

Parallel Session
Ecology V

MODELLING AND CONTROL OF COFFEE BERRY BORER INFESTATION

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Keywords: Epidemiological model, Optimisation, *Hypothenemus hampei*, Integrated pest management, Tropical agriculture.

Coffee plays an important role in the economic growth of many developing countries. Coffee production throughout the world is affected by several pests and diseases. Among these pests, the coffee berry borer (CBB), *Hypothenemus hampei*, is considered as the most important pest economically. The CBB is a beetle that feeds and spends its development cycle in the coffee berries, causing direct crop losses and a lowering of the coffee quality. Mature females are responsible for the dispersal of the population: they emerge from the berries to colonise and lay their eggs in new berries, while males and juvenile stages remain inside the berries. Several control methods have been developed to fight these insects: pesticides, but also cultural practices, biological control and trapping. Our global aim is to design and assess the efficiency of control strategies, with a focus on alternatives to pesticides.

To tackle this issue, we developed a mathematical model that describes the infestation dynamics of coffee berries by CBB, based on the insect life-cycle and including the berry availability during a cropping season. We aim at maximising the yield at the end of cropping season, while minimising the CBB population and the control costs. We show the existence of an optimal solution and solve the problem numerically. Numerical simulations are provided to illustrate our results.

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AN AGRICULTURAL CONTROL OF *RADOPHOLUS SIMILIS* IN BANANA PLANTATIONS

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Keywords: Epidemiological model, Optimisation, Plant-parasitic nematode, Integrated pest management, Tropical agriculture.

Radopholus similis is the major parasitic nematode of banana and plantain plants worldwide. *R. Similis* feeds on the root tissues and causes damages going from simple root lesions, reducing the crop yield, to the fall of seedlings. Hence, *R. similis* is one of the most regulated plant pests. Its control mainly relies on toxic nematicides, but with limited efficiency. Our global aim is to design more efficient and sustainable control strategies, including alternative methods to nematicides.

Our approach is based on a hybrid model describing the plant-nematode interactions over several cropping seasons. During the inter-season, in the absence of host, the pest population undergoes a rapid decay. A longer inter-season duration reduces the pest population the following season, which is correlated with the seasonal crop yield. However, longer inter-season durations also decrease the number of cropping seasons during a fixed time horizon, and potentially the multi-seasonal yield.

An optimisation problem is therefore formulated to determine the inter-season duration that maximises the multi-seasonal yield. Two cases are considered: a fixed or a variable inter-season duration. The existence of an optimal solution is proven and its location is computed. Numerical simulations are provided to illustrate our results.

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SPATIAL DISPERSAL PATTERNS OF CITRUS DISEASE (HLB) AND ITS VECTOR

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Keywords: Huanglongbing (HLB), Epidemiology, Spatial Dispersion, Psyllids.

Plant and animal diseases have significant ecological and economic impacts. Specifically, the citrus disease Huanglongbing (HLB) is one of the most important yield damage for the citriculture worldwide [1, 2]. The natural transmission in the field is given by a vector insect, the Asian citrus psyllid (ACP), also known as *Diaphorina citri* Kuwayama. There are no curative methods for HLB and the best solution has been the elimination of symptomatic infected plants and the control of vector population. It is known that the primary means of attraction and reproduction of psyllids is through the shoots of plants, in which the deposition of eggs is made only in young plant tissues. Older plants and young can have different levels of flush, what results in different levels of attraction to the vector of this disease. Furthermore, there are other different factors which can attract these arthropods; yellow color: growers use yellow sticky traps for monitoring the activity of adults and; host plant volatiles: studies have showed the preference and repulse of psyllids for some odorants [3]. We propose a simulation model (Individual-Based Modeling [4]) to evaluate the spatial dispersal of psyllids on the citrus plantations due to the different factors of attraction. It's intended to discuss, corroborate and give further insights about the control of HLB.

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References

- [1] J. M. Bové (2006) *Huanglongbing: a destructive, newly-emerging, century-old disease of citrus*. Journal of Plant Pathology, 88, 7–37.
- [2] T. R. Gottwald, 2010. *Current epidemiological understanding of citrus huanglongbing*. Annual Review Phytopathology, 48, 119–139.
- [3] I. V. Coutinho-Abreu, L. Forster, T. Guda, A. Ray, 2014. *Odorants for surveillance and control of the asian citrus psyllid (Diaphorina citri)*. PLoS ONE, 9, 1–7

- [4] V. Grimm and S.F. Railsback, *Individual-based Modeling and Ecology*. Princeton University Press, Princeton and Oxford, 2005.

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VIRUSES THAT MODIFY PLANTS: MANIPULATION OF VECTOR DENSITY AND TRANSMISSION AT SEVERAL SCALES

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Keywords: Plant viruses, Non-persistent transmission, Aphids.

Disease from plant viruses is an important constraint on global food production. A majority of plant viruses are non-persistently transmitted (NPT) i.e. are carried between plants on the piercing mouth-parts (stylets) of aphids. It has frequently been observed that NPT viruses modulate plant phenotypes (VMPP) such as attractiveness to aphids. To fully understand virus epidemics and how they are promoted by VMPPs, we developed a framework that separates aphid probing vs feeding behaviour and distinguishes local (wingless) from longer-distance (winged) dispersal. Our results show that the changing balance in winged and wingless aphid densities is critical for virus epidemics because it leads to distinct spatial scales of transmission. A practical objective is to use such insights to disrupt the transmission processes of this diverse and abundant group of viruses.

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SUSTAINABLE MANAGEMENT OF ROOT-KNOT NEMATODES BY MODELLING AND OPTIMIZING RESISTANCE DEPLOYMENT

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Keywords: Epidemiology, Nematode, Resistance.

Root-knot nematodes (RKNs) of the genus *Meloidogyne* are soil-borne, little mobile, polyphagous pests which threaten important sheltered crops such as vegetables or small fruits. They attack plant roots to feed and reproduce and have a major impact on crop yield. Most eco-friendly plant protection strategies are based on the use of resistant crops. Resistance is usually associated with a hypersensitivity reaction (HR), a rapid and localized cell death in the infected plant in response to a pathogenic attack. In the family *Solanaceae*, there are two major resistance genes (R genes) with different modes of action: an early HR when the nematode enters the root system and a late HR when the nematode creates its feeding site. The emergence of virulent nematode variants, which are adapted to the resistance, challenges the durability of such methods. Because virulent root-knot nematodes exhibit a reduced fitness on susceptible crops, combining both resistant and susceptible plants can help increase the efficacy and sustainability of resistance-based nematode control. We carried out a preliminary study to investigate the best rotations of susceptible and resistant cultivars over cropping seasons in terms of yield and resistance durability. The resistance considered was associated with early HR. For this purpose, we developed a semi discrete model describing the plant root growth and nematode population dynamics within and between cropping season, including the plant nematode interactions. Our aim in this study is to implement and compare the action of both R genes. We will first compare the optimal deployment strategies of resistant crops for both R genes. Then we will determine the best rotations based on both resistant cultivars.

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