

SUPPORTING INFORMATION

Genome-wide transcriptional signatures of migratory flight activity in a globally invasive insect pest

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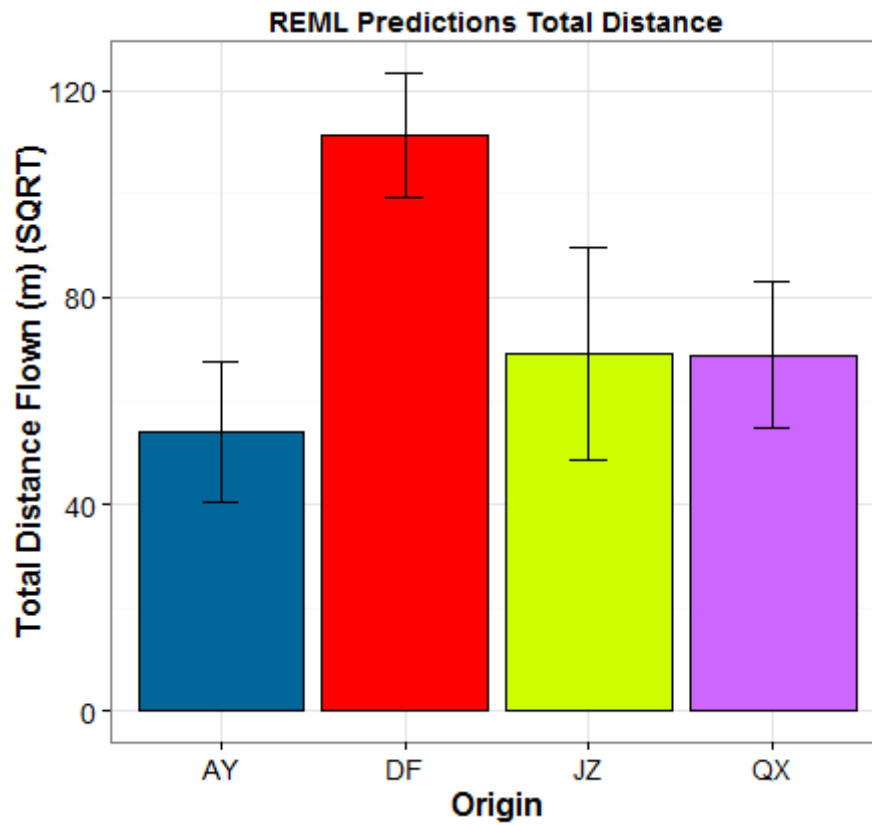


Figure S1. REML estimations of total distance flown by Chinese populations. Total distance flown is square root transformed and error bars are 95% CIs. Adult moths from Dafeng flew significantly further than the other three populations ($P < 0.001$) supported by non-overlapping 95% CIs.

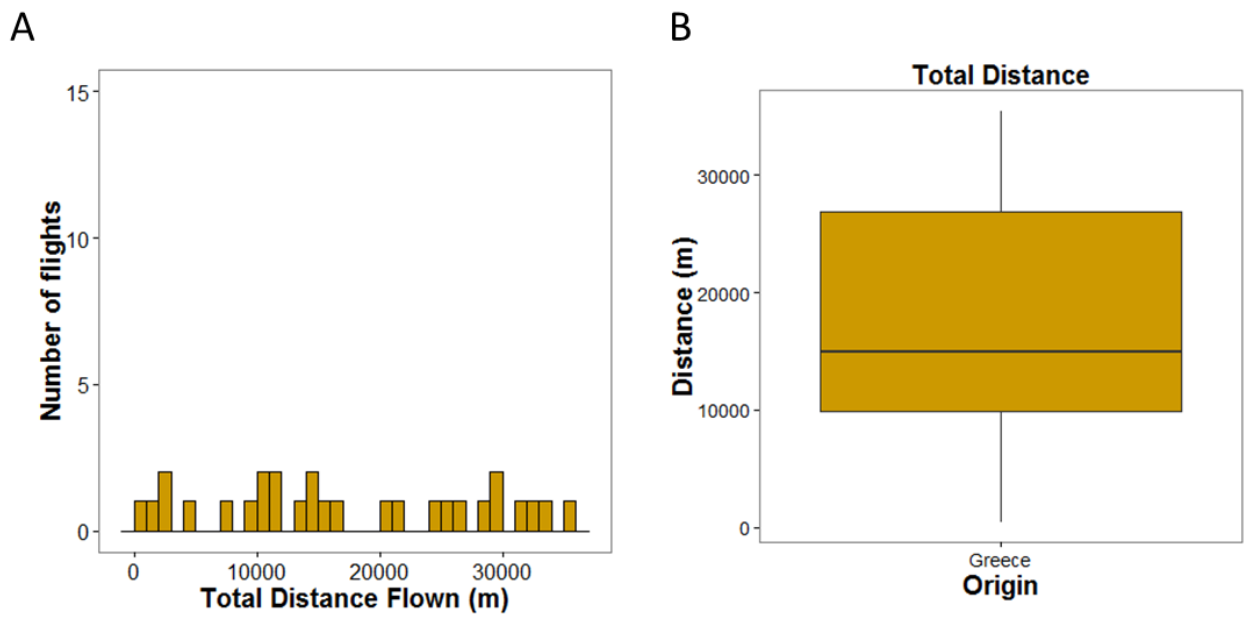


Figure S2. Flight performance of *H. armigera* from northern Greece. The (A) distribution and (B) boxplot of total distance flown are shown ($n = 28$). Only female moths from the Greek population were flown.

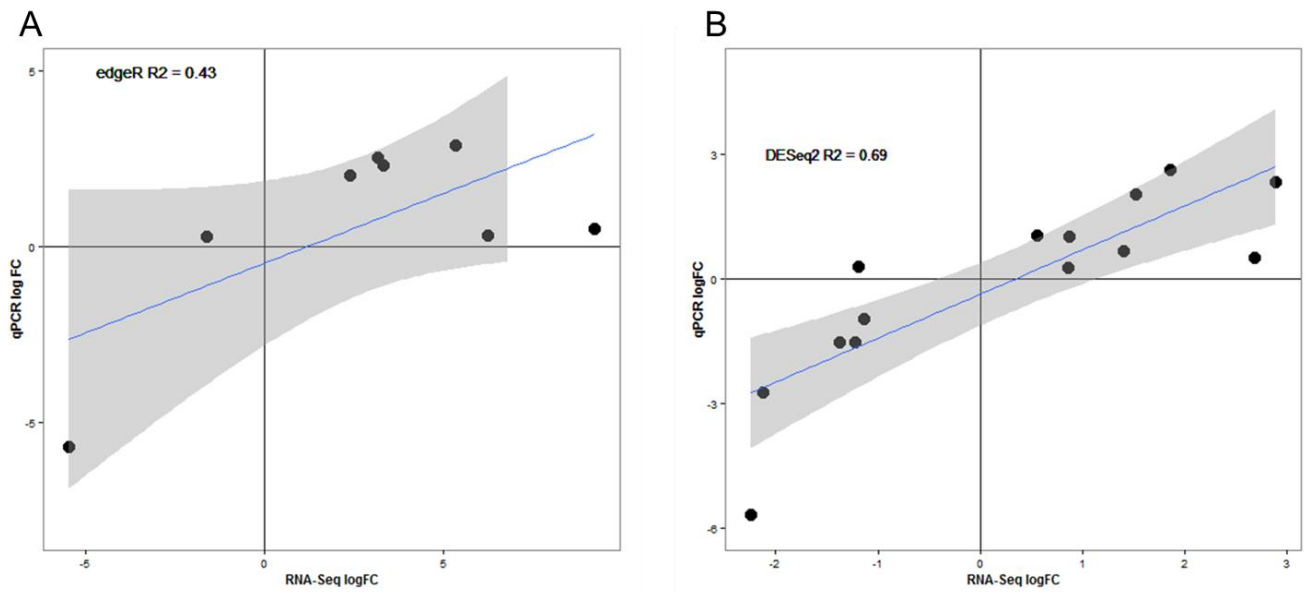


Figure S3. Validation of RNA-seq by qPCR. Individual qPCR fold-changes are plotted against RNA-seq values per expression package (A) edgeR and (B) DESeq2. Only instances in which the transcript was significantly expressed in the RNA-seq data (FDR < 0.1) are plotted. Fold-changes are log₂-transformed. A simple linear regression line is presented (with 95% CIs) with the corresponding R² value for each package.

Table S1. Information on the origin and generation of each *H. armigera* collection used in either flight mill, RNA-seq and/or qPCR experiments.

Country of origin	Population	Reference coordinates
China	Dafeng	33.19°N, 120.50°E
China	Anyang	36.10°N, 114.20°E
China	Jingzhou	30.14°N, 111.73°E
China	Qiuxian	36.81°N, 115.16°E
China	Wangjiang	30.14°N, 116.66°E
Greece	Greece	41°N, 023°E
Laboratory	Bayer	-

Table S2. Output of explanatory variables from full REML model for total distance flown by Chinese *H. armigera*.

Fixed term	F statistic	n.d.f	d.d.f	F-test P
population	4.73	3	60.6	0.005
sex	0.48	1	32.4	0.492
population*sex	0.27	3	63.4	0.844

Constant + population + sex + population*sex (night + mill + night*mill)

Table S3. Output of explanatory variables from full REML model investigating total distance flown by Dafeng *H. armigera* versus three other Chinese populations.

Fixed term	F statistic	n.d.f	d.d.f	F-test P
dafeng	13.47	1	56.9	13.47
dafeng*rest	0.38	2	61.6	0.38
sex	0.48	1	32.4	0.48
dafeng*sex	0.63	1	64.6	0.63
dafeng*rest*sex	0.09	2	63.3	0.09

Constant + dafeng + dafeng*rest +sex +dafeng*sex + dafeng*rest*sex (night + mill + night*mill)

Table S4. Primer information for target and control genes used to validate and analyse expression in *H. armigera*.

Type	Gene description	gene name	Primer Fwd (5'-3')	Primer Rev (5'-3')	Efficiency
target	obp6	HaOG200803	TGAGCAAAGTTCACGCCACA	GGGTAACTCCGTGCTCCTTA	0.93
target	obp3	HaOG200802	GACCAAGCTGCAGAAGTTCG	ATTCAGTGCAGCGCATGTCT	0.79
target	BMORI:retinoid-inducible serine carboxypeptidase-like isoform X1	HaOG202884	TTCAAAGCTGGACCCAGACG	CTGACTGTCCGGCAGCATT	0.81
target	BMORI:nucleoside diphosphate kinase 7-like	HaOG216795	TGAAGATGCGCGAATGATGC	CCGTGAGAGTTGAGCGGAAT	1.08
target	BMORI:neuropeptide receptor B3 precursor	HaOG206273	CGATACCAGCCAGTGTGAGG	AGTGATGACAAGAAGGCCCG	0.76
target	BMORI:myofilin isoform A	HaOG212567	ATCATACTGTCTTCCCTCAACTTTT	GAAGCCCCCTGCTGTTATTCAA	0.79
target	HaLipase28	HaOG200555	CATAACGCGACCATGATGCC	CCTTGACCGTAGTGAGCGAG	1.06
target	BMORI:collagen alpha-1(II) chain-like	HaOG215487	ATATCCGGTCCAGGTGGGTC	TAGGGTTCAATCCGTTACCGC	0.83
target	BMORI:apolipoporphins isoform X2	HaOG211110	GTCAGGATCTTGCGTGCCT	AGACCTCAATGCTGTAGCCG	0.85
target	BMORI:acyl-coenzyme A dehydrogenase	HaOG201695	CGCCAAACCAGAGAACAAGC	CCAGCTGCGTACTTGTAAAC	0.78
target	BMORI:putative fatty acyl-CoA reductase CG5065-like	HaOG214659	GCGTCGAGAACAAAGTCACAC	ATAGCTTTCAGACGCTGGCT	0.89
target	BMORI:3-oxoacyl-[acyl-carrier-protein] reductase chloroplastic-like	HaOG211178	ATACTCCGCATCGAAGGCTG	TCAGTTTTACGGGTCCAGG	0.97
target	BMORI:elongation of very long chain fatty acids protein 2-like	HaOG206659	AGGTGGTCACGGAACCTTGA	TCTTAACACTGGGGACCGCT	1.04
target	BMORI:acyl-CoA Delta(11) desaturase	HaOG215659	CGGCCAGAATTCCCTTCTCC	CGTTGTGAGGGTCTGCATCT	0.94
target	BMORI:3-hydroxyacyl-CoA dehydrogenase	HaOG208751	GCAAGGATACTCCCGGCTTT	GCATCGCCTCTCTCCAACAT	0.74
target	BMORI:probable peroxisomal acyl-coenzyme A oxidase 1-like	HaOG208389	TGAAGCCTGATGCTGGTGAG	TCGAGGCTATGGCGATGAAC	0.97
control	elongation factor	Yan <i>et al.</i> (2013)	GAAGTCAAGTCCGTGGAGATG	GACCTGTGCTGTGAAGTCG	0.88
control	actin	Wang <i>et al.</i> (2013)	TCCAGCCCTCATTCTTGGGTAT	CAAGTCCTTACGGATGTCAACA	0.87

Table S5. GO-term enrichment analysis of genes up-regulated in long-distance phenotypes of *H. armigera*.

GO-ID	Term	Category	FDR	#Test	#Ref
GO:0006189	'de novo' IMP biosynthetic process	P	4.41E-08	6	3
GO:0055114	oxidation-reduction process	P	1.03E-05	28	974
GO:0044282	small molecule catabolic process	P	1.71E-05	9	71
GO:1901606	alpha-amino acid catabolic process	P	5.22E-04	6	35
GO:0009072	aromatic amino acid family metabolic process	P	5.22E-04	5	18
GO:0006564	L-serine biosynthetic process	P	8.05E-04	3	1
GO:0006164	purine nucleotide biosynthetic process	P	5.42E-03	7	91
GO:0016742	hydroxymethyl-, formyl- and related transferase activity	F	8.06E-03	3	5
GO:0030170	pyridoxal phosphate binding	F	1.42E-02	5	45
GO:0050662	coenzyme binding	F	1.57E-02	9	199
GO:0006546	glycine catabolic process	P	1.90E-02	3	8
GO:0006760	folic acid-containing compound metabolic process	P	2.38E-02	3	9
GO:0016903	oxidoreductase activity, acting on the aldehyde or oxo group of donors	F	3.43E-02	5	58
GO:0016823	hydrolase activity, acting on acid carbon-carbon bonds, in ketonic substances	F	3.43E-02	2	1
GO:0035999	tetrahydrofolate interconversion	P	3.43E-02	2	1
GO:0004488	methylenetetrahydrofolate dehydrogenase (NADP+) activity	F	3.43E-02	2	1
GO:0042219	cellular modified amino acid catabolic process	P	3.43E-02	2	1
GO:0006144	purine nucleobase metabolic process	P	4.82E-02	3	13

*GO, gene ontology; FDR, false discovery rate