



A modelling framework for pest population dynamics and management: An application to the grape berry moth



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ABSTRACT

Physiologically based demographic models are important tools for the development of sustainable pest management as they can realistically describe the spatio-temporal dynamics of population abundance as function of environmental forcing variables, e.g. temperature and resource availability. The physiological based model presented here is based on a stochastic demographic model for a stage-structured population that has application to a wide range of species across different taxa. The species life-history strategies are described in terms of a set of biodemographic rate functions dependent from the biological characteristics of the species and their environmental driver variables. Model application required parameter estimation of the biodemographic rate functions at two levels: assessing physiological responses at the per capita level and/or using population time series data for rate functions estimation. To explore the usefulness of the modelling framework in pest management, we consider the case study of the grape berry moth *Lobesia botrana*, a major pest in European vineyard. Most of the model parameters were estimated from data in the literature. An unpublished dataset of population dynamics collected in a vineyard in the Veneto region (Italy) over three years was used to estimate the mortality function. Model validation was performed with a set of independent data.

Model simulations provided realistic trajectories of population dynamics obtained with a limited dataset of initial conditions. The suitability of the model as a tool for decision support for grape berry moth management is discussed.

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1. Introduction

Ecological disruption due to pest control, agronomic practices and climate change affect all aspects of system sustainability, including farmer health and food safety, and ecologically based pest management methods must be developed to manage these systems sustainably. Considerable progress has accrued in the area of pesticide efficacy, application techniques and related policy (e.g., Directive 2009/128/EC on the sustainable use of pesticides in Europe). However, the crucial unresolved issue remains of how to define sustainable pest management and how to implement it in time and space. Key to correcting this lacuna at the local,

regional and national level are decision support tools based on pest population dynamics and trophic interaction models describing the dynamics in the agro-ecosystems, the procedures for scenario assessment and knowledge-based decision making. Considerable progress has been made in this area, but the discussion on the approaches and the technological solutions to be used for the development of decision support tools requires further clarity.

Since the 1970s, multidisciplinary research involving biologists, ecologists, entomologists and plant pathologists, mathematicians and meteorologists has developed useful tools to meet some of these multiple objectives aided in the United States by the NSF/EPA/USDA funded IPM projects (Norton and Holling, 1977, pp. 253–316). Getz and Gutierrez (1982) reviewed the origins of systems analysis in crop protection and integrated pest management (CP/IPM) that integrated developments in physiology (De Wit and Goudriaan, 1974), population dynamics (e.g., Gilbert and Gutierrez, 1973; Gutierrez et al., 1977; Wang et al., 1977) and economics (Regev et al., 1976), and that had later application to

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a wide range of crop systems (e.g., alfalfa, cotton, cassava, olive, grape). Innovative elements of this work led to the development of an integrated approach to support sustainable integrated pest management (IPM) programs, but despite wide application, the methods remain largely underutilised by the vast majority of agricultural researchers and extension personnel, and in most cases, decisions continue to be taken without the support of quantitative tools.

Mechanistic approaches based on weather-driven ecological models were used to evaluate the spatio-temporal dynamics of pest populations as forced by the crucial driving role on pest population dynamics played by meteo-climatic features as well as other physical-biological characteristics of the agricultural landscape (Gutierrez, 1996). Mechanistic models for population dynamics based on physiological responses at individual level to environmental driving variables have been proposed since the 1970s (Gutierrez, 1996; Gutierrez et al., 1975; McDonald et al., 1989; Metz and Diekmann, 1986; Wang et al., 1977; De Wit and Goudriaan, 1974). These models have been defined as physiologically based demographic models (PBDMs) (Gutierrez et al., 2010) and offer several advantages for developing sustainable crop production systems (Gilioli and Mariani, 2011). For example:

- (i) they account for the non-linear relationships between environmental forcing variables (e.g., temperature) and the biological processes enabling the population dynamics to be described realistically;
- (ii) they enable the evaluation of the effects of biological and ecological variability on population dynamics, especially in complex systems over geographic space and time required for area-wide pest management (Gutierrez et al., 2012);
- (iii) they capture within the same modelling framework processes at different trophic levels and the trophic interactions and their consequences in simple trophic web (Gutierrez and Baumgaertner, 1984);
- (iv) they allow fine-scale predictions of the phenology and population dynamics at different spatial scales using ecologically meaningful state variables directly related to the pest impact on plants density and biomass fundamental for decision making in pest control and management of invasive species (Gutierrez and Ponti, 2013; Pasquali et al., 2015) and
- (v) they allow the exploration of complex scenarios in which no simple (i.e., linear) conclusions can be drawn, for example evaluating the effects of management options based on different techniques and tactic-strategy of implementation at different scales, or the large scale impact of drivers of ecosystem change (Gilioli and Mariani, 2011; Gilioli et al., 2014; Gutierrez and Ponti, 2013).

These characteristics make PBDMs particularly useful for the development of decision support systems in IPM. In particular, PBDMs are suitable for management problems characterised by heterogeneity and complexity related to the interaction among processes affecting the interactions of systems components (e.g. plant, pest, as affected by the biotic and abiotic environment), at different spatial scales (micro, meso and macro-scales), requiring different information for decision making at tactical, strategic and policy levels.

The modelling framework reported here is a particularisation, for a suitable choice of the biodemographic functions, of the most general mathematical framework presented in Buffoni and Pasquali (2007), which allows obtaining the distribution of individuals in an age-stage structured population in time and physiological age. Buffoni and Pasquali (2007) used Eulerian formalism based on the Fokker-Planck (or forward Kolmogorov) equation (Gardiner, 1985, p. 117) to formulate a nonlinear stochastic model to describe the

population dynamics of a species characterised by either a continuous size structure or a discontinuous stage structure that includes the dispersion effects of the individuals during the development. Numerical approximation and analysis of existence and stability of equilibrium states of the stochastic Eulerian model were discussed by Buffoni and Pasquali (2007). Properties and advantages of the forward Kolmogorov model compared with other age structured models are illustrated in Buffoni et al. (1990a,b, 1996) and Di Cola et al. (1998, 1999). This modelling framework can be used to model a population characterised by a discontinuous stage structure with continuous time- and age-structure within a stage with the biodemographic functions dependent on time through temperature. Specifically, the rate functions for fecundity and mortality are driven by biotic variables. The mathematical and biological characteristics of this modelling framework fall under the ambit of the PBDM.

Here we develop a model to simulate the population dynamics of the grape berry moth (*L. botrana* Den. & Schiff.) (Lepidoptera Tortricidae), the most important pest of grape (*Vitis vinifera* L.) in the Mediterranean basin (CABI, 2014). The pest attacks more than 27 families of berry producing plants, but despite its wide host range, it causes economic damage only to grapevine (CABI, 2014). The original geographical distribution follows a clear Palearctic pattern and currently includes Southern and Middle Europe, Northern and Western Africa, Middle East, West Asia (CABI, 2014; Maher and Thiéry, 2006; Thiéry and Moreau, 2005; Venette et al., 2003), South America and localised in Northern California (Varela et al., 2010) before its eradication. *L. botrana* is regarded as a potentially serious pest on a worldwide scale for all the vine-growing areas that are presently unaffected (CABI, 2014).

Demographic modelling approaches for *L. botrana* aiming at tactical decision making have lacked a fully mechanistic description of the demographic process (Schmidt et al., 2001, 2003). Most prior models for *L. botrana* used to support IPM practices have been phenological models (Baumgärtner and Baronio, 1988; Hardman, 2012) that predict the time of appearance of developmental stages and are used to facilitate timing of sampling and control operations. Even if temperature dependent development rate and stage-age structure are included in such phenological models, they do not produce realistic projections of *L. botrana* population dynamics, that are indispensable for pest control decision making based threshold levels of stage-specific abundance (Hardman, 2012). Recently, analytical models for *L. botrana* population dynamics have been developed; they may provide strategic evaluation of control measures even if are ill-suited for tactical decision making (Ainseba et al., 2011; Picart and Milner, 2014). Only Gutierrez et al. (2012) developed a fully mechanistic, physiologically based description of the dynamics of grapevine and of *L. botrana* population dynamics. This model used a distributed maturation time model (Vansickle, 1977) and was designed to simulate the dynamics and potential geographic distribution and relative abundance of the moth in California, the continental USA and Mexico. It also served as the basis for a strategic analysis of the timing of mating disruption pheromone for pest control.

In contrast to Gutierrez et al. (2012), the goal of our model development, parameterisation and model output is for use in field decision support for IPM practice implementation. Our modelling framework focuses on tactical application of field-based PBDM applications that require field calibration and validation before they are used. Estimation of the biodemographic functions using a bottom-up approach are based on literature data on the life-history biology of *L. botrana*, summarised in Gutierrez et al. (2012). The simplifying assumption of this and prior models is the parameters of the biodemographic functions are time-invariant. In this paper, we estimate the mortality rate using unpublished field data on the dynamics of *L. botrana* life stages, collected at Colognola ai Colli

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