

# Is *Helicoverpa armigera* (Lepidoptera: Noctuidae) in Brazil? First detailed molecular detection report

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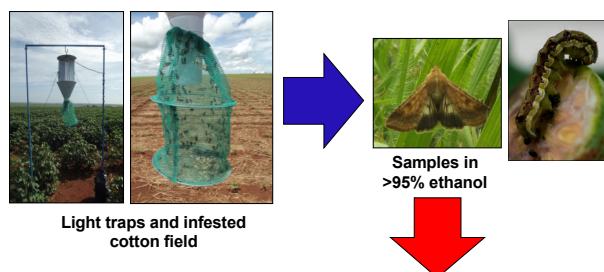
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## BACKGROUND

The cotton bollworm *Helicoverpa armigera* (Hübner) (Lepidoptera: Noctuidae) is a quarantine agricultural pest for the American continents. In different regions of Brazil during the 2011/12 and 2012/13 growing seasons *Heliothinae* larvae were observed attacking the main annual crops (cotton, maize and soybeans). It is thought that this pest invaded the American continents ~1.5 million years ago leading to the founding of current *Helicoverpa zea* (Boddie) populations. This relatively recent divergence is evident via hybridisation under laboratory conditions. Despite periodic interceptions of *H. armigera* into North America, this species is not believed to have successfully established in the New World. We provide for the first time detailed molecular evidence that *H. armigera* is in Brazil with individuals being detected in the State of Mato Grosso.

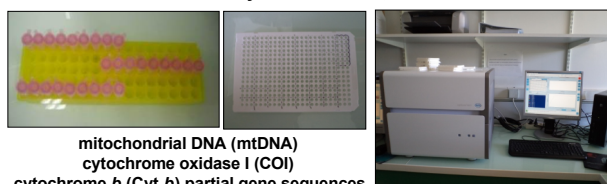
## METHODOLOGY

**1. Heliothinae samples were collected from** Center-East (Primavera do Leste) and South (Pedra Preta) region of Mato Grosso State, Brazil



Light traps and infested cotton field

**2. Molecular characterisation of partial mitochondrial DNA genes and Exon-Primed Intron-Crossing (EPIC) PCR marker analyses were performed by** CSIRO Ecosystem Sciences, Australia



mitochondrial DNA (mtDNA) cytochrome oxidase I (COI) cytochrome b (Cyt b) partial gene sequences

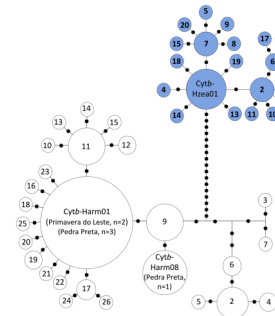


**3. Brazilian samples were compared with** global *H. armigera* and *H. zea* COI and Cyt b haplotype distribution patterns – see published paper for relevant GenBank Accession Numbers and Point 5 of this poster for details of the number of samples from each location.

## RESULTS

**4. Genotypes of 6 *H. armigera* from Brazil, 1 *H. zea* sampled in 2006 from** Mato Grosso (MG), and an Old World *H. armigera* (GR) using RpL11, DDC and RpS6 exon-primed intron-crossing (EPIC) PCR markers

Sample	COI	Cyt b	RpL11 (bp)	DDC (bp)	RpS6 (bp)	Possible Matriline
Brazil-04	Harm01	Harm01	297/297	208/218	266/268	1
Brazil-07	Harm01	Harm01	297/297	208/208	269/271	1
Brazil-10	Harm01	Harm01	297/297	206/206	270/275	2
Brazil-11	Harm01	Harm08	297/297	211/213	265/271	3
Brazil-13	Harm01	Harm01	297/297	x/x	x/x	N.D.
Brazil-14	Harm01	Harm01	x/x	204/221	247/247	4
<i>H. zea</i> (MG)	Hzea06	Hzea01	297/297	206/206	270/270	Control
<i>H. arm</i> (GR)	N.D.	N.D.	x/x	204/206	264/270	Control



Global *Helicoverpa armigera* and *H. zea* Cyt b haplotype distribution patterns including the Brazilian *H. armigera* Cytb-Harm01 and Cytb-Harm08 haplotypes, and relevant GenBank Accession numbers.

**5. Partial mtDNA Cyt b haplotype network of *H. armigera* based on 434bp.** A total of 26 haplotypes were identified from 255 individuals sampled from India (n=90), Pakistan (n=10), China (n=34), Burkina Faso (35), Uganda (24), Australia (56), and Brazil (6). Numbers of individuals within each haplotype are: 1 (n=162), 2 (n=10), 3 (n=1), 4 (n=2), 5 (n=1), 6 (n=3), 7 (n=1), 8 (n=18), 9 (n=17), 10 (n=1), 11 (n=19), 12 (n=2), 13-16 (n=1 each), 17 (n=4), 18 (n=1), 19 (n=2), 20-26 (n=1 each). Number of SNPs differentiating haplotypes are indicated by black circles.

## CONCLUSIONS

- *H. armigera* is present in Brazil with at least four matriline.
- Based on small sample size, there is currently no evidence of introgression between *H. armigera* and *H. zea* populations in Brazil.

