NATIVE BUDWORM POPULATIONS MAYBE REGIONALLY DISTINCT

Ary A. Hoffmann and Stephen W. McKechnie[1]

Department of Genetics and Human Variation, La Trobe University, Bundoora, 3183 and [1]Department of Genetics and Developmental Biology, Monash University, Clayton, 3168

Outbreaks of native budworm, *Helicoverpa punctigera*, often arise after egglaying by emigrant moths from distant populations. We would be in a better position to control this pest if (i) we could find genetic differences among populations allowing identification of moth origins, and (ii) if we understood the nature and extent of heritable regional differences for ecologically important traits. Towards this end we looked for genetic differences among moth populations originating from widespread Australian sites.

Moths were provided from five sites by *Helicoverpa* workers: Warrnambool (Vic), Birdsville (Inland), Geraldton (WA), Emerald (Qld) and Narrabri (NSW). Duplicate lines were initiated with more than 100 moths from each site. They were established within 5 months of each other on artificial diet at 25° C on a 16 hr light:8 hr dark cycle, and at a census size of about 100 adults. Using the polymerase chain reaction a small hypervariable region of mitochondrial DNA was amplified and 250 bases of nucleotide sequence was determined for individual moths. Fifty first-instar larvae from each line were placed individually on artificial diet at 19° C and fresh diet was added once before pupation. Individuals were weighed 5-6 days after pupation. Time to pupation and eclosion was scored. Adults were weighed directly after eclosion, wings were mounted on slides, and measurements made.

The most common DNA sequence from the 20 moths examined is given in Table 1. Variation among the moths occurred at five positions within this sequence and these differences are also shown. The same technique gave sequence from one *Helicoverpa armigera* moth (Table 1). *H.armigera* differed from the *H.punctigera* consensus sequence at 31 sites, resulting in an 88% level of homology. The variation detected among the *H.punctigera* from the laboratory populations is summarised by listing only the nucleotides present at the variable sites (Table 2). Five different genetic types were detected, and all but one of these were unique to specific populations. Each population sample was monomorphic for its own type, except for two different types in the Warrnambool (Vic) sample. One moth type from the Warrnambool population was the same as from the Emerald (Qld) population. Clearly our sample sizes so far are too small and are only from laboratory populations. Because of the laboratory history we cannot exclude the possibility that founder effects have significantly reduced the mtDNA variation and by chance resulted in little sharing of genetic types across the samples. Nonetheless these limited data are encouraging in our search for genetic markers associated with geographical regions. If regional differentiation for this marker proves to be the case for *H.punctigera* we might expect the same DNA sequence to be even more useful as a region-of-origin marker for *H.armigera*. The latter species is believed to be less migratory than *H.punctigera* which would decrease the likelihood of gene exchange leading to genetic homogeneity. We are now taking samples directly from the field and we will monitor genetic types in the Narrabri region for changes through several seasons.

Only quantitative data for non-diapausing pupae are presented. Statistical analysis indicated significant differences among the populations for a number of

traits including biomass, development time and wing measurements (Figure 1). Sex effects were also significant for some traits reflecting differences in wing markings and a faster eclosion time for females. Warrnambool and Narrabri tend to have slower development times than the other populations, while Birdsville and Narrabri tend to have smaller black spots on their forewings. Warrnambool males tend to be heavier than those of the other populations, while Emerald and Narrabri females tend to be relatively heavier. There were also population differences in the proportion of larvae entering diapause, which varied from 70% for Emerald to 26% for Geraldton. The quantitative data should be regarded as preliminary but suggest heritable divergence between *H.punctigera* populations for morphological and life-history traits. The smaller size and more rapid development of the Birdsville population could be associated with a higher migratory tendency in moths from inland sites where food plants are more ephemeral. These quantitative results indicate that care should be taken when experimental data from laboratory studies are used to predict population dynamics and crop damage in cotton growing areas. The region of origin of the experimental population needs to be considered.

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TABLE 1: DNA sequence and sequence variation in a segment of the AT-rich region of *Helicoverpa punctigera* and *Helicoverpa armigera*

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Consensus AATTTTTATTATTTATTATTATATAAAAAATTATTAAAAATGGTTTAATA 50
H.punct.                          G
H.armig.      A      X            G           C          T  G

          TCTAATTTAATAAATAAATTACTTATATATATATATATATATATATTAAA 100

           A G        TG    G   T     A

          TATTTAATTTATTAATATAATTATTAATATAATAAATTATTAAAAAATTA 150

                        T A

          ATATTAATTATATTAATATGATATTATATAAATTAATATTAATTGTTTAT 200
           C     C              G                 C
             X                TTAG               AC
          TATTATTTAGTTTTTAATATTATTATTATGAAAAAGAATAAAAGAAAATT 250

            A                  A       X       XXXX         AA
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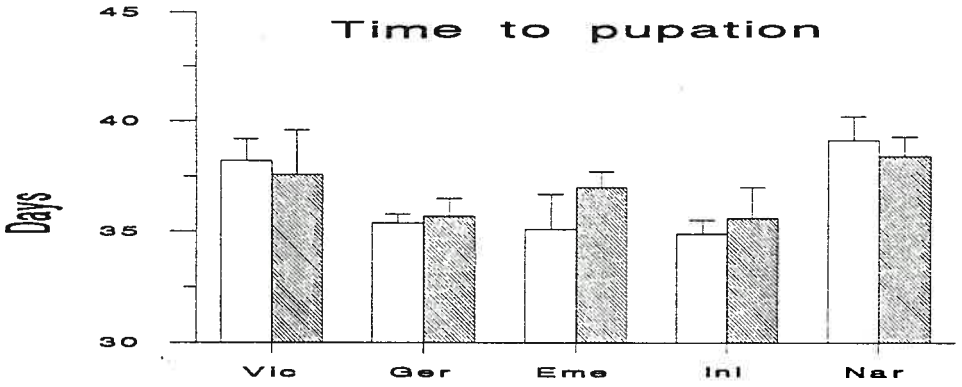
A = adenine; T = thymine; C: cytosine; G = guanine
(X = deletion; underlined base = insertion)

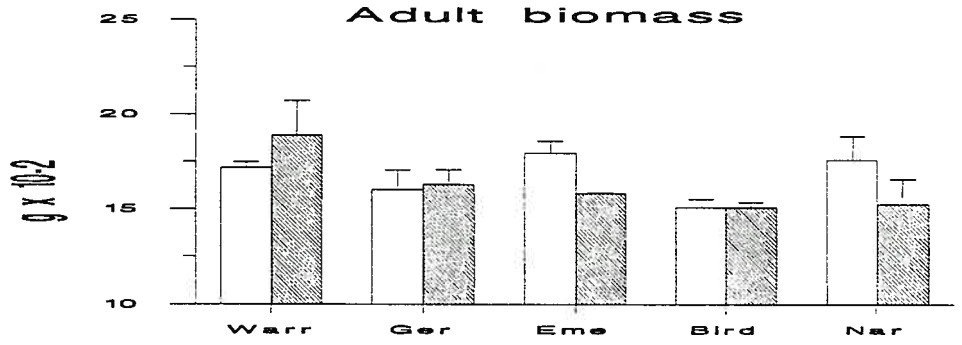
A sequence of 250 base pairs of the most common genetic type (Consensus) is shown. Letters immediately under this sequence show the sites and alternate bases which occurred in different *H.punctigera*. Letters two lines below indicate the different bases that occurred at these positions in the homologous sequence from one *H.armigera* moth.

TABLE 2: Genetic types of 20 *H. punctigera* from five laboratory populations

Population	Moth #	Base Position 25	152	158	173	190
Narrabri:	18	A	T	T	A	C
	53	A	T	T	A	C
	54	A	T	T	A	C
	55	A	T	T	A	C
Birdsville:	16	A	T	C	A	T
	26	A	T	C	A	T
	27	A	T	C	A	T
	75	A	T	C	A	T
Geraldton:	11	G	T	T	G	T
	13	G	T	T	G	T
	14	G	T	T	G	T
	24	G	T	T	G	?
	29	G	T	T	G	T
Warrnmb'l:	31	A	C	T	A	T
	33	?	C	T	A	T
	38	A	T	T	A	T
	72	A	C	T	A	T
Emerald:	3	A	T	T	A	T
	20	A	T	T	A	T
	30	?	T	T	A	T



Open bars represent females;
hatched bars males.



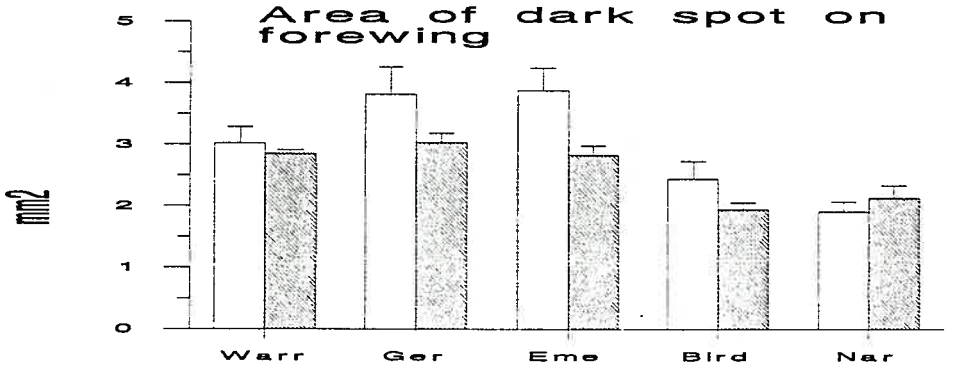


FIGURE 1. Population means for time to pupation, adult biomass and area of dark spot scored at 19°C. Error bars are standard errors based on the two replicate lines.