

**11-Population genomics to detect local adaptation: application to Bti resistance monitoring in mosquitoes at a regional scale**

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Identification of genes involved in local adaptation is particularly challenging in species functioning as a network of inter-connected populations undergoing frequent extinction-recolonisation, because populations are submitted to contrasted evolutionary pressures. Using AFLP markers, population genetic structure of the mosquito *Aedes rusticus* was analyzed in five geographical areas of the French Rhône-Alpes region, including sites treated with the bio-insecticide *Bacillus thuringiensis* subsp. *israelensis* (Bti) for more than 15 years. Most of the genetic variability was found within populations, with no significant variation among geographical areas, although variation among populations within areas was significant. Pairwise  $F_{ST}$  values were significant and no isolation-by-distance was observed, suggesting a metapopulation structure in this species at the regional scale. Bti treatment had no effect on genetic structure, and within-population diversity levels were not significantly higher in non-treated compared with treated sites, suggesting that these are rapidly re-colonized by a diversified population of migrants after Bti treatment. However, signatures of positive selection associated with Bti treatment were detected for five loci, even though standard toxicological bioassays performed on field-collected larvae showed no significant difference in mortality between Bti-treated and non-treated sites. The absence of resistant phenotypes may result from the polygenic basis of resistance mechanisms to Bti, together with a high resistance cost measured in a laboratory selected mosquito strain. We also showed that selected mosquitoes are only moderately resistant to the full commercial Bti mixture, but show high levels of resistance to separate Bti toxins. This suggests that monitoring resistance in field populations should require evaluating mosquito resistance to individual Bti toxins, rather than to full commercial Bti mixture. We propose new methods for monitoring Bti resistance evolution in mosquito populations, in order to detect resistance at the very early steps of its appearance, when bioassays using Bti fail to detect resistance.

**12-Can Deuterium stable isotopes be used to infer geographical origins of an auxiliary hoverfly and a pest moth?**Lucie Raymond<sup>1,2</sup>, Philippe Menozzi<sup>3</sup>, Andrew J. Hamilton<sup>4</sup>, Jean-Pierre Sarthou<sup>1,2</sup>, Noelline Tsafack<sup>1,2,3</sup>, Aude Vialatte<sup>1,2</sup>, Sergine Ponsard<sup>5,6</sup>, and Annie Ouin<sup>1,2</sup>

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Deuterium  $\delta D$  isotopic analysis is increasingly being used to trace wildlife movement, and undoubtedly has much to offer in this respect but questions still remain as to the feasibility and practicality of the method in ecology. Here we report our attempt to determine the geographic origin of an auxiliary hoverfly, *Episyrphus balteatus*, in South-western France and a pest moth, *Helicoverpa armigera* in Western Africa. We used quantile regression to calculate the minimum separation distance, based on the International Atomic Energy Agency / World Meteorological Organization (IAEA / WMO) data, at which two insects could be said to originate from different latitudes with a given degree of confidence. Our results revealed greater variability of hoverfly adults  $\delta D$  in autumn than in spring. From this we infer an autumnal migration of the auxiliary hoverfly species. Despite the complications encountered in Europe, the minimum separation distance model proved a useful first step to get a first range of possible origins of *E. balteatus* and its application to other arthropod species in Europe warrants investigation. The lack of IAEA / WMO data in western Africa prevents the calculation of a minimum separation distance for the pest moth. The interpretation of water simulated  $\delta D$  in the study area in Western Africa and preliminary results on wild moth advocate for a restricted use of stable isotope to infer the geographical origin of the pest moth.