

Table S1 Quantitative PCR primers

Primer name	Sequence from 5' to 3'	Amplification product length
<i>CYP6B74</i>	F: GAGCTAACTTGTTCCACGCC R: CGAAGACACAGGCCGTTATG	225
<i>CYP6AB112</i>	F: TACCAGCACTCGGAAACCAT R: TCGCTTCCAAGGTGTGATCT	214
<i>CYP6AB113</i>	F: TTTGGTTTCCTTACACGCCG R: TCATCCTCAGGGTCGAATCG	170
<i>CYP6AB114</i>	F: TCGGCCGGAGAGATTTAGTC R: ACCCGACTTTGGCTCAACTA	206
<i>CYP6AB115</i>	F: TTCAGATCAACACGTCCGGA R: AACAAACCGCCACAAATCTCC	170
<i>CYP6AB116</i>	F: GATGACACGTCCACATTCCG R: AAAGCGACCGTATGCCTTTC	252
<i>CYP6AB117</i>	F: GCTGCTAAACCAACACACGA R: GCGTAGAAAATGTTGGGCCA	209
<i>CYP6AN35</i>	F: ACCAGCCCTCATCATCAGAG R: GCAGCTTCCAAGTATCACCG	152
<i>β-actin</i>	F: CTTTCACCACCACCGCTG R: CGCAAGATTCCATACCCA	222

Table S2 Best BLASTp matches for *G. molesta* P450s

Gene name	ORF length	Best BLASTp match				
		Name	Accession number	Species	E-value	Percent identity
<i>CYP6B74</i>	1497	cytochrome P450 6B45	ADE05578.1	<i>Manduca sexta</i>	0	54.92
<i>CYP6AB112</i>	1593	cytochrome P450 6B2c	AXP17138.1	<i>Cydia pomonella</i>	0	87.61
<i>CYP6AB113</i>	1530	escape protein 2	AXP17154.1	<i>Cydia pomonella</i>	0	75.50
<i>CYP6AB114</i>	1536	cytochrome p450 CYP6AB14	ASO97998.1	<i>Vanessa tameamea</i>	0	69.45
<i>CYP6AB115</i>	1536	CYP6AB47	AHW57301.1	<i>Chilo suppressalis</i>	0	69.03
<i>CYP6AB116</i>	1530	CYP6AB7	ABL60877.1	<i>Depressaria pastinacella</i>	0	63.53
<i>CYP6AB117</i>	1551	Cytochrome P450 6B2b	AXP17131.1	<i>Cydia pomonella</i>	0	80.57
<i>CYP6AN35</i>	1533	Cytochrome P450 CYP6AN19	ASX93976.1	<i>Zygaena filipendulae</i>	0	58.62

Table S3 Physicochemical properties of *G. molesta* P450s

Gene name	CYP6B74	CYP6AB112	CYP6AB113	CYP6AB114	CYP6AB115	CYP6AB116	CYP6AB117	CYP6AN35
Number of AA	498	530	509	511	511	509	516	510
Molecular weight	58047.2	60754.95	58261.07	58496.04	58267.78	57365.67	59752.42	58195.37
Theoretical pI	8.84	8.35	6.55	8.82	8.57	8.77	7.61	8.82
Total number of negatively charged residues (Asp + Glu)	61	67	63	64	64	54	67	63
Total number of positively charged residues (Arg + Lys)	69	70	61	70	68	61	68	71
Instability index	36.62	38.77	37.22	35.79	34.96	39.57	36.35	34.77
Aliphatic index	84.56	85.36	89.02	90.84	89.55	94.09	90.41	85.47
Grand average of hydropathicity	-0.319	-0.348	-0.229	-0.166	-0.167	-0.075	-0.156	-0.258
Formula	C ₂₆₃₆ H ₄₀₉₆ N ₆ 90O ₇₃₇ S ₂₅	C ₂₇₄₆ H ₄₂₈₇ N ₇₄₁ O	C ₂₆₃₁ H ₄₁₁₈ N ₇₀₈ O	C ₂₆₆₆ H ₄₁₈₄ N ₆₉₈ O	C ₂₆₄₉ H ₄₁₆₄ N ₆₉₂ O	C ₂₆₀₁ H ₄₀₉₇ N ₆₉₃ O	C ₂₇₄₉ H ₄₂₆₁ N ₆₉₅ O	C ₂₆₃₃ H ₄₁₃₂ N ₆₉₆ O
		777S ₂₀	749S ₁₉	738S ₂₁	739S ₂₃	724S ₂₂	756S ₁₉	745S ₂₃

Table S4 Signal peptides of *G. molesta* P450s

Gene name	Max C	Max Y	Max S	Mean S	Mean D	Cleavage site	Signal peptide
<i>CYP6B74</i>	18 (0.627)	18 (0.775)	11 (0.984)	1-17 (0.953)	1-17 (0.872)	17-18	YES
<i>CYP6AB1</i> 12	23 (0.214)	23 (0.228)	12 (0.431)	1-22 (0.253)	1-22 (0.238)	-	NO
<i>CYP6AB1</i> 13	20 (0.253)	20 (0.296)	12 (0.461)	1-19 (0.336)	1-19 (0.312)	-	NO
<i>CYP6AB1</i> 14	22 (0.165)	22 (0.224)	13 (0.548)	1-21 (0.319)	1-21 (0.262)	-	NO
<i>CYP6AB1</i> 15	22 (0.199)	13 (0.242)	1 (0.639)	1-12 (0.401)	1-12 (0.306)	-	NO
<i>CYP6AB1</i> 16	26 (0.146)	26 (0.340)	13 (0.928)	1-25 (0.761)	1-25 (0.567)	25-26	YES
<i>CYP6AB1</i> 17	33 (0.183)	23 (0.333)	15 (0.863)	1-22 (0.728)	1-22 (0.547)	22-23	YES
<i>CYP6AN3</i> 5	21 (0.173)	21 (0.336)	6 (0.737)	1-20 (0.647)	1-20 (0.504)	20-21	YES



Figure S1 Multiple-sequence alignment of *G. molesta* cytochrome P450s.

Note: The following species (with GenBank accession numbers) were examined: *C. pomonella* (AXP17138.1 *CYP6B2C*), *M. sexta* (ADE05585.1 *CYP6AB13*, ADE05584.1 *CYP6AN5*), *Bombyx mori* (NP_001077080.1 *CYP6AE2*). The newly identified 8 genes belong to the cytochrome P450 family. The conserved region of cytochrome P450s is marked, such as ‘WXXXR’, ‘EXXRXX’, ‘PXXFXPXX’, ‘FXXGXXXCXG’ and ‘A/GGXDETT/S’.