Effects of Elevated CO_2 Concentration on Host Adaptability and Chlorantraniliprole Susceptibility in *Spodoptera frugiperda*

Supplement Table S1

Primers of detoxification enzyme genes used in the quantitative real-time PCR.

Identification	Primer Sequence (5′ → 3′)	
	Forward	Reverse
RPL10-insects	TGGGTAAGAAGAAGGCTACG	TGTTGATGCGGATGACAT
RPL13-JIA	GCCTTAACCCTGCTTTTGCTAG	GCTTCGCCCTTCAATACCTTC
CYP-19543	TGCCGCACCTACCACCAAA	TGCCCAAGTAAGAGCCAACG
CYP-17259	CTTACGCCTTTGTTCTCATCCG	CGTCAGGGCTCGCACTTCA
CYP-05919	ATGGCAAGTACGAATGGTGGA	CGGCTATCAGGCGAAAGAAA
CYP-22092	TGTTCGTGTTCTTCGCTGCTG	TCTCCTCCTGCGCCTTCCT
CYP-10853	GAAGTGTTCAGTGATCGTGGCG	AAACCGATTCCTCAAGGCTGT
CE-12593	AATGCCGAATCCTTGTCCG	TGATGATGGCTTCAGGGTGG

CE-20560	ACGACGAATGGCGGGAAGT	GGTGCCGTGGCGTAAGGTAT
CE-13095	TTCGTTACGGTCAACCACCC	GCTGCCTTCCACAACATCTAAAA
CE-21185	ACCTGTGCCTGAAGGGTCG	GTTGTTTGGGTGGTGGTGTTG
CE-12962-	AGATAGCATTCTGTTTGGACCCG	CCCAGCGATATGAGGCAGTTTT
ABC-01998	GCATCGCAGGTTAGGACAC	TTCACAGCAAACGGCACAG
ABC-02885	ACCTCATAGCACGATCACC	AAACGGCTTCCTTTACTGA
ABC-18240	AATGTCCACCCGTTTCTAC	TACTAACCATCGCACTGAC
ABC-22158	GAACGAGCATTCGACGACAAT	CGGCAAACCAGCTAACATCAG
UGT-18136	CCATTGCTCTACCCAGGGATT	TGGCACATCTGGTCCAAACA
UGT-17742	AAAAGGCAACCCTACCCAT	CTTAGCGGCCAGTTCACAA

Supplement Table S2

Toxicity effect of Chlorantraniliprole on 3rd larvae of *S.frugiperda* under elevated CO_2 and ambient CO_2.

Treatment	Concentration response regression equation	χ^2	P	LC$_{50}$(mg L^{-1}) 95% CI
F_AW_A	y=4.2826+0.7447x	51.9652	0.0001	9.19 (1.57 - 59.67)
F_EW_A	y=4.4479+0.7901x	39.6400	0.0001	5.00(0.32 - 9.55)

Note: 95% CI, 95% confident intervals; LC$_{50}$, the concentration of Chlorantraniliprole.

Supplement Table S3
Summary of the transcriptome sequencing data.

Sample	Total Clean Reads (M)	Clean Reads Q20 (%)	Clean Reads Q30 (%)	Clean Reads Ratio (%)	Total Mapping (%)
$F_AW_A\_1$	41.99	97.1	92.59	95.83	69.25
$F_AW_A\_2$	42.37	97.18	92.7	95.66	69.03
$F_AW_A\_3$	42.47	97.13	92.56	96.92	67.51
$F_EW_E\_1$	42.3	97.16	92.62	96.52	67.28
$F_EW_E\_2$	42.18	97.29	92.95	96.25	68.49
$F_EW_E\_3$	42.39	97.25	92.81	96.74	67.25
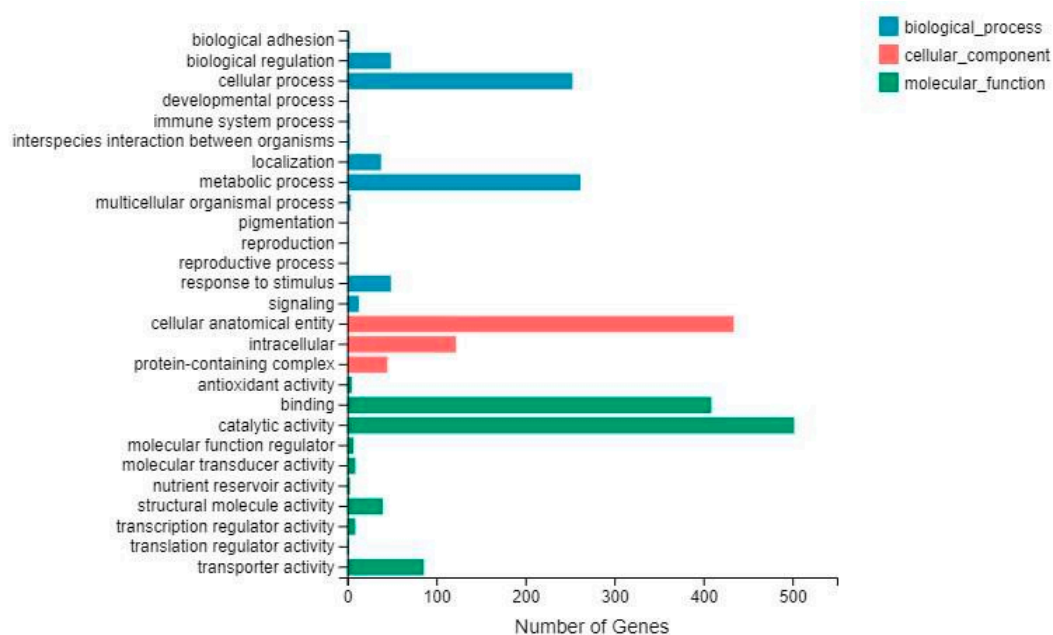
Supplement Figure S1. GO gene function classifications of DEGs in comparison groups.

Gene function classifications of DEGs in $F_A W_A$ versus $F_E W_E$. Note: The X-axis represents the

number of genes annotated to GO entries and the Y-axis represents the GO functional classification.
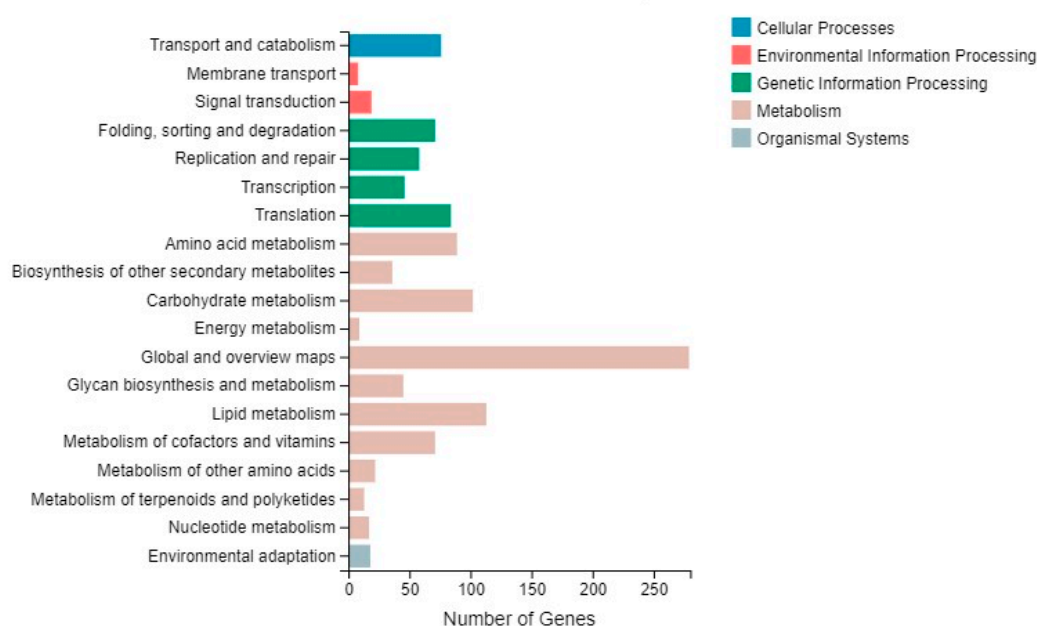
Supplement Figure S2. KEGG gene function classifications of DEGs in comparison groups.

Gene function classifications of DEGs in $F_A W_A$ versus $F_E W_E$. ***Note***: X-axis is the number of genes

annotated to a particular KEGG Pathway category and Y-axis is the KEGG Pathway category.