Supplementary Information

Molecular signature of domestication in the arboviral vector *Aedes aegypti*

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Supplementary Methods.

We also estimated the ratio of Ka/Ks by gene in each population using the PAML package v4.10.6 (1). For this analysis, we derived 539,298 gene nucleotide alignments with the vcf2fasta package (https://github.com/santiagosnchez/vcf2fasta) from protein coding genes with at least 1 SNP in each population. Then, each alignment was translated into amino acids sequences with transeq from the EMBOSS package v6.6.0.0 (2), and their corresponding codon alignments were created with the pal2nal.pl program v14 (3). A total of 162 protein coding genes were removed from this analysis due to the presence of multiples indels affecting the positions of codons, resulting in a final dataset of 539,136 codon alignments. A ML phylogenetic tree was reconstructed for each codon alignment with FastTree v2.1 (4) and the GTR+GAMMA model. The one-ratio model (M0) was used to calculate the ka/ks ratio average for the whole gene over all branches in the phylogeny with the codeml program from the PAML package (1). The Ka/Ks ratio of a gene was the average Ka/Ks ratios calculated within the gene. PAML detected 2.5-fold times more sites under selection than the improved K2P Li's method. However, ~37% of the Ka/Ks ratios detected with PAML exhibit standard deviations >10, suggesting either a high divergence among individuals within a population or an overestimation of the Ka/Ks ratio per gene.

References:

1. Yang Z. PAML 4: Phylogenetic analysis by maximum likelihood. Mol Biol Evol. 2007;24(8).

2. Rice P, Longden I, Bleasby A. EMBOSS: the European molecular biology open software suite. Trends Genet. 1154 2000;16:276-277.

3. Suyama M, Torrents D, Bork P. PAL2NAL: robust conversion of protein sequence alignments into the corresponding codon alignments. Nucleic Acids Res. 2006;34:W609-12.

4.Price MN, Dehal PS, Arkin AP. FastTree2- Approximately Maximum-Likelihood Trees for large Alignments. 1158 PLoS One 2010;5(3):e9490.

Supplementary Data Files Content:

Supplementary Data 1. 1,030 SNP outliers associated to 2,266 genes detected with Pcadapt (VCF format). Available at: https://github.com/naborlozada/Aaegypti_domestication.

Supplementary Data 2. Matrix with pN/pS ratio values for all 13,503 protein-coding genes annotated in AaegL5 for each *Ae. aegypti*'s population (TXT). Available at: https://github.com/naborlozada/Aaegypti_domestication.

Supplementary Data 3. Position of SNPs in AaegL5 obtained from the literature and VectorBase (TXT). Available at: https://github.com/naborlozada/Aaegypti_domestication.

Supplementary Data 4. Phylogenetic tree of populations (NEWICK format), and a phylogenetic tree of individuals (NEWICK format). This PDF document.

Supplementary Data 5. Matrix with pN/pS ratio (PAML approach) values for all 13,503 protein-coding genes annotated in AaegL5 for each *Ae. aegypti* population (TXT). Available at: https://github.com/naborlozada/Aaegypti_domestication.

Supplementary Data 6. Sequences of new detected nrEVEs (FASTA format). This PDF document.

Supplementary Data 4. Pylogenetic tree of individuals (NEWICK format).

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Supplementary Data 4. Pylogenetic tree of populations (NEWICK format).

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Supplementary Data 6. Sequences of new detected nrEVEs (FASTA format).

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