Supplementary Table S1. Tests for Hardy-Weinberg equilibrium of genotypes at three *Vssc* mutation sites in *Aedes aegypti* from the field (Shah Alam), the laboratory (B3F3 IMR) and bioassayed female individuals (dead and alive).

Mutation/Population	Genotype			n	X²	P-value
V1016G	**TT**	**TG**	**GG**		**df=1**	**(0.05)**
Field	30	39	11	80	0.089	0.766
Colony	34	36	10	80	0.010	0.922
Bioassay	25	47	8	80	4.253	**0.039**
F1534C	**TT**	**TG**	**GG**			
Field	11	43	26	80	1.043	0.307
Colony	16	44	20	80	0.845	0.358
Bioassay	8	47	25	80	4.253	**0.039**
S989P	**TT**	**TC**	**CC**			
Field	30	39	11	80	0.089	0.766
Colony	34	36	10	80	0.010	0.922
Bioassay	25	47	8	80	4.253	**0.039**

Supplementary Material S1

DNA sequences for 27 individuals of *Aedes albopictus* for a small section of the voltage-sensitive sodium channel gene (*Vssc*) from S6, domain III from Shah Alam, Selangor, Malaysia. The wildtype state at codon 1534 is TTC (Phenylalanine) and is shaded in yellow. Sample E09 has a non-synonymous homozygous mutation at codon 1534 and would code for Leucine (shaded in green). Samples A10, B07, F10 are heterozygotes at codon 1534 (TTC/TTG) and are shaded in blue (IUPAC code S for C/G appears in the sequence). Synonymous mutations (TTT and TTC) were found at codon 1528, some of which comprised heterozygotes (IUPAC code Y for C/T) and are highlighted in grey. Sample E07 was heterozygous at position three in codon 1539 (IUPAC code Y for C/T) and is highlighted in grey, but it is a synonymous mutation. Samples A01, B05, B10, C6 and E4 were heterozygotes at codon 1544 position three (IUPAC code Y for C/T) and are highlighted in grey. The T is a synonymous mutation (Isoleucine). The same five samples were also heterozygous at codon 1561, position 3 (IUPAC code K for G/T), another synonymous mutation (Serine) and shaded in red. Another heterozygote occurs at position three, codon 1547 in sample B08 (IUPAC code Y for C/T). The alternatives are again synonymous (Isoleucine). Sample G09 is heterozygous at codon 1582, position three (IUPAC code R for A/G), but the mutation is synonymous (Leucine). Bases unable to be called accurately (N) are highlighted in pink.

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             1        10        20        30        40        50        60
IMRSASA01    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASA10    CTACATGTACCTCTACTTTGTGTTCTTCATCATCTTSGGGTCGTTCTTCACCCTCAACCT
IMRSASB05    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASB07    CTACATGTACCTCTACTTTGTGTTCTTCATCATCTTSGGGTCGTTCTTCACCCTCAACCT
IMRSASB08    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASB10    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASC01    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASC03    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASC06    CTACATGTACCTCTACTTTGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASD01    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASD03    CTACATGTACCTCTACTTTGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASE02    CTACATGTACCTCTACTTTGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASE04    CTACATGTACCTCTACTTTGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASE07    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACYCTCAACCT
IMRSASE09    CTACATGTACCTCTACTTTGTGTTCTTCATCATCTTGGGGTCGTTCTTCACCCTCAACCT
IMRSASF03    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASF05    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACYCTCAACCT
IMRSASF08    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASF10    CTACATGTACCTCTACTTTGTGTTCTTCATCATCTTSGGGTCGTTCTTCACCCTCAACCT
IMRSASG01    CTACATGTACCTCTACTTCGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASG04    CTACATGTACCTCTACTTCGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASG06    CTACATGTACCTCTACTTNGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASG09    CTACATGTACCTCTACTTCGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTYAAYCT
IMRSASH02    CTACATGTACCTCTACTTTGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASH05    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASH07    CTACATGTACCTCTACTTYGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
IMRSASH10    CTACATGTACCTCTACTTCGTGTTCTTCATCATCTTCGGGTCGTTCTTCACCCTCAACCT
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                 |        70        80        90       100       110       120
IMRSASA01   GTTCATYGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCKCT
IMRSASA10   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASB05   GTTCATYGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCKCT
IMRSASB07   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASB08   GTTCATCGGTGTCATYATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASB10   GTTCATYGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCKCT
IMRSASC01   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAARAAAGCCGGTGGCTCGCT
IMRSASC03   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASC06   GTTCATYGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCKCT
IMRSASD01   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASD03   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASE02   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASE04   GTTCATYGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCKCT
IMRSASE07   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASE09   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASF03   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASF05   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASF08   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASF10   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASG01   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASG04   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASG06   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASG09   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASH02   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASH05   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASH07   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCCGGTGGCTCGCT
IMRSASH10   GTTCATCGGTGTCATCATCGACAACTTCAACGAGCAGAAGAAGAAAGCYGGTGGCTCGCT

                 |       130       140       150       160       170       180
IMRSASA01   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASA10   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASB05   GGAAATGTTCATGACRGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASB07   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASB08   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASB10   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASC01   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASC03   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASC06   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAA----------------
IMRSASD01   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASD03   GGAAATGTTCATGACRGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASE02   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASE04   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASE07   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASE09   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAA-----------
IMRSASF03   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASF05   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASF08   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASF10   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGA-------------
IMRSASG01   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASG04   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASG06   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASG09   RGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASH02   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASH05   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
IMRSASH07   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAA----------------
IMRSASH10   GGAAATGTTCATGACGGAGGATCAGAAAAAGTACTACAACGCAATGAAAAAGATGGGCTC
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