Steady state concentration for a phenotype structured problem modelling the evolutionary adaptation of pathogens

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Résumé

We aim to analyse the concentration property, in the phenotype trait space, of the steady state solutions of an integro-differential model representing the evolutionary epidemiology of plant pathogens facing host population with quantitative disease resistance.
Our motivation comes from the fact that modeling the epidemiology and the evolution of pathogens has long been addressed through analysis of invasibility assuming that epidemiological and evolutionary time scales are distinct. These analysis ignore short-term evolutionary and epidemiological dynamics despite the major interests of these dynamics in agro-ecosytems. Deriving sustainable management strategies of resistance gene to plant pathogens is one of the many examples where one want to make quantitative predictions far away from the epidemiological equilibrium. Up to date, most of the modelling approaches devoted to design sustainable strategies of resistance management tackle the case of qualitative resistance based on gene for gene interactions that triggers host immunity to the disease. Few works consider adaptation to quantitative resistances that reduce pathogen aggressiveness instead of conferring immunity. Pathogen aggressiveness is determined experimentally by plant pathologists by measuring life history traits which described the disease life cycle: the infection efficiency, the latency time, the sporulation period and the rate of spore production.
In this work, we used integro-differential equations to model both the epidemiological and the evolutionary dynamics of spore-producing pathogens in a homogeneous host population. The host population is subdivided into compartments (Susceptible or healthy host tissue (S), Infected tissue (i) and Airborne spores (A)) by explicitly

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integrating dedicated life-history traits of the pathogens as well as the life cycle of the pathogen by taking into account the age since infection. An integral operator with kernel m describing mutations from a pathogen strain with phenotypic value y $\in$ R N to another one with phenotypic value x $\in$ R N . More specifically, we investigate the concentration properties in the phenotype trait space of model stationary states when the mutation kernel m depends on a small parameter $\epsilon >$ 0 and is highly concentrated.