Mechanisms behind population responses to variable thermal environments: experiments and model-based analyses of the role of intraspecific phenotypic variation

Anne-Lise Boixel^{*†1}, Erik Svensson², Frédéric Suffert¹, and Michaël Chelle³

¹UMR BIOGER (biologie et gestion des risques en agriculture) – Institut National de la Recherche Agronomique, AgroParisTech, Université Paris-Saclay,Sorbonne Universités – Campus AgroParisTech BP01 F-78850 Thiverval-Grignon, France

²Evolutionary Ecology Unit, Department of Biology, Lund University – Sölvegatan 37, 223 62 Lund, Sweden

³UMR ECOSYS (écologie fonctionnelle et écotoxicologie des agroécosystèmes) – Institut National de la Recherche Agronomique, AgroParisTech, Université Paris-Saclay,Sorbonne Universités – Route de la Ferme F-78850 Thiverval-Grignon, France

Abstract

Foliar pathogens inhabit environments exhibiting drastic thermal changes and a high degree of patchiness. Although temperature strongly affects individual growth and ecological processes that drive disease development, the mechanisms that underpin population dynamics in response to thermal variations are not fully understood due to a lack of knowledge of inter-individual variations in thermal responses, phenotypic plasticity and the thermal environment actually perceived by each individual. To explore consequences of inter-individual variations and thermal patchy structure on the adaptive responses of populations, we developed a spatially explicit individual-based model addressing these problems. In our model, we simulate temporal changes in the phenotypic composition of a population in response to thermal variations occurring in a patchy environment. We have performed numerical simulations tailored to field and greenhouse selection experiments all specifically focusing on the wheat pathogen Zymoseptoria tritici and its foliar environment. Three general and complementary results from our simulation outputs of population dynamics and ecological processes will be presented: (i) quantitative impacts of three oversimplifications regarding phenotypic diversity, plasticity and environmental characterisation currently adopted in disease prediction models; (ii) the role of inter-individual variation on the dynamics and the adaptive potential of populations and (iii) the influence of spatio-temporal thermal heterogeneity on maintenance of phenotypic diversity. This flexible modelling framework operates based on individual reaction norms and as such can be easily applied to other biological systems. It establishes a quantitative framework for increasing our understanding of how environmental signals, inter-individual phenotypic variations and ecological processes interact and influence both population and evolutionary dynamics.

^{*}Speaker

[†]Corresponding author: anne-lise.boixel@inra.fr