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**ABSTRACT**

Owing to their evolutionary potential, plant pathogens are able to rapidly adapt to genetically-controlled plant resistance, often resulting in resistance breakdown and major epidemics in agricultural crops. Various deployment strategies have been proposed to improve resistance management. Globally, these rely on careful selection of resistance sources and their combination at various spatio-temporal scales (e.g. via gene pyramiding, crop rotations and mixtures, landscape mosaics). However, testing and optimising these strategies using controlled experiments at large spatio-temporal scales is logistically challenging. Mathematical models provide an alternative investigative tool, and many have been developed to explore resistance deployment strategies under various contexts. This review analyses 67 modelling studies in light of specific model structures (e.g. demographic or demo-genetic, spatial or not), underlying assumptions (e.g. whether pre-adapted pathogens are present before resistance deployment) and evaluation criteria (e.g. resistance durability, disease control, cost-effectiveness). It highlights major research findings and discusses challenges for future modelling efforts.

Key words: adaptation, durability, evolution, host-microbe interaction, immunity, simulation.

# Introduction: Why we need to manage resistance deployment and how models can help

Deployment of plant resistance is a relatively low input, cost-effective way to protect agricultural crops from plant pathogens (67, 125). Plant resistance has been used in plant breeding programs to control diseases of various crops (e.g. (4, 6, 58)). However, pathogens have frequently evolved to quickly break down resistance following field deployment (37, 51, 106), sometimes resulting in catastrophic epidemics and massive use of pesticides. High pathogen evolutionary potential, coupled with the standardisation and intensification of modern agriculture across large cultivated areas has generally led to recurrent cycles of resistance deployment followed by rapid pathogen adaptation, often described as boom and bust cycles (78). When the resistance of a cultivar becomes ineffective, economic losses can be considerable because of the direct impact of epidemics and the cost of alternative control methods. Moreover, breeding for resistance is costly, time consuming and often constrained by the limited availability of genetic resistance sources (40, 147). Resistance genes should therefore be considered as an exhaustible resource deserving careful stewardship.

The design and implementation of strategies that improve **resistance durability** would therefore be of great benefit to agricultural productivity, sustainability and profitability. However, a key point is that **resistance durability** and **epidemiological control** are not necessarily correlated (13, 52). Thus, any strategy designed to control the emergence of **resistance-adapted pathogens** in agro-ecosystems has the potential to conflict with epidemic control both in the short-term (from standing pathogenic variants) and the long-term, should resistance break down.

Pathogen spread and adaptation is favoured by the low host genetic diversity that is representative of intensive agricultural systems (124). Therefore, many proposed strategies rely on the selection of diverse resistance sources and their spatio-temporal deployment to engineer biodiverse cropping systems (9, 13, 77, 84, 125). The goal is to confront pathogens with eco-evolutionary challenges and thus avoid or delay their adaptation to plant resistance, while maintaining effective epidemiological protection (15, 147). Particularly for airborne plant pathogens, deployment strategies are more likely to be effective if implemented across landscapes at large spatial scales (40). However, experimental tests of landscape-based strategies are rarely feasible for obvious practical reasons (but see (26, 57, 150)).

To overcome the difficulties of experimentation with plant resistance deployment at large spatio-temporal scales, numerous mathematical models have been developed (see sidebar: “Complementarity between models, experiments and observations”). However, models are typically faced with the challenge of combining several aspects of resistance deployment (e.g. type of plant-pathogen interaction; spatio-temporal scale of deployment; section 1), incorporating realistic parameters and assumptions with respect to epidemiological and evolutionary processes (section 2), and generating usable outputs (section 3). In this review, we identified 67 studies that used models to assess or optimise

deployment strategies (Table 1 & details in Supplemental Table S1). Our aim is to provide a comprehensive overview of these modelling approaches, noting that the diversity of model structures, assumptions and outputs make direct comparisons difficult. Regardless, we examine their main features from both epidemiological and evolutionary perspectives and highlight major findings of relevance to **resistance durability** and **epidemiological control**.

# 1. Modelling resistance deployment from gene to landscape scales

The main strategies considered in plant resistance deployment act across scales from genes to landscapes. They rely on the appropriate choice of resistance sources, which can be combined in the same cultivar (gene pyramiding), alternated within rotations, mixed within fields, or segregated across a mosaic of fields (Figure 1). Since these have been extensively described in previous reviews (9, 13, 84, 125, 147), we focus on mathematical models developed to assess, compare and improve these strategies (Table 1 & Supplemental Table S1). We note that the evolutionary processes underlying pathogen and pest adaptation to plant resistance are analogous to those associated with the emergence of resistance to chemicals. Therefore, the deployment strategies we consider have counterparts for the management of resistance to pesticides in crops, drugs used for the treatment of animals and humans, as well as vaccines (for reviews see (109, 110, 128, 136)).

## A. Choosing appropriate resistance sources

The smallest scale that impacts deployment lies in the choice of resistance sources to be deployed. Plant resistance has often been classified as either **qualitative complete** or **quantitative partial**, although considerable empirical evidence suggests that this dichotomy should be revised (see sidebar: "Should the traditional dichotomy of plant resistance be reconsidered?").

### Modelling qualitative and quantitative resistance

**Qualitative resistance** usually refers to 'major resistance genes', which code for specific host proteins able to recognise a specific pathogen molecular pattern or effector. Such 'gene-for-gene' interactions are traditionally modelled using a 2-by-2 matrix describing the occurrence of disease as an outcome of the interaction between host **genotype** (with or without the resistance gene) and pathogen **genotype** (**non-adapted** or **adapted**) (34) (Figure 2d). Only **resistance-adapted pathogens** can infect resistant hosts. Depending on whether or not they are present in the initial pathogen population, they may have to appear (e.g. via immigration from distant areas, mutation or recombination, section 2B). In this context, pathogen adaptation leads to **resistance breakdown**, i.e. complete restoration of pathogen infectivity on resistant hosts. However, adaptation is often penalised by a **fitness** cost on susceptible hosts (59, 67, 139), resulting in decreased ability of **resistance-adapted pathogens** to infect susceptible hosts compared to **non-adapted genotypes** (130). Inclusion of a **fitness** cost parameter makes the plant-pathogen interaction matrix (Figure 2b) relevant

for both the 'gene-for-gene' (Figure 2d) and 'matching allele' (Figure 2e) concepts (1, 116, 129). Indeed, the classic matching allele concept states that pathogen adaptation to a new host makes infection of the other host impossible (i.e. the **fitness** cost is maximal).

**Quantitative resistance** traditionally refers to the additive effects of multiple 'minor resistance genes', resulting in a continuous distribution of pathogen adaptation (20, 90, 123). From the plant perspective, pathogen adaptation corresponds to an erosion phenomenon (9, 78, 105) (Figure 2ac). **Quantitative resistance** is classically considered to be **partially efficient**, i.e. resistant hosts can be infected by **maladapted pathogens**, although disease development is reduced. Models with compartmental architecture (section 2A) can disentangle the effect of **partial resistance** on different **pathogenicity traits**: plant infection rate by pathogen propagules (e.g. fungal or bacterial spores, insect vectors carrying viral particles), latent and infectious periods, and propagule production rate (Figure 3a). According to the few modelling studies which have compared the performance of **quantitative resistance** against different **pathogenicity traits**, from a disease management perspective, the most promising target trait for **quantitative resistance** is latent period, followed by infection rate and propagule production rate (72, 113).

However, **qualitative resistance** is not always **complete**, and **quantitative resistance** is not necessarily **partial** (see the sidebar titled "Should the traditional dichotomy of plant resistance be reconsidered?"). For example, many **qualitative resistance** genes actually allow some infection, whether they may be partially broken down, environmentally sensitive, developmentally-regulated, or simply weak (19, 91, 123). In models, inclusion of a resistance efficiency parameter in the plant-pathogen interaction matrix (Figure 2b) allows the representation of **partially efficient qualitative resistance**.

### Deployed resistance sources must be inherently hard to break down

One of the few models accounting for the molecular mechanisms of pathogen adaptation to resistance highlighted the effect of the number, nature (transition or transversion) and rate of the required mutations and associated **fitness** costs on the **durability** of major resistance genes (31). The impact of mutation rate and **fitness** cost has also been demonstrated in models focusing on phenotypic aspects of **qualitative resistance** ((32, 33, 111); see also section 2B). Similarly, for **quantitative resistance**, models indicate that strong **fitness** costs of pathogen adaptation slow down resistance erosion (72, 101, 103). However, resistance erosion is sensitive to pathogen mutational processes (i.e. the number of mutations required to completely erode **quantitative resistance**) (8). Collectively, these results support the importance of identifying and deploying resistance sources that are inherently hard to break down. These findings have been confirmed experimentally for plant viruses (49, 78, 108).

High resistance efficiency (i.e. the targeted **pathogenicity trait** is drastically reduced for **maladapted pathogens**) reduces pathogen epidemiological impact (104, 113, 118). However, the effect of this parameter on **resistance durability** is less well documented, probably

because it is generally associated with **quantitative resistance**, for which defining **durability** is still a challenge (section 3B). A study on pesticide resistance showed that high application doses slow the appearance of **adapted pathogens**, but hasten their invasion once present (45). These conclusions agree with results obtained for **partially efficient** major genes when **resistance-adapted pathogens** are initially present (21, 107).

## B. Spatio-temporal strategies for deploying different resistance sources

### Resistance genes can be combined at plant scale

Multiple resistance sources can be stacked into a single plant **genotype**, as a "pyramid" (29, 35, 82). Although different resistance types can be combined, published models have mostly focused on pyramids of major resistance genes (Figure 3b). In line with theoretical predictions (9, 67, 84) and results obtained with single genes (section 1A), models have shown that the **durability** of this strategy increases with the number of mutations required to break down all the genes composing the pyramid, and the strength of associated **fitness** costs (28, 31, 111, 113). However, **durability** of pyramids can be compromised if pyramid gene components are simultaneously deployed individually (73, 117) or if pathogens **adapted** to one or more of these components are already present in the population (73) (see also section 2B). Pyramid cultivars must therefore be deployed carefully, especially because their **breakdown** results in the emergence of **multi-adapted pathogens**.

Extensive empirical evidence has demonstrated the efficacy of combining **qualitative** and **quantitative resistance** in a pyramid (11, 85, 98, 108) but few models have investigated these scenarios. These models have shown that the **breakdown** of a major resistance gene can be delayed when pyramided with the appropriate **quantitative resistance**. Promising target traits include latent period (113) and pathogen effective population size (i.e. the size of an idealized population showing the same degree of randomness in allele frequencies as the real population, noting that small effective sizes amplify genetic drift; section 2B) (114). Several sources of **quantitative resistance** may also be pyramided (60, 123). The only model investigating this scenario highlighted the potential of targeting **pathogenicity traits** whose evolution is constrained by trade-offs (i.e. evolution to improve one trait penalises another trait) (8).

### Resistance genes can be segregated at field and landscape scales

At field scale, varieties carrying different resistance sources (or resistant and susceptible varieties) can be cultivated in the same patch, simultaneously in mixtures or alternating within rotations. Crop varieties can also be segregated into a mosaic of fields within a broader regional strategy (78, 84). Furthermore, varying the different components of mixtures, rotations and mosaics, their relative proportions and their spatial (for mixtures and mosaics) or temporal (for rotations and mosaics) organisation offer a multitude of deployment options (Figure 4).

The value of combining cultivars in mixtures or mosaics is likely to increase with the number and heterogeneity of components. Given **fitness** costs of pathogen adaptation to different hosts, heterogeneous host populations are expected to favour diversifying selection, i.e. to select for higher pathogen specialization (5). This should result in reduced disease spread owing to (i) a dilution effect (i.e. reduced colonization rate of a specialized pathogen in host cultivars to which it is adapted due to increased distance among these hosts, with the remainder of the host population acting as a propagule sink), (ii) a barrier effect (i.e. hosts of a given **genotype** acting as physical barriers to pathogen spread owing to their architecture); and (iii) a competition effect (i.e. different pathogen **genotypes** competing for the same host individual) (14, 54, 143). In accordance with empirical results (38, 48), models confirm the potential for dilution effects by showing that the amount of disease in mixtures is often smaller than the arithmetic mean of the amount of disease obtained from these components in pure stands (50, 53, 65, 66, 118). Assuming **fitness** costs of adaptation to different components, models have also demonstrated that higher numbers of mixture components amplify dilution effects (28, 80) and delay the emergence of **multi-adapted pathogens** through competition with more specialised pathogens (44, 61, 65). In addition to dilution, barrier and competition effects, mixtures and to a lesser extent mosaics may facilitate plant immune system activation via various mechanisms including induced resistance (149). Induced resistance (for any kind of pathogen) or cross protection (for viruses) can occur when a cultivar becomes resistant to a **resistance-adapted pathogen** when previously challenged by a **non-adapted pathogen** coming from another cultivar (148). The only model we are aware of that has investigated induced resistance in mixtures highlighted the impact of the size of the area protected by induced resistance, and of the duration and level of protection on disease reduction (64).

In practice, the spatial organisation of a mixture is often linked to the degree of heterogeneity of its components. Multiline cultivars differing in only a few genes (10), non-fixed populations showing high genetic diversity (e.g. landraces), and mixtures of different cultivars from the same species (143) may be sown after mixing seeds, resulting in completely random mixtures. Conversely, intercropping different species (7), as well as some cultivar mixtures, often require planting in blocks or rows to facilitate crop segregation at harvest (83, 150). Accordingly, mixtures are qualitatively similar to mosaics (hence the term “field mosaic” sometimes used), the main difference being the average distance between components (the size of a genetic unit), noting that this distance must match the scale of pathogen dispersal for effective disease management (41, 119). In fact, results obtained from studies of mixtures and mosaics are likely to be highly correlated (86). This is especially true for non-spatial models where the scale of host population structure could be interchangeably represented as a field or a landscape (Table 1).

Models have found that when **resistance-adapted pathogens** are initially absent, high proportions of resistant hosts in a field or broader region with low aggregation of cultivars (or weak connectivity between hosts of a given cultivar) favour good disease control (39, 47, 72,

96, 99, 103, 104, 111, 118, 122, 127, 138, 146). However, intermediate proportions of resistant cultivars are often preferable when **adapted pathogens** are initially present, with the precise proportion that maximises disease control being sensitive to their initial frequency (32, 94). This U-shape effect is in line with the effect of the proportion of resistance on its **durability** (17, 103, 111, 135). The U shape is attributable to the fact that high proportions of resistance considerably reduce pathogen population size (resulting in a low probability of appearance of **adapted** mutants), while small proportions minimise selection pressure and reduce the probability that an **adapted pathogen** successfully disperses to a resistant field. With respect to spatial aggregation, in contrast to its effect on disease control, well-mixed landscapes (i.e. low aggregation) tend to have a higher probability of **resistance breakdown**, as this increases the interface between resistant and susceptible components, and thus the exposure of resistant hosts to potential **adapted pathogens** emerging from susceptible cultivars (17, 103, 111).

The effect of cultivar rotations on **resistance durability** is less well documented than the effect of mixtures and mosaics, especially in models. Nevertheless, one expectation is that for each rotation cycle, the number of components, their degree of heterogeneity and temporal sequence all affect pathogen survival (equivalent to dispersal in time; (12)) in a conceptually analogous way to pathogen spatial dispersal in mixtures and mosaics. Accordingly, models predict that resistance will be more durable when used in small proportion (92) and with a rapid turnover (111) within the temporal sequence. Furthermore, while most landscape-scale studies use a static landscape (i.e. crop allocation to fields is fixed), some models have demonstrated that resistance deployment can be improved by temporal variation in the proportion of resistance in the landscape (28, 33, 70). This finding emphasises the potential of dynamic mosaics where the number and spatial location of resistant fields vary in time (Figure 4).

In addition to the strategies discussed above, resistance deployment can benefit from complementary control methods (83). Any control method which reduces the effective or census size of the pathogen population (e.g. chemical applications, biological control, removal of infected crop residues and other agronomic practices) should increase **resistance durability**, provided that the pathogen does not adapt to this additional control method (16).

The diversity of resistance types, spatio-temporal scales of deployment and complementary control methods result in an extensive range of possibilities whose combinations merit further investigation. Based on the few results from modelling studies, some combinations are expected to maximize both **epidemiological control** and **resistance durability**, like rotations and mosaics (28, 33, 111) or rotations and mixtures (145). Other combinations are yet to be explored, like those involving different types of resistance (e.g. **complete** and **partial**, **qualitative** and **quantitative**) at different spatio-temporal scales via pyramids (Figure 3), mosaics, mixtures and rotations (Figure 4). Models are powerful tools to

assess and compare deployment options. Nevertheless, a clear understanding of their structure and assumptions is essential to make appropriate interpretations and comparisons.

## 2. Model structure and assumptions

Following the long-standing tradition of compartmental models in theoretical epidemiology (55), diverse models have been developed to investigate resistance deployment. They are mainly distinguished by how the genetic and spatio-temporal structures of host and pathogen populations are modelled and how epidemiology and evolution are accounted for.

### A. Modelling epidemics

The basic 'SIR model' consists of a set of coupled non-linear ordinary differential equations (ODE) representing the temporal dynamics of S(t), I(t) and R(t), respectively the numbers of 'susceptible' (i.e. healthy in this context), 'infected' and 'removed' (i.e. epidemiologically inactive) individuals in the host population (75). For pathogens such as viruses that trigger systemic infection, host individuals are often entire plants. For other pathogens such as fungi that trigger localised clonal lesions, individuals may be considered as plant tissue units such as a leaf or part thereof (Supplemental Table S1). If the basic SIR model considers a population of genetically identical hosts, compartmental models can handle several host **genotypes** by including dedicated compartments for each plant cultivar. Such models remain purely demographic from the pathogen perspective, as a single pathogen strain characterised by a unique set of **pathogenicity traits** (e.g. transmission rate, infection rate; see section 1A) is considered (Table 1a). ODE naturally apply to tropical crops with continuous planting and harvest throughout the year. Nevertheless, seasonality of temperate climates (as well as cultivar rotations, section 1B) can be represented in semi-discrete models. They undergo continuous ODE dynamics, and experience discrete dynamics at given time points, typically at pathogen overwintering ((76); see also Supplemental Table S1). Regardless of their structures, ODE rely on a **deterministic** framework where a set of given inputs invariably yields the same outputs. However, epidemic dynamics as well as pathogen demography are impacted by uncertainty affecting individual life events (**demographic stochasticity**) or imposed by the environment (**environmental stochasticity**) (67). **Demographic stochasticity** is typically important during the initial phase of an epidemic. Using **stochastic** SIR models is then a way to account for the probability of epidemic extinction when the number of infected hosts is small.

### B. Accounting for pathogen evolution

Addressing questions about **resistance durability** requires modelling of pathogen evolution. Historically, theoretical studies of pathogen evolution mainly relied on the framework of adaptive dynamics (25). Assuming that a single pathogen strain is present at its endemic steady state, the method determines under what conditions a second mutant strain, introduced at low frequency, will invade the population. Adaptive dynamics supposes that

epidemiological and evolutionary processes do not interfere with each other or act at different time-scales. It essentially focuses on long-term predictions for endemic diseases and has been used to study pathogen evolution in response to resistance deployment (Table 1b). For example, the effect of resistance genes targeting different **pathogenicity traits** on the evolution of virus multiplication rates has been investigated (134, 137). Through computation of stable evolutionary equilibria, it is possible to resolve evolutionary trade-offs like those between virulence (in this context, virulence refers to host damage caused by pathogen infection) and transmission (36, 131), survival and transmission (131), generalism and specialisation (102). However, in agro-ecosystems, interest is generally focused on short-term epidemics, which impacts both pathogen population size and composition. Day and Proulx (24) and Day and Gandon (23) introduced a framework to simultaneously model the dynamics of epidemics and evolution for any **pathogenicity trait**. This approach, termed evolutionary epidemiology, is inspired by quantitative genetics and is well suited to model the evolution of quantitative traits. To date, it has been applied to study the erosion of **quantitative resistance** targeting different **pathogenicity traits** (27, 72).

As for plant cultivars, multiple pathogen strains are considered in multi-strain compartmental models. By doing so, models explicitly switch from demographic to demo-genetic representations of the pathogen population (Table 1c). Many models solely consider the effect of selection, and assume that all pathogen **genotypes** are initially present, with **adapted genotypes** initially present at low frequencies. These assumptions ignore the time required for the appearance and establishment of adaptive mutations in pathogen populations (135). While this may be an acceptable assumption for pathogens with large population sizes, it can considerably overestimate the speed of adaptation of pathogens with smaller effective population sizes, especially for strategies involving gene pyramids (section 1B).

A further step is to explicitly model the effects of mutation or migration on the establishment of **resistance-adapted pathogens** that are initially absent. Taking into account the classical genetic mutation rate (number of genetic mutations/generation/nucleotide) is difficult as it requires correct identification of the genetic architecture (number, type, location and phenotypic effects of genetic mutations) underlying phenotypic trait variation. Presently, this knowledge is only considered for virus adaption to major resistance genes using the concept of mutation-selection balance (28, 32, 33). For most pathogens, the links between **genotype** and **phenotype** are ignored. Most models instead consider a phenotypic mutation rate representing a displacement into the pathogen phenotypic space (e.g. (8, 72, 73, 96, 113)). Empirically largely unknown, this rate theoretically integrates the phenotypic effects of genetic mutations into the multi-dimensional space of **pathogenicity traits** as well as potential correlations within and between host **genotypes**. Immigration of pathogen strains from external sources has also been considered as an alternative source of new genetic variants (71, 135). While the rate of appearance of new genetic variants via mutation depends

on the size of the pathogen population, with immigration this rate is generally constant and independent of the epidemiological status of the system.

Besides mutation, genetic recombination (occurring during virus replication, bacterial conjugation, transformation and transduction, or fungal sexual cycle), also generates new variants. For example, recombination can accelerate pathogen adaptation via the re-assortment of adaptive mutations controlled by independent loci. This enables the emergence of **multi-adapted pathogens** and thus favours the **breakdown** of resistance pyramids. Thus, ignoring its role can result in severe bias (2). Only few models (70, 117, 144) included recombination to study the emergence of **multi-adapted genotypes** of a pathogen having one sexual phase at the beginning of each cropping season (Table 1).

**Demographic stochasticity** shapes the effect of these evolutionary processes and can be dealt with **stochastic** models. This is of particular importance when (i) events are inherently rare (e.g. due to low mutation rates), and (ii) pathogen population size is low (e.g. just after a mutant strain appears). Therefore, depending on subtle interactions between effective population size ($Ne$), selection coefficient ($s$) and mutation rate ($\mu$), the evolutionary dynamics of a population can be mainly **deterministic** or **stochastic** (115). For example, if $Ne \times \mu \ll 1$, the waiting time of mutations conferring adaptation could be substantial and is thus subjected to large random fluctuations that can hardly be ignored if **adapted pathogens** are initially absent. If $Ne \times s \ll 1$, genetic drift generates random fluctuations in pathogen genetic diversity, with the potential to purge variants regardless of their selective value. Most models reviewed here ignore the effect of genetic drift (Table 1). Dealing with such evolutionary force requires specific consideration of $Ne$ and its variation, especially bottlenecks from which only some individuals will be randomly sampled and survive to reproduce (18). Lo Iacono, et al. (71) used the size of the infected host population as an indirect proxy of such variation, whereas other authors have explicitly modelled bottlenecks occurring at crop harvest and during the off-season (73, 103, 113, 144, 145), during intra-plant movement in viral infection (114) and during viral transmission by insect vectors (31).

### C. Representing the spatial structure of host populations.

In non-spatial models (Table 1), each infected individual is equally likely to establish an infectious contact with any other healthy individual, regardless of its geographic location. Accounting for space is critical for accurate assessment of deployment strategies relying on the spatial segregation of different cultivars (e.g. mixtures and rotations, section 1B), especially when the pathogen disperses primarily at short distances compared to field size.

New compartments leading to more realistic contact structures between individuals can be introduced in spatially-implicit models. A metapopulation of well-mixed host patches where pathogen spread rates differ within and between patches provides a typical example (42). Addressing this question more deeply requires spatially-explicit approaches, where pathogen dispersal is represented using reaction-diffusion equations (RDE; (46)) or via dedicated kernels (89) within integro-differential equations (IDE). Notably, dispersal kernels

allow explicit representation of long-distance infection events (79). In any case, variables of interest depend on a vector of spatial coordinates x in addition to time t (e.g. $S(t,x)$, $I(t,x)$), providing a straightforward way to investigate the effect of habitat geometry (e.g. spatial aggregation, section 1B). **Stochastic** models are often used to randomly segregate pathogen propagules across different landscape elements. They are also used to explicitly consider **environmental stochasticity** associated with random fluctuations of cultivar allocations (73, 145), or pesticide treatments (71, 96) year after year in different parts of the landscape.

# 3. Model outputs: criteria to assess deployment strategies

As described for fungicide application (136), assessment of resistance deployment strategies depends strongly on evaluation criteria. Importantly, the objectives of different stakeholders (e.g. growers, breeders) are not always compatible. Indeed, minimising epidemiological impacts, maximising **resistance durability**, and minimising costs of disease management are all sensible targets that may lead to different optimal strategies (103, 111, 135). This section considers potential key variables used in models (Table 1 & Supplemental Table S1) for assessing resistance deployment strategies from epidemiological, evolutionary and socio-economic perspectives.

## A. Epidemiological outputs

Epidemiological outputs characterise the ability of deployment strategies to reduce disease impact in a given region over a given time period (15). In the field, disease impact is classically evaluated using the proportion of infected hosts (disease prevalence; (75)) or a quantitative assessment of symptoms on infected hosts (disease severity; (75)). In models, disease impact is usually measured by the proportion of infected individuals (i.e. infection units, Section 2A), equating to prevalence when an individual is a single plant, or severity when an individual is an infection site. Thus, prevalence and severity can only be distinguished when plant architecture is explicitly modelled in terms of number of infection sites per plant (e.g. (39, 144-146)). Because prevalence and severity change in time, the challenge is to summarize them using representative point estimates to compare different deployment options. One approach focuses on epidemiological status at the end of a given period (118, 122, 127) or at stable evolutionary equilibrium (80, 94, 134, 137). Another approach relies on the integration of prevalence or severity over time into an area under disease progress curve (AUDPC; (28, 32, 33, 111, 113)).

Alternatively, the number of infected hosts can be deduced from the number of healthy hosts (94, 100, 134, 137). Similar to the computation of AUDPC, the dynamic of healthy hosts may be integrated over time into a variable representing the cumulative amount of photosynthetic tissue, assumed to be proportional to crop growth and yield (141). Modelling studies variously refer to this as healthy area duration (HAD; (103)), healthy surface (72, 99, 104), green leaf area (113) or green area canopy duration (107). Depending on the study objectives, AUDPCs and HAD-like variables may be computed for the whole host population

or individually for each cultivar (e.g. (107)), and for the whole simulation run or for specific periods (e.g. before and after **resistance breakdown**; (103, 111)). It may be expressed in absolute value, or relative to a reference context, for example to assess, compared to a fully susceptible landscape, the additional number of healthy hosts resulting from resistance deployment (71, 72, 135) or the intensity of epidemics (28, 32, 33).

Finally, the dynamic of infected hosts in a region can be summarized by other metrics like the speed of the epidemic expansion front (121, 133, 138), the total distance travelled (104), or the final area covered by epidemics (122, 127).

### B. Evolutionary outputs

Evolutionary outputs mainly assess the ability of deployment strategies to prevent or slow down pathogen adaptation and are often summarized by **resistance durability**. In models where pathogen **genotypes** are classified as **non-adapted** or **adapted** (section 1A), **resistance durability** has been calculated using criteria such as the point in time when resistant hosts become as severely affected as susceptible hosts (107), when **adapted pathogens** first appear (31), or when their prevalence (56, 111, 113) or frequency in the pathogen population (16, 73, 74, 96, 107, 135) exceed an arbitrary threshold. The value of this threshold determines which of the three characteristic phases of **resistance breakdown** is targeted. These phases, analogous to an ecological invasion process of the cropping landscape by **adapted pathogens**, consist of: i) introduction via immigration or appearance (via mutation, recombination, horizontal gene transfer or sexual reproduction), ii) establishment, when extinction becomes unlikely despite potential competition with **non-adapted pathogens**, and iii) spread (or propagation) within the formerly resistant host population, potentially causing severe yield losses. Thus, model results can be significantly impacted by the chosen threshold above which resistance is considered to have been broken down (74), but also by model assumptions (e.g. whether or not **adapted pathogens** are initially present; (73); see also section 2B). When several resistance genes are deployed, and in particular for pyramid cultivars, resistance durability can also be assessed based on the dynamics of the **multi-adapted pathogen** (21, 44, 65, 66, 111).

Measuring pathogen adaptation to resistance when it is continuously distributed is still a challenge. The few approaches that have been proposed rely on the speed of pathogen evolution (102) or of resistance erosion (113), and on the time point when the proportion of healthy hosts drops below an arbitrary threshold (16, 101, 103).

### C. Socio-economic outputs

Despite the importance of identifying deployment strategies that are not only efficient and durable but also cost-effective and feasible for growers, socio-economic factors are rarely accounted for in resistance deployment models. Although planting density, growth rate and contribution to crop yield are often assumed to be uniform, this is rarely the case in practice. For potato late blight in the Netherlands (96) and blackleg of winter oilseed rape (69, 70), crop yield was computed as a function of crop cultivar, disease severity and climatic variables.

Accounting for yield enables the resolution of trade-offs between the reduction of damage resulting from the use of resistant cultivars and associated costs, like reduced growth (96) or smaller yield (140) of resistant varieties. However, yield data are generally not available and can be challenging to estimate (or predict), particularly the yield of a cultivar carrying a broken down resistance.

Organisational and social aspects (e.g. feasibility criteria accounting for farming practices) of resistance deployment have rarely been considered. Yet, these factors drive farmers' decisions and have considerable impact on the adoption of a deployment strategy, as illustrated for potato late blight (95). Milne, et al. (81) predict that adoption of a resistant maize cultivar producing a Bacillus-thuringiensis toxin (Bt, offering better protection against European corn borers but potentially more expensive to grow) by farmers depends on their communication network and sensitivity to risk. In this context, the use of visual interfaces and model-based scenarios can help communicate results to the farmer community and stimulate stakeholder discussions in workshops on plant resistance management (e.g. (97)).

## General conclusions

Models of resistance deployment can be used to deliver insights into the epidemiological, evolutionary and economic performance of deployment strategies (e.g. gene pyramiding, crop rotations, cultivar mixtures, landscape mosaics), at spatio-temporal scales beyond the scope of empirical experimentation. However, it is important to note that the models reviewed here are not designed to precisely predict **resistance durability** or the level of **epidemiological control** in real-world systems. Rather their purpose is to identify key parameters, provide mechanistic insight into the consequences of different deployment strategies and allow decision makers to understand their relative merits (43).

Given this focus, is it possible to use the models to collectively identify a single 'best' strategy for resistance deployment? The diversity of assumptions underlying the different modelling approaches, of scenarios considered and of evaluation criteria used makes it almost impossible to rank strategies. Based on the very few studies that allow such a comparison "all other things being equal", pyramiding seems the most epidemiologically-efficient and evolutionarily-durable strategy to deploy **complete resistance** in the absence of pre-adapted pathogen **genotypes** (73, 111) (Figure 5). However, pyramiding can suffer important limitations as (i) it is challenging to effectively identify the existence of pre-adapted **genotypes** that could be maintained at very low frequencies; (ii) other cultivars or wild relatives can represent evolutionary steps facilitating the adaptation of the pathogen population; and (iii) several precious genetic resources are lost at the same time when a pyramid is overcome. Mosaics and rotations are alternative solutions to cope with these limitations and are predicted to be more efficient (28, 111) and durable (73) when **resistance-adapted genotypes** are present prior to resistance deployment. In addition, by increasing the overall diversity of the crop, these strategies confer a portfolio effect, i.e. increased resilience to other biotic and abiotic constraints. These conclusions should not be overgeneralized to any crop production

situation and pathosystem as they have mostly been obtained in specific contexts. This brings us face-to-face with the modeler's dilemma – it is not possible to maximize generality, realism and precision in the same model (68).

To conclude, we argue that there is no universal strategy. The optimal deployment approach depends on the desired objective, the epidemiological and evolutionary context, and the pathosystem considered, among others. This is in line with what Mundt wrote in a recent review (85): "There are multiple approaches to increasing **durability of resistance** […], none of which should be considered inherently superior to the other, and all of which likely benefit from being combined". We hope this review paves the way for future modelling investigations towards more efficient, sustainable, cost-effective and feasible deployment of plant resistance.

## Summary points

- During the last twenty years there has been a paradigm shift from the idea of "durable resistance" to "durable management of resistance". This implies that **durability** is no longer considered as an intrinsic property of a resistance gene but rather the result of a clever combination of effects operating at different scales. Accordingly, plant resistance against pathogens must be carefully designed (by breeders) and organised in space and time (by farmers) to be both efficient and durable in spite of pathogen evolutionary potential.
- The multiplicity of deployment strategies, resulting from the huge diversity of choices made from gene to landscape scales (Figure 1), impedes their comparison with empirical experimentation. In this context, models provide powerful tools to explore possible deployment options (Figures 2, 3, 4) and can help identify promising strategies (Figure 5) which, in turn, may be amenable to experimental verification.
- The profusion of modelling approaches offers a wide range of possibilities to model epidemics while accounting for pathogen evolution and spatiotemporal organisation of host plants (Table 1 and Supplemental Table S1). Their epidemiological, evolutionary and socio-economic outputs allow the evaluation of deployment options with respect to multiple criteria.
- There is no 'silver bullet' deployment strategy: optimal deployment approaches will vary depending on the desired objective, the epidemiological and evolutionary context, and the pathosystem considered. Any deployment option will have its own advantages and drawbacks, thus there is likely to be benefit from hybrid strategies.

## Future challenges

- Future models should encompass the diversity of plant immunity mechanisms (including tolerance, which reduces pathogen-induced host damage without affecting pathogen development) and consider the full range of pathogen adaptation mechanisms.

- Recognizing that predictions about real world systems often require relatively complex models, we must take advantage of computers current capacity to model complex resistance deployment scenarios that combine different deployment options and complementary control measures at multiple spatio-temporal scales. Such scenarios should also include adaptive strategies that are continuously updated based on real-time data.
- A unified modelling framework will help compare deployment strategies "all other things being equal", and understand the impact of ecological, epidemiological, evolutionary and genetic factors for a diversity of pathosystems. This is one of the objectives of the model *landsepi*, freely accessible through an R package (112).
- More efforts should be made to collect and share epidemiological datasets to help calibrate and validate models with empirical data.
- Models must account for socio-economic and organisational constraints of real farming systems in order to identify solutions that are both feasible and likely to be adopted by breeders and growers.
- Results and recommendations need to be communicated to relevant stakeholders in a way that information is accessible and likely to be acted upon. The use of dedicated pedagogical interfaces facilitates such interactions ((97), see also an interface for *landsepi* in Related Resources).

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## Annotated references

Chabas et al. 2018: predictions based on a theoretical model on pathogen evolutionary emergence are tested experimentally using bacteriophages.

Djian-Caporalino et al. 2014: an experimental comparison of pyramiding, rotation and mixture strategies to deploy pepper resistance against nematodes.

Djidjou-Demasse R, Moury B, Fabre F. 2017: this model shows that mosaics are more efficient than pyramids when resistance-adapted pathogens pre-exist.

Kermack & McKendrick 1927: a seminal paper developing compartmental models in human epidemiology.

Lof ME, de Vallavieille-Pope C, van der Werf W. 2017: this model compares different deployment strategies with and without pre-existence of resistance-adapted pathogens.

Papaïx et al 2018: This model shows that epidemiological control and resistance durability are not necessarily correlated.

Rex Consortium 2013: strategies to manage resistance to xenobiotics are compared based on theoretical models and experimental studies.

Rimbaud L, Papaïx J, Barrett LG, Burdon JJ, Thrall PH. 2018: in this model, pyramids are the most durable strategy when resistance-adapted pathogens do not pre-exist.

Rimbaud L, Papaïx J, Rey J-F. 2018: a freely accessible R package (*landsepi*) proposing a unified modelling framework to compare deployment strategies.

van den Bosch & Gilligan 2003: this model shows that the optimal proportion of resistance depends on how durability is measured.

# Related Resources

1. Prototype of a shiny pedagogical interface for the model *landsepi*: https://shiny.biosp.inrae.fr/app_direct/landsepi/
2. Tepekule B, Uecker H, Derungs I, Frenoy A, Bonhoeffer S. 2017. Modeling antibiotic treatment in hospitals: A systematic approach shows benefits of combination therapy over cycling, mixing, and mono-drug therapies. *PLoS Comput. Biol.* 13: e1005745

## Terms and definitions

- Resistance-adapted pathogen: a pathogen variant adapted to a plant resistance gene. Also referred to as “infective”, “virulent” and “resistance-breaking” in other contexts.
- Complete resistance: a resistance which completely blocks the infectious cycle of **non-adapted pathogens** (e.g. by preventing infection or the production of propagules).
- Demographic stochasticity: refers to the intrinsic uncertainty associated with the life events of each individual in a population (reproduction, dispersal, mutation, death).
- Deterministic: a framework where a set of given inputs invariably yields the same outputs. Deterministic models inform on mean output tendencies.
- Stochastic: a framework where random events are accounted for. Stochastic models inform on mean tendencies and variability of the outputs.
- Environmental stochasticity: refers to random perturbations imposed to a population by its environment.
- Epidemiological control: reduction in disease impact on the host in a given region and during a given period.
- Fitness: ability to transmit genes to the next generation. Here, pathogen fitness is mostly the relative adaptation to different host **genotypes**.
- Genotype: here, plant genotype refers to the set of susceptibility/resistance genes, and pathogen genotype refers to the set of **pathogenicity** genes.
- Maladapted pathogen: a pathogen variant not fully adapted to plant resistance, i.e. infection is possible although the resulting disease is reduced.
- Multi-adapted pathogen: a pathogen variant adapted to several resistance genes. Also referred to as “multi-virulent” and “superpathogen” in other contexts.
- Non-adapted pathogen: a pathogen variant not adapted to plant resistance. Also referred to as “avirulent” or “wild-type” in other contexts.
- Partial resistance: a resistance for which infection by **maladapted pathogens** is not blocked but reduced, resulting in the attenuation of **pathogenicity traits**.
- Pathogenicity trait: a measure of pathogen ability to develop and spread (e.g. infection, reproduction and survival rates, latent and infectious periods) (62).
- Phenotype: here it refers to the occurrence (and amount) of disease, and is mostly determined by the plant-pathogen-environment interaction.
- Qualitative: distributed in discrete classes (by homology with statistics).
- Quantitative: continuously distributed (by homology with statistics).
- Resistance breakdown: loss of effectiveness (complete or partial, sudden or gradual) of plant resistance as a consequence of pathogen adaptation.
- Resistance durability: Initially defined as “the time during which a given resistance remains effective in spite of an environment favourable to disease” (51, 52); the term has since gained a wide range of accepted usages (section 3B).

# Sidebars

**Sidebar 1: Complementarity between models, experiments and observations.**

Numerical experiments performed using computer models represent an alternative way of generating results while circumventing logistical, financial, legal and ethical constraints associated with traditional experiments in laboratory of field conditions (30). Models are powerful tools to predict epidemics and guide disease management. With respect to the use of plant resistance, a huge number of deployment strategies can now be tested via such models thanks to the growing capacity of modern computers, even if the number of possible calculations will always be limited by the "computational cost" (i.e. the time required to perform the calculations). However, we are now confronted with the difficulty of manipulating, analysing and synthesising results obtained from high dimension systems. And more fundamentally, modelling is insufficient on its own. Modellers need empirical knowledge and data acquired from experimental and observational approaches in the laboratory or the field, to develop their model, calibrate its parameters and validate or test its predictions.

**Sidebar 2**: **Should the traditional dichotomy of plant resistance be reconsidered?**

Plant resistance is traditionally classified into two distinct categories. On one hand, **qualitative resistance** is described as monogenic (conferred by a single 'major' resistance gene typically coding for an NLR [nucleotide-binding domain leucine-rich repeat containing] protein), **complete**, race-specific (i.e. effective only for some strains of a pathogen species) and often considered as non-durable. On the other hand, **quantitative resistance** is described as polygenic (conferred by the additive action of several 'minor' resistance genes), **partial**, race non-specific and often hypothesised as durable. However, over-simplification sometimes leads to erroneous assumptions, and several excellent reviews have pointed out exceptions to this long-standing dichotomy (90, 91, 123), such as the wheat gene *Lr34* against rusts and the barley gene *mlo* against powdery mildew (these genes do not belong to the NLR family, and confer almost **complete**, race non-specific and durable resistances). Consequently, we think it is important to disentangle the **phenotype** (**complete** *vs* **partial**), specificity, genetic inheritance (monogenic *vs* polygenic), molecular mechanism and **durability** of a resistance. Furthermore, we argue that pathogen **genotypes** can be structured **qualitatively** (i.e. in discrete classes: either **adapted** or not to the resistance) or **quantitatively** (i.e. continuously: more or less adapted). Corresponding modelling approaches are illustrated in Figure 2.

# Figure legends

[**Note to Annual Reviews: Figure 1 was originally drawn by the first author of this article and was re-designed by GRAPHIC Business at our request. We entirely created figures 2 to 5 for this article. All figures are not based on any previously published image.**]

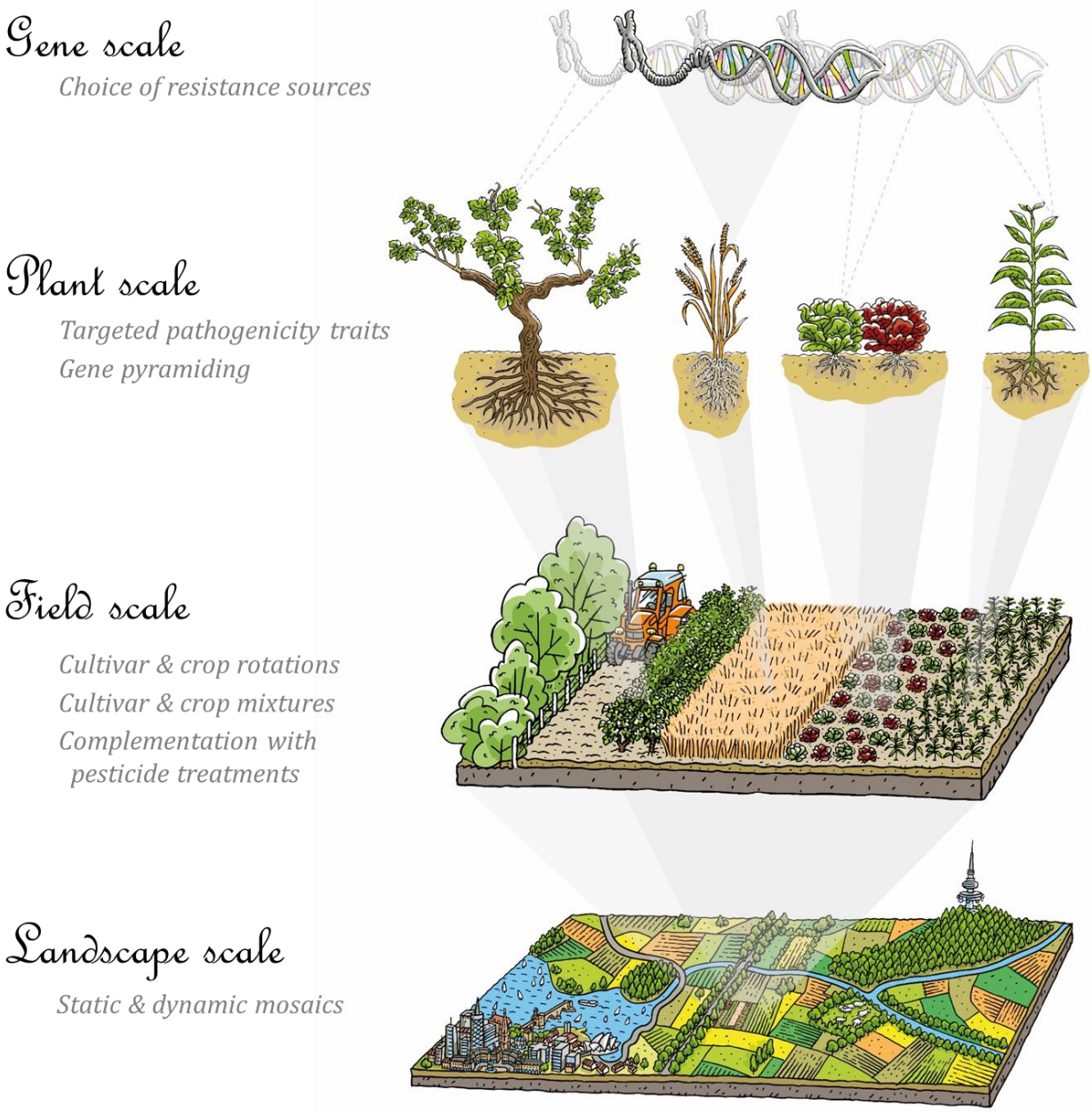


**Figure 1. Nested scales of plant resistance deployment.** A global deployment strategy is the combination of: 1) the appropriate selection of effective genetic resistance sources (e.g. **qualitative** or **quantitative**, **complete** or **partial**) and 2) their spatio-temporal deployment at

plant, field and landscape scales with the aim of mitigating pathogen spread and evolution. Such deployment may be complemented by agronomic practices, biological control and chemical treatments. Possible options available at each scale are indicated.

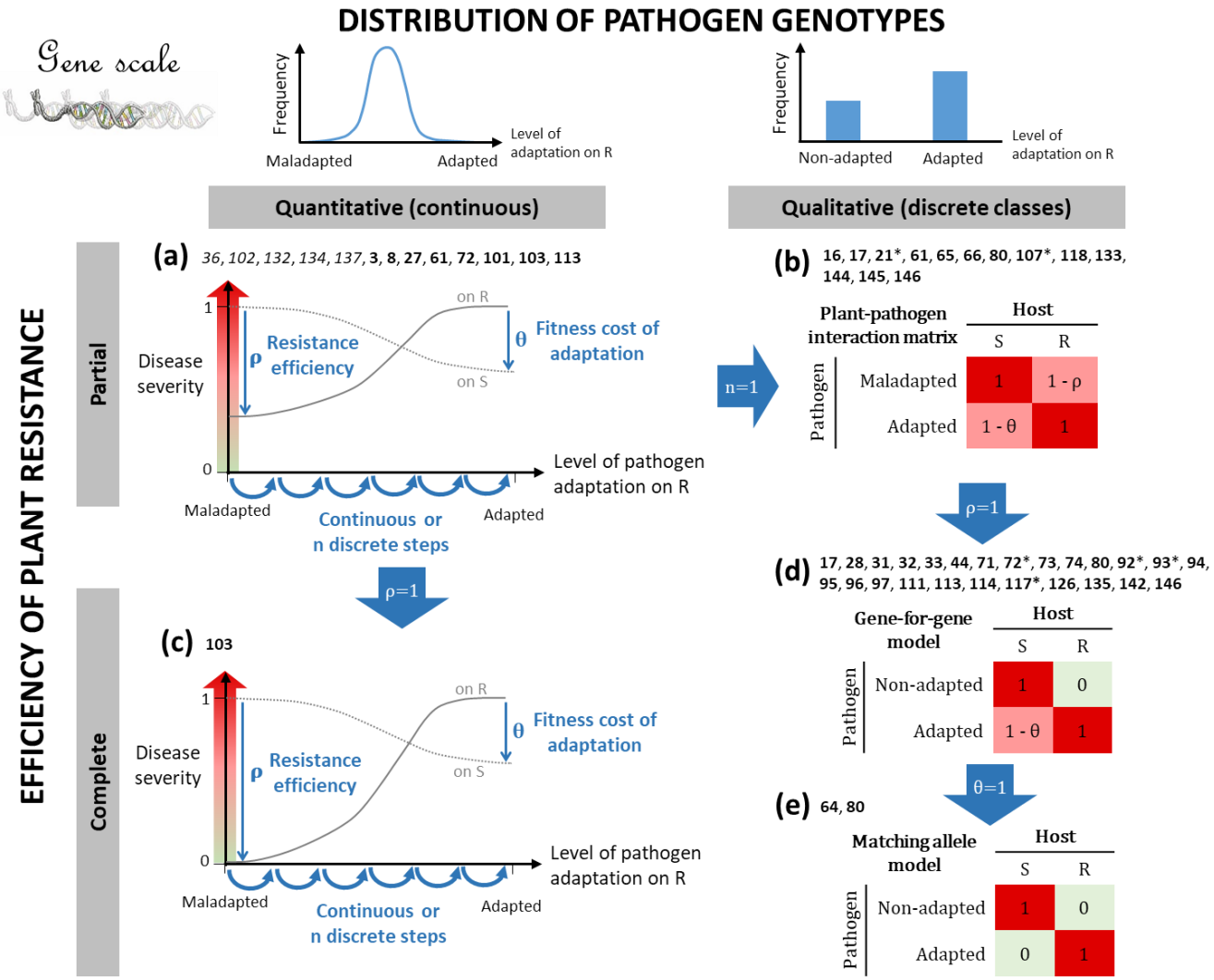


**Figure 2. Modelling the phenotype of plant-pathogen interactions for resistance deployment.** The **quantitative** description of plant-pathogen interactions provides a general framework (a). Parameters of interest in plant resistance deployment are indicated in bold blue text. In this depiction, the degree of pathogen adaptation to the resistance source is distributed continuously in the population. Gradual pathogen adaptation via continuous mutation or n discrete adaptive steps (each step involving one or more genetic mutations) results in resistance erosion, with a potential **fitness** cost (θ) paid on susceptible hosts. When the pathogen population is split into two genotypic classes (**adapted** or **non-adapted** to the resistance), resistance is broken down in a single step (i.e. n=1), resulting in a simple matrix which describes a gene-for-gene interaction (b). Independent of the distribution of pathogen **genotypes**, resistance can be **partial** (i.e. infection is possible with reduced efficiency $\rho<1$; a and b) or **complete** (i.e. it provides total immunity, $\rho=1$; c to e). Numbers refer to adaptive

dynamic (italic) and demo-genetic (bold) models listed in Table 1 that have used these formalisations. Symbol '*' indicates models where **resistance-adapted pathogens** suffer the **fitness** cost on both susceptible and resistant hosts (21, 72, 92, 93, 107, 117).

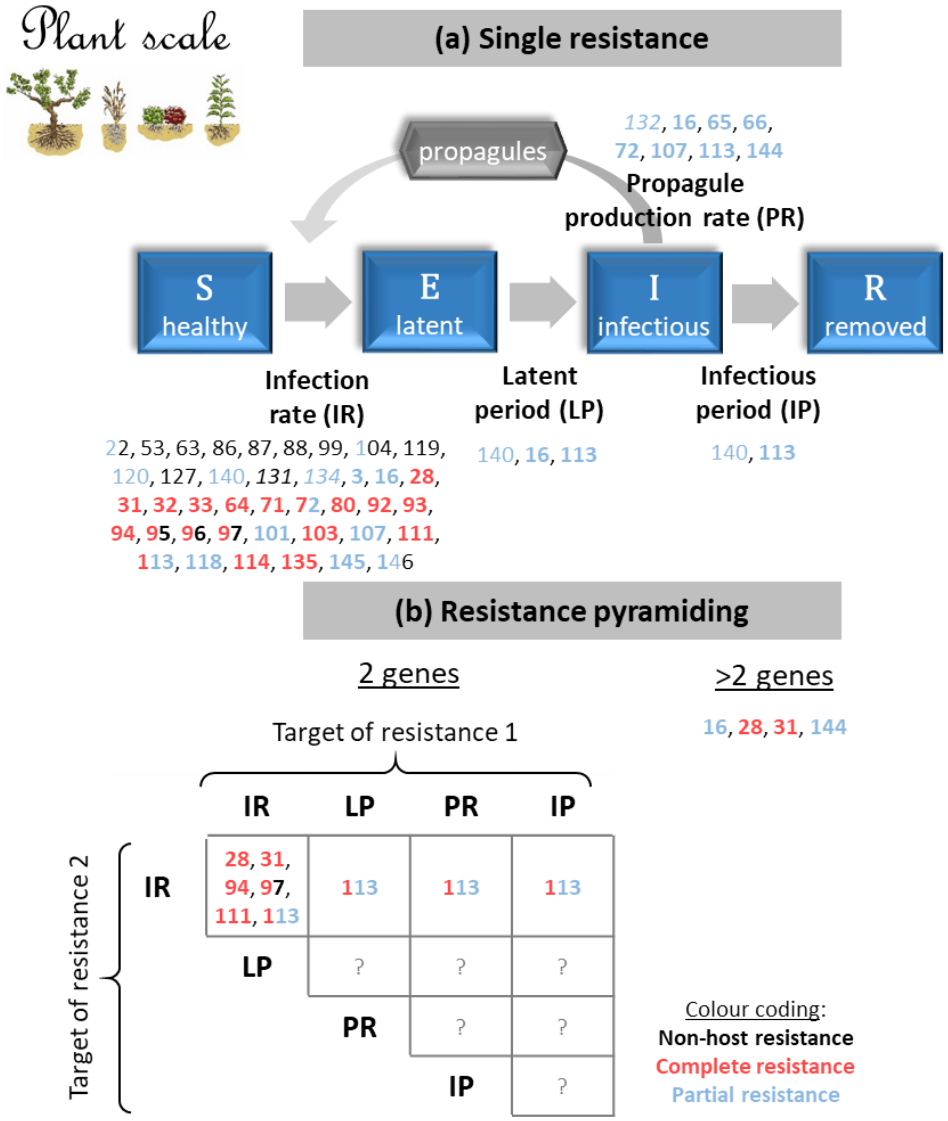


**Figure 3. Modelling resistance deployment options at plant scale.** Different resistance types have varying phenotypic effects on plants when challenged by a pathogen: lower infection and propagule production rates (IR and PR respectively), shorter infectious period (IP), or longer latent period (LP). Potentially, all these **pathogenicity traits** could be completely or partially impeded by plant resistance, but in published models **complete resistance** has mostly been associated with infection rate. Different sources of resistance can be stacked into the genome of a single plant as a pyramid. Numbers refer to demographic (normal font), adaptive dynamic (italic) and demo-genetic (bold) SEIR models listed in Table 1 and representing a wide range of pathosystems.

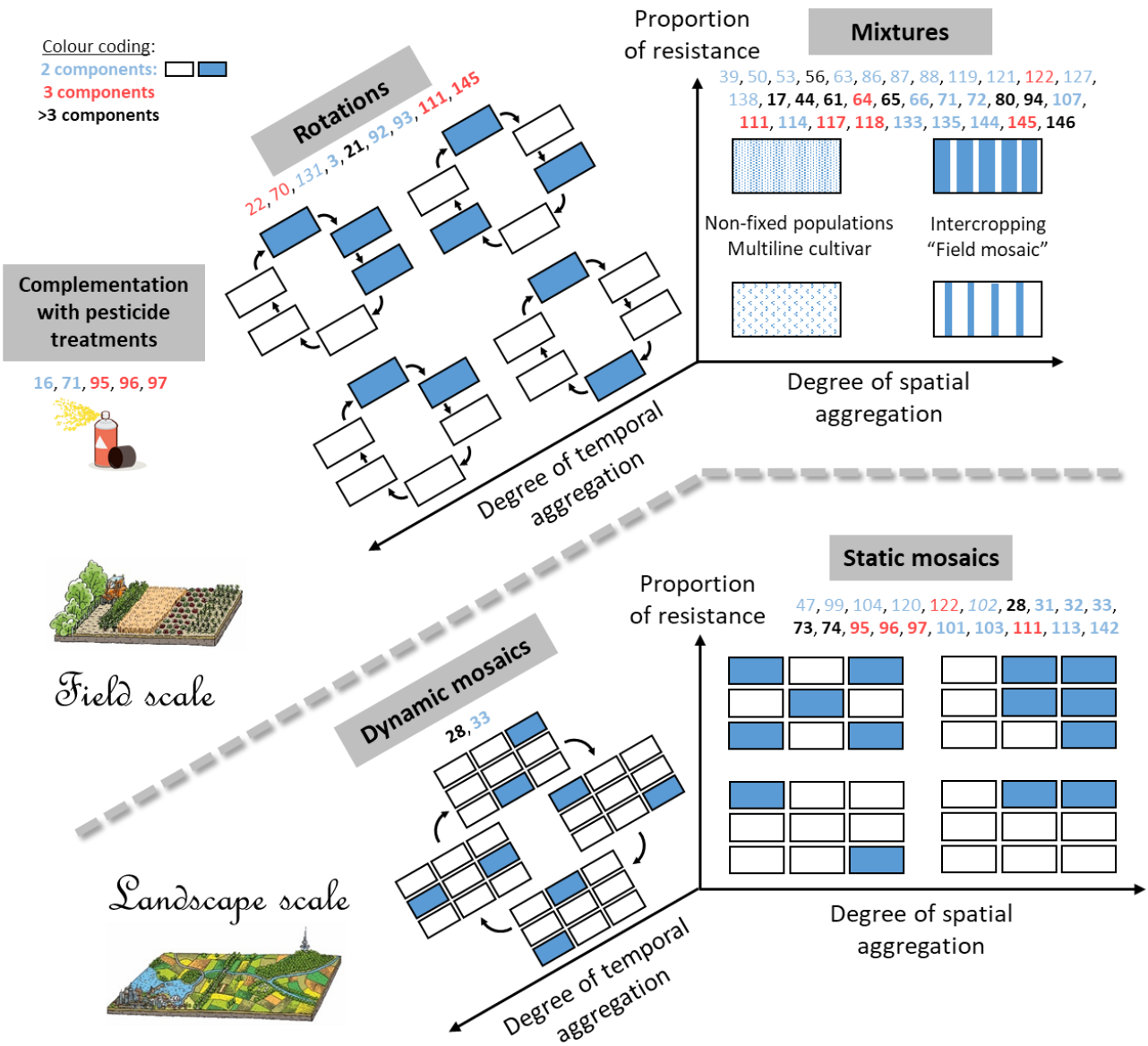


**Figure 4. Modelling resistance deployment options at field and landscape scales.** Field-scale strategies mostly include mixtures and rotations, which can vary with regard to the relative proportion of each component and their degree of aggregation in space (mixtures) or time (rotations). These may be complemented with other control methods (e.g. pesticide treatments). Landscape-scale strategies refer to mosaics of fields where resistance is deployed in controlled proportions and degree of spatio-temporal aggregation. Numbers refer to demographic (normal font), adaptive dynamic (italic) and demo-genetic (bold) models listed in Table 1 that have explored these different options.

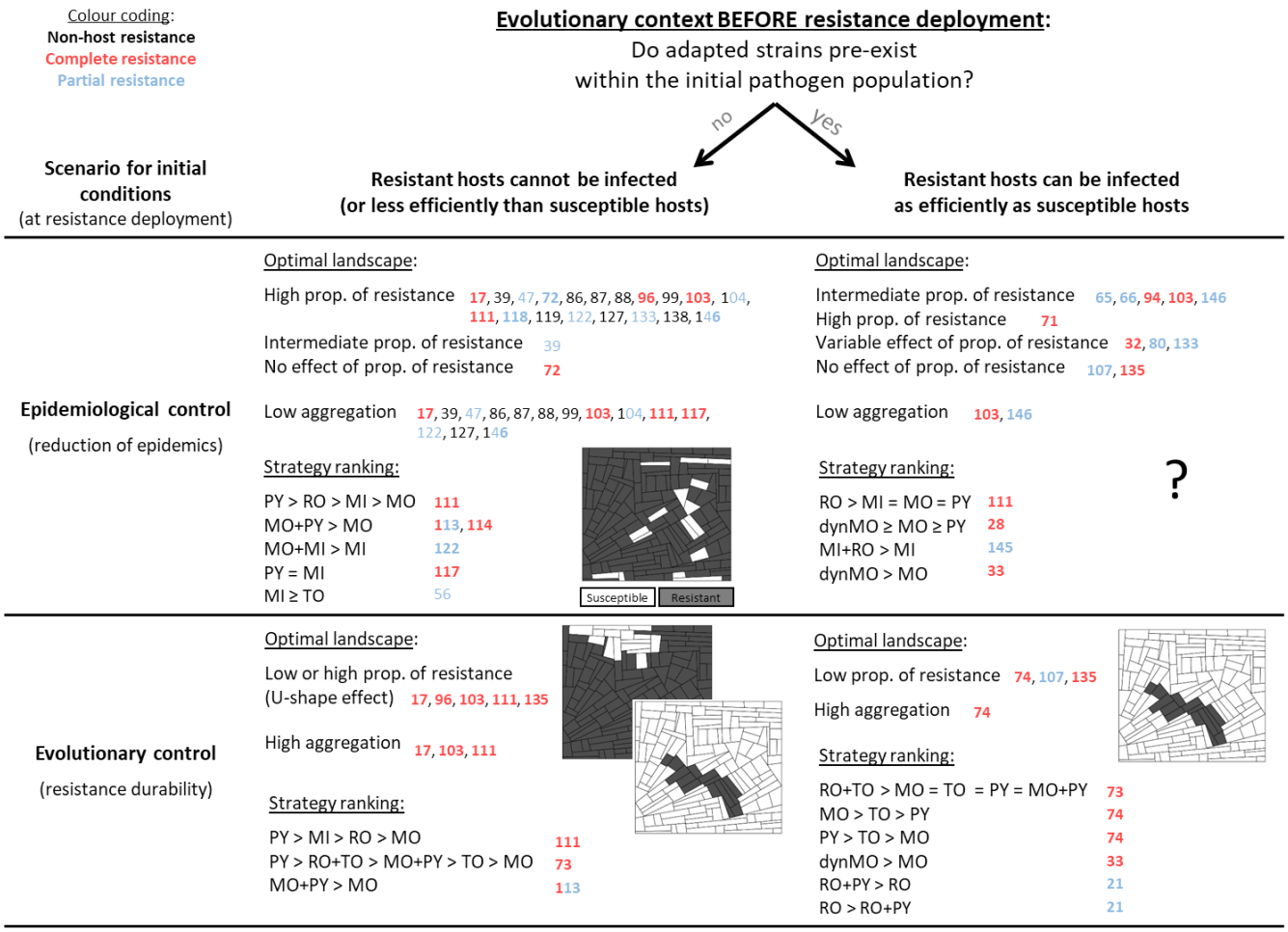


**Figure 5. What models tell us about optimal landscape organisations and deployment strategies to manage plant resistance with respect to epidemiological and evolutionary disease control.** Conclusions considerably differ depending on the existence or absence of **resistance-adapted genotypes** in the pathogen population prior to resistance deployment. Illustrations are examples of optimal landscape organisations. PY: gene pyramiding; TO: turnover of cultivars; RO: cultivar rotation; MI: cultivar mixture; MO: landscape mosaic; dynMO: dynamic mosaic; '+' stands for combination. Numbers refer to demographic (normal font) and demo-genetic (**bold**) models listed in Table 1 and representing different pathosystems.

**Table 1. List of mathematical models used to test, optimise or compare plant resistance deployment strategies against pathogens (a & c) or predict their evolutionary consequences (b).** A detailed version is in Supplemental Table S1.

| Deployment strategy[a] | Resistance efficiency[b] | Distribution of pathogen genotypes[c] | Model structure[d] | Evolution mechanisms[e] | Pre-existence of adapted pathogens | Host spatial structure[f] | Seasonality[g] | OUTPUTS[h] | | | References |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | Epidemiological | Evolutionary | Socio-Economical | |
| **(a) Purely demographic models** | | | | | | | | | | | |
| MI | Non-host | | DE | | no | SE | no | x | | | (63) |
| MI* | Non-host | | DE | | no | SE | no | x | | | (53, 86-88) |
| MI | Non-host | | IDE | | no | SE | no | x | | | (121) |
| MI | Non-host | | ODE | | no | SE | no | x | | | (127) |
| MI | Non-host | | other | | no | | no | x | | | (138) |
| MO+RO | Non-host | | other | | no | SE | yes | x | | | (70) |
| MI | Non-host | | RDE+STOCH | | no | SE | no | x | | | (119) |
| MO | Non-host | | STOCH | | no | SE | no | x | | | (99) |
| MI | Non-host or Partial | | DE+STOCH | | no | SE | no | x | | | (39) |
| RO | Non-host or Partial | | ODE | | no | | no | x | | | (22) |
| MO | Non-host or Partial | | STOCH | | no | SE | no | x | | | (104) |
| MO or MO+MI | Non-host or Partial | | IDE+STOCH | | no | SE | no | x | | | (122) |
| MI | Partial | | ODE | | no | | no | x | | | (50) |
| TO or MI | Partial | | ODE | | no | | yes | x | | | (56) |
| MI* | Partial | | ODE+STOCH | | no | | no | | | x | (140) |
| MO | Partial | | ODE+STOCH | | no | | no | x | | x | (120) |
| MO | Partial | | other | | no | SE | yes | x | | | (47) |
| **(b) Demo-genetic models of adaptive dynamics** | | | | | | | | | | | |
| RO | Non-host | Continuous | ODE | S-M | no | | yes | | x | | (131) |
| Pure stand or MO | Non-host or Partial | Continuous | ODE | S-M | no | | no | | x | | (36) |
| MO | Partial | Continuous | DE | S-M | no | SE | no | | x | | (102) |
| MI* | Partial | Continuous | ODE | S-M | no | | no | | x | | (132) |
| Pure stand | Partial | Continuous | ODE | S-M | no | | no | x | x | | (134, 137) |

| (c) Demo-genetic models | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| MO | Non-host or Complete | Classes | ODE | S-M | no | SE | yes | x | x | x | (95, 96) |
| MO or MO+PY | Non-host or Complete | Classes | ODE | S-M | no | SE | yes | x | | x | (97) |
| TO or MO or PY or MO+PY | Complete | Classes | IDE+STOCH | S-M-D | yes/no | SE | yes | | x | | (73) |
| MI* or MI*+PY | Complete | Classes | ODE | S | yes | | no | x | | | (94) |
| MO | Complete | Classes | ODE | S | yes | SI | yes | x | | | (32) |
| MO or dynMO | Complete | Classes | ODE | S | yes | SI | yes | x | x | | (33) |
| MI* | Complete | Classes | ODE | S-I-M | yes/no | | no | x | x | | (135) |
| MO or dynMO or PY or dynMO+PY | Complete | Classes | ODE | S-M | yes | SI | yes | x | | | (28) |
| RO | Complete | Classes | ODE | S-M | yes | | yes | x | | | (92, 93) |
| MO+PY | Complete | Classes | ODE (within plant) STOCH (between plant) | S-M-D | no | | no | | x | | (31) |
| MO or MI | Complete | Classes | ODE+STOCH | S-I-M-D | yes | | no | x | | | (71) |
| MI | Complete | Classes | other | S | yes | | no | | x | | (44) |
| TO or MO or PY or MO+PY | Complete | Classes | other | S | yes | SI | yes | | x | | (74) |
| MI* | Complete | Classes | other | S-M | yes | | no | | x | | (126) |
| MI or MI+PY | Complete | Classes | RDE | S-R | only single mutants | SE | yes | x | x | | (117) |
| MO | Complete | Classes | STOCH | S-M | no | SE | no | | x | | (142) |
| MO or MI or RO or PY | Complete | Classes | STOCH | S-M-D | no | SE | yes | x | x | | (111) |
| MO | Complete | Continuous | STOCH | S-M-D | no | SE | yes | x | x | | (103) |
| MI | Complete+Induced R | Classes | DE | | yes | SE | no | x | | | (64) |
| MI | Complete or Partial | Classes | ODE | S | yes | | no | x | x | | (80) |
| MI | Complete or Partial | Classes | STOCH | S-M | no | SI | no | x | x | | (17) |
| MO or MI | Complete or Partial | Classes or Continuous | IDE | S-M | no | | no | x | | | (72) |
| MI or MI+PY | Complete or Complete+Partial | Classes or Classes+Continuous | DE | S | yes | | no | | x | | (61) |
| MI* or MI*+PY | Complete or Complete+Partial | Classes | STOCH | S-M-D | yes | | no | x | | | (114) |
| MO or MO+PY | Complete or Partial or Complete+Partial | Classes or Continuous or Classes+Continuous | STOCH | S-M-D | no | SE | yes | x | x | | (113) |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| MI | Non-host or Partial | Classes | STOCH | S | yes/no | SE | no | x | | | (146) |
| RO | Non-host or Partial | Continuous | ODE | S-M | no | | yes | x | x | x | (3) |
| MI | Partial | Classes | DE | S | yes | SE | yes | x | x | | (65, 66) |
| MI* | Partial | Classes | ODE | S | yes | | yes | x | x | | (107) |
| PY+Fungicides | Partial | Classes | ODE | S-M | no | | yes | | x | | (16) |
| MI | Partial | Classes | other | S | yes/no | | no | x | | x | (133) |
| MI | Partial | Classes | RDE | S | yes | SE | no | x | | | (118) |
| Pure stand or RO or RO+PY | Partial | Classes | STOCH | S-R | yes | | yes | x | x | | (21) |
| MI or MI+RO | Partial | Classes | STOCH | S-D | yes | SE | yes | x | | | (145) |
| PY+MI | Partial | Classes | STOCH | S-R-D | only single mutants | SE | yes | | x | | (144) |
| Pure stand | Partial | Continuous | IDE | S-M | no | | no | | x | | (27) |
| Pure stand or PY | Partial | Continuous | STOCH | S-M | no | | no | x | x | | (8) |
| MO | Partial | Continuous | STOCH | S-M-D | no | SE | yes | | x | | (101) |

[a] TO: turnover, MO: mosaic, dynMO: dynamic mosaic, MI: mixture, RO: rotation, PY: pyramiding. Symbol '+' stands for combination, and symbol '*' indicates models where mosaics and mixtures cannot be distinguished.

[b] Resistance may be completely or partially efficient. 'non-host' is indicated when a cultivar is completely resistant to a pathogen without evolution (i.e. the pathogen can never adapt and infect such host). Symbol '+' stands for combination.

[c] A distribution in classes refers to qualitative resistance (to which a pathogen adapts via a sudden breakdown), a continuous distribution refers to quantitative resistance (to which a pathogen gradually adapts via erosion). Symbol '+' stands for combination.

[d] DE: difference equations, ODE: ordinary differential equations, IDE: integro-differential equations, RDE: reaction-diffusion equations, STOCH: stochastic equations (accounting for demographic stochasticity). Symbol '+' stands for combination.

[e] S: selection, I: immigration, M: mutation, D: genetic drift, R: recombination

[f] SE: spatially-explicit, SI: spatially-implicit, blank for non spatial models.

[g] seasonality refers to a periodic host dynamic imposing a recurrent reduction in pathogen population size (but not necessarily with genetic drift).

[h] Epidemiological, evolutionary and socio-economical outputs used in modelling studies, relative to plant health and pathogen population size, pathogen population genetic composition, and crop yield or economic profit, respectively.

# SUPPORTING INFORMATION

**Table S1.** List of mathematical models used to test, optimise or compare plant resistance deployment strategies against pathogens of cultivated crops, or predict their evolutionary consequences. Table S1 is a comprehensive version of Table 1 including additional details, for every modelling study, on:

- the pathosystem considered;
- the deployment strategy (e.g. scale of host population and infection unit, numbers of host and pathogen genotypes, number of resistance sources)
- model structure (e.g. continuous or discrete-time, sources of demographic and environmental stochasticity, state variables, fitness cost of pathogen adaptation and of plant resistance);
- model outputs.