

Table. S1 Gene names of orthologous candidate reference genes (*RPL10*, *GADPH*, *EF1*, and *ACT1*), potential orthologous Cry toxin target genes, species, GenBank accession numbers and primer sequences for the amplification of the respective *Chrysodeixis includens* genes.

Gene name (abbreviation)	Species	GenBank accession number	Primer sequence	Amplification efficiency % (E)	Correlation coefficient (R ²)
<i>Ribosomal Protein L10 (RPL10)</i>	<i>Spodoptera exigua</i>	JF728812.1	5' TCTGCGTCGTGCCAAGTT 3'	101.41	0.997
	<i>Chrysodeixis includens</i>	MT879133	5' AGGGCCGTACTTGACGTTG 3'		
<i>Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)</i>	<i>Spodoptera litura</i>	DQ192234.1	5' ACTACACCGAGGAGCAGGT 3'	101.98	0.996
	<i>Chrysodeixis includens</i>	MT879136	5' AGCCGAACCTCGTTGTCTGT 3'		
<i>Elongation Factor 1 (EF1)</i>	<i>Spodoptera litura</i>	HQ012003.2	5' TTGCCTGCAAATTCGCCG 3'	101.88	0.998
	<i>Chrysodeixis includens</i>	MT879131	5' ACGCACAGAGGCTTGGAA 3'		
β -Actin 1 (<i>ACT1</i>)	<i>Spodoptera litura</i>	KC866373.1	5' TTGCCGGCAACAAGGAAC 3'	109.14	0.996
	<i>Chrysodeixis includens</i>	MT879129	5' CGGTGGCGTCAAATGCTT 3'		
<i>ATP-binding cassette subfamily C2 transporter (ABCC2)</i>	<i>Spodoptera frugiperda</i>	AU038740.1	5' AGGACCGGTTCTTGTGGA 3'	95.71	0.974
	<i>Chrysodeixis includens</i>	MT879134	5' AACGGGCGCTGGAAAGT 3'		
<i>ATP-binding cassette subfamily C3 transporter (ABCC3)</i>	<i>Spodoptera frugiperda</i>	AU038741.1	5' TGCCGCTTCCAACCAACT 3'	101.11	0.994
	<i>Chrysodeixis includens</i>	MT879135	5' AGGGCTGCATCAACGGT 3'		
<i>Membrane-bound alkaline phosphatase (mALP)</i>	<i>Lymantria dispar</i>	AAD31183.1	5' GCCGCCAAAATCGTTGCA 3'	109.70	0.998
	<i>Chrysodeixis includens</i>	MT879132	5' TGGGCTTCTCCTGGAGT 3'		
<i>Aminopeptidase N1 (APN1)</i>	<i>Plutella xylostella</i>	AAS75551.1	5' TGTGCTCCTCGTTCACGT 3'	103.00	0.997
	<i>Chrysodeixis includens</i>	MT879125	5' AGCGCCAGTGGTGAAAGT 3'		
<i>Aminopeptidase N2 (APN2)</i>	<i>Lymantria dispar</i>	AAL26894.1	5' TCACGCGATGTTCCCTCA 3'	95.00	0.993
	<i>Chrysodeixis includens</i>	MT879126	5' ATGGTTCCGAAGTGGCCA 3'		
<i>Aminopeptidase N3 (APN3)</i>	<i>Lymantria dispar</i>	AAL26895.1	5' AACGTTGGGGCAGTGCT 3'	92.40	0.998
	<i>Chrysodeixis includens</i>	MT879127	5' ATGTGCCACGTGGGGTT 3'		
<i>Aminopeptidase N4 (APN4)</i>	<i>Plutella xylostella</i>	AHF20243.2	5' ACGCACCTTGGATCGCT 3'	108.30	0.996
	<i>Chrysodeixis includens</i>	MT879128	5' GCGGTTGACAACAGCTGT 3'		
<i>Cadherin (CAD)</i>	<i>Helicoverpa armigera</i>	ACZ06062.1	5' TTTGTTACAGTGCGTGCG 3'	99.80	0.987
	<i>Chrysodeixis includens</i>	MT879130	5' TCACGAAGTCTTCCGGCA 3'		

Table. S2 Toxicity (LC₅₀-and LC₉₅-values) of Cry1Ac and Cry1F to neonates of soybean looper Benzon strain and the respective goodness of fit calculated for the non-linear regressions used

Toxin	N ¹	LC ₅₀ (ng cm ⁻²)	95% CI ²	LC ₉₅ (ng cm ⁻²)	95% CI	Slope (±SE ³)	df ⁴	R ²	SS ⁵	Sy.x ⁶
Cry1Ac	288	10.41	7.970 - 13.44	44.56	26.54 - 92.27	2.025 (0.40)	17	0.966	1367	8.967
Cry1F	324	194.7	88.44 - 425.7	4,967	2,534 - 10,605	0.909 (0.10)	22	0.954	1545	8.379

¹ N: Number of individuals tested; ² CI: confidence interval; ³ SE: standard error; ⁴ df: degree of freedom; ⁵ SS: sum of squares; ⁶ Sy.x: standard deviation of the residuals