



Population genetics for characterisation of non-susceptible *Cydia pomonella* strains against *Cydia pomonella* granulovirus (CpGV)

MAX-PLANCK-GESELLSCHAFT



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Cydia pomonella

The Codling moth *Cydia pomonella* (Linnaeus) (Lep., Tortricidae) is the most serious pest of apple and pear worldwide. Without any control damage by larvae can reach 95%. An adult female lays 30-60 eggs. Hatched larvae enter the fruits and tunnel into the core where they feed on developing seeds. Entrance and exit holes are filled with frass. In Europe, *C. pomonella* has 2 generations per year, however, under warm climates a third generation is possible.



Adult *Cydia pomonella* on apple



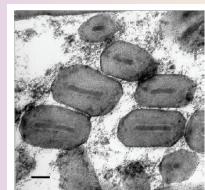
Larva is damaging the seeds inside an apple



Damaged apple

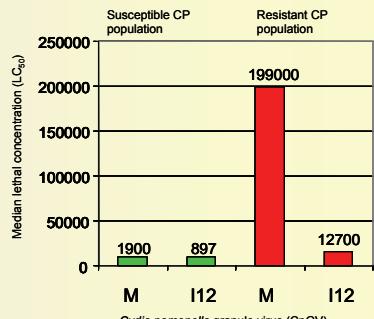
Granulovirus

The *Cydia pomonella* granulovirus (CpGV) belongs to the family *Baculoviridae*, genus *Granulovirus*. It's a double-stranded DNA virus, infecting the larval stage of its host *C. pomonella*. After oral ingestion by the larva the virus occlusion bodies disintegrate in the alkaline environment of the midgut and initiate infection of the midgut epithelium cells. From there the infection spreads to the tracheal system, the fat body and other tissues. The larvae dies 5-7 days after infection. CpGV is a widely used bio-insecticide in Codling moth control programs.



CpGV-occlusion bodies

Foto: Dr. A. Hüger, BBA Darmstadt



Mortality of susceptible and resistant *C. pomonella* populations after infection with CpGV-M and CpGVI12 in a 7-days-bioassay (J. JEHLE, unpublished).

The problem

Since 2003, an increasing number of Codling moth populations have been observed in Germany and France showing an up to thousand fold decreased susceptibility to CpGV, making biocontrol by CpGV almost impossible. A spread of this phenomenon is a severe threat to efficient control of the Codling moth, particularly in organic apple production. Even though, insect resistance to pesticides is a well-studied phenomenon, this is the first time resistance to an entomopathogenic virus has been reported.

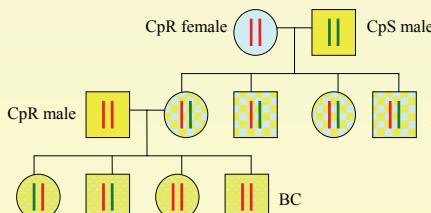
Planned investigations on genetic mechanisms of resistance

In order to evaluate further management of putative resistant *C. pomonella* populations, information about the genetics and mechanism of resistance are essential. Therefore, experiments to gain information about the inheritance pattern of resistance as well as bioassays with larvae of a susceptible and a resistant strain, will be carried out.

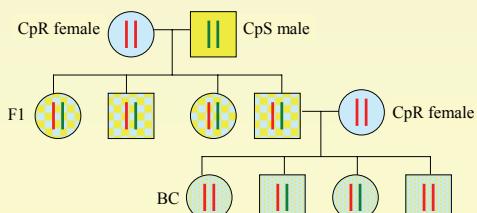
An unambiguous **diagnostic marker** will be developed to separate sensitive strains from non-sensitive strains. **Microsatellite** markers and **SNPs** (single nucleotide polymorphism) shall serve as diagnostic markers to distinguish sensitive and non-susceptible strains.

Mapping of traits involved in resistance will be performed. Involved loci will be identified with the help of **AFLPs** (amplified fragment length polymorphism). Loci coupled to susceptibility can help to elucidate resistance mechanisms.

A **cDNA-AFLP-analysis** (copyDNA-amplified fragment length polymorphism) will be performed to display differences in expression rate of particular genes. If there are differences between sensitive and non-sensitive strains, the genes will be isolated and sequenced. Putative sequence homologies give the direction of the functional sense of the mentioned gene and further conclusion of the mechanisms of the susceptibility of CpGV.



Crossing scheme from the female informative crossing. A resistant Cp female crosses with a susceptible Cp male. The hybrid female progeny are backcrossed with a resistant male. All the resulting F2-offsprings will be analysed.



Crossing scheme from the male informative crossing. A resistant Cp male crosses with a susceptible Cp female. The hybrid male progeny are backcrossed with a resistant female. All the resulting F2-offsprings will be analysed.

Acknowledgements

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