Helicoverpa armigera: truly polyphagous

Interbreeding in *Helicoverpa armigera* populations from different host plants estimated by resistance status and microsatellite markers

J. ACHALEKE [1], T. BREVAULT [1], L. BLONDIN [2] and J.M. VASSAL [2]

[1] CIRAD-IRAD, Station de Garoua, BP 415
Garoua, Cameroun
thierry.brevault@cirad.fr

[2] UMR CBGP, Campus International de Baillarguet,
TA 40/L, 34398 Montpellier Cedex 5, France
jean-michel.vassal@cirad.fr

Introduction

Due to the high polpyhagy of larvae, *Helicoverpa armigera (Hübner)* constitutes a major pest for a large range of cultivated plants worldwide. In Central Africa savannas, this noctuid is a major pest of cotton and vegetable crops (particularly tomato). Following diagnosis of *H. armigera* resistance to pyrethroids in Cameroon, the situation has led to cypermethrin failure in cotton fields (Brevault and Achaleke, 2005).

H. armigera larva in cotton flower (Photo T. Brévault).

In order to establish the epidemiological profile of resistance, we defined two objectives: to compare resistance frequencies in *H. armigera* populations from different host plants in the same locality in the course of the season and investigate by microsatellite markers genetic structure of populations from different host plants collected at the same time within the same locality.

Material and methods

Resistance survey

Collection of larvae

The resistance survey was conducted in the locality of Pitoa (9°39 N, 13°50 E) from the following host plants: cotton (*Gossypium hirsutum*), maize (*Zea mays*), tomato (*Lycopersicum esculentum*) and weed hosts (*Cleome sp.* and *Hyptis suaveolens*).

Vial tests

Assessment of *H. armigera* susceptibility to pyrethroid insecticides was carried out through vial tests (Mc Cutchen *et al.*, 1989). Two treatments were tested in the laboratory in 30 ml vials: 10 acetone treated vials (control) and 30 vials each treated with 30 µg of cypermethrin. Tests were replicated at least twice. G-test was then performed to statistically compare resistance frequencies ($P<0.05$).

H. armigera damage on tomato fruit (Photo T. Bévault).

H. armigera larva on Cleome viscosa weed (Photo T. Brévault).

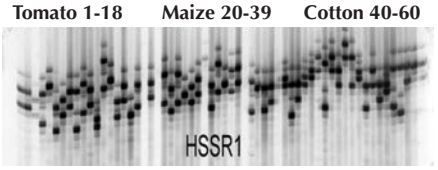
H. armigera larva on maize corp (Photo T. Brévault).

H. armigera larva on Hyptis suaveolens weed (Photo T. Brévault).

Genetic analysis of population samples

DNA extraction and microsatellite analysis

In September 2003, larval samples were collected from tomato, cotton and maize in the same locality, Dakar (10°63′ N, 14°29′ E). DNA for microsatellite analysis was extracted from larval cuticule using Qiagen protocole. Six microsatellite loci were used to analyse the differents *H. armigera* individuals.



Autoradiographic film showing bands of amplified DNA at HarSSR1 locus. Genotype defined by allele's number of base pairs.

Results

Resistance survey

The general trend in the succession and colonisation of *H. armigera* in nothern Cameroon is *Cleome spp* (June), maize (July – August), cotton (August – October) and finally, tomato and maize as off season hosts around irrigated areas (Fig. 1).

Our survey finding showed that resistance frequencies of *H. armigera* populations in treated *versus* non treated hosts are not significantly different (NS*, $P>0.05$). On the other hand, the temporal picture of resistance status further indicates a progressive seasonal increase in both non treated *versus* treated hosts plants (Fig. 2).

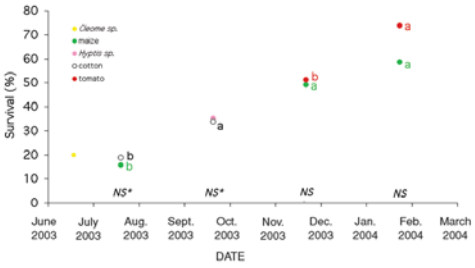


Figure 2. Resistance status of *H. armigera* populations over time in different host plants, in Pitoa (2003/04 season).

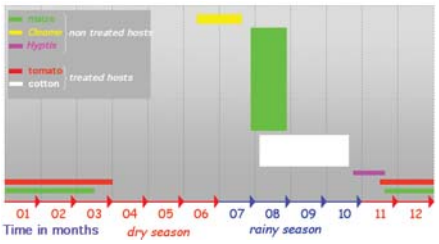


Figure 1. Host plant succession cycle of *H. armigera* in North Cameroon. Band thickeness is approximately proportionate to the host abundance.

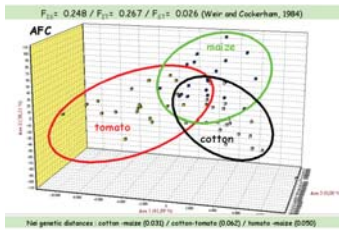


Figure 3. Genetic distances between populations from different host plants (Dakar, Cameroon, September 2003).

Genetic analysis of population samples

Examination of allele's frequencies at six microsatellite loci as well did not yield any significant difference. The low Fst value indicates low difference between the populations and the calculation of genetic distance between populations gave small distances (Fig. 3).

Conclusion

The simultaneous progression of resistance frequencies in populations of refuge and treated hosts over the season indicates that the same pest population could colonize the succession of different host plants. The seasonal increase in resistances is therefore due to the continuous infestations of resistance genes through seasonal successions.

According to the refuge model (Madden *et al.*, 1995), maize and *Cleome* are potential reservoirs hosts of *H. armigera* and supply susceptible genes that can dilute resistance genes from treated fields. These alternate non treated hosts therefore naturally could contribute to resistance management.

References

Brévault, T., Achaleke J., 2005. Status of pyrethroid resistance in the cotton bollworm, *Helicoverpa armigera*, in Cameroon. *Resistant Pest Management Newsletter* (in press).

Madden A.D., Holt J., Armes N.J., 1995. The role of uncultivated hosts in the spread of pyrethroid resistance in *Helicoverpa armigera* populations in Andhra Pradesh, India: a simulation approach. *Ecological Modelling*, 82, 1, 61-74.

Mc Cutchen B.F., Plapp F.W. Jr., Nemec S.J., Campanhola C., 1989. Developmement of diagnostic monitoring techniques for larval pyrethroid resistance in *Helicoverpa spp.* (Lepidoptera: noctuidae) in cotton. *Journal of Econonomic Entomology*, 82, 1502-1507.

Weir B.S., Cockerham C.C., 1984. Estimating F-statistics for the analysis of population structure. *Evolution*, 38, 1358-1370.

Design and production, DIC, CIRAD - Fax: +33 4 67 61 55 13 - October 2005