Disentangling the effects of pathogen sexual reproduction on the effectiveness and durability of resistance deployment strategies: *Plasmopara viticola* as a case study.

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1 Introduction

The deployment of resistant cultivars in agricultural landscapes is a low-input and cost-effective way to protect crops from plant pathogens. However, resistant cultivars have often been quickly overcome by pathogens following their deployment by farmers (McDonald & Linde, 2002). Indeed, when a single resistant cultivar is widely cultivated over a large geographic area, as commonly do in modern agriculture, the pathogen population may rapidly adapt to the resistance gene deployed. Ultimately, this may result in recurrent cycles of resistance deployment followed by rapid pathogen adaptation, often described as boom-and-bust cycles (McDonald & Linde, 2002). Several strategies have been proposed to promote a more durable management of resistant cultivars. These strategies rely on the management of host genetic diversity (McDonald, 2010, 2014; Zhan et al., 2015) with the aim to confront pathogens with eco-evolutionary challenges and thus avoid or delay their adaptation to plant resistance (evolutionary control), while maintaining effective disease protection (epidemiological control). Host genetic diversity can be introduced in time through crop rotations (*e.g.* recurring succession of different crops in the same field) (Curl, 1963). Host genetic diversity can also be introduced in space. Resistant cultivars can be combined within the same field in cultivar mixtures (Mundt et al., 2002; Wolfe, 1985) or cultivated in different fields in landscape mosaics (Burdon et al., 2014; Zhan et al., 2015). Finally, several resistance sources can be stacked in the same cultivar by plant breeders through pyramiding (Fuchs, 2017).

Given the diversity of deployment options, comparing and identifying an optimal deployment strategy in a given epidemiological context is not straightforward. In addition, the assessment of resistance deployment strategies depends strongly on the objectives of different stakeholders (*e.g.* growers, breeders), which are not always compatible. For example, any strategy designed to prevent or slow down the emergence of resistance-adapted pathogens in agro-ecosystems does not necessarily provide an efficient epidemic control. Finally, particularly for airborne plant pathogens that may disperse over several kilometres (Gilligan, 2008), deployment strategies are more likely to be effective if implemented across landscapes at large spatial scales, which makes logistically challenging the experimental tests (but see Djian-Caporalino et al., 2014; Koller et al., 2018; Lohaus et al., 2000). To overcome these difficulties, numerous mathematical models have been developed to assess the evolutionary and epidemiological outcomes associated to different resistance deployment strategies (reviewed by Rimbaud et al., 2021). These models can also be used to find optimal resistance deployment strategies for a given epidemiological context. However, so far, most of these models focused on pathogens that reproduce purely asexually. Within these pathosystems new pathogen variants, possibly more adapted to the deployed source of resistance, are generated through mutation or are already present (possibly at small frequency) at the beginning of the simulated period (see Rimbaud et al., 2021 and citation therein).

Besides purely asexual reproduction, some pathogens include in their life cycle at least one sexual cycle per growing season (mixed reproduction system) or even only sexual cycles (purely sexual reproduction system). Of the 43 plant pathogens analysed by McDonald & Linde (2002), only 17 (40%) present purely asexual reproduction, while the remaining 26 pathogens present different forms of reproduction (*e.g.* mixed or purely sexual).

The impact of pathogen reproduction system on the effectiveness of resistance deployment strategies remains only partially understood. Indeed, three mechanisms linked to sexual reproduction could affect the effectiveness of resistance deployment strategies. Firstly, **genetic recombination**, occurring during sexual reproduction, can efficiently create favourable gene combinations that would be accessible only through sequential mutation events in purely asexual reproduction. Recombination can then favour the emergence of multi-adapted pathogens (able to overcome all the deployed resistance genes) and thus the breakdown of resistance pyramids (Rimbaud et al., 2021; Uecker, 2017). However, whether recombination will effectively favour breakdown also depends on subtle interactions between, on one side, mutation and recombination rates, and, on the other side, pathogen population size (Althaus & Bonhoeffer, 2005). Secondly, sexual reproduction often results in the formation of specialized structures that may persist in a state of **dormancy** and potentially survive in the soil for many years (Clément et al., 2010; Shang et al., 2000). By distributing the germination dynamics of sexual spores in time, dormancy possibly impacts the efficacy of crop rotation as a means of pathogen control (Shang et al., 2000). Indeed, the success of rotation largely depends on its duration relative to the timing of pathogen emergence, which, for sexual spore, depends on dormancy duration. Thirdly, sexual and asexual spores may differ in **dispersal abilities**, which are likely to affect the effectiveness of resistance deployment strategies such as

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mixture and mosaic (Papaïx et al., 2018; Sapoukhina et al., 2010; Watkinson-Powell et al., 2020). Indeed, to successfully control a disease, the scale of the deployed strategy should matches the spatial scale of the epidemic, which is closely related to spore dispersal ability (Gilligan et al., 2007). Crucially, ignoring sexual reproduction for pathosystems presenting mixed or purely sexual reproduction systems can result in severe bias in the analysis and comparison of resistance deployment strategies (Arenas et al., 2018).

So far, only a few models (Crété et al., 2020; Lô-Pelzer et al., 2010; Sapoukhina et al., 2009; Xu, 2012) simulated a pathogen having mixed reproduction system. Crété and colleagues (2020) investigated how different rotation strategies will affect the evolution of fungal pathogen virulence and the breakdown of crop resistance with a model explicitly considering pathogen sexual reproduction in combination to asexual reproduction. Xu (2012) developed a model to study the dynamics of fungal virulence in mixtures of perennial crops, focusing on the effects of cost of virulence and pathogen mixed reproduction system on the emergence and persistence of multi-adapted pathogen in the population. Sapoukhina and colleagues (2009) formulated a model for ascertaining the effect of spatial composition of the host population (organised in mixtures of simple or pyramided resistant and susceptible genotypes) on the spread of a pathogen that alternates between multiple cycles of asexual reproduction during the epidemic phase and a single cycle of sexual reproduction at the end of host growing season. On the one hand, the over mentioned models focused on just one or two resistance deployment strategies, which limits a global assessment of the wide range of spatio-temporal deployment options. On the other hand, they mainly focus on sexual recombination, ignoring the possibility for the sexual spores to *i*) stay in the soil for multiple seasons before germination and *ii*) have a different dispersal ability from asexual spores.

2 Model development

In the present work, we compare the four main categories of deployment strategies (rotation, pyramiding, mixture and mosaic) for situations where two qualitative resistance genes are deployed. Qualitative resistance refers to major resistance gene, which codes for specific host proteins able to recognize a specific pathogen molecular pattern or effector (Flor, 1971). Host infection is thus a binary outcome determined by the interaction between host genotype (with or without resistance gene) and pathogen genotype (non-adapted or adapted). Using a generic spatially explicit stochastic model, we aim to shed light on the mechanisms linked to pathogen sexual reproduction and their effects on the evolutionary and epidemiological outcomes across the considered resistance deployment strategies. In particular, we adapted a previously developed model (Rimbaud et al., 2018), which simulates the spread of epidemics across an agricultural landscape and the evolution of a pathogen in response to the deployment of host resistance, to include pathogen mixed reproduction system. The model is implemented in the R package {*landsepi*} (https://cran.rproject.org/web/packages/landsepi/index.html) . The new model (Fig. 1), is flexible enough to vary resistance deployment strategy and pathogen life cycle.

Here, we investigate the impact of three mechanisms linked to sexual reproduction (*i.e.* recombination, dormancy and dispersal dimorphism) on the effectiveness and durability of different resistance deployment strategies against the case of downy mildew of grapevine. Downy mildew epidemics on grapevine, caused by the oomycete *Plasmopara viticola*, are typical examples of polycyclic diseases caused by pathogens combining sexual and asexual reproduction cycles (Gessler et al., 2011; Wong et al., 2001). In particular, *P. viticola* combines several cycle of asexual reproduction during host growing season and a single cycle of sexual reproduction at the end of the host growing season. Sexual spores of *P. viticola* may remain viable in the soil for at least 65 months after they are produced (Caffi et al., 2011). After germination, sexual spores are distributed from the soil to the grapevine canopy by rain-splashes, thus presenting a smaller dispersal ability than asexual spore, which are transported by air masses (Gessler et al., 2011). Downy mildew represent a real threat for grapevines in all vine-growing areas of the world, leading to significant yield losses (Gessler et al., 2011). Over the past years, breeders have been engaged in breeding programs for resistance to grapevine downy mildew, resulting in the creation of several resistant varieties, with the aim of lowering pesticides application to grapevines. However, *P. viticola* has already shown high evolutionary potential, as proven by the appearance of fungicide resistance (Blum et al., 2010; Chen et al., 2007) and breakdown of some deployed resistances (Delmas et al., 2016; Peressotti et al., 2010).

3 Conclusions

In this context, the presented model facilitates the comparison of different resistance deployment strategies to evaluate their ability to promote evolutionary and/or epidemiological control for the *P. viticola*-grapevine pathosystem.

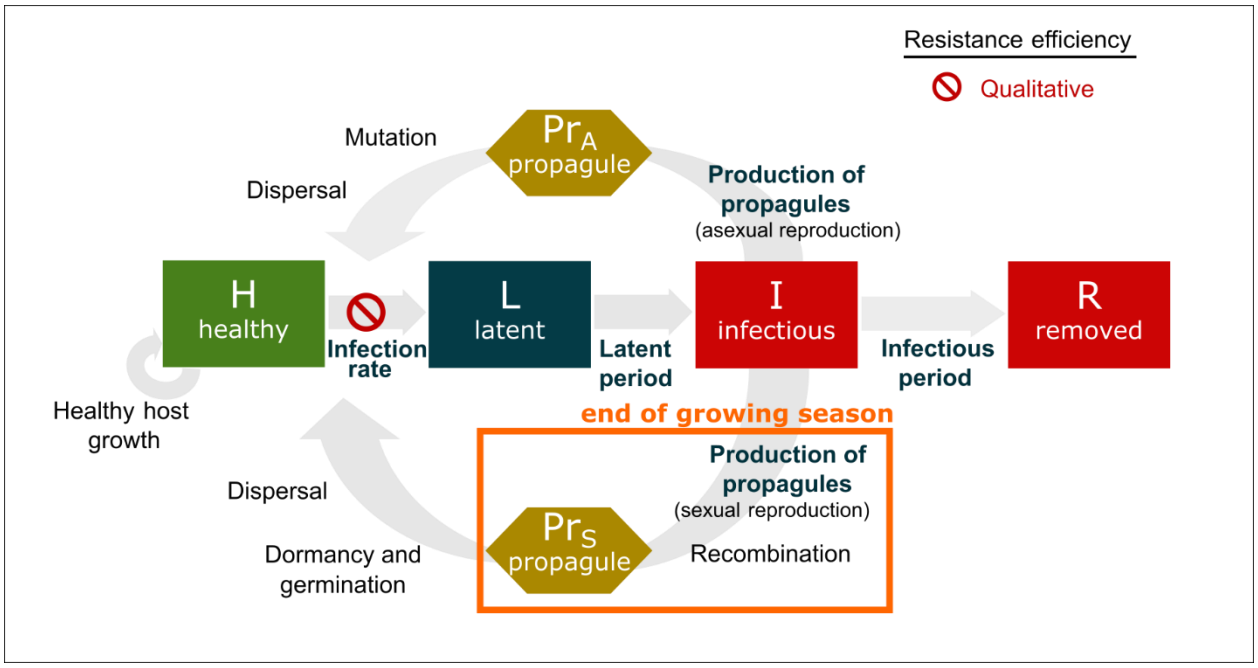

Figure 1: **Architecture of the simulation model**. During growing season, healthy hosts can be contaminated by pathogen propagules (both generated through asexual or sexual reproduction) and may become infected. Following a latent period, infectious hosts start producing new propagules trough asexual reproduction, which may mutate and disperse across the landscape. At the end of the infectious period, infected hosts become epidemiologically inactive. At the end of the growing season, infectious hosts start producing propagules through sexual reproduction. Sexual spores stay dormant in the soil and germinate in the following host growing seasons. After germination, spores disperse across the landscape. Qualitative resistance prevents transition to the latently infected state. Green boxes indicate healthy hosts which contribute to crop yield and host growth, in contrast to diseased plants (*i.e.* symptomatic, red boxes) or those with latent infections (dark blue box).

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