MODELLING THE EVOLUTIONARY EPIDEMIOLOGY OF SPORE PRODUCING PATHOGENS

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- The sustainable management of plant disease has two goals:
  - Reducing severity and frequency of disease epidemics (immediate epidemiological goal),
  - Reducing the rate of evolution of new patho-types (longer-term evolutionary).

Here, we model epidemiological and evolutionary dynamics of spore-producing pathogens in a homogeneous host population.

The model considers a continuum of different pathogen strains (denoted by their phenotypic value $\boldsymbol{x}$). On quantitatively resistant hosts, pathogen exhibit a continuous distribution of their disease phenotype: all the pathogen strains cause infection but each with its own level of quantitative pathogenicity.

Quantitative traits of pathogenicity of strain $\boldsymbol{x}$:
(i) $\beta(x)$, infection efficiency,
(ii) $\tau(x)$, latent period,
(iii) $p(x)$, sporulation rate,
(iv) $l(x)$, infectious period.

Fitness.
The fitness of the pathogen with phenotypic value $\boldsymbol{x}$ is given by the fitness function $\boldsymbol{\psi}$ above.

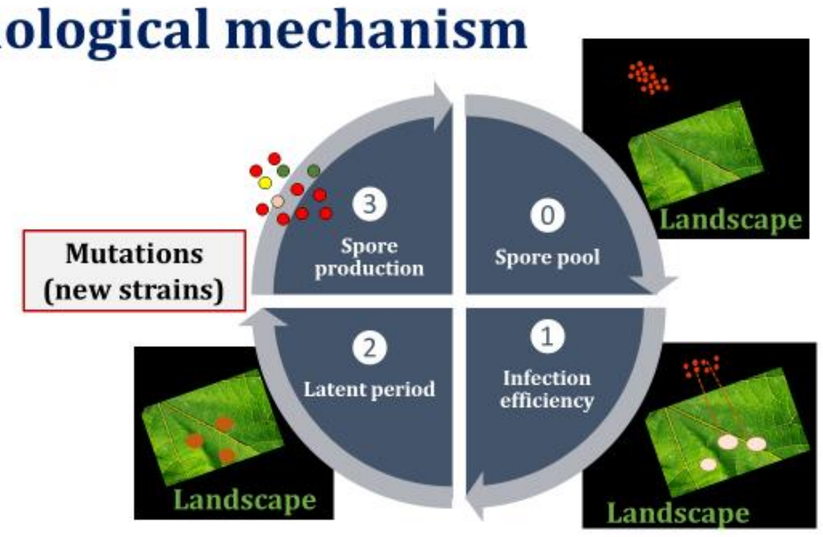
Evolutionary Strategy (ES).
The set of the fitness function maximum points is called the ES-set.
And each element of that set is called an ES-phenotypic value.

Evolutionary Stable Strategy (ESS): it's a phenotypic value such that, when the vast majority of the individuals has it, no rare mutant with a different phenotype can increase in numbers.

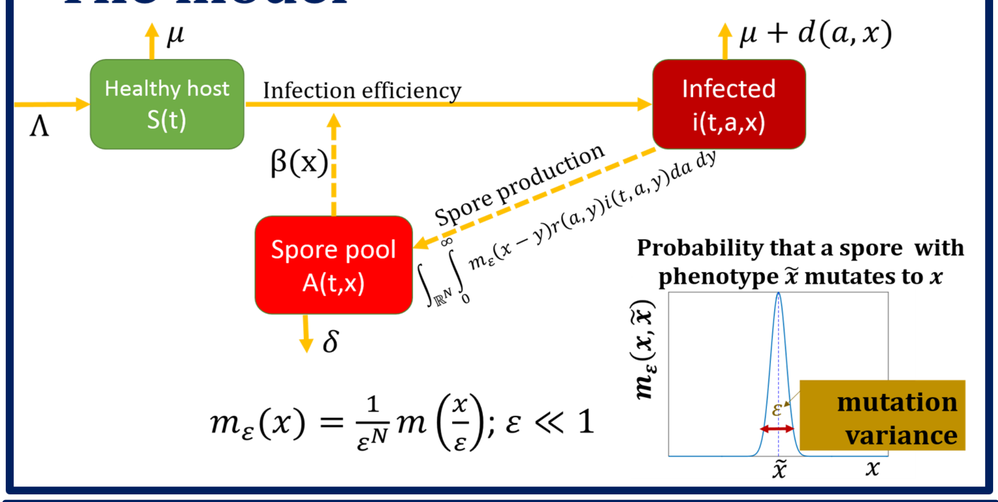
By using a suitable order, defined on the set of phenotypic values which maximize the fitness function, we characterize the ESS-phenotypic value.

Figure 1. Grapevine infected by downy mildew.

Biological mechanism



The model



$$m_\varepsilon(x) = \frac{1}{\varepsilon^N} m\left(\frac{x}{\varepsilon}\right); \varepsilon \ll 1$$

Fitness function

Infection efficiency

$$\Psi(x) := \frac{\beta(x)}{\delta} \int_0^\infty r(a,x)\, e^{-\mu a} \mathrm{d}a$$

$$r(a,x) := p(x)\chi_{[\tau(x),\tau(x)+l(x)]}(a)$$

Sporulation rate — Latent period — Infectious period

The phenotype x^* *is* ***ES*** *if* x^* *maximize* Ψ

MAIN RESULTS

- **The biological endemic steady state of the model, when it exists, is unique.**
- **At the evolutionary equilibrium, the pathogen population is typically concentrated around the well-characterized ESS-phenotypic value (using the fitness function ψ).**

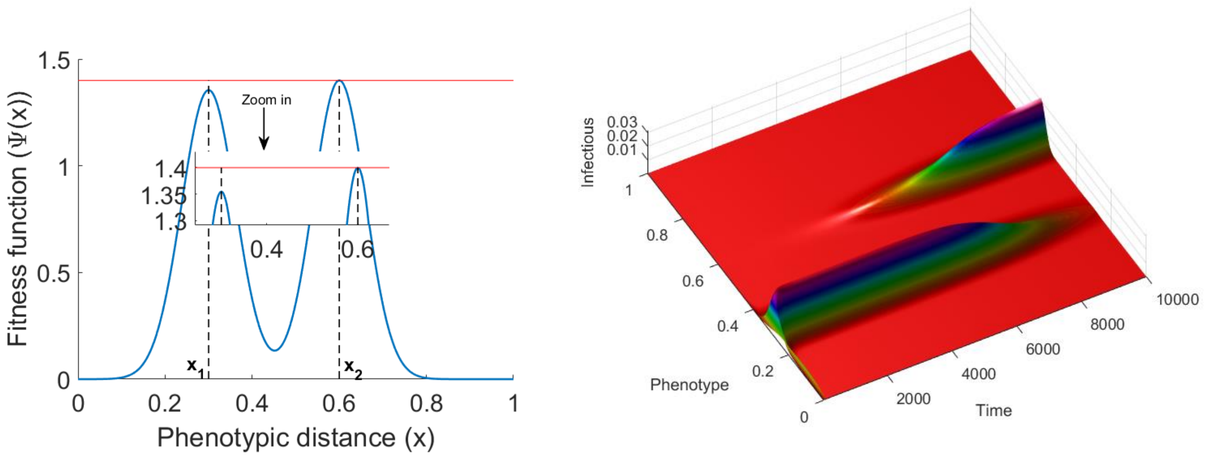


Figure2: (Left) The fitness function ψ with respect to the phenotypic value space. The fitness function is maximized by a single phenotypic value x_2 and the phenotypic value x_1 is close to the maximum of the fitness function, i.e. $\psi(x_1) \approx \psi(x_2)$ (as illustrated by the zoom in). In this case, x_2 is the ESS-phenotypic value. (Right) Dynamics of infectious tissues with respect to the phenotypic value space. Initially (i.e. at $t = 0$), the pathogen population is essentially concentrated around the phenotypic value x_1. With the time and due to mutations in the space of phenotypic values, the pathogen population will typically concentrate around the ESS-phenotypic value x_2. Notice that the concentration process around the phenotypic value x_2 is preceding by some co-existence of both phenotypes x_1 and x_2.

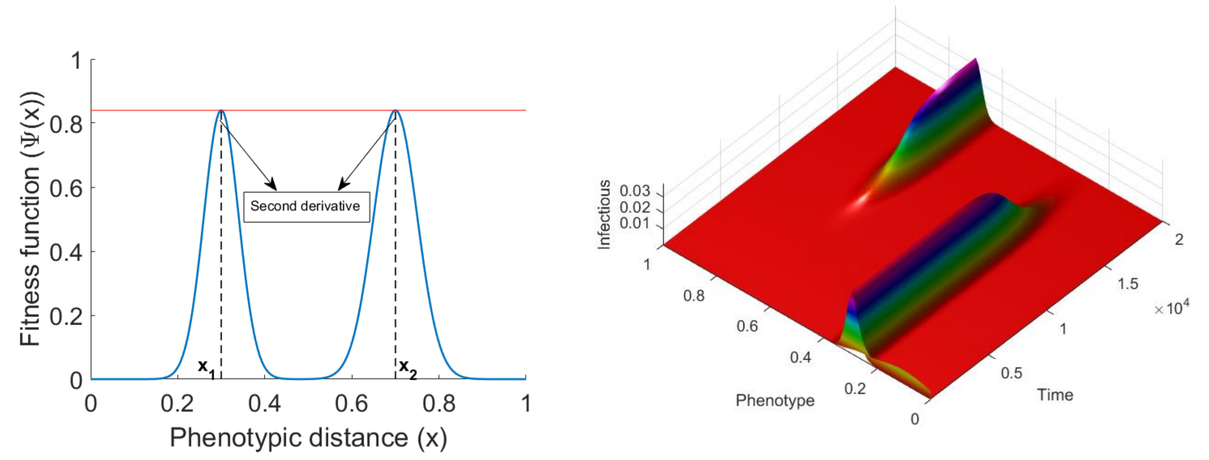


Figure3: (Left) The fitness function ψ with respect to the phenotypic values space. The fitness function is maximized by two phenotypic value x_1 and x_2. The phenotypic values x_1 and x_2 differ by their respective second derivative of the fitness function: $\psi''(x_2) > \psi''(x_1)$. According to a suitable order defined on the set of the fitness function maximum points, x_2 is then the ESS-phenotypic value. (Right) Dynamics of infectious tissues with respect to the phenotypic value space. Initially (i.e. at time $t = 0$), the pathogen population is essentially concentrated around the phenotypic value x_2. Before reaching the ESS-phenotypic value x_2, the pathogen population can evolve during long time around the phenotypic value x_1 followed by a co-existence of both phenotypes x_1 and x_2. This is because in this current case the phenotypic value x_1 is much more close to the ESS-phenotypic value x_2 than in the case of **Figure 2**.

Acknowledgments

R. D-D's work was funded by the CIVB and the EU in the framework of the Marie-Curie FP7 COFUND People Programme, through the award of an AgreenSkills/AgreenSkills+ fellowship.

Further information

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