Novel receptor interaction of *Bacillus thuringiensis* Cry1Da_7 and Cry1B.868 proteins allow control of resistant fall armyworm, *Spodoptera frugiperda* (J.E. Smith)

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*Running title: New insecticidal proteins to combat *Bt*-resistant fall armyworm

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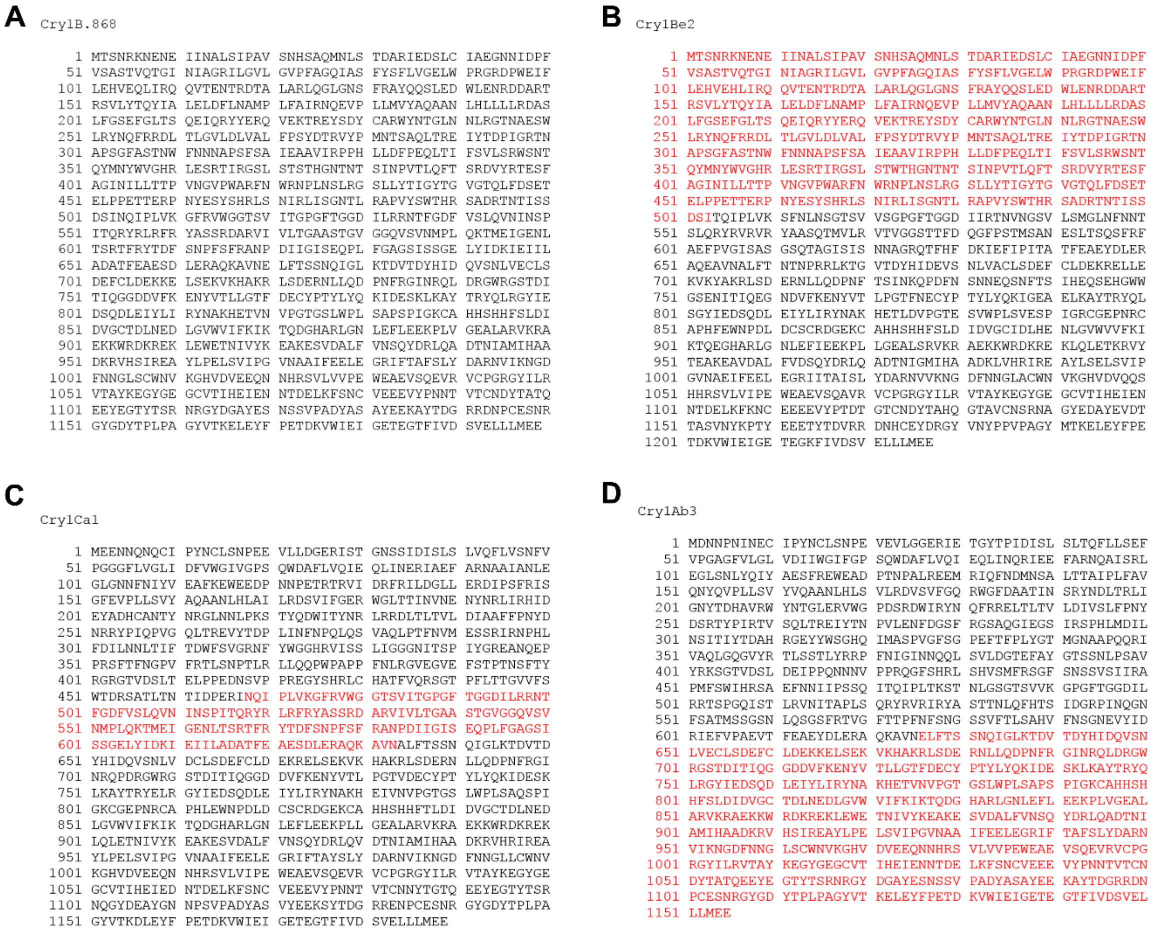
Supplementary Figure 1.



A Cry1B.868

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 101 LEHVEQLIRQ QVTENTRDTA LARLQGLGNS FRAYQQSLED WLENRDDART
 151 RSVLYTQYIA LELDFLNAMP LFAIRNQEVP LLMVYAQAAN LHLLLLRDAS
 201 LFGSEFGLTS QEIQRYYERQ VEKTREYSDY CARWYNTGLN NLRGTNAESW
 251 LRYNQFRRDL TLGVLDLVAL FPSYDTRVYP MNTSAQLTRE IYTDPIGRTN
 301 APSGFASTNW FNNNAPSFSA IEAAVIRPPH LLDFPEQLTI FSVLSRWSNT
 351 QYMNYWVGHR LESRTIRGSL STSTHGNTNT SINPVTLQFT SRDVYRTESF
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 951 DKRVHSIREA YLPELSVIPG VNAAIFEELE GRIFTAFSLY DARNVIKNGD
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1051 VTAYKEGYGE GCVTIHEIEN NTDELKFSNC VEEEVYPNNT VTCNDYTATQ
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B Cry1Be2

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C

Cry1Ca1

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 101 GLGNNFNIYV EAFKEWEEDP NNPETRTRVI DRFRILDGLL ERDIPSFRIS
 151 GFEVPLLSVY AQAANLHLAI LRDSVIFGER WGLTTINVNE NYNRLIRHID
 201 EYADHCANTY NRGLNNLPKS TYQDWITYNR LRRDLTLTVL DIAAFFPNYD
 251 NRRYPIQPVG QLTREVYTDP LINFNPQLQS VAQLPTFNVM ESSRIRNPHL
 301 FDILNNLTIF TDWFSVGRNF YWGGHRVISS LIGGGNITSP IYGREANQEP
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 951 YLPELSVIPG VNAAIFEELE GRIFTAYSLY DARNVIKNGD FNNGLLCWNV
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1051 GCVTIHEIED NTDELKFSNC VEEEVYPNNT VTCNNYTGTQ EEYEGTYTSR
1101 NQGYDEAYGN NPSVPADYAS VYEEKSYTDG RRENPCESNR GYGDYTPLPA
1151 GYVTKDLEYF PETDKVWIEI GETEGTFIVD SVELLLMEE
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D

Cry1Ab3

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 401 YRKSGTVDSL DEIPPQNNNV PPRQGFSHRL SHVSMFRSGF SNSSVSIIRA
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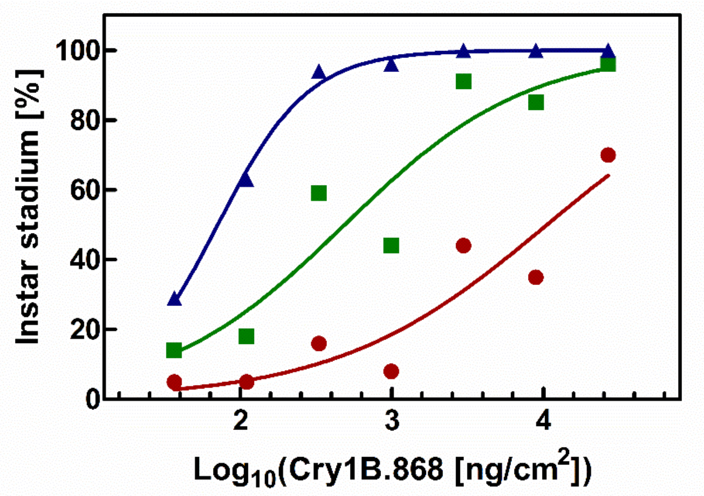
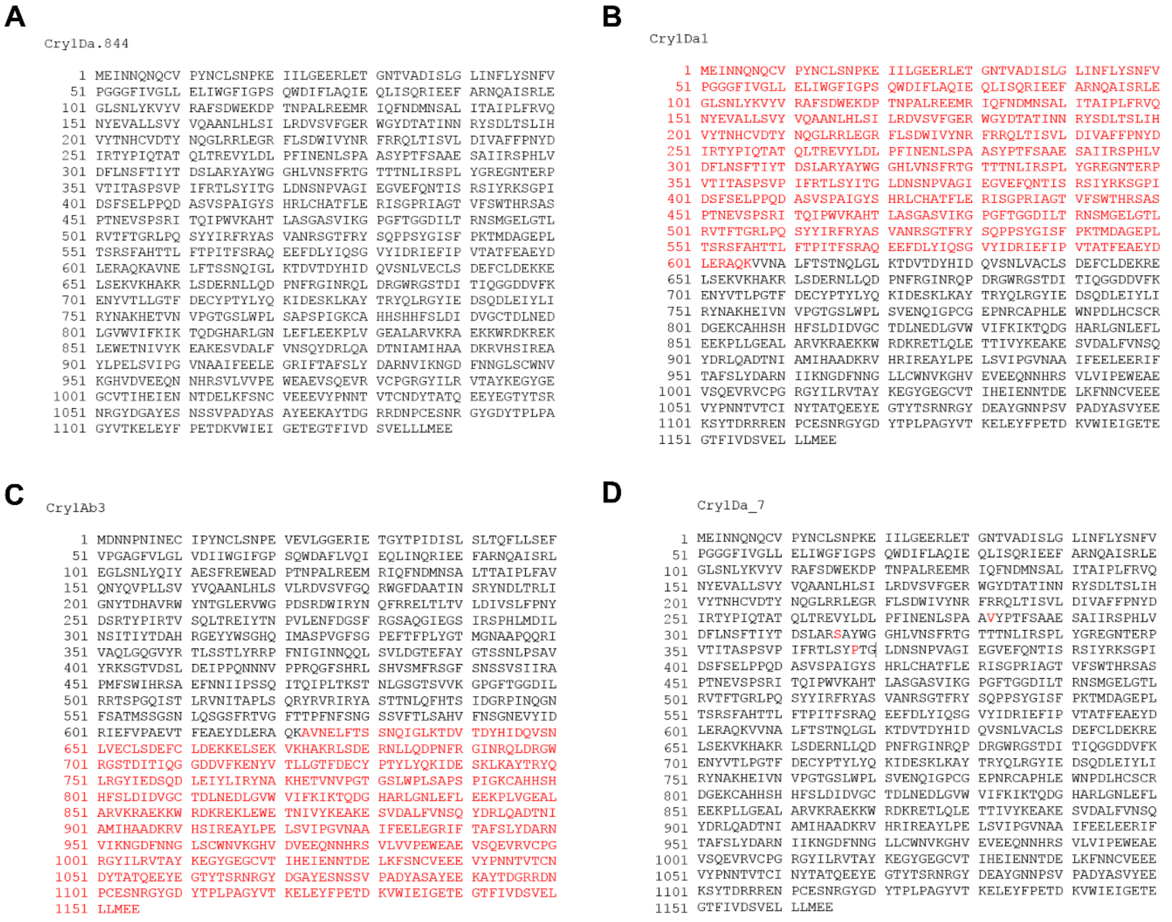
Supplementary Figure 2.



Supplementary Figure 3.

Protein	Slope	MIC$_{50}$ (µg/cm2)	95% CI
Cry1Be2	1.55	3.23	2.16 – 5.06
Cry1B.868	1.63	0.43	0.28 – 0.62

Supplementary Figure 4.



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Cry1Da.844

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 201 VYTNHCVDTY NQGLRRLEGR FLSDWIVYNR FRRQLTISVL DIVAFFPNYD
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 301 DFLNSFTIYT DSLARYAYWG GHLVNSFRTG TTTNLIRSPL YGREGNTERP
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B

Cry1Da1

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C

Cry1Ab3

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 101 EGLSNLYQIY AESFREWEAD PTNPALREEM RIQFNDMNSA LTTAIPLFAV
 151 QNYQVPLLSV YVQAANLHLS VLRDVSVFGQ RWGFDAATIN SRYNDLTRLI
 201 GNYTDHAVRW YNTGLERVWG PDSRDWIRYN QFRRELTLTV LDIVSLFPNY
 251 DSRTYPIRTV SQLTREIYTN PVLENFDGSF RGSAQGIEGS IRSPHLMDIL
 301 NSITIYTDAH RGEYYWSGHQ IMASPVGFSG PEFTFPLYGT MGNAAPQQRI
 351 VAQLGQGVYR TLSSTLYRRP FNIGINNQQL SVLDGTEFAY GTSSNLPSAV
 401 YRKSGTVDSL DEIPPQNNNV PPRQGFSHRL SHVSMFRSGF SNSSVSIIRA
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1151 LLMEE
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D

Cry1Da_7

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1151 GTFIVDSVEL LLMEE
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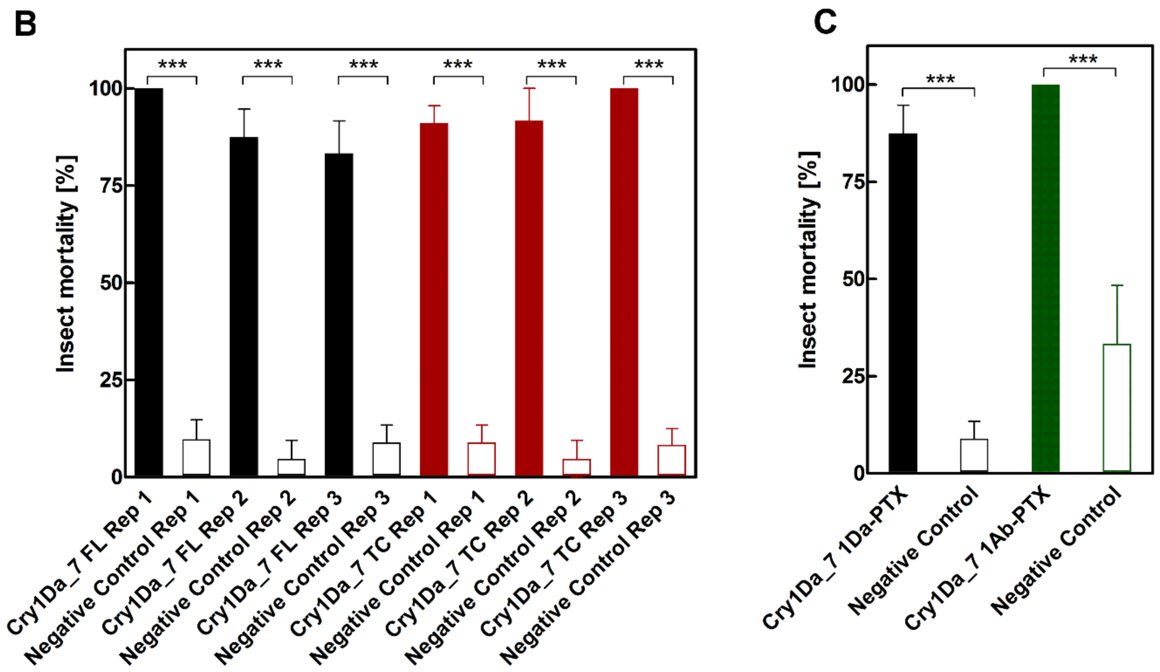
Supplementary Figure 5.

A

Active core (D1-3)	Mutations in active core	PTX domain (D4-7)	Protein form tested	Insect	Slope	IC_{50} [µg/cm^2]	95% CI
Cry1Da_7	S282V,Y316S,I368P	Cry1Ab	full-length	CEW	4.03	0.063	0.051 – 0.078
Cry1Da	N/A	Cry1Ab	full-length	CEW	1.56	3.28	2.26 – 4.96



Supplementary Figure 6.

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HHHHH

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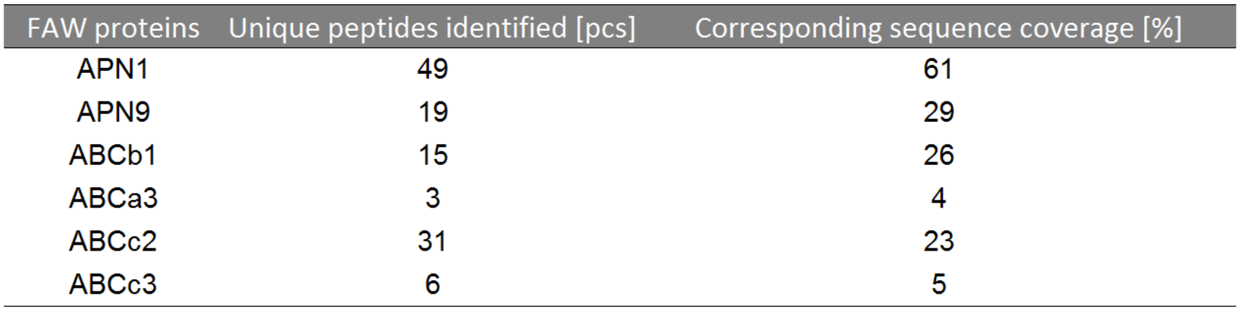
Supplementary Figure 7.



FAW proteins	Unique peptides identified [pcs]	Corresponding sequence coverage [%]
APN1	49	61
APN9	19	29
ABCb1	15	26
ABCa3	3	4
ABCc2	31	23
ABCc3	6	5

FIGURE LEGENDS

SUPPL. FIG 1. Amino acid sequence of the chimeric Cry1B.868 protein. Segments of the Cry1Be2, Cry1Ca1, and Cry1Ab3 sequences comprising Cry1B.868 are highlighted in red.

SUPPL. FIG 2. Concentration-response feeding assays demonstrating insecticidal activity of Cry1B.868 toward fall armyworm (FAW), *Spodoptera frugiperda*. Symbols are as follows, red circle, percent of dead insects; green square, percent of FAW larvae that have not molted to 2nd instar stadium; blue triangle, percent of FAW larvae that have not molted to 3rd instar stadium.

SUPPL. FIG 3. Specific insecticidal activity of the parent, Cry1Be2, and chimeric Cry1B.868 proteins on FAW.

SUPPL. FIG 4. Amino acid sequence of the chimeric Cry1Da.844 and Cry1Da_7 proteins. Segments of the Cry1Da1 and Cry1Ab3 sequences comprising Cry1Da.844 (A-C) as well as the three amino acid substitutions in Cry1Da_7 (D) are highlighted in red.

SUPPL. FIG 5. Specific insecticidal activity of the modified Cry1Da_7. (A) Assessment of the specific activity improvement against CEW via comparative analysis between Cry1Da and the modified Cry1Da_7, **(B)** FAW activity of 345 ng/cm^2 Cry1Da_7 before and after removing the protoxin domain via trypsin treatment, **(C)** FAW activity of the 345 ng/cm^2 Cry1Da_7 active core outfitted with Cry1Da vs. Cry1Ab protoxin domain (PTX).

SUPPL. FIG 6. FAW receptor sequences.

SUPPL. FIG 7. Proteomics data analysis indicating the presence of relevant *Bt* receptors in the FAW BBM sample. The columns indicate the protein ID, the number of unique peptides identified by proteomics and the corresponding percent of coverage in the full-length receptor sequence.