

What insect resistance against fungal biopesticides can teach us about G x E in host-pathogen interactions

Tinsley, Matt C.¹; Mangan, Rosie¹; Polanczyk, Ricardo A.²; Bussière, Luc F.³

¹Biological and Environmental Sciences, Stirling University, Stirling, UK.

²Universidade Estadual Paulista (UNESP). Campus de Jaboticabal. Faculdade de Ciências Agrárias e Veterinárias (FCAV), Brasil.

³University of Gothenburg, Department of Biological & Environmental Sciences, Gothenburg, Sweden.

Corresponding author: matthew.tinsley@stir.ac.uk

Pathogens frequently place strong selection on host populations to evolve resistance. Nevertheless, natural host populations frequently contain considerable genetic variation for pathogen defence traits. This raises fundamental questions about what factors maintain this genetic variation, and in some applied settings demands understanding of how this evolutionary potential can be managed.

Insect pests represent an ever-present threat to agricultural production. Farmers are increasingly adopting biological pesticides formulated from the pathogens of insects to enable a move away from ecologically damaging chemical insecticides. However, as biopesticide use increases, so does selection pressure on target insects to evolve resistance. We investigated the potential for the major lepidopteran agricultural pest *Helicoverpa armigera* to evolve resistance against fungal pathogens used as biocontrol agents. We then tested how this evolutionary potential could be managed in agricultural landscapes by investigating genotype by environment interactions for pathogen susceptibility. We assessed how simultaneous manipulation of fungal pathogen strain and the crop plant on which larvae feed decreases selection consistency to prevent resistance evolution.

First, we identified multiple fungal isolates that kill *H. armigera* and studied the impact of field conditions on viability and virulence of spores. Then we quantified host genetic variation for fungal isolate susceptibility using 2198 *H. armigera* larvae from 32 females mated to 18 males. Larvae were reared on 1 of 3 plants (soybean, maize, or tomato) and inoculated with 1 of 3 fungal isolate treatments (*Metarhizium*, *Beauveria* or a control). We demonstrate that *H. armigera* populations harbour extensive genetic variation for fungal pathogen resistance, which if not appropriately managed could facilitate biopesticide resistance evolution. However, we show that selection for resistance is inconsistent between different fungal isolates, an effect enhanced by applying spores to larvae feeding on different crop species. Perhaps surprisingly, the efficacy of resistance genotypes in preventing insect death was more strongly affected by the diet of the larvae than it was by the pathogen strain.

We argue this knowledge could be used in agriculture to develop practical solutions for long term proactive biopesticide resistance management.