

# COMPETITION PROCESSES, A TOOL TO MODEL PATHOGEN ADAPTATION TIME

R. Bourget<sup>a,b</sup>, L. Chaumont<sup>a</sup> and N. Sapoukhina<sup>b</sup>

<sup>a</sup>LAREMA, Département de Mathématiques  
Université d'Angers, UFR Sciences  
2 Boulevard Lavoisier - 49045, Angers, France  
bourget@math.univ-angers.fr  
loic.chaumont@univ-angers.fr

<sup>b</sup>INRA/ACO/UA UMR077 PaVé, IFR149  
BP 60057, F-49071 Beaucouzé, France  
natalia.sapoukhina@angers.inra.fr

In many biological contexts, humans try to control harmful populations by introducing resistance into their habitat. However, this strategy is rarely durable because of swift pathogen adaptation to a new hostile environment. Multi-resistance is thought to be a way to delay pathogen adaptation. To understand the population adaptation to multi-resistance, we were interested in the impact of the structure of multi-resistant environment on the waiting time before emergence of a multi-virulent mutant.

We formulated and analyzed a stochastic population model based on competition processes with mutation, migration and recombination. We included a fitness cost for mutants overcoming resistance. To estimate the emergence time, we performed numerical simulations in which we vary pathogens life history traits and the environment structure.

The numerical simulation showed the strong dependence of the emergence time on the environment structure. In the case of diversified environment including mono-resistant and susceptible areas, emergence time is a parabolic function of the fraction of resistant area. The emergence time was longer for low and high resistant area fractions, because of induced low migration and mutation probabilities. For multi-resistant environment, emergence time increases with the increase of number of resistances and with the decrease of the transition environments proportion.

The results of the model provide insight into our understanding the interplay between used disease control strategy and the pathogen evolution rate to overcome the resistance. The model can be used for designing control strategies preventing rapid adaptation of harmful populations.

**Keywords:** pathogen evolution, multi-resistance, stochastic model