

Objectives and Rationale

The false codling moth (FCM), *Thaumatotibia leucotreta* (Meyrick), is a polyphagous pest attacking many crops of economic importance and is listed as a quarantine pest for most of our export markets. Here we aim to investigate the gene flow of FCM in orchards and non-orchards across South Africa to identify potential movement pathways and possible host races. In addition, the possibility of refugia will be explored in the Western Cape Province and kinship analyses will be used to track moths and provide estimates of dispersal.

Methods

Fruit suspected to be infested with FCM larvae were collected, cut open and all larvae collected. All samples collected were stored in alcohol for subsequent identification and genetic analyses.

Key Results

FCM have been collected from the Western, Eastern and Limpopo provinces (N=21) and from multiple hosts (citrus, peaches and pomegranates). FCM identification was confirmed by an expert. Collections of FCM from orchards and home gardens were however delayed by several months due to covid-19 lockdown. During lockdown DNA extraction protocols for double-digest restriction-site associated DNA sequencing was discussed with manufacturers of extraction kits to optimise yield and quality of DNA used as starting material for SNPs.

Conclusion and Discussion

No conclusions can be made at this stage, and is typical of this type of molecular work. The library preparation can only start once sufficient samples have been collected. We have requested an extension on this project to ensure good coverage to address our core project objectives and in light of covid-19 lockdown restrictions hampering sampling. The PhD student will continue sourcing FCM samples including samples from at least four acorn sites (alternative host plants) in the Western Cape.