Resistance to *Cydia pomonella* granulovirus: Novel findings on its distribution and diversity

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Abstract

The codling moth (CM) Cydia pomonella *L. is a nearly worldwide pest on pome fruits. Without effective control the larvae cause tremendous yield losses and serious economic damage in apple, pear and walnut orchards. With the isolation of the* C. pomonella *granulovirus (CpGV), originally found in Mexico in 1963, a very specific and highly efficient pathogen for codling moth control was discovered (Tanada, 1964). Since its first registration as a biopesticide in the late 1980s in Switzerland, several CpGV products have been registered worldwide; most of them derived from the original Mexican CpGV-M isolate (Huber, 1998). CpGV products have been successfully used in organic and integrated pome fruit production for more than 15 years. In 2004, local codling moth populations with significant reduced susceptibility towards CpGV-M were first observed in orchards in south-west Germany (Fritsch et al., 2005) and latery in France (Sauphanor et al., 2006). Since then, further cases of resistance were reported from commercial apple orchards in Germany, France, Italy, Switzerland, the Netherlands, Austria (Asser-Kaiser et al., 2007, Schmitt et al., 2013) and an experimental orchard in the Czech Rebublic (Zichová et al., 2013).*

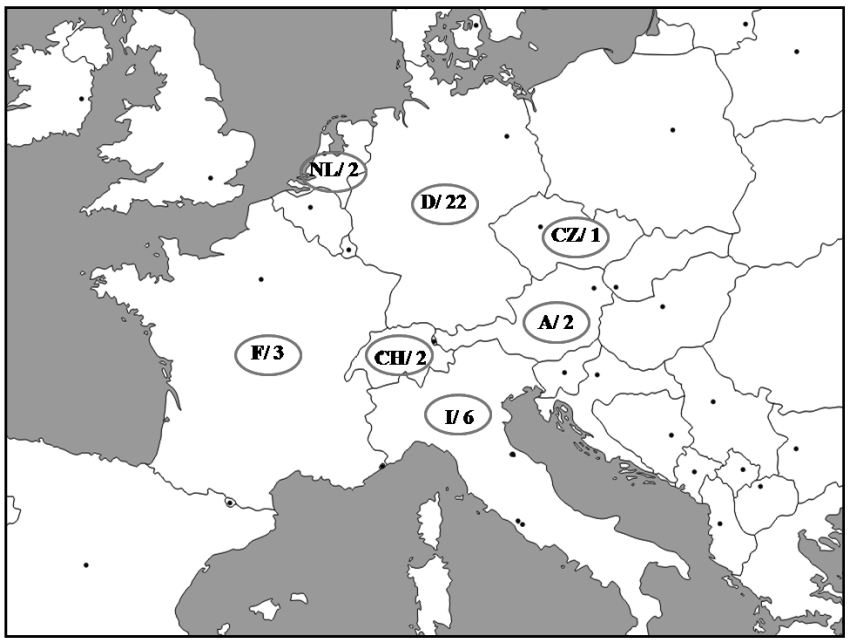

Figure 1: Number of resistant CM populations currently observed in different European countries until 2013.

In the years 2003 to 2008, 47 colonies of CM were collected as diapausing larvae in six European countries and their F1 generations were tested for resistance in laboratory bioassays by means of LC_{50} estimations and/or using a single diagnostic concentration of

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CpGV-M (Schmitt *et al*., 2013). For 33 CM colonies, a reduced susceptibility to CpGV-M was confirmed, independent of the country origin. Some field populations of CM varied significantly with respect to the resistance levels and even exceeded resistance levels in terms of LC_{50} of 10,000-fold in comparison to susceptible codling moth populations (Asser-Kaiser *et al*., 2007). Resistance of CM to CpGV-M is geographically widely spread but locally concentrated in single orchards exposed to repeated CpGV applications.

In summary, a total of 38 CM populations with resistance to CpGV-M were observed in seven European countries (Figure 1).

Single pair crossing experiments and genetic analysis of several CM populations revealed that the resistance to CpGV-M was sex-linked through the inheritance of a single dominant resistance allele located on the Z chromosome, which enables the rapid selection of resistance in these CM populations (Asser-Kaiser *et al*. 2007, 2010).

Recently, improved CpGV products based on resistance overcoming CpGV isolates were selected and eventually registered in different European countries. Nowadays, they are successfully applied in the vast majority of orchards with resistance to CpGV-M (Zingg 2008). Nevertheless, two resistant CM colonies were observed from different locations in Germany, where the application of a new resistance overcoming CpGV product still failed to control CM.

Crossing experiments between individuals of these colonies and a susceptible CM laboratory strain indicated that the inheritance of CpGV resistance of these populations did not follow the previously described pattern of Z-linked dominance. In order to elucidate this mode of inheritance to different methods: (i) repeated single pair crossings followed by family selection and (ii) successive mass crossing experiments under virus pressure were carried out to establish genetically homogenous CM strains. Subsequent reciprocal backcrossing experiments with the resulting homogenous resistant strains and a susceptible laboratory CM strain followed by bioassays fitted to a dominant autosomal inheritance model.

Further naturally occurring CpGV isolates are able to successfully overcome this second type of resistance. This was tested in several years in these orchards. Hence the available biodiversity of CpGV isolates appears to be sufficient to control all known resistant CM populations.

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