

# A population model for the peach fruit moth, *Carposina sasakii* Matsumura (Lepidoptera: Carposinidae), in a Korean orchard system

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## ABSTRACT

A population model for the peach fruit moth, *Carposina sasakii* Matsumura, was constructed to understand the population dynamics of this pest species and to develop an effective management strategy for various orchard (apple, peach, apple + peach) systems. The model was structured by the five developmental stages of *C. sasakii*: egg, larva, pupa, larval-cocoon (overwintering larva), and adult. The model consisted of a series of component models: (1) a bimodal spring adult emergence model, (2) an adult oviposition model, (3) stage emergence models of eggs, larvae, and pupae, (4) a larval survival rate model in fruits, (5) a larval-cocoon formation model, and (6) an insecticide effect model. Simulations using the model described the typical patterns of *C. sasakii* adult abundance in various orchard systems well, and was specific to the composition of host plants: three adult abundance peaks (first peak, mid-season peak, and last peak) a year with decreased peaks after the first peak in monoculture orchards of late apple, two adult peaks a year with a much higher last peak in monoculture orchards of early peach, and three adult peaks a year with much higher later peaks in mixed orchards of late apple and early peach. The average deviation between model outputs and actual records for first and second adult peak dates was 2.8 and 3.9 d, respectively, in simulations without an insecticide effect. The deviation decreased when insecticide effects were incorporated into the model. We also performed a sensitivity analysis of our model, and suggest possible applications of the model.

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## 1. Introduction

The peach fruit moth, *Carposina sasakii* Matsumura (Lepidoptera: Carposinidae), is one of the major insect pests of fruit trees in Korea, attacking the fruits directly (Kim and Yiem, 1981; Lee et al., 1984; Choi et al., 2008). *C. sasakii* has one to two generations in Korea (Kim et al., 2000). The full-grown larvae (larval-cocoons) overwinter in the soil, escape from cocoons in the spring, and make pupal-cocoons. Adults emerge beginning in early June, and lay eggs on fruits such as apple and peach. Larvae bore into the fruits and feed on the fruit flesh. Mature larvae escape from fruits and enter into one of two developmental phases: they either become non-diapausing pupal-cocoons on the soil surface and emerge as adults later in the season, or they become diapausing larval-cocoons in the soil and overwinter.

The complex population dynamics of *C. sasakii* in orchards are characterized by several factors. First, they have a bimodal spring adult emergence pattern (Kim et al., 2000); overwintered larvae emerge as adults over several months with the first major peak in late June and a second smaller peak in late July. Second, temporal larval survivorship dynamics differ according to fruit cultivar and fruit age (Kim and Lee, 2002): no larvae survive in young fruits of late apple cultivars, while larvae can develop in early apple cultivars. In peaches, larvae can survive in young fruits of both early and late cultivars with much higher survivorship in the early cultivar. Finally, both univoltine and multivoltine groups exist. The univoltine group comprises first generation larval brood that feed on fruits and remain as fully grown diapausing larvae upon escape from the fruits. The multivoltine group comprises first generation larval brood that develop into adults and produce the summer larval brood. A short day length triggers diapause induction at the middle-aged larval stage (Toshima et al., 1961), and diapausing larvae appear from early August (Lee et al., 1984). Under natural conditions, 50% of the mature larvae that escape from fruits in mid-August enter diapause (Toshima et al., 1961; Lee et al., 1984). Thus, diapause induction timing also affects the population dynamics of *C. sasakii*.

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Because of the complexity discussed above, it is challenging to predict *C. sasakii* population dynamics empirically. Thus, a *C. sasakii* population dynamics model that integrates the major factors discussed above is critical to understand the population dynamics of this pest species and to design effective management strategies. Our goal was to construct a full population model for *C. sasakii* by incorporating sub-models including a bimodal spring emergence model (Kim et al., 2000), a stage emergence model (Kim et al., 2001), and an oviposition model (Kim and Lee, 2003). Additional sub-models including models for larval-cocoon formation, larval survival, and insecticide model were also developed and incorporated into the full model.

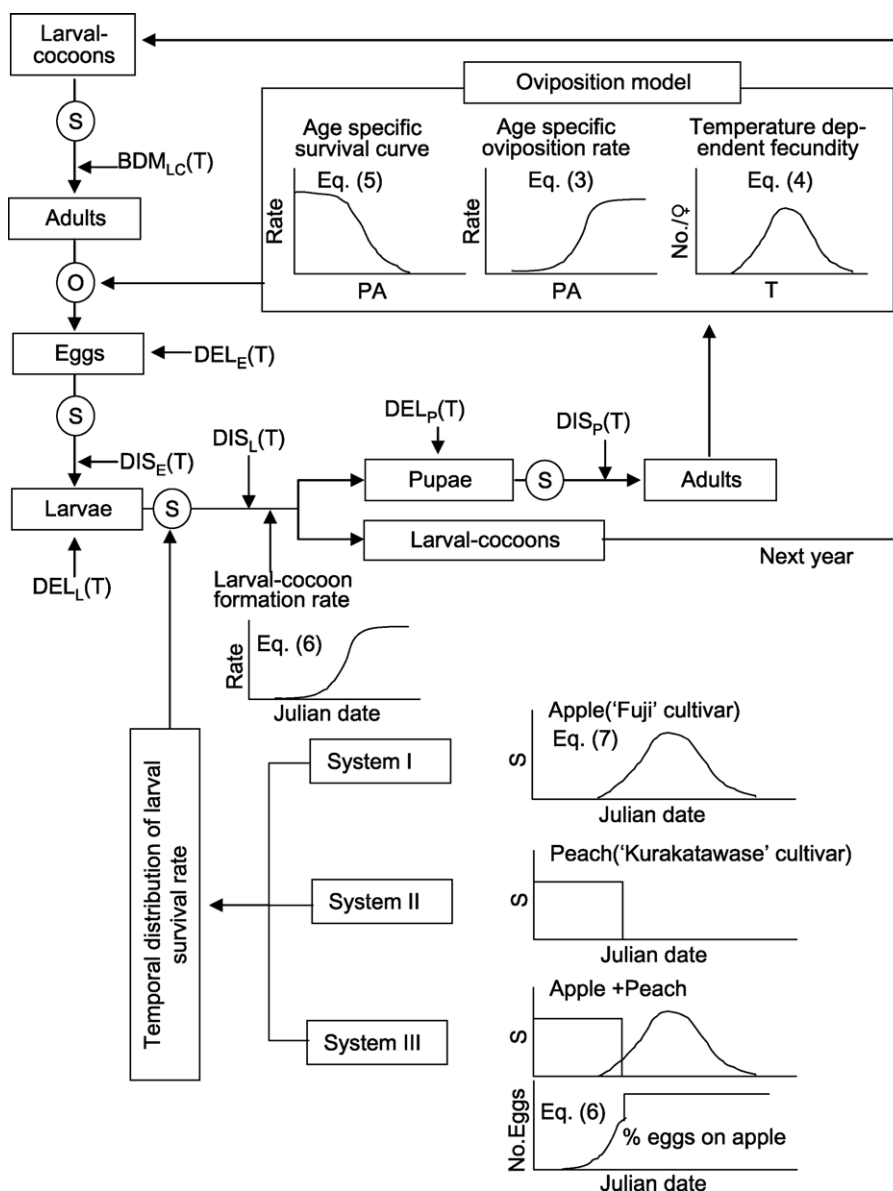
## 2. Model description

### 2.1. Model overview

The *C. sasakii* population model was constructed to include five developmental stages (Fig. 1): egg, larva, pupa, larval-cocoon

(overwintering larva), and adult. Each stage was divided into separate cohorts of individuals that entered the stage on a given day and were treated as different age groups in the stage (Curry and Feldman, 1987). However, the larval-cocoon stage, from which the model starts, consisted of a single cohort because it is the overwintering stage; we made the assumption that individuals in this stage are physiologically identical (Kim et al., 2000). The model consisted of a number of component models: a temperature-dependent development rate and development distribution models for each stage, an adult oviposition model (age-specific oviposition rate, age-specific survival rate, and temperature-dependent total fecundity), a larval survival rate model incorporating host plant effects, a larval-cocoon formation model, and an insecticide effect model.

At any given time, each cohort is characterized by two state variables (Shaffer and Gold, 1985):  $a_{ij}(t)$ , the physiological age of cohort  $j$  within stage  $i$  at time  $t$ ; and  $N_{ij}(t, a)$ , the number of individuals in the cohort which are of physiological age  $a$  at time  $t$ . The output of the model is  $N_i(t)$ , the total number in stage  $i$  at time  $t$ , which is obtained simply by summing over the cohorts.



**Fig. 1.** Schematic diagram of the population simulation model for *C. sasakii*. BDM: bimodal distribution model (Eq. (1)), DEL: development model (Eq. (2)), DIS: distribution model of development time (Eq. (3)), T: temperature, S: survival rate, O: oviposition model, and PA: physiological age. Also, LC, E, L, and P indicate larval-cocoons, eggs, larvae, and pupae, respectively. The corresponding functions were chosen since they provided a statistically good fit for the empirical data.

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