Gene expression in midgut cells of type II resistant *Cydia pomonella* larvae exposed to resistance breaking/non-breaking Cydia pomonella granulovirus isolates

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The codling moth (CM, *Cydia pomonella* L.) is a major pest affecting worldwide pome fruit production. Besides chemical agents, biological agents like Cydia pomonella granulovirus (CpGV) are being used to effectively control CM and prevent production loss. Fruits can be sprayed with viral occlusion bodies (OBs), causing infections once eaten.

A type I termed resistance against the widely used Mexican isolate CpGV-M has been observed since 2005. Target of this resistance is a repetitive 24 bp insertion in the viral gene *pe38*. Therefore, new resistance breaking CpGV isolates were needed. Resistance breaking isolates include the English isolate CpGV-E2 and the Canadian isolate CpGV-S, both of which are being used to circumvent type I resistance.

A novel type of resistance was documented for a field derived laboratory strain of CM named CpR5M. This type II resistant CM strain is resistant to CpGV-M and CpGV-S but remains infectious for CpGV-E2. Interestingly, a recombinant CpGV-M (bacCpGVΔpe38$_M^{pe38S::GFP}$) with its *pe38* replaced by the *pe38* of CpGV-S breaks this type II resistance. The mechanism of this novel type of resistance is expected to be a midgut-related blockade, as CpR5M is not affected by oral ingestion of CpGV-S but shows high mortality when injected into the hemolymph.

To study the unknown mechanisms involved in type II resistance on transcription and replication levels, a series of infection experiments were conducted on CpR5M larvae with the baculovirus isolates CpGV-S, -M, -E2 (resistance breaking, positive control), as well as bacCpGVΔpe38$_M^{pe38S::GFP}$. Three days post infection (dpi) midguts of the infected larvae were isolated in order to perform RNA extractions from individual tissue samples. Afterwards, the quality, quantity and integrity of the extracted RNA are going to be determined via RNA Integrity Number (RIN).

Some of the RNA will be reverse transcribed and submitted to qPCRs to quantify the gene expression levels of selected early, late and very late expressed viral genes. The high quality RNA samples are intended for RNAseq with the goal of performing an extensive analysis of host cell transcriptomes to gain a better understanding of the type II resistance.