Objectives and Rationale

The development of novel control methods for false codling moth (FCM), Thaumatotibia leucotreta (Meyrick) is an urgent priority for several fruit kinds to maintain current and emerging market access. Here we aim to develop a new genomic and transcriptomic toolkit for FCM in order to support novel population control methods and better understand the rapid evolution of, and constraints on, pesticide resistance and environmental stress adaptation and potential interactions between these.

Methods

For the dose response curve, FCM larvae were exposed to five different concentrations (4, 8, 12, 16, 50 mg/ 100mL) of spinetoram and placed at two different temperatures (22 and 28˚C). The percentage mortality was monitored in three replicated experiments with 60 individuals at each concentration. Based on the novel dose response curve, FCM larvae were exposed to 4mg/ 100mL and acclimated to two temperatures (22 and 28˚C) before assessing their life history traits, metabolic rate and survival. Adults were flash frozen and stored at -80˚C for downstream gene expression. In addition, INQABA Biotechnological Industries were identified for whole genome sequencing.

Key Results

Survival was significantly different between the different acclimation temperatures, but there was no difference in metabolic rate between the control and pesticide treatments ($F=1.63$, $p=0.21$) or between the two acclimation temperatures ($F=0.26$, $p=0.61$). FCM were sent to INQABA Biotechnological Industries for whole genome sequencing on the Illumina miSeq platform (long reads) as well as the PacBio Sequel II platform.

Conclusion and Discussion

Temperature has a clear effect on the efficacy of the active insecticide ingredient and future work should investigate this aspect in light of insecticide resistance development and variation in environmental conditions among farming regions.