Estimation of demographic parameters of an insect pest in apple-orchards landscape, from genetic data

Emily Walker, Etienne E. Klein, Lionel Roques, Pierre Franck

To cite this version:

Emily Walker, Etienne E. Klein, Lionel Roques, Pierre Franck. Estimation of demographic parameters of an insect pest in apple-orchards landscape, from genetic data. 4. International Statistical Ecology Conference (ISEC 2014), Jul 2014, Montpellier, France. 1 p. hal-02795599

HAL Id: hal-02795599
https://hal.inrae.fr/hal-02795599

Submitted on 5 Jun 2020

4th International Statistical Ecology Conference
Montpellier, France
1-4 July 2014

Book of abstracts

Estimation of demographic parameters of an insect pest in apple-orchards landscape, from genetic data

Emily Walker (1), Etienne Klein (1), Lionel Roques (1), Pierre Franck (2)

(1) INRA, Biostatistiques et Processus Spatiaux - BioSP, Domaine St Paul, Site Agroparc, 84914 Avignon

Mily.walker@gmail.com / Emily.walker@paca.inra.rf

Etienne.klein@paca.inra.fr

Lionel.roques@avignon.inra.fr

(2) INRA, Plantes et Systèmes de culture Horticoles - PSH, Domaine St Paul, Site Agroparc, 84914 Avignon

Pierre.franck@paca.inra.fr

In the context of agrosystem management in order to reduce the use of pesticides, we aim to understand population dynamics at the landscape scale of the codling moth (*Cydia pomonella*), an insect pest in apple orchards.
To analyse statistically the genetic markers data (22 microsatellites) obtained from a thousand georeferenced individuals (sampled in 51 different orchards), we developed a spatially explicit metapopulation model. The objective is to estimate population sizes and migration rates as functions of landscape factors (spatial heterogeneities). First the structure of homogeneous genetic groups are analysed from genetic marker data, according to numerical Bayesian approach, with a non-supervised clustering method (STRUCTURE). Second the estimated sub-populations allelic frequencies are used as inputs of a mechanistic-statistical model to estimate dispersion in the heterogeneous landscape. The model associates a reaction-diffusion model for the mechanistic description of insect movements with a population genetic model for the statistical modelling of marker data.

Keywords

Metapopulation dynamics, Spatial ecology, Molecular ecology, Landscape genetics