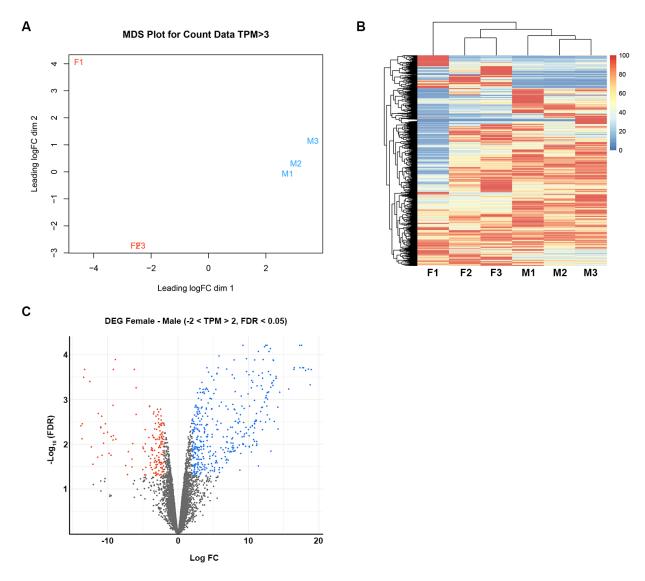
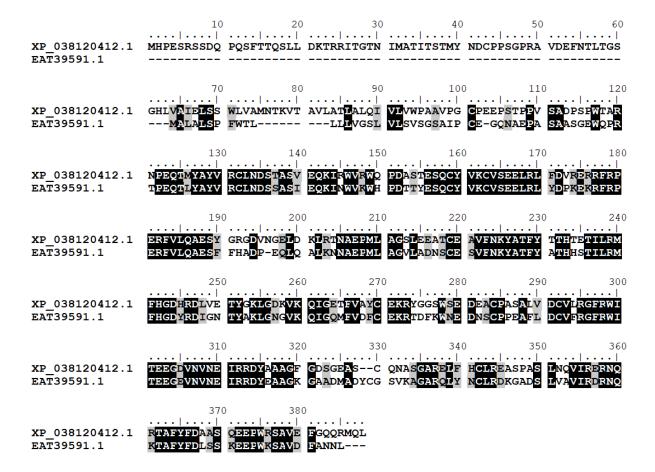
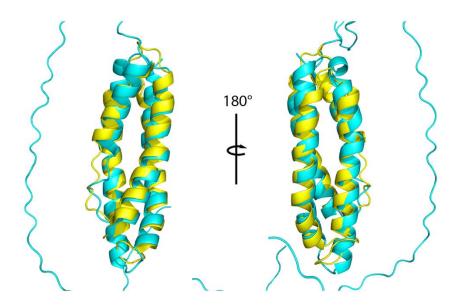
Supplementary Figures



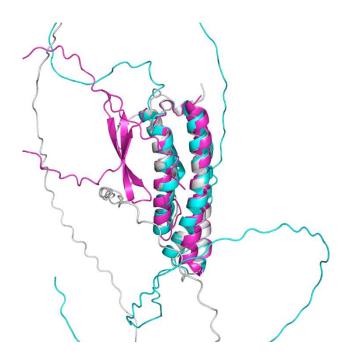
Supplementary figure 1: (A): Multidimensional plot based on the CDS identified in the salivary glands of females (F) and males (M) *C. quinquefasciatus* mosquitoes. (B): Heat map plot of the normalized TPM of each CDS identified in females (F) and males (M) *C. quinquefasciatus* mosquitoes. (C): Volcano plot of the CDS differentially expressed between female and male mosquitoes. The female down-regulated transcripts are shown in red while the up-regulated ones are represented in blue.



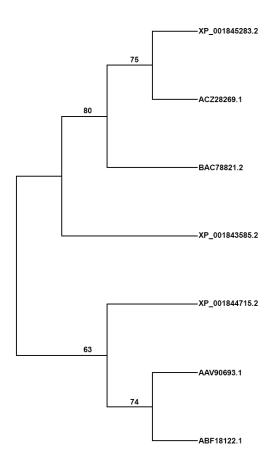
Supplementary figure 2: Amino acid alignment of the D7 proteins from *C. quinquefasciatus* (XP_038120412.1) and the juvenile hormone binding D7 from *Ae. aegypti* (EAT39591.1). Identical and similar residues are boxed.



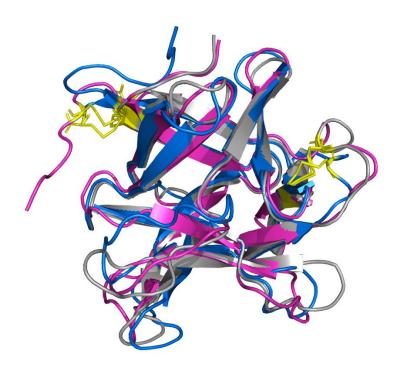
Supplementary figure 3: Structural superposition of albicin (yellow, PDB: 6XKE), the salivary complement inhibitor from *An. albimanus*, with the C-terminal region of aegyptin (cyan), the platelet aggregation inhibitor from *Ae. aegypti*. Aegyptin structure was modeled using AlphaFold2.



Supplementary figure 4: Superposition of XM_001845231 from *C. quinquefasciatus* (pink), aegyptin (cyan) from *Ae. aegypti* and AAPI from *An. stephensi* (gray). The three structures were modeled using AlphaFold2.



Supplementary figure 5: Phylogenetic tree of the 30 kDa salivary allergens from Diptera vectors. The numbers at the base of branches indicates the concordance between 500 bootstraps replicates. The three was constructed using the Maximum likelihood method with the Jones-Taylor-Thornton (JTT) model using MEGA11.



Supplementary figure 6: Superposition of putative salivary proteins containing the β -trefoil domain from *C. quinquefasciatus*. The crystal structure of CqDVP-2 (PDB: 7KC8) is shown in pink, while the alphafold model of XP_038107904.1 (blue) classified as a WRP protein and XP_038112911.1 (grey) from the 15.3 kDa protein family. Cysteine residues are represented as yellow sticks.

Supplementary Table 1: Relative quantification of putative CDS coding for long or short D7 proteins

CDS	Average TPM in	Average TPM in	Protein
	Female	Male	family
XM_038258283.1	64497.91	6.09	D7 LONG
XM_001865378.2	49918.57	2.85	D7 LONG
XM_038251030.1	11581.13	175.82	D7 LONG
XM_038255328.1	6391.33	61.74	D7 LONG
XM_038255191.1	2248.46	0.01	D7 LONG
XM_038251031.1	31.94	0.28	D7 LONG
Cq-contig_13280	11.82	5.51	D7 LONG
XM_038264484.1	70.82	27.55	D7 LONG
XM_001865373.2	3780.23	0.49	D7 SHORT
XM_038251032.1	3609.12	0.32	D7 SHORT
XM_038256440.1	1134.02	0.30	D7 SHORT
Cq-contig_16889	1052.61	0.13	D7 SHORT
Cq-contig_990	40.21	0.04	D7 SHORT

Supplementary files 1 and 2: The hyperlinked excel spreadsheet and the associated files can be downloaded as a single zip file fromhttps://proj-bip-prod-publicread.s3.amazonaws.com/transcriptome/C_quinquefasciatus_sialome_2022/CQ_SUPPLEMENTARY_FI

LES.zip