

THE FRAMEWORK PROGRAMME FOR RESEARCH AND INNOVATION

HORIZON 2020

PROJECT DELIVERABLE REPORT

Deliverable D2.4: Use of highly resolving molecular tools to assess the seasonal population dynamics of *Cc*



**Fruit Flies In-silico
Prevention & Management**

FF • IPM

Project Title:

In-silico boosted, pest prevention and off-season focused IPM against new and emerging fruit flies ('OFF-Season' FF-IPM)

SFS-2018-2

1 Summary

The Mediterranean fruit fly (*Ceratitis capitata*) is a pest species of major concern in the fruit trade and has exhibited a large range expansion from Africa into Europe and continents worldwide. Because of the warming climate, it appears to be spreading northwards in Europe and has been reported well north of the Mediterranean region.

Deliverable 2.4 provide novel data that contribute to better understanding of the annual and seasonal genetic variation of *C. capitata* in different invasion/establishment scenarios within Europe. Additionally, we want to investigate whether *C. capitata* specimens occurring at the margin of the current distribution range or in isolated pockets are derived from established or transient populations.

We bring forward evidence of annual variation in genetic structure in natural populations of *C. capitata* in multiple locations in core and marginal populations. For some cases, there may be historically documented events being the cause of the observed patterns like the SIT application in Opuzen (Croatia) in 2010-2011 resulting in a suppression of the local population followed by shifts in the dominant genotype. In other cases (Molise, Italy), the cause of this annual variation is not obvious. Changes in population genetic composition are not accompanied by decreased genetic diversity which excludes a large-scale bottleneck as a cause. However, small bottlenecks induced by insecticide use or stochasticity in the environment accompanied by an influx of immigrants could explain temporal variation in genetic structure in some cases.

In neither of the studied natural core and marginal populations did we find evidence for variation in genetic composition between flies trapped in the early season versus the late season. Most likely, overlap between generations of *C. capitata* within one activity period is hampering genetic differentiation between early and late season flies.

In the one case study of isolated populations (Vienna, Austria) we show that isolated, small allotments with mixed fruits and vegetables can harbor a surprisingly diverse population with significant and independent year-to-year variation. Here, unfavorable conditions, causing large, annual fluctuations in medfly abundance together with occasional import of new medfly genotypes are likely driving the observed genetic variation over successive years. Moreover, in the two locations samples we observe clear differences in the observed patterns demonstrating a clear isolation and very limited gene flow between the sites.