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

17th February 2017

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 adslkj adslk jasd

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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 [1]

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]	AOAc	BFAc	GNAg	BFAg	CMAg	GAAg	UGAg	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 CMAg 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.

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[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.
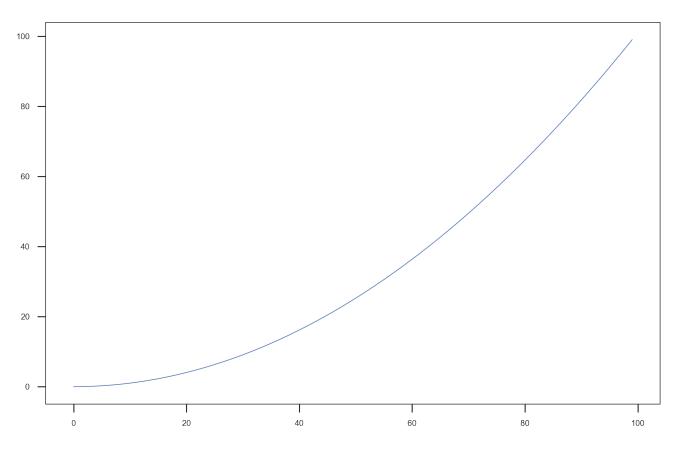
TODO

Foo	Bar	Baz
1	a	True
2	b	False

Table 2. This is a table.

Discussion

TODO

Methods

TODO

References

[1] Nandita R. Garud et al. 'Recent Selective Sweeps in North American Drosophila melanogaster Show Signatures of Soft Sweeps'. In: *PLoS Genetics* 11.2 (2015), pp. 1–32. ISSN: 15537404. arXiv: 1303.0906.