

The work "Impact of ploidy and pathogen life cycle on resistance durability" by Saubin et al. aims to assess the impact of ploidy on the epidemics of plant pathogens. The study of plant pathogens is an issue of great interest in agricultural sciences and many economic implications.

After reading the abstract and the Section introduction, my first impression was that the manuscript was concerned with developing resistant host strategies to prevent resistance breakdown. The authors also highlight that the current approach couples population dynamics and population genetics. However, from my perspective, the approach used in the manuscript resembles more those of ecological models.

Metapopulation models to assess the genetic diversity of pathogens whose epidemiology follows standard dynamics such as SIR or SIS are not new. In those approaches, the hosts are represented as groups (compartments) whose states evolve, i.e., the landscape is not static.

Many aspects of the evolutionary dynamics of the model are unclear, and for me, it is quite challenging to understand the meaning and motivation of the results. Below I enumerate my main concerns:

- 1) Does the model allow the coexistence of different strains in the susceptible compartment?
- 2) As I can understand from Figure 1, the answer to question 1) is yes. In this case, the within-host dynamics, supposedly provided by Eqs. (1) and (2) is not clear. Different strains might compete within the same host, i.e., they do not independently evolve as there is competition for "space".
- 3) In the abstract, it is said, "A major component of deployment hosts strategies is the proportion of resistant hosts in the landscape". Nevertheless, this problem is not addressed in the paper. What is the point to not consider a consistent metapopulation model, in which the number of compartments can be made large, and not only two or three, as assumed in the current formulation?
- 4) Different topologies (migration network) could be considered as a metapopulation model of many compartments is built. The topology of migration networks is also a significant component in epidemics, especially in plant pathogens' epidemics.
- 5) Both pathogens and hosts are static entities. They do not effectively evolve as they do not mutate or change state. Are those assumptions reasonable in the time scale considered in the simulations?