Epidemiological, evolutionary and economic outcomes associated to the coexistence of monogenic and pyramided resistant cultivars in agricultural landscapes: a case-study with the management of downy mildew in wine growing areas

Marta Zaffaroni, Loup Rimbaud, Julien Papaïx, Jean-François Rey, Laurent Deliere, Anne-Sophie Miclot, Adeline Ugaglia, Frédéric Fabre

Epidemiological, evolutionary and economic outcomes associated to the coexistence of monogenic and pyramided resistant cultivars in agricultural landscapes: a case-study with the management of downy mildew in wine growing areas.

Marta Zaffaroni, Loup Rimbaud, Julien Papaïx, Jean-François Rey, Laurent Delière, Anne-Sophie Miclot, Adeline Ugaglia and Frédéric Fabre

Downy mildew represents a real threat for grapevines in all vine-growing areas of the world, leading to significant yield losses and massive recourse of fungicides. 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. At present, growers can plant monogenic (with mainly the resistance factors Rpv1, Rpv3 but also Rpv10 and Rpv12) or pyramided cultivars (mainly cumulating Rpv1 and Rpv3). Currently, the resistance factors Rpv1 and Rpv3 start to be deployed in France. These two resistance factors can be deployed in: (i) monogenic cultivars sown in the same field (mixture strategy), (ii) monogenic cultivars sown in different fields (mosaic strategy), (iii) pyramided cultivars (pyramid strategy) and (iv) in hybrid strategies that combine the three previous basic strategies. Here, we used the spatially explicit stochastic model *landsepi* to investigate the epidemiological, evolutionary and economic outcomes associated to these deployment strategies. Our results particularly highlight the risks for resistance durability associated to the coexistence of monogenic and pyramided cultivars in the same landscape. Finally, we discuss how the model *landsepi* has been used to design deployment scenarios and discuss their outcomes with the staff of a cooperative cellar growing nearly 2000 ha of grapevine in South-western France.

Epidemiological and evolutionary outcomes associated to the coexistence of monogenic and pyramided resistant cultivars in agricultural landscapes

Marta Zaffaroni[1,3], Loup Rimbaud[2], Julien Papaïx[3], Jean-François Rey[3], Laurent Delière[1], anne-Sophie Miclot[1], Adeline Ugaglia[1] & **Frédéric Fabre**[1]

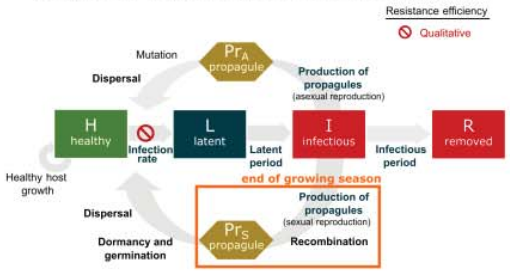
[1] INRAE – SAVE, 33882 Villenave d'Ornon, France, [2] INRAE – Pathologie Végétale, 84140, Montfavet, France [3] INRAE – BioSP, 84914, Avignon, France

1 Introduction & objectives

- The deployment of resistant cultivars in agricultural landscapes is an effective way to protect crops from plant pathogens, but pathogens may quickly adapt to the deployed resistance [1]. The way resistant cultivars are deploy impact their efficiency in maintaining an effective disease protection over short and long terms.
- Downy mildew is a real threat for grapevines in all vine-growing areas of the world. Breeders have been engaged in breeding programs for resistance to grapevine downy mildew, resulting in the creation of several resistant varieties. At present, growers in France can start to plant monogenic (with mainly the resistance factors Rpv1, Rpv3) or pyramided cultivars (mainly cumulating Rpv1 and Rpv3).
- What is the best strategy to deploy these monogenic and pyramided cultivars in agricultural landscapes ? Growers can deploy (i) only monogenic cultivars sown in the same field (***mixture strategy***), (ii) only monogenic cultivars sown in different fields (***mosaic strategy***), (iii) only pyramided cultivars (***pyramid strategy***) or (iv) choose ***hybrid strategy*** that combine the three previous basic strategies. Here, we used the spatially explicit stochastic model *landsepi [2,3]* to investigate the epidemiological and evolutionary outcomes associated to these strategies.

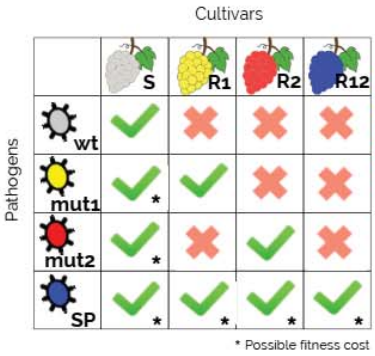
2 *landsepi*, a demo-genetic spatially-explicit temporal stochastic model

Pathogen epidemic and evolutionary dynamics

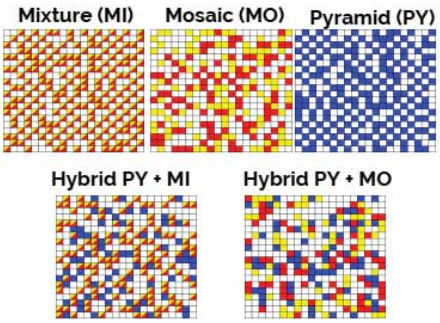


The R package *landespi* provides a modelling framework to compare plant resistance deployment strategies and understand the impact of epidemiological, evolutionary and genetic factors for a wide range of pathosystems.

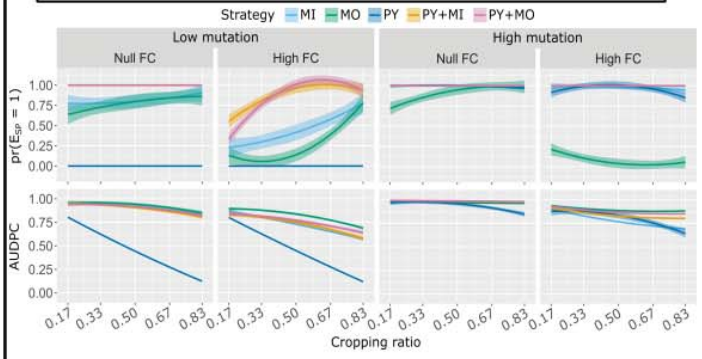
Gene-for-gene interaction



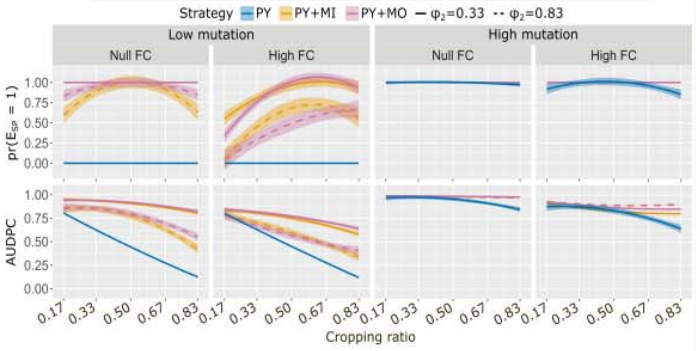
Epidemics in a diversified landscape of 400 fields



3 Hybrid strategies reduce the advantage of resistance genes pyramiding . . .



4 . . . even for low proportion of monogenic cultivars



Factors studied : ❶ **Cropping ratio** : proportion of fields with R cultivars ; ❷ **FC** : fitness cost
❸ **Mutation rate** (2 levels) ; ❹ **Strategies** (5 levels) ; ❺ **Proportion φ_2**: relative proportion of fields with R12 cultivars

Outcomes: ❶ **Evolutionary outcomes** : pr(E_{SP}=1), probability of superpathogen SP pathogen establishment ; ❷ **Epidemiological outcomes** : AUDPC, relative AUDPC during 30 years at landscape scale

5 Conclusions

- Knowledge of the mutation probability determines if the pyramiding strategy provides a substantial benefit over mixture and mosaic strategies.
- Going further a study of Lof and colleagues (2017) [4], we showed that, at low mutation probability, deploying hybrid strategies drastically decreases the advantage of resistance genes pyramiding, even for low proportion of monogenic cultivars.
- Socio-economic studies are needed to asses how regulatory policies could be mobilize to manage resistance cultivars deployment in agricultural landscapes in order to preserve the advantage of resistance genes pyramiding.

FINANCIAL SUPPORT
This work benefited from OFB Ecophyto "Leviers territoriaux" (Project Médée, 2020–2023) and from ANR (project COMBINE, 2023-2026).

LINKS
Web app: https://shiny.biosp.inrae.fr/app_direct/landsepi/
R package: https://cran.r-project.org/web/packages/landsepi/index.html

REFERENCES
[1] Rimbaud L. et al. (2021) Annu. Rev. Phytopathol. 59:125-152. [2] Rimbaud L. et al (2018) PLoS Comput. Biol. 14:e1006067. [3] Zaffaroni M., et al. (2022), Bioarxiv, https://doi.org/10.1101/2022.02.02.573679 [4] Lof M., et al. (2017) Phytopathology, 107 (5).