*	CM*Ag*	GA*Ag*	UG*Ag*	KE	GW	L995F	L995S
2,390,177 G>A	R254K	NA	0	0	0	0	32	21	0	0	0	NA	NA
2,391,228 G>C	V402L	NA	0	7	0	0	0	0	0	0	0	NA	NA
2,391,228 G>T	V402L	NA	0	7	0	0	0	0	0	0	0	NA	NA
2,399,997 G>C	D466H	NA	0	0	0	0	7	0	0	0	0	NA	NA
2,400,071 G>A	M490I	NA	0	0	0	0	0	0	0	18	0	NA	NA
2,400,071 G>T	M490I	NA	0	0	0	0	0	0	0	0	0	NA	NA
2,416,980 C>T	T791M	NA	0	1	13	14	0	0	0	0	0	NA	NA
2,422,651 T>C	L995S	NA	0	0	0	0	15	64	100	76	0	NA	NA
2,422,652 A>T	L995F	NA	86	85	100	100	53	36	0	0	0	NA	NA
2,424,384 C>T	A1125V	NA	9	0	0	0	0	0	0	0	0	NA	NA
2,425,077 G>A	V1254I	NA	0	0	0	0	0	0	0	0	5	NA	NA
2,429,617 T>C	I1527T	NA	0	14	0	0	0	0	0	0	0	NA	NA
2,429,745 A>T*	N1570Y	NA	0	26	10	22	6	0	0	0	0	NA	NA
2,429,897 A>G	E1597G	NA	0	0	6	4	0	0	0	0	0	NA	NA
2,429,915 A>C	K1603T	NA	0	5	0	0	0	0	0	0	0	NA	NA
2,430,424 G>T	A1746S	NA	0	0	11	13	0	0	0	0	0	NA	NA
2,430,817 G>A	V1853I	NA	0	0	8	5	0	0	0	0	0	NA	NA
2,430,863 T>C	I1868T	NA	0	0	18	25	0	0	0	0	0	NA	NA
2,430,880 C>T	P1874S	NA	0	21	0	0	0	0	0	0	0	NA	NA
2,430,881 C>T	P1874L	NA	0	7	45	26	0	0	0	0	0	NA	NA
2,431,061 C>T	A1934V	NA	0	12	0	0	0	0	0	0	0	NA	NA
2,431,079 T>C	I1940T	NA	0	4	0	0	7	0	0	0	0	NA	NA

Table 1. Non-synonymous mutations in the voltage-gated sodium channel gene. All mutations are at 5% frequency or above in one or more of the 9 Ag1000G phase 1 populations, with the exception of 2,400,071 G>T which is at 0.4% frequency in the CM*Ag* population but is included because another mutation (2,400,071 G>A) is found at the same position causing the same amino acid substitution (M490I). Substitutions marked with an asterisk (*) failed conservative variant filters applied genome-wide in the Ag1000G phase 1 AR3 callset, but appeared sound on manual inspection of read alignments.

[1]Position relative to AgamP3 reference sequence, chromosome arm 2L.
[2]Codon numbering according to transcript AGAP004707-RA in geneset AgamP4.4.
[3]Codon numbering according to @@TODO.

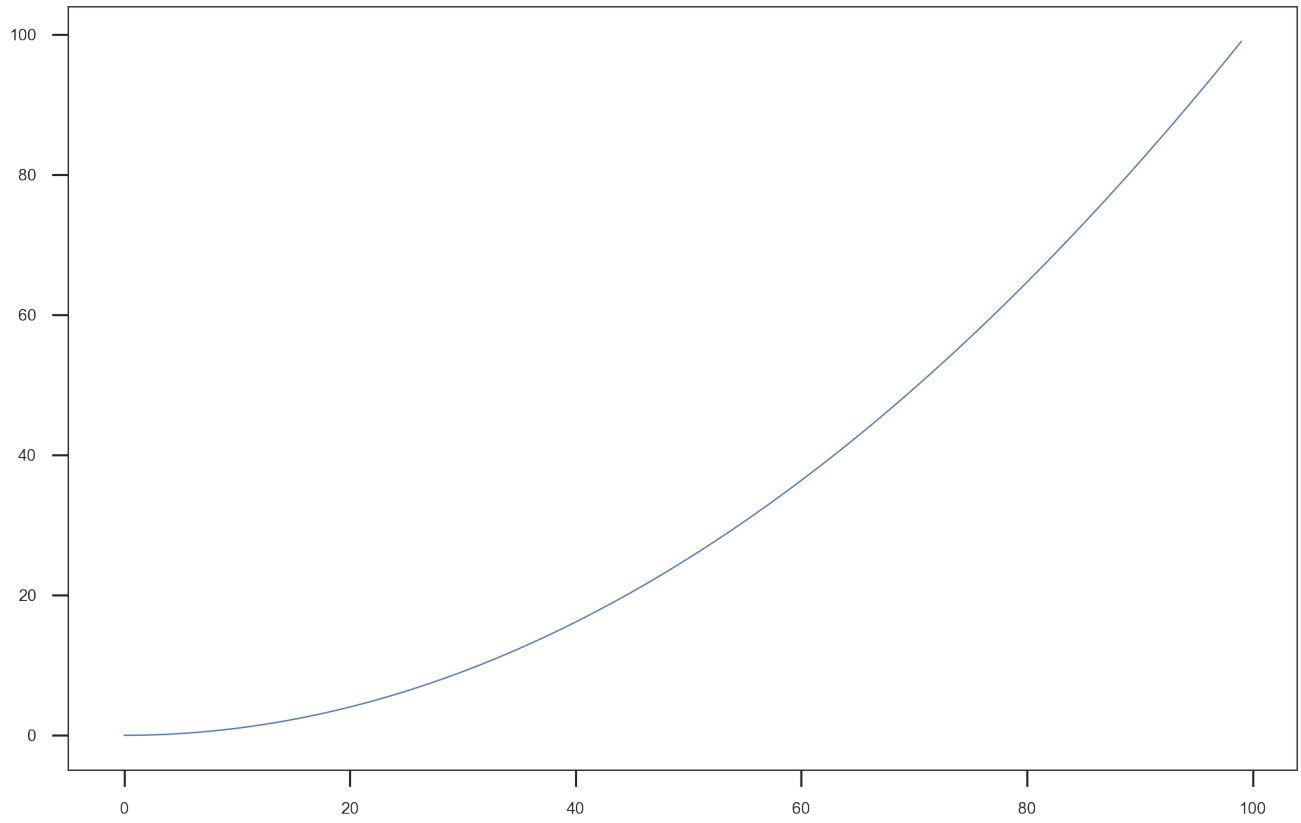

Figure 1. Demo figure.

TODO

Foo	Bar	Baz
1	a	True
2	b	False

Table 2. This is a table.

Discussion

TODO

Methods

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